IPI Entry	Gene Symbol	Protein Name	Protein Probability	Protein Coverage (%)	# of Unique Sequences	# of Identified Peptides	Total # of Identified Spectra	# of Proteins in Entry	Mean Control	Mean 1 µg/mL	Mean 10 µg/mL	Mean 100 µg/mL	SEM Control	SEM 1 µg/mL	SEM 10 µg/mL	SEM 100 µg/mL	CV(%) Control	CV(%) 1 µg/mL	CV(%) 10 µg/mL	CV(%) 100 µg/mL	Fold Change 1 µg/mL vs. Control	P 1 µg/mL vs. Control	Fold Change 10 µg/mL vs. Control	P 10 µg/mL vs. Control	Fold Change 100 µg/mL vs. Control	P 100 µg/mL vs. Control	Fold Change 10 µg/mL vs. 1 µg/mL	P 10 µg/mL vs. 1 µg/mL	Fold Change 100 µg/mL vs. 1 µg/mL	P 100 µg/mL vs. 1 µg/mL	Fold Change 100 µg/mL vs. 10 µg/mL	P 100 µg/mL vs. 10 µg/mL
				Peptide Sequence	Peptide Charge	Peptide Probability	# of Spectra																									
IPI00000001	STAU1	isoform Long of Double-stranded RNA-binding protein Staufen homolog 1	100.0%	9.7	4	4	4	4	4,068,753	4,449,999	3,873,776	4,720,824	481,489	332,999	318,190	196,830	26.5	16.7	18.4	9.3	1.1	0.5	-1.1	0.7	1.2	0.2	-1.1	0.2	1.1	0.5	1.2	0.05
IPI00218609	STAU1	isoform Short of Double-stranded RNA-binding protein Staufen homolog 1	100.0%	11.3	4	4	4	4	4,068,753	4,449,999	3,873,776	4,720,824	481,489	332,999	318,190	196,830	26.5	16.7	18.4	9.3	1.1	0.5	-1.1	0.7	1.2	0.2	-1.1	0.2	1.1	0.5	1.2	0.05
IPI00641873	STAU1	Staufen, RNA binding protein, homolog 1	100.0%	11.3	4	4	4	4	4,068,753	4,449,999	3,873,776	4,720,824	481,489	332,999	318,190	196,830	26.5	16.7	18.4	9.3	1.1	0.5	-1.1	0.7	1.2	0.2	-1.1	0.2	1.1	0.5	1.2	0.05
IPI00643664	STAU1	double-stranded RNA-binding protein Staufen homolog 1 isoform c	100.0%	11.2	4	4	4	4	4,068,753	4,449,999	3,873,776	4,720,824	481,489	332,999	318,190	196,830	26.5	16.7	18.4	9.3	1.1	0.5	-1.1	0.7	1.2	0.2	-1.1	0.2	1.1	0.5	1.2	0.05
				ELLYGGTSPTAETILK	2	100.0%	1																									
				LLSELDQQSTEMPR	2	99.9%	1																									
				NAAENMLEILGFK	2	100.0%	1																									
				VSVGEFVGEGEGK	2	80.3%	1																									
IPI00000015	SRSF4	Serine/arginine-rich splicing factor 4	100.0%	6.7	3	3	3	2	4,264,984	4,733,812	4,459,362	5,317,313	635,719	458,296	371,822	337,910	33.3	21.7	18.6	14.2	1.1	0.6	1.0	0.8	1.2	0.2	-1.1	0.7	1.1	0.3	1.2	0.1
IPI01015447	SRSF4	47 kDa protein	100.0%	8.1	3	3	3	2	4,264,984	4,733,812	4,459,362	5,317,313	635,719	458,296	371,822	337,910	33.3	21.7	18.6	14.2	1.1	0.6	1.0	0.8	1.2	0.2	-1.1	0.7	1.1	0.3	1.2	0.1
				LIVENLSSR	2	99.9%	1																									
				NGYGFVEFDDLR	2	91.9%	1																									
				QAGEVTYADAHK	2	100.0%	1																									
IPI00000023	GABRG2	Gamma-aminobutyric acid receptor subunit gamma-2	97.5%	5.1	1	1	1	4	159,711	161,103	138,262	134,749	17,929	25,258	21,291	7,315	25.1	35.1	34.4	12.1	1.0	1	-1.2	0.5	-1.2	0.2	-1.2	0.5	-1.2	0.4	-1.0	0.9
IPI00396250	GABRG2	gamma-aminobutyric acid receptor subunit gamma-2 isoform 3 precursor	97.5%	4.7	1	1	1	4	159,711	161,103	138,262	134,749	17,929	25,258	21,291	7,315	25.1	35.1	34.4	12.1	1.0	1	-1.2	0.5	-1.2	0.2	-1.2	0.5	-1.2	0.4	-1.0	0.9
IPI00419200	GABRG2	gamma-aminobutyric acid receptor subunit gamma-2 isoform 1 precursor	97.5%	5.1	1	1	1	4	159,711	161,103	138,262	134,749	17,929	25,258	21,291	7,315	25.1	35.1	34.4	12.1	1.0	1	-1.2	0.5	-1.2	0.2	-1.2	0.5	-1.2	0.4	-1.0	0.9
IPI00982076	GABRG2	cDNA FLJ59748, highly similar to Gamma-aminobutyric-acid receptor gamma-2 sub	97.5%	6.5	1	1	1	4	159,711	161,103	138,262	134,749	17,929	25,258	21,291	7,315	25.1	35.1	34.4	12.1	1.0	1	-1.2	0.5	-1.2	0.2	-1.2	0.5	-1.2	0.4	-1.0	0.9
				NTTEVVKTTSGDYVVMSVYFDLSR	3	97.5%	1																									
IPI00000024	PCDH1	isoform 1 of Protocadherin-1	99.6%	2.6	1	1	1	6	359,650	378,968	498,332	430,347	72,590	47,494	75,619	21,243	45.1	28.0	33.9	11.0	1.1	0.8	1.4	0.2	1.2	0.4	1.3	0.2	1.1	0.4	-1.2	0.4
IPI00872579	PCDH1	isoform 2 of Protocadherin-1	99.6%	2.3	1	1	1	6	359,650	378,968	498,332	430,347	72,590	47,494	75,619	21,243	45.1	28.0	33.9	11.0	1.1	0.8	1.4	0.2	1.2	0.4	1.3	0.2	1.1	0.4	-1.2	0.4
IPI00914969	PCDH1	isoform 3 of Protocadherin-1	99.6%	2.7	1	1	1	6	359,650	378,968	498,332	430,347	72,590	47,494	75,619	21,243	45.1	28.0	33.9	11.0	1.1	0.8	1.4	0.2	1.2	0.4	1.3	0.2	1.1	0.4	-1.2	0.4
IPI00964741	PCDH1	cDNA FLJ77464, highly similar to Homo sapiens protocadherin 1 (cadherin-like 1) (F	99.6%	2.6	1	1	1	6	359,650	378,968	498,332	430,347	72,590	47,494	75,619	21,243	45.1	28.0	33.9	11.0	1.1	0.8	1.4	0.2	1.2	0.4	1.3	0.2	1.1	0.4	-1.2	0.4
IPI00965876	PCDH1	Uncharacterized protein	99.6%	7.3	1	1	1	6	359,650	378,968	498,332	430,347	72,590	47,494	75,619	21,243	45.1	28.0	33.9	11.0	1.1	0.8	1.4	0.2	1.2	0.4	1.3	0.2	1.1	0.4	-1.2	0.4
IPI00968042	PCDH1	cDNA FLJ53887, highly similar to Protocadherin-1	99.6%	2.7	1	1	1	6	359,650	378,968	498,332	430,347	72,590	47,494	75,619	21,243	45.1	28.0	33.9	11.0	1.1	0.8	1.4	0.2	1.2	0.4	1.3	0.2	1.1	0.4	-1.2	0.4
				VPEEQPPNTLIGSLAADYGFPDVGHLYK	3	99.6%	1																									
IPI00000041	RHOB	Rho-related GTP-binding protein RhoB	100.0%	16.8	2	2	2	1	811,228	717,145	753,096	788,244	106,966	28,586	64,513	36,459	29.5	8.9	19.2	10.3	-1.1	0.4	-1.1	0.7	-1.0	0.8	1.1	0.6	1.1	0.2	1.0	0.6
				DEFPEVYVPTVFENYVADIEVDGK	2	100.0%	1																									
				TCLLIVFSK	2	95.7%	1																									
IPI00000051	PFDN1	Prefoldin subunit 1	99.3%	9.0	1	1	1	2	2,985,365	3,602,765	3,520,925	3,703,675	290,749	379,530	399,707	434,443	21.8	23.6	25.4	26.2	1.2	0.2	1.2	0.3	1.2	0.2	-1.0	0.9	1.0	0.9	1.1	0.8
IPI00974249	PFDN1	Uncharacterized protein	99.3%	9.4	1	1	1	2	2,985,365	3,602,765	3,520,925	3,703,675	290,749	379,530	399,707	434,443	21.8	23.6	25.4	26.2	1.2	0.2	1.2	0.3	1.2	0.2	-1.0	0.9	1.0	0.9	1.1	0.8
				LADIQIEQLNR	2	99.3%	1																									
IPI00000105	MVP	Major vault protein	100.0%	29.8	20	21	23	1	81,454,455	85,923,765	78,738,387	92,549,329	5,406,853	4,112,333	4,508,561	4,387,433	14.8	10.7	12.8	10.6	1.1	0.5	-1.0	0.7	1.1	0.1	-1.1	0.3	1.1	0.3	1.2	0.06
				ALQPLEEGEDEEK	2	93.7%	1																									
				AQLELEVSK	2	98.8%	1																									
				AQQLAEVEVK	2	99.3%	1																									
				AQQLAEVEVKK	2	99.5%	1																									
				DAQGLVLFDVTGQVR	2	100.0%	1																									
				DLAVAGPEMQVK	2	99.9%	2																									
				ELLELEALSMAVESTGTAK	3	100.0%	1																									
				GAVASVTFDDFHK	2	100.0%	1																									
				GPLEYVPSAK	2	99.9%	1																									
				HYCTVANPVSR	2	100.0%	1																									
				IEGEGSVLQAK	2	99.9%	1																									
				ILDQSEAEK	2	99.6%	1																									
				IPPYHYIHVLDQNSNVSR	3	100.0%	1																									
				LAQDPFPLYPGEVLEK	2	100.0%	2																									
				LFSVPDFVGDACK	2	86.8%	1																									
				QAIPLDENEGIYVQDVK	2	100.0%	1																									
				QAIPLDENEGIYVQDVK	3	99.9%	1																									
				QMTEAIGPSTIR	2	99.7%	1																									
				TAVFGFETSEAK	2	100.0%	1																									
				VASGPSPGEGISPQSAQAPQAPGDNHVVPVLR	3	100.0%	1																									
				VPHNAAVQVYDYR	3	94.7%	1																									
IPI00000184	SCOC	isoform 1 of Short coiled-coil protein	99.3%	11.3	1	1	1	5	311,165	349,280	375,949	464,730	28,758	38,322	33,963	33,705	20.7	24.5	20.2	16.2	1.1	0.4	1.2	0.2	1.5	0.008	1.1	0.6	1.3	0.05	1.2	0.1
IPI00396594	SCOC	isoform 2 of Short coiled-coil protein	99.3%	14.8	1	1	1	5	311,165	349,280	375,949	464,730	28,758	38,322	33,963	33,705	20.7	24.5	20.2	16.2	1.1	0.4	1.2	0.2	1.5	0.008	1.1	0.6	1.3	0.05	1.2	0.1
IPI00893763	SCOC	isoform 3 of Short coiled-coil protein	99.3%	14.9	1	1	1	5	311,165	349,280	375,949	464,730	28,758	38,322	33,963	33,705	20.7	24.5	20.2	16.2	1.1	0.4	1.2	0.2	1.5	0.008	1.1	0.6	1.3	0.05	1.2	0.1
IPI00929604	SCOC	short coiled-coil protein isoform 2	99.3%	11.4	1	1	1	5	311,165	349,280	375,949	464,730	28,758	38,322	33,963	33,705	20.7	24.5	20.2	16.2	1.1	0.4	1.2	0.2	1.5	0.008	1.1	0.6	1.3	0.05	1.2	0.1
IPI00963819	SCOC	9 kDa protein	99.3%	22.0	1	1	1	5	311,165	349,280	375,949	464,730	28,758	38,322	33,963	33,705	20.7	24.5	20.2	16.2	1.1	0.4	1.2	0.2	1.5	0.008	1.1	0.6	1.3	0.05	1.2	0.1
				LINQVLELQHTLEDLSAR	3	99.3%	1																									
IPI00000190	CD81	CD81 antigen	94.9%	6.8	1	1	1	7	1,121,656	1,154,857	779,873	1,114,063	133,279	104,077	85,540	120,618	26.6	20.2	24.5	24.2	1.0	0.8	-1.4	0.06	-1.0	1	-1.5	0.02	-1.0	0.8	1.4	0.05
IPI00657752	CD81	Uncharacterized protein	94.9%	5.8	1	1	1	7	1,121,656	1,154,857	779,873	1,114,063	133,279	104,077	85,540	120,618	26.6	20.2	24.5	24.2	1.0	0.8	-1.4	0.06	-1.0	1	-1.5	0.02	-1.0	0.8	1.4	0.05
IPI00978459	CD81	Uncharacterized protein	94.9%	6.6	1	1	1	7	1,121,656	1,154,857	779,873	1,114,063	133,279	104,077	85,540	120,618	26.6	20.2	24.5	24.2	1.0	0.8	-1.4	0.06	-1.0	1	-1.5	0.02	-1.0	0.8	1.4	0.05
IPI00979139	CD81	24 kDa protein	94.9%	7.1	1	1	1	7	1,121,656	1,154,857	779,873	1,114,063	133,279	104,077	85,540	120,618	26.6	20.2	24.5	24.2	1.0	0.8	-1.4	0.06	-1.0	1	-1.5	0.02	-1.0	0.8	1.4	0.05
IPI00979839	CD81	Protein	94.9%	7.2	1	1	1	7	1,121,656	1,154,857	779,873	1,114,063	133,279	104,077	85,540	120,618	26.6	20.2	24.5	24.2	1.0	0.8	-1.4	0.06	-1.0	1	-1.5	0.02	-1.0	0.8	1.4	0.05
IPI00981672	CD81	Uncharacterized protein	94.9%	7.7	1	1	1	7	1,121,656	1,154,857	779,873	1,114,063	133,279	104,077	85,540	120,618	26.6	20.2	24.5	24.2	1.0	0.8	-1.4	0.06	-1.0	1	-1.5	0.02	-1.0	0.8	1.4	0.05
IPI00983214	CD81	Uncharacterized protein	94.9%	9.7	1	1	1	7	1,121,656	1,154,857	779,873	1,114,063	133,279	104,077	85,540	120,618	26.6	20.2	24.5	24.2	1.0	0.8	-1.4	0.06	-1.0	1	-1.5	0.02	-1.0	0.8	1.4	0.05
				NNLCPSGSNIISNLFK	2	94.9%	1																									
IPI00000192	SON	isoform F of Protein SON	99.8%	1.2	2	2	2	9	1,038,179	1,085,657	1,093,833	1,112,027	79,150	55,963	65,507	39,260	17.1	11.5	13.4	7.9	1.0	0.6	1.1	0.6	1.1	0.4	1.0	0.9	1.0	0.7	1.0	0.8
IPI00217930	SON	isoform J of Protein SON	99.8%	1.2	2	2	2	9	1,038,179	1,085,657	1,093,833	1,112,027	79,150	55,963	65,507	39,260	17.1	11.5	13.4	7.9	1.0	0.6	1.1	0.6	1.1	0.4	1.0	0.9	1.0	0.7	1.0	0.8
IPI00218618	SON	isoform B of Protein SON	99.8%	1.2	2	2	2	9	1,038,179	1,085,657	1,093,833	1,112,027	79,150	55,963	65,507	39,260	17.1	11.5	13.4	7.9	1.0	0.6	1.1	0.6	1.1	0.4	1.0	0.9	1.0	0.7	1.0	0.8
IPI00218619	SON	isoform C of Protein SON	99.8%	1.2	2	2	2	9	1,038,179	1,085,657	1,093,833	1,112,027	79,150	55,963	65,507	39,260	17.1	11.5	13.4	7.9	1.0	0.6	1.1	0.6	1.1	0.4	1.0	0.9	1.0	0.7	1.0	0.8
IPI00218620	SON	isoform D of Protein SON	99.8%	1.1	2	2	2	9	1,038,179	1,085,657	1,093,833	1,112,027	79,150	55,963	65,507	39,260	17.1	11.5	13.4	7.9	1.0	0.6	1.1	0.6	1.1	0.4	1.0	0.9	1.0	0.7	1.0	0.8
IPI00218621	SON	isoform E of Protein SON	99.8%	1.3	2	2	2	9	1,038,179	1,085,657	1,093,833	1,112,027	79,150	55,963	65,507	39,260	17.1	11.5	13.4	7.9	1.0	0.6	1.1	0.6	1.1	0.4	1.0	0.9	1.0	0.7	1.0	0.8
IPI00218622	SON	isoform G of Protein SON	99.8%	1.2	2	2	2	9	1,038,179	1,085,657	1,093,833	1,112,027	79,150	55,963	65,507	39,260	17.1	11.5	13.4	7.9	1.0	0.6	1.1	0.6	1.1	0.4	1.0	0.9	1.0	0.7	1.0	0.8
IPI00218624	SON	isoform I of Protein SON	99.8%	1.1	2	2	2	9	1,038,179	1,085,657	1,093,833	1,112,027	79,150	55,963	65,507	39,260	17.1	11.5	13.4	7.9	1.0	0.6	1.1	0.6	1.1	0.4	1.0	0.9	1.0	0.7	1.0	0.8
IPI00748258	SON	isoform A of Protein SON	99.8%	1.3	2	2	2	9	1,038,179	1,085,657	1,093,833	1,112,027	79,150	55,963	65,507	39,260	17.1	11.5	13.4	7.9	1.0	0.6	1.1	0.6	1.1	0.4	1.0	0.9	1.0	0.7	1.0	0.8
				AGIEGPLLASDVGR	2	99.6%	1																									
				IEEVLSGVLDTELR	2	83.8%	1																									
IPI00000230	TPM1	tropomyosin alpha-1 chain isoform 2	100.0%	9.5	3	3	5	9	887,996	902,026	849,457	1,014,189	70,514	45,439	61,777	28,577	17.8	11.3	16.3	6.3	1.0	0.9	-1.0	0.7	1.1	0.1	-1.1	0.5	1.1	0.07	1.2	0.04
IPI00014581	TPM1	isoform 1 of Tropomyosin alpha-1 chain	100.0%	9.5	3	3	5	9	887,996	902,026	849,457	1,014,189	70,514	45,439	61,777	28,577	17.8	11.3	16.3	6.3	1.0	0.9	-1.0	0.7	1.1	0.1	-1.1	0.5	1.1	0.07	1.2	0.04
IPI00018853	TPM1	Tropomyosin isoform	100.0%	11.1	3	3	5	9	887,996	902,026	849,457	1,014,189	70,514	45,439	61,777	28,577	17.8	11.3	16.3	6.3	1.0	0.9	-1.0	0.7	1.1	0.1	-1.1	0.5	1.1	0.07	1.2	0.04
IPI00216135	TPM1	isoform 3 of Tropomyosin alpha-1 chain	100.0%	9.5	3	3	5	9	887,996	902,026	849,457	1,014,189	70,514	45,439	61,777	28,577	17.8	11.3	16.3	6.3	1.0	0.9	-1.0	0.7	1.1	0.1	-1.1	0.5	1.1	0.07	1.2	0.04
IPI00296039	TPM1	isoform 4 of Tropomyosin alpha-1 chain	100.0%	9.5	3	3	5	9	887,996	902,026	849,457	1,014,189	70,514	45,439	61,777	28,577	17.8	11.3	16.3	6.3	1.0	0.9	-1.0	0.7	1.1	0.1	-1.1	0.5	1.1	0.07	1.2	0.04
IPI00604537	TPM1	tropomyosin alpha-1 chain isoform 3	100.0%	9.5	3	3	5	9	887,996	902,026	849,457	1,014,189	70,514	45,439	61,777	28,577	17.8	11.3	16.3	6.3	1.0	0.9	-1.0	0.7	1.1	0.1	-1.1	0.5	1.1	0.07	1.2	0.04
IPI00915324	TPM1	isoform 6 of Tropomyosin alpha-1 chain	100.0%	9.5	3	3	5	9	887,996	902,026	849,457	1,014,189	70,514	45,439	61,777	28,577	17.8	11.3	16.3	6.3	1.0	0.9	-1.0	0.7	1.1	0.1	-1.1	0.5	1.1	0.07	1.2	0.04
IPI00940343	TPM1	cDNA FLJ16459 fis, clone BRCAN2002473, moderately similar to Tropomyosin, fibr	100.0%	8.3	3	3	5	9	887,996	902,026	849,457	1,014,189	70,514	45,439	61,777	28,577	17.8	11.3	16.3	6.3	1.0	0.9	-1.0	0.7	1.1	0.1	-1.1	0.5	1.1	0.07	1.2	0.04
IPI00970818	TPM1	tropomyosin alpha-1 chain isoform 5	100.0%	9.5	3	3	5	9	887,996	902,026	849,457	1,014,189	70,514	45,439	61,777	28,577	17.8	11.3	16.3	6.3	1.0	0.9	-1.0	0.7	1.1	0.1	-1.1	0.5	1.1	0.07	1.2	0.04
				AQKDEEKMEIQEIQLK	3	92.3%	1																									
				IQLVEEELDR	2	100.0%	2																									
				RIQLVEEELDR	2	100.0%	2																									
IPI00000279	ZC3H15	Similar to Zinc finger CCCH domain-containing protein 15	99.5%	2.3	1	1	1	3	444,999	402,573	468,116	421,053	20,067	18,598	49,181	26,636	10.1	10.3	23.5	14.2	-1.1	0.2	1.1	0.7	-1.1	0.5	1.2	0.3	1.0	0.6	-1.1	0.4
IPI00909823	ZC3H15	cDNA FLJ60710, highly similar to Homo sapiens likely ortholog of mouse immediate	99.5%	6.2	1	1	1	3	444,999	402,573	468,116	421,053	20,067	18,598	49,181	26,636	10.1	10.3	23.5	14.2	-1.1	0.2	1.1	0.7	-1.1	0.5	1.2	0.3	1.0	0.6	-1.1	0.4
IPI01010979	ZC3H15	45 kDa protein	99.5%	2.6	1	1	1	3	444,999	402,573	468,116	421,053	20,067	18,598	49,181	26,636	10.1	10.3	23.5	14.2	-1.1	0.2	1.1	0.7	-1.1	0.5	1.2	0.3	1.0	0.6	-1.1	0.4
				ITLESFLAWK	2	99.5%	1																									
IPI00000335	HINT2	Histidine triad nucleotide-binding protein 2, mitochondrial	99.5%	22.1	2	2	2	1	9,691,900	8,723,680	9,260,540	9,729,810	419,192	287,529	405,498	174,926	9.7	7.4	9.8	4.0	-1.1	0.09	-1.0	0.5	1.0	0.9	1.1	0.3	1.1	0.02	1.1	0.3
				AQQATPGGAAPTIFSR	2	96.8%	1																									
				ISQAEEEDQQLLGHLLLVAK	3	99.5%	1																									
IPI00000477	ARPC2	Uncharacterized protein	99.4%	20.0	2	2	2	2	817,193	814,344	833,095	973,509	63,356	42,616	48,493	55,069	17.3	11.7	13.0	12.7	-1.0	1	1.0	0.8	1.2	0.1	1.0	0.8	1.2	0.05	1.2	0.09
IPI00005161	ARPC2	Actin-related protein 2/3 complex subunit 2	99.4%	13.3	2	2	2	2	817,193	814,344	833,095	973,509	63,356	42,616	48,493	55,069	17.3	11.7	13.0	12.7	-1.0	1	1.0	0.8	1.2	0.1	1.0	0.8	1.2	0.05	1.2	0.09
				ELQAHGADELLK	2	93.3%	1																									
				VYGSFLVNPESGYNVSLLYDLENLPASK	2	99.4%	1																									
IPI00000494	RPL5	60S ribosomal protein L5	100.0%	16.2	4	4	5	2	24,993,645	25,520,100	23,560,225	26,460,280	1,442,255	915,957	1,219,687	672,870	12.9	8.0	11.6	5.7	1.0	0.8	-1.1	0.5	1.1	0.4	-1.1	0.2	1.0	0.4	1.1	0.07
IPI00640037	RPL5	cDNA FLJ38496 fis, clone FELIV1000137, highly similar to 60S RIBOSOMAL PROT	100.0%	19.4	4	4	5	2	24,993,645	25,520,100	23,560,225	26,460,280	1,442,255	915,957	1,219,687	672,870	12.9	8.0	11.6	5.7	1.0	0.8	-1.1	0.5	1.1	0.4	-1.1	0.2	1.0	0.4	1.1	0.07
				GAVDGGLSIPHSTK	2	100.0%	1																									
				HIMGQNVADYMR	2	100.0%	2																									
				RFPGYDSESK	2	88.1%	1																									
				YLMEEDEDAYKK	3	99.8%	1																									
IPI00000513	CDH1	E-cadherin	100.0%	11.3	6	6	9	1	8,248,961	7,970,909	8,613,647	9,301,785	468,772	422,182	469,591	242,300	12.7	11.8	12.2	5.8	-1.0	0.7	1.0	0.6	1.1	0.08	1.1	0.3	1.2	0.03	1.1	0.2
				DNVYYYDEEGGGEEDQDFDLSQLHR	3	99.6%	1																									
				DTANWLEINPDTGAISTR	2	100.0%	2																									
				ITYRIWRDTANWLEINPDTGAISTR	3	95.9%	1																									
				MALEVGDYK	2	100.0%	2																									
				NTGVISVVTTGLDR	2	100.0%	2																									
				YLPRPANPDEIGNFIDENLK	3	100.0%	1																									
IPI00000581	OTUB1	cDNA FLJ56307, highly similar to Ubiquitin thioesterase protein OTUB1	100.0%	21.1	5	6	7	3	7,893,174	8,001,722	7,858,327	9,232,363	742,924	338,863	479,936	304,384	21.1	9.5	13.7	7.4	1.0	0.9	-1.0	1	1.2	0.1	-1.0	0.8	1.2	0.03	1.2	0.04
IPI00939174	OTUB1	isoform 1 of Ubiquitin thioesterase OTUB1	100.0%	24.0	5	6	7	3	7,893,174	8,001,722	7,858,327	9,232,363	742,924	338,863	479,936	304,384	21.1	9.5	13.7	7.4	1.0	0.9	-1.0	1	1.2	0.1	-1.0	0.8	1.2	0.03	1.2	0.04
IPI01012383	OTUB1	28 kDa protein	100.0%	27.0	5	6	7	3	7,893,174	8,001,722	7,858,327	9,232,363	742,924	338,863	479,936	304,384	21.1	9.5	13.7	7.4	1.0	0.9	-1.0	1	1.2	0.1	-1.0	0.8	1.2	0.03	1.2	0.04
				AFGFSHLEALLDDSKELQR	3	100.0%	2																									
				EYAEDDNIYQQK	2	99.9%	1																									
				FFEHFIEGGR	2	96.7%	1																									
				FFEHFIEGGR	3	99.6%	1																									
				IQQEIAVQNPLVSER	2	100.0%	1																									
				LLTSGYLQR	2	99.9%	1																									
IPI00000643	BAG2	BAG family molecular chaperone regulator 2	98.7%	5.2	1	1	1	1	10,501,420	10,120,090	11,239,750	11,853,780	1,593,568	1,050,583	787,248	545,999	33.9	23.2	15.7	10.3	-1.0	0.8	1.1	0.7	1.1	0.5	1.1	0.4	1.2	0.2	1.1	0.5
				LLESLDQLELR	2	98.7%	1																									
IPI00000684	UAP1	isoform AGX2 of UDP-N-acetylhexosamine pyrophosphorylase	99.7%	8.1	3	3	3	4	2,860,183	3,174,453	2,957,820	3,693,053	300,070	126,044	292,515	125,050	23.5	8.9	22.1	7.6	1.1	0.4	1.0	0.8	1.3	0.03	-1.1	0.5	1.2	0.02	1.2	0.05
IPI00217816	UAP1	isoform AGX1 of UDP-N-acetylhexosamine pyrophosphorylase	99.7%	8.3	3	3	3	4	2,860,183	3,174,453	2,957,820	3,693,053	300,070	126,044	292,515	125,050	23.5	8.9	22.1	7.6	1.1	0.4	1.0	0.8	1.3	0.03	-1.1	0.5	1.2	0.02	1.2	0.05
IPI00607787	UAP1	isoform 3 of UDP-N-acetylhexosamine pyrophosphorylase	99.7%	8.1	3	3	3	4	2,860,183	3,174,453	2,957,820	3,693,053	300,070	126,044	292,515	125,050	23.5	8.9	22.1	7.6	1.1	0.4	1.0	0.8	1.3	0.03	-1.1	0.5	1.2	0.02	1.2	0.05
IPI00646967	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	99.7%	19.1	3	3	3	4	2,860,183	3,174,453	2,957,820	3,693,053	300,070	126,044	292,515	125,050	23.5	8.9	22.1	7.6	1.1	0.4	1.0	0.8	1.3	0.03	-1.1	0.5	1.2	0.02	1.2	0.05
				DQDQLQAWESEGLFQISQNK	3	95.8%	1																									
				TLFQIQAER	2	91.8%	1																									
				VAVLLLAGGQGTR	2	92.8%	1																									
IPI00000690	AIFM1	isoform 1 of Apoptosis-inducing factor 1, mitochondrial	100.0%	6.2	3	3	3	2	3,942,002	4,121,791	3,714,271	4,334,314	383,282	109,431	230,964	190,003	21.7	5.9	13.9	9.8	1.0	0.7	-1.1	0.6	1.1	0.4	-1.1	0.1	1.1	0.4	1.2	0.07
IPI00157908	AIFM1	isoform 3 of Apoptosis-inducing factor 1, mitochondrial	100.0%	6.2	3	3	3	2	3,942,002	4,121,791	3,714,271	4,334,314	383,282	109,431	230,964	190,003	21.7	5.9	13.9	9.8	1.0	0.7	-1.1	0.6	1.1	0.4	-1.1	0.1	1.1	0.4	1.2	0.07
				ALGTEVIQLFPEK	2	96.6%	1																									
				ISGLGLTPEQK	2	99.0%	1																									
				TGGLEIDSDFGGFR	2	99.2%	1																									
IPI00000695	GNA14	Guanine nucleotide-binding protein subunit alpha-14	100.0%	5.4	1	2	3	1	439,085	429,635	475,854	526,204	59,353	31,983	52,267	14,218	30.2	16.7	24.6	6.0	-1.0	0.9	1.1	0.7	1.2	0.2	1.1	0.5	1.2	0.02	1.1	0.4

				VPTTGIIEYPFDLENIIFR	2	100.0%	2																								
				VPTTGIIEYPFDLENIIFR	3	100.0%	1																								
IPI00000706	DAGLA	Sn1-specific diacylglycerol lipase alpha	91.8%	1.5	1	1	1	1	1,256,996	1,322,196	1,339,660	1,375,179	40,767	132,082	80,759	131,916	7.3	22.3	13.5	21.5	1.1	0.7	1.1	0.4	1.1	0.4	1.0	0.9	1.0	0.8	1.0	0.8
				DLVPRIGLSQLEGFRR	3	91.8%	1																								
IPI00000760	DDAH2	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	99.5%	4.9	1	1	1	1	3,687,000	4,080,510	3,945,200	4,436,830	192,325	177,888	383,122	244,759	11.7	9.8	21.7	12.3	1.1	0.2	1.1	0.6	1.2	0.04	-1.0	0.8	1.1	0.3	1.1	0.3
				GGGDLPNSQEALQK	2	99.5%	1																								
IPI00000792	CRYZ	Quinone oxidoreductase	100.0%	29.2	5	5	5	1	16,652,086	17,348,150	18,492,333	20,683,226	1,994,429	783,561	1,676,028	569,671	26.8	10.1	20.3	6.2	1.0	0.8	1.1	0.5	1.2	0.1	1.1	0.6	1.2	0.009	1.1	0.3
				DLSLLSHGGR	2	99.3%	1																								
				EEFQQYAAALQAGMEIGWLKPVIGSQYPLEK	3	99.4%	1																								
				KPLLPYTPGSDVAGVIEAVGDNASAFK	3	99.9%	1																								
				VAEAHENIIHGSGATGK	3	100.0%	1																								
				VFEFGGPEVLK	2	100.0%	1																								
IPI00000807	MYO5A	isoform 1 of Myosin-Va	90.1%	0.8	1	1	1	4	194,518	189,059	185,504	165,617	27,213	13,831	15,938	8,768	31.3	16.4	19.2	11.8	-1.0	0.9	-1.0	0.8	-1.2	0.4	-1.0	0.9	-1.1	0.2	-1.1	0.3
IPI00873959	MYO5A	isoform 2 of Myosin-Va	90.1%	0.8	1	1	1	4	194,518	189,059	185,504	165,617	27,213	13,831	15,938	8,768	31.3	16.4	19.2	11.8	-1.0	0.9	-1.0	0.8	-1.2	0.4	-1.0	0.9	-1.1	0.2	-1.1	0.3
IPI00936879	MYO5A	Uncharacterized protein	90.1%	0.8	1	1	1	4	194,518	189,059	185,504	165,617	27,213	13,831	15,938	8,768	31.3	16.4	19.2	11.8	-1.0	0.9	-1.0	0.8	-1.2	0.4	-1.0	0.9	-1.1	0.2	-1.1	0.3
IPI01010015	MYO5A	Myosin Va	90.1%	1.0	1	1	1	4	194,518	189,059	185,504	165,617	27,213	13,831	15,938	8,768	31.3	16.4	19.2	11.8	-1.0	0.9	-1.0	0.8	-1.2	0.4	-1.0	0.9	-1.1	0.2	-1.1	0.3
				LTNENLDLMEQLEK	2	90.1%	1																								
IPI00000811	PSMB6	Proteasome subunit beta type-6	100.0%	21.3	4	4	6	1	12,959,398	13,626,400	12,636,663	14,592,493	795,384	717,773	774,955	377,693	13.7	11.8	13.7	5.8	1.1	0.6	-1.0	0.8	1.1	0.1	-1.1	0.4	1.1	0.3	1.2	0.05
				GAGPAPAWGPEAFTPDWESR	2	99.8%	1																								
				LAAIAESGVER	2	99.9%	2																								
				QVLLGDQIPK	2	98.7%	1																								
				TTTGSYIANR	2	99.9%	2																								
IPI00000816	YWHAE	isoform 1 of 14-3-3 protein epsilon	100.0%	62.8	17	22	31	1	161,524,895	164,766,647	157,914,573	182,843,150	########	4,506,285	########	5,333,372	15.7	6.1	15.2	6.5	1.0	0.8	-1.0	0.8	1.1	0.1	-1.0	0.6	1.1	0.03	1.2	0.07
				AAFDDAIAELDTLSEESYK	2	100.0%	2																								
				AAFDDAIAELDTLSEESYK	3	100.0%	2																								
				AASDIAMTELPPTHPIR	2	100.0%	1																								
				AASDIAMTELPPTHPIR	3	100.0%	3																								
				DNLTLWTSDMQGDGEEQNKEALQDVEDENQ	2	99.8%	1																								
				DNLTLWTSDMQGDGEEQNKEALQDVEDENQ	3	100.0%	1																								
				EAAENSLVAYK	2	100.0%	1																								
				HLIPAANTGESK	2	100.0%	2																								
				IISSIEQK	2	98.2%	1																								
				IISSIEQKEENK	2	99.7%	1																								
				IISSIEQKEENKGGEDK	3	99.6%	1																								
				LAEQAERYDEMVESMK	3	100.0%	2																								
				LAEQAERYDEMVESMKK	3	100.0%	1																								
				LICCDILDVLDK	2	100.0%	1																								
				LICCDILDVLDKHLIPAANTGESK	3	100.0%	1																								
				VAGMDVELTVEER	2	100.0%	2																								
				YDEMVESMK	2	100.0%	1																								
				YDEMVESMKK	2	99.9%	1																								
				YDEMVESMKK	3	99.9%	1																								
				YLAEFATGNDR	2	100.0%	2																								
				YLAEFATGNDRK	2	100.0%	2																								
				YLAEFATGNDRK	3	99.9%	1																								
IPI00000858	RDBP	cDNA FLJ56180, highly similar to Negative elongation factor E	92.4%	3.1	1	1	1	4	1,339,348	1,351,658	1,354,070	1,374,968	59,538	27,622	46,961	38,831	9.9	4.6	7.8	6.3	1.0	0.9	1.0	0.9	1.0	0.6	1.0	1	1.0	0.6	1.0	0.7
IPI00642023	RDBP	RD RNA binding protein	92.4%	7.6	1	1	1	4	1,339,348	1,351,658	1,354,070	1,374,968	59,538	27,622	46,961	38,831	9.9	4.6	7.8	6.3	1.0	0.9	1.0	0.9	1.0	0.6	1.0	1	1.0	0.6	1.0	0.7
IPI00922214	RDBP	cDNA FLJ56553, highly similar to Negative elongation factor E	92.4%	3.6	1	1	1	4	1,339,348	1,351,658	1,354,070	1,374,968	59,538	27,622	46,961	38,831	9.9	4.6	7.8	6.3	1.0	0.9	1.0	0.9	1.0	0.6	1.0	1	1.0	0.6	1.0	0.7
IPI00941607	RDBP	Negative elongation factor E	92.4%	3.2	1	1	1	4	1,339,348	1,351,658	1,354,070	1,374,968	59,538	27,622	46,961	38,831	9.9	4.6	7.8	6.3	1.0	0.9	1.0	0.9	1.0	0.6	1.0	1	1.0	0.6	1.0	0.7
				SLYESFVSSSDR	2	92.4%	1																								
IPI00000861	LASP1	isoform 1 of LIM and SH3 domain protein 1	100.0%	33.0	10	11	14	1	26,982,338	27,896,714	25,209,321	30,458,775	2,202,055	1,050,440	1,105,096	800,011	18.3	8.4	9.8	5.9	1.0	0.7	-1.1	0.5	1.1	0.2	-1.1	0.1	1.1	0.09	1.2	0.005
				GFSVVADTPELQR	2	100.0%	2																								
				IVYPTEK	2	97.7%	1																								
				KPYCNAHYPK	2	99.4%	1																								
				KPYCNAHYPK	3	99.4%	1																								
				LKQQSELQSQVR	3	95.4%	1																								
				MGPSGGEGMEPER	2	99.7%	1																								
				MGPSGGEGMEPERR	2	93.1%	1																								
				QQSELQSQVR	2	100.0%	2																								
				QSFTMVADTPENLR	2	100.0%	1																								
				TQDQISNIK	2	100.0%	2																								
				YHEEFEK	2	89.9%	1																								
IPI00000873	VARS	Valyl-tRNA synthetase	100.0%	10.0	7	7	8	2	8,788,807	8,813,114	9,352,595	10,172,619	610,211	431,067	510,319	128,408	15.5	10.9	12.2	2.8	1.0	1	1.1	0.5	1.2	0.09	1.1	0.4	1.2	0.03	1.1	0.2
IPI00893918	VARS	Valyl-tRNA synthetase	100.0%	10.0	7	7	8	2	8,788,807	8,813,114	9,352,595	10,172,619	610,211	431,067	510,319	128,408	15.5	10.9	12.2	2.8	1.0	1	1.1	0.5	1.2	0.09	1.1	0.4	1.2	0.03	1.1	0.2
				GDLRILPEAHQR	3	88.5%	1																								
				HGLEAISIMDSR	2	99.7%	1																								
				LLSPFMPFVTEELFQR	2	100.0%	2																								
				LPALEQGPGGLWVWGATAVAQLLWPAGLGGPGGSR	3	81.9%	1																								
				SLPIVFDEFVDMDFGTGAVK	2	100.0%	1																								
				SSAQDPQAVLGALGR	2	99.7%	1																								
				VQGSDSDEEVVVATTR	2	92.4%	1																								
IPI00000874	PRDX1	Peroxiredoxin-1	100.0%	70.9	16	17	23	1	88,015,545	89,690,477	84,578,061	99,393,829	6,593,248	3,892,755	4,589,883	4,116,390	16.8	9.7	12.1	9.3	1.0	0.8	-1.0	0.7	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.04
				ADEGISFR	1	96.9%	1																								
				ADEGISFR	2	99.3%	1																								
				ATAVMPDGQFK	2	100.0%	2																								
				DISLSDYK	1	98.4%	1																								
				GLFIIDDK	2	100.0%	2																								
				GLFIIDDKGILR	2	98.7%	1																								
				HGEVCPAGWKPGSDTIKPDVQK	3	100.0%	1																								
				KQGGLGPMNIPLVSDPK	3	100.0%	1																								
				KQGGLGPMNIPLVSDPKR	3	100.0%	2																								
				LNCQVIGASVDSHFCHLAWVNTPK	3	99.8%	1																								
				LVQAFQFTDK	2	100.0%	2																								
				QGGLGPMNIPLVSDPK	2	100.0%	1																								
				QGGLGPMNIPLVSDPKR	3	100.0%	1																								
				QITVNDLPVGR	2	100.0%	2																								
				RTIAQDYGVLK	2	99.5%	1																								
				SKEYFSK	1	85.1%	1																								
				TIAQDYGVLK	2	100.0%	2																								
IPI00000875	EEF1G	cDNA FLJ56389, highly similar to Elongation factor 1-gamma	100.0%	25.9	12	13	15	2	32,566,393	32,792,472	31,209,340	36,459,438	2,152,325	1,163,127	1,827,978	1,179,363	14.8	7.9	13.1	7.2	1.0	0.9	-1.0	0.6	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.04
IPI00937615	EEF1G	Elongation factor 1-gamma	100.0%	28.8	12	13	15	2	32,566,393	32,792,472	31,209,340	36,459,438	2,152,325	1,163,127	1,827,978	1,179,363	14.8	7.9	13.1	7.2	1.0	0.9	-1.0	0.6	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.04
				AKDPFAHLPK	3	99.9%	1																								
				ALIAAQYSGAQVR	2	100.0%	2																								
				AVLGEVK	1	92.6%	1																								
				EYFSWEGAFQHVGK	2	99.9%	1																								
				ILGLLDAYLK	2	100.0%	2																								
				KAAAPAPEEEMDECEQALAAEPK	3	99.9%	1																								
				KLDPGSEETQTLVR	2	100.0%	1																								
				KLDPGSEETQTLVR	3	100.0%	1																								
				LDPGSEETQTLVR	2	100.0%	1																								
				STFVLDEFKR	3	99.5%	1																								
				TFLVGER	2	99.4%	1																								
				TPEFLR	2	85.4%	1																								
				WFLTCINQPQFR	2	100.0%	1																								
IPI00000877	HYOU1	Hypoxia up-regulated protein 1	100.0%	24.2	16	18	21	4	22,670,653	22,421,795	22,683,775	25,498,723	2,336,205	954,287	1,311,765	885,242	23.0	9.5	12.9	7.8	-1.0	0.9	1.0	1	1.1	0.3	1.0	0.9	1.1	0.05	1.1	0.1
IPI00922838	HYOU1	cDNA FLJ56074, highly similar to 150 kDa oxygen-regulated protein	100.0%	24.7	16	18	21	4	22,670,653	22,421,795	22,683,775	25,498,723	2,336,205	954,287	1,311,765	885,242	23.0	9.5	12.9	7.8	-1.0	0.9	1.0	1	1.1	0.3	1.0	0.9	1.1	0.05	1.1	0.1
IPI01010461	HYOU1	94 kDa protein	100.0%	28.5	16	18	21	4	22,670,653	22,421,795	22,683,775	25,498,723	2,336,205	954,287	1,311,765	885,242	23.0	9.5	12.9	7.8	-1.0	0.9	1.0	1	1.1	0.3	1.0	0.9	1.1	0.05	1.1	0.1
IPI01011324	HYOU1	cDNA FLJ45395 fis, clone BRHIP3027191, highly similar to 150 kDa oxygen-regulat	100.0%	24.4	16	18	21	4	22,670,653	22,421,795	22,683,775	25,498,723	2,336,205	954,287	1,311,765	885,242	23.0	9.5	12.9	7.8	-1.0	0.9	1.0	1	1.1	0.3	1.0	0.9	1.1	0.05	1.1	0.1
				AANSLEAFIFETQDK	2	100.0%	1																								
				DAVVYPILVEFTR	2	100.0%	2																								
				EVEEEPGIHSLK	2	100.0%	1																								
				LAGLFNEQR	2	98.2%	1																								
				LCQGLFFR	2	98.5%	1																								
				LGNTISSLFGGGTTPDAK	2	100.0%	1																								
				LIPEMDQIFTEVEMTTLEK	2	100.0%	2																								
				LIPEMDQIFTEVEMTTLEK	3	100.0%	1																								
				LPATEKPVLLSK	3	99.6%	1																								
				LSAASTWLEDEGVGATTVMLK	2	100.0%	2																								
				LSAASTWLEDEGVGATTVMLK	3	100.0%	1																								
				NINADEAAAMGAVYQAAALSK	3	99.9%	1																								
				RAVLQAAR	2	92.1%	1																								
				TLGGLEMELR	2	99.8%	1																								
				TVLSANADHMAQIEGLMDDVDFK	3	100.0%	1																								
				VEFEELCADLFER	2	100.0%	1																								
				VESVFETLVEDSAEEESTLTK	2	100.0%	1																								
				VLQLINDNTATALSYGVFR	2	99.6%	1																								
IPI00000949	CRYM	Mu-crystallin homolog	99.6%	16.9	3	3	3	2	9,121,555	9,330,871	9,020,907	10,207,898	775,739	433,161	612,257	243,199	19.0	10.4	15.2	5.3	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.1	1.1	0.1
IPI00556050	CRYM	mu-crystallin homolog isoform 2	99.6%	19.5	3	3	3	2	9,121,555	9,330,871	9,020,907	10,207,898	775,739	433,161	612,257	243,199	19.0	10.4	15.2	5.3	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.1	1.1	0.1
				ESGDVLLSGAEIFAELGEVIK	2	93.1%	1																								
				GYLGVMPAYSAAEDALTTK	2	95.6%	1																								
				SLGMAVEDTVAAK	2	98.4%	1																								
IPI00001146	LSM6	U6 snRNA-associated Sm-like protein LSm6	96.1%	13.8	1	1	1	1	1,997,020	1,926,880	2,104,000	2,081,660	289,725	125,780	132,322	97,540	32.4	14.6	14.1	10.5	-1.0	0.8	1.1	0.7	1.0	0.8	1.1	0.4	1.1	0.4	-1.0	0.9
				GNNVLYISTQK	2	96.1%	1																								
IPI00001159	GCN1L1	Translational activator GCN1	100.0%	4.4	8	8	8	1	20,778,607	24,199,094	23,211,358	25,183,716	2,808,045	1,230,259	1,646,544	1,224,481	30.2	11.4	15.9	10.9	1.2	0.3	1.1	0.5	1.2	0.2	-1.0	0.6	1.0	0.6	1.1	0.4
				AIITALGVER	2	94.6%	1																								
				FVHFIDAPSLALIMPIVQR	3	99.9%	1																								
				ILPEIIPILEEGLR	2	99.3%	1																								
				LSVADSQAEAK	2	97.3%	1																								
				LVLPSLLAALEEESWR	2	100.0%	1																								
				NPEILAIAPVLLDALTDPSR	2	99.3%	1																								
				VDPLFTELLNGIR	2	96.0%	1																								
				VLAFLSSVAGDALTR	2	99.9%	1																								
IPI00001466	EML4	Echinoderm microtubule-associated protein-like 4	100.0%	3.9	3	3	3	3	5,157,874	5,302,015	5,057,434	5,923,778	532,824	299,413	509,056	281,142	23.1	12.6	22.5	10.6	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.2	0.2
IPI00854834	EML4	echinoderm microtubule-associated protein-like 4 isoform b	100.0%	4.1	3	3	3	3	5,157,874	5,302,015	5,057,434	5,923,778	532,824	299,413	509,056	281,142	23.1	12.6	22.5	10.6	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.2	0.2
IPI00893067	EML4	Uncharacterized protein	100.0%	3.8	3	3	3	3	5,157,874	5,302,015	5,057,434	5,923,778	532,824	299,413	509,056	281,142	23.1	12.6	22.5	10.6	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.2	0.2
				ADQFLVGTSR	2	95.9%	1																								
				LSLPQNETVADTTLTK	2	99.9%	1																								

				VQQQEDEITVLK	2	99.9%	1																									
IPI00001539	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	100.0%	25.2	6	6	6	1	34,367,110	33,293,360	33,545,680	37,222,320	2,072,019	1,237,436	2,088,212	1,845,504	13.5	8.3	13.9	11.1	-1.0	0.7	-1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.1	1.1	0.2
				AANDAGYFNDEMAPIEVK	2	100.0%	1																									
				DFTATDLSEFAAK	2	99.3%	1																									
				ITAHLVHELR	2	99.0%	1																									
				IVGYFVSGCDPSIMGIGPVPAISGALKK	3	94.6%	1																									
				TNVNGGAIALGHPLGGSGSR	3	100.0%	1																									
				TPFGAYGGLLK	2	100.0%	1																									
IPI00001589	TIMM13	Mitochondrial import inner membrane translocase subunit Tim13	100.0%	26.3	2	2	3	1	11,139,060	11,360,960	10,928,770	11,788,440	1,135,296	742,752	716,120	511,972	22.8	14.6	14.7	9.7	1.0	0.9	-1.0	0.9	1.1	0.6	-1.0	0.7	1.0	0.6	1.1	0.4
				LDPGLIMEQVK	2	100.0%	1																									
				VQIAVANAQELLQR	2	100.0%	2																									
IPI00001639	KPNB1	Importin subunit beta-1	100.0%	28.1	18	19	21	1	144,856,598	144,824,185	138,295,631	166,446,450	########	4,502,777	9,495,172	4,362,915	20.2	7.0	15.4	5.9	-1.0	1	-1.0	0.7	1.1	0.2	-1.0	0.6	1.1	0.009	1.2	0.03
				AAVENLPTFLVELSR	2	100.0%	1																									
				EHIKNPDWR	3	87.2%	1																									
				ESCLEAYTGIVQGLK	2	94.0%	1																									
				GALQYLVPILTQTLTK	2	100.0%	1																									
				GALQYLVPILTQTLTK	3	100.0%	1																									
				HFIMQVVCEATQCPDTR	3	100.0%	1																									
				LAATNALLNSLEFTK	2	100.0%	2																									
				LLETTDRPDGHQNNLR	3	100.0%	1																									
				LQQVLQMESHIQSTSDR	3	100.0%	1																									
				NSLTSKDPDIK	2	94.8%	1																									
				PMIHELLTEGR	3	99.4%	1																									
				SSAYESLMEIVK	2	100.0%	2																									
				TTLVIMER	2	99.9%	1																									
				TVSPDRLELEAAQK	2	92.7%	1																									
				VAALQNLVK	2	99.7%	1																									
				VQHQDALQISDVVMASLLR	3	100.0%	1																									
				WLAIDANAR	2	85.7%	1																									
				YLEVVLNTLQQASQAQVDK	3	100.0%	1																									
				YMEAFKPFLGIGLK	3	99.9%	1																									
IPI00001661	RCC1	regulator of chromosome condensation isoform a	100.0%	17.9	5	5	5	3	4,967,701	5,883,931	4,841,579	5,994,001	573,502	409,837	411,813	385,726	25.8	15.6	19.0	14.4	1.2	0.2	-1.0	0.9	1.2	0.2	-1.2	0.1	1.0	0.8	1.2	0.08
IPI00747309	RCC1	Regulator of chromosome condensation	100.0%	19.2	5	5	5	3	4,967,701	5,883,931	4,841,579	5,994,001	573,502	409,837	411,813	385,726	25.8	15.6	19.0	14.4	1.2	0.2	-1.0	0.9	1.2	0.2	-1.2	0.1	1.0	0.8	1.2	0.08
IPI00787306	RCC1	regulator of chromosome condensation isoform b	100.0%	18.5	5	5	5	3	4,967,701	5,883,931	4,841,579	5,994,001	573,502	409,837	411,813	385,726	25.8	15.6	19.0	14.4	1.2	0.2	-1.0	0.9	1.2	0.2	-1.2	0.1	1.0	0.8	1.2	0.08
				LGLGEGAEEK	2	98.6%	1																									
				SHSTEPGLVLTLGQGDVGQLGLGENVMER	3	100.0%	1																									
				SMVPVQVQLDVPVVK	2	100.0%	1																									
				VPELFANR	2	92.5%	1																									
				VVQVSAGDSHTAALTDDGR	3	98.2%	1																									
IPI00001676	NPLOC4	isoform 2 of Nuclear protein localization protein 4 homolog	100.0%	5.2	2	3	3	3	1,832,787	1,797,679	1,907,673	2,108,229	231,795	91,604	211,450	128,846	28.3	11.4	24.8	13.7	-1.0	0.9	1.0	0.8	1.2	0.3	1.1	0.6	1.2	0.09	1.1	0.4
IPI00290543	NPLOC4	isoform 1 of Nuclear protein localization protein 4 homolog	100.0%	5.3	2	3	3	3	1,832,787	1,797,679	1,907,673	2,108,229	231,795	91,604	211,450	128,846	28.3	11.4	24.8	13.7	-1.0	0.9	1.0	0.8	1.2	0.3	1.1	0.6	1.2	0.09	1.1	0.4
IPI00975546	NPLOC4	Uncharacterized protein	100.0%	5.2	2	3	3	3	1,832,787	1,797,679	1,907,673	2,108,229	231,795	91,604	211,450	128,846	28.3	11.4	24.8	13.7	-1.0	0.9	1.0	0.8	1.2	0.3	1.1	0.6	1.2	0.09	1.1	0.4
				VFGAPNVVEDEIDQYLSK	2	100.0%	1																									
				VFGAPNVVEDEIDQYLSK	3	92.8%	1																									
				VGWIFTDLVSEDTR	2	100.0%	1																									
IPI00001690	CUL7	Cullin-7	98.0%	1.8	1	1	1	2	1,521,590	1,462,335	1,437,400	1,496,260	138,281	146,783	221,871	116,626	20.3	22.4	34.5	17.4	-1.0	0.8	-1.1	0.8	-1.0	0.9	-1.0	0.9	1.0	0.9	1.0	0.8
IPI00955011	CUL7	cullin-7 isoform 1	98.0%	1.7	1	1	1	2	1,521,590	1,462,335	1,437,400	1,496,260	138,281	146,783	221,871	116,626	20.3	22.4	34.5	17.4	-1.0	0.8	-1.1	0.8	-1.0	0.9	-1.0	0.9	1.0	0.9	1.0	0.8
				GLVSSLGKGSACSSTDVLSCILHLLGKGTLR	3	98.0%	1																									
IPI00001699	PYCARD	isoform 1 of Apoptosis-associated speck-like protein containing a CARD	100.0%	21.5	3	3	5	3	2,340,821	2,081,959	2,214,066	2,817,543	303,347	140,199	144,411	90,027	29.0	15.1	14.6	7.1	-1.1	0.5	-1.1	0.7	1.2	0.2	1.1	0.5	1.4	0.002	1.3	0.008
IPI00221360	PYCARD	isoform 2 of Apoptosis-associated speck-like protein containing a CARD	100.0%	23.9	3	3	5	3	2,340,821	2,081,959	2,214,066	2,817,543	303,347	140,199	144,411	90,027	29.0	15.1	14.6	7.1	-1.1	0.5	-1.1	0.7	1.2	0.2	1.1	0.5	1.4	0.002	1.3	0.008
IPI00221362	PYCARD	isoform 3 of Apoptosis-associated speck-like protein containing a CARD	100.0%	31.1	3	3	5	3	2,340,821	2,081,959	2,214,066	2,817,543	303,347	140,199	144,411	90,027	29.0	15.1	14.6	7.1	-1.1	0.5	-1.1	0.7	1.2	0.2	1.1	0.5	1.4	0.002	1.3	0.008
				DAILDALENLTAEELKK	3	92.8%	1																									
				VLTDEQYQAVR	2	99.9%	2																									
				VTNVEWLLDALYGK	2	100.0%	2																									
IPI00001734	PSAT1	Phosphoserine aminotransferase	100.0%	14.5	5	5	5	2	12,884,163	13,868,688	14,065,005	16,339,841	1,126,823	608,982	576,784	524,813	19.6	9.8	9.2	7.2	1.1	0.5	1.1	0.4	1.3	0.02	1.0	0.8	1.2	0.02	1.2	0.02
IPI00219478	PSAT1	isoform 2 of Phosphoserine aminotransferase	100.0%	18.5	5	5	5	2	12,884,163	13,868,688	14,065,005	16,339,841	1,126,823	608,982	576,784	524,813	19.6	9.8	9.2	7.2	1.1	0.5	1.1	0.4	1.3	0.02	1.0	0.8	1.2	0.02	1.2	0.02
				ELLAVPDNYK	2	93.9%	1																									
				FGTINIVHPK	3	94.7%	1																									
				FLEMHQL	2	92.2%	1																									
				IINNTENLVR	2	99.9%	1																									
				VIFLQGGGCGQFSAVPLNLIGLK	2	99.1%	1																									
IPI00025879	MYH1	Myosin-1	97.3%	0.9	1	1	1	3	1,726,900	1,903,383	1,961,383	2,068,138	182,846	62,874	219,439	176,633	23.7	7.4	25.0	19.1	1.1	0.4	1.1	0.4	1.2	0.2	1.0	0.8	1.1	0.4	1.1	0.7
IPI00001753	MYH4	Myosin-4	97.3%	0.9	1	1	1	3	1,726,900	1,903,383	1,961,383	2,068,138	182,846	62,874	219,439	176,633	23.7	7.4	25.0	19.1	1.1	0.4	1.1	0.4	1.2	0.2	1.0	0.8	1.1	0.4	1.1	0.7
IPI00302329	MYH8	Myosin-8	97.3%	0.9	1	1	1	3	1,726,900	1,903,383	1,961,383	2,068,138	182,846	62,874	219,439	176,633	23.7	7.4	25.0	19.1	1.1	0.4	1.1	0.4	1.2	0.2	1.0	0.8	1.1	0.4	1.1	0.7
				VQLLHTQNTSLINTKKK	3	96.4%	1																									
IPI00001754	F11R	Junctional adhesion molecule A	93.8%	12.0	2	2	2	4	4,071,720	3,870,179	3,798,244	4,516,738	433,431	230,846	239,724	283,615	23.8	13.3	14.1	14.0	-1.1	0.7	-1.1	0.6	1.1	0.4	-1.0	0.8	1.2	0.1	1.2	0.09
IPI00069985	F11R	Junction adhesion molecule	93.8%	13.9	2	2	2	4	4,071,720	3,870,179	3,798,244	4,516,738	433,431	230,846	239,724	283,615	23.8	13.3	14.1	14.0	-1.1	0.7	-1.1	0.6	1.1	0.4	-1.0	0.8	1.2	0.1	1.2	0.09
IPI00922511	F11R	cDNA FLJ54854, highly similar to Junctional adhesion molecule A	93.8%	11.9	2	2	2	4	4,071,720	3,870,179	3,798,244	4,516,738	433,431	230,846	239,724	283,615	23.8	13.3	14.1	14.0	-1.1	0.7	-1.1	0.6	1.1	0.4	-1.0	0.8	1.2	0.1	1.2	0.09
IPI00940512	F11R	Uncharacterized protein	93.8%	12.9	2	2	2	4	4,071,720	3,870,179	3,798,244	4,516,738	433,431	230,846	239,724	283,615	23.8	13.3	14.1	14.0	-1.1	0.7	-1.1	0.6	1.1	0.4	-1.0	0.8	1.2	0.1	1.2	0.09
				LIVLVPPSKPTVNIPSSATIGNR	3	93.5%	1																									
				NGYGTPMTSNAVR	2	93.8%	1																									
IPI00001757	RBM8A	isoform 1 of RNA-binding protein 8A	100.0%	17.2	2	2	2	2	3,015,580	3,499,900	3,434,420	3,431,910	181,713	111,555	173,321	171,031	13.5	7.1	11.3	11.1	1.2	0.05	1.1	0.1	1.1	0.1	-1.0	0.8	-1.0	0.7	-1.0	1
IPI00216659	RBM8A	isoform 2 of RNA-binding protein 8A	100.0%	17.3	2	2	2	2	3,015,580	3,499,900	3,434,420	3,431,910	181,713	111,555	173,321	171,031	13.5	7.1	11.3	11.1	1.2	0.05	1.1	0.1	1.1	0.1	-1.0	0.8	-1.0	0.7	-1.0	1
				GYTLVEYETYK	2	100.0%	1																									
				MREDYDSVEQDGDEPGPQR	3	100.0%	1																									
IPI00001871	PAWR	PRKC apoptosis WT1 regulator protein	99.9%	9.7	2	2	2	1	8,257,152	8,826,508	8,314,689	8,748,445	555,605	262,173	1,028,248	447,541	15.1	6.6	27.7	11.4	1.1	0.4	1.0	1	1.1	0.5	-1.1	0.7	-1.0	0.9	1.1	0.7
				DANVSGTLVSSSTLEK	2	99.2%	1																									
				TSSGLGGSTTDFLEEWK	2	98.5%	1																									
IPI00001922	ST14	Suppressor of tumorigenicity 14 protein	99.9%	6.4	3	3	3	1	4,722,310	4,743,673	4,573,535	5,175,130	477,642	399,983	572,944	305,820	22.6	18.9	28.0	13.2	1.0	1	-1.0	0.8	1.1	0.4	-1.0	0.8	1.1	0.4	1.1	0.4
				IFQAGVVSWGDGCAQR	2	98.9%	1																									
				SQFVVTSNSNK	2	99.7%	1																									
				WVVLAAVLIGLLLVLLGIGFLVWHLQYR	3	80.2%	1																									
IPI00001960	CLIC4	Chloride intracellular channel protein 4	99.6%	12.3	2	2	2	3	3,077,566	2,953,813	2,839,260	3,098,463	209,934	139,181	164,569	48,650	15.3	10.5	13.0	3.5	-1.0	0.6	-1.1	0.4	1.0	0.9	-1.0	0.6	1.0	0.4	1.1	0.2
IPI00903323	CLIC4	cDNA FLJ38640 fis, clone HHDPC2003472, highly similar to CHLORIDE INTRACEL	99.6%	13.3	2	2	2	3	3,077,566	2,953,813	2,839,260	3,098,463	209,934	139,181	164,569	48,650	15.3	10.5	13.0	3.5	-1.0	0.6	-1.1	0.4	1.0	0.9	-1.0	0.6	1.0	0.4	1.1	0.2
IPI01010396	CLIC4	cDNA FLJ10762 fis, clone NT2RP4000008, moderately similar to CHLORINE CHAN	99.6%	14.9	2	2	2	3	3,077,566	2,953,813	2,839,260	3,098,463	209,934	139,181	164,569	48,650	15.3	10.5	13.0	3.5	-1.0	0.6	-1.1	0.4	1.0	0.9	-1.0	0.6	1.0	0.4	1.1	0.2
				FLDGNEMTLADCNLLPK	2	99.6%	1																									
				HPESNTAGMDIFAK	2	95.9%	1																									
IPI00002134	PSMD5	26S proteasome non-ATPase regulatory subunit 5	100.0%	17.3	6	7	8	1	18,009,514	18,539,505	16,776,680	20,543,643	1,799,505	215,686	945,115	489,251	22.3	2.6	12.6	5.3	1.0	0.8	-1.1	0.6	1.1	0.2	-1.1	0.1	1.1	0.006	1.2	0.008
				ELTGEDVLVR	2	97.4%	1																									
				ILTLSQIGR	2	96.9%	1																									
				ISLTQAGLEALFESNLLDDLK	2	100.0%	2																									
				ISLTQAGLEALFESNLLDDLK	3	100.0%	1																									
				IVENSDAVTEILNNAELLK	2	100.0%	1																									
				LMFNSPGFVEYVVDR	2	98.8%	1																									
				TIAEIFGNPNYLR	2	100.0%	1																									
IPI00644667	SAR1A	SAR1 gene homolog A	99.9%	9.1	1	1	1	5	1,596,592	1,613,902	1,440,367	1,403,663	204,238	99,176	72,673	97,040	28.6	13.7	11.3	15.5	1.0	0.9	-1.1	0.5	-1.1	0.4	-1.1	0.2	-1.1	0.2	-1.0	0.8
IPI00002149	SAR1B	GTP-binding protein SAR1b	99.9%	5.6	1	1	1	5	1,596,592	1,613,902	1,440,367	1,403,663	204,238	99,176	72,673	97,040	28.6	13.7	11.3	15.5	1.0	0.9	-1.1	0.5	-1.1	0.4	-1.1	0.2	-1.1	0.2	-1.0	0.8
IPI00964410	SAR1B	Uncharacterized protein	99.9%	10.7	1	1	1	5	1,596,592	1,613,902	1,440,367	1,403,663	204,238	99,176	72,673	97,040	28.6	13.7	11.3	15.5	1.0	0.9	-1.1	0.5	-1.1	0.4	-1.1	0.2	-1.1	0.2	-1.0	0.8
IPI00966157	SAR1B	Uncharacterized protein	99.9%	6.5	1	1	1	5	1,596,592	1,613,902	1,440,367	1,403,663	204,238	99,176	72,673	97,040	28.6	13.7	11.3	15.5	1.0	0.9	-1.1	0.5	-1.1	0.4	-1.1	0.2	-1.1	0.2	-1.0	0.8
IPI00968137	SAR1B	Uncharacterized protein	99.9%	7.6	1	1	1	5	1,596,592	1,613,902	1,440,367	1,403,663	204,238	99,176	72,673	97,040	28.6	13.7	11.3	15.5	1.0	0.9	-1.1	0.5	-1.1	0.4	-1.1	0.2	-1.1	0.2	-1.0	0.8
				LVFLGLDNAGK	2	99.4%	1																									
IPI00002203	BCCIP	isoform 1 of BRCA2 and CDKN1A-interacting protein	100.0%	24.5	5	5	5	1	33,698,808	39,525,123	37,274,809	40,504,918	6,812,153	4,607,000	3,799,372	3,034,858	45.2	26.1	22.8	16.8	1.2	0.5	1.1	0.7	1.2	0.4	-1.1	0.7	1.0	0.9	1.1	0.5
				APVNTAELTDLLIQQNHIGSVIK	3	100.0%	1																									
				FINVPPQIALPMYQQLQK	3	98.8%	1																									
				KGTQCVEQIQELVLR	3	81.5%	1																									
				TVMLIPGDK	2	98.6%	1																									
				WSFDDVPMTPLR	2	99.9%	1																									
IPI00002212	STK24	isoform B of Serine/threonine-protein kinase 24	100.0%	13.8	5	5	6	5	3,510,651	3,289,378	3,501,467	3,978,598	483,289	174,247	240,431	211,735	30.8	11.9	15.4	11.9	-1.1	0.7	-1.0	1	1.1	0.4	1.1	0.5	1.2	0.04	1.1	0.2
IPI00641189	STK24	cDNA FLJ61159, highly similar to Serine/threonine-protein kinase 24	100.0%	14.8	5	5	6	5	3,510,651	3,289,378	3,501,467	3,978,598	483,289	174,247	240,431	211,735	30.8	11.9	15.4	11.9	-1.1	0.7	-1.0	1	1.1	0.4	1.1	0.5	1.2	0.04	1.1	0.2
IPI00909904	STK24	cDNA FLJ61383, highly similar to Serine/threonine-protein kinase 24	100.0%	13.6	5	5	6	5	3,510,651	3,289,378	3,501,467	3,978,598	483,289	174,247	240,431	211,735	30.8	11.9	15.4	11.9	-1.1	0.7	-1.0	1	1.1	0.4	1.1	0.5	1.2	0.04	1.1	0.2
IPI00981772	STK24	isoform A of Serine/threonine-protein kinase 24	100.0%	14.2	5	5	6	5	3,510,651	3,289,378	3,501,467	3,978,598	483,289	174,247	240,431	211,735	30.8	11.9	15.4	11.9	-1.1	0.7	-1.0	1	1.1	0.4	1.1	0.5	1.2	0.04	1.1	0.2
IPI00640104	STK24	Uncharacterized protein	100.0%	13.9	5	5	6	5	3,510,651	3,289,378	3,501,467	3,978,598	483,289	174,247	240,431	211,735	30.8	11.9	15.4	11.9	-1.1	0.7	-1.0	1	1.1	0.4	1.1	0.5	1.2	0.04	1.1	0.2
				ADIWSLGITAIELAR	2	100.0%	2																									
				LADFGVAGQLTDTQIK	2	99.5%	1																									
				LADFGVAGQLTDTQIKR	3	99.9%	1																									
				RPFSQCLSTIISPLFAELK	3	82.3%	1																									
				TSYLTELIDR	2	99.8%	1																									
IPI00002214	KPNA2	Importin subunit alpha-2	100.0%	6.6	2	2	2	2	3,360,450	3,428,670	2,861,840	3,565,065	253,135	231,951	188,798	181,879	16.8	15.1	14.8	11.4	1.0	0.8	-1.2	0.2	1.1	0.5	-1.2	0.09	1.0	0.7	1.2	0.03
IPI00789457	KPNA2	Karyopherin alpha 2	100.0%	6.6	2	2	2	2	3,360,450	3,428,670	2,861,840	3,565,065	253,135	231,951	188,798	181,879	16.8	15.1	14.8	11.4	1.0	0.8	-1.2	0.2	1.1	0.5	-1.2	0.09	1.0	0.7	1.2	0.03
				NKNPAPPIDAVEQILPTLVR	3	100.0%	1																									
				NNQGTVNWSVDDIVK	2	100.0%	1																									
IPI00002221	SZT2	isoform 1 of Protein SZT2	94.5%	0.8	1	1	1	2	1,577,080	1,421,085	1,762,720	1,437,270	168,553	104,201	150,890	134,334	23.9	16.4	19.1	20.9	-1.1	0.5	1.1	0.4	-1.1	0.5	1.2	0.1	1.0	0.9	-1.2	0.1
IPI00970827	SZT2	isoform 3 of Protein SZT2	94.5%	0.8	1	1	1	2	1,577,080	1,421,085	1,762,720	1,437,270	168,553	104,201	150,890	134,334	23.9	16.4	19.1	20.9	-1.1	0.5	1.1	0.4	-1.1	0.5	1.2	0.1	1.0	0.9	-1.2	0.1
				EEEFEQLTQVIRCPVVVDSSSAQNGAPR	3	94.5%	1																									
IPI00002236	MFGE8	cDNA FLJ59612, highly similar to Lactadherin	96.7%	3.8	1	1	1	4	2,728,173	2,768,440	2,628,010	2,985,845	132,588	111,095	141,933	107,032	10.9	9.0	12.1	8.0	1.0	0.8	-1.0	0.6	1.1	0.2	-1.1	0.5	1.1	0.2	1.1	0.08
IPI00334005	MFGE8	isoform 3 of Lactadherin	96.7%	3.9	1	1	1	4	2,728,173	2,768,440	2,628,010	2,985,845	132,588	111,095	141,933	107,032	10.9	9.0	12.1	8.0	1.0	0.8	-1.0	0.6	1.1	0.2	-1.1	0.5	1.1	0.2	1.1	0.08
IPI00966900	MFGE8	isoform 1 of Lactadherin	96.7%	3.4	1	1	1	4	2,728,173	2,768,440	2,628,010	2,985,845	132,588	111,095	141,933	107,032	10.9	9.0	12.1	8.0	1.0	0.8	-1.0	0.6	1.1	0.2	-1.1	0.5	1.1	0.2	1.1	0.08
IPI01015593	MFGE8	cDNA FLJ38589 fis, clone HCHON2010074, highly similar to LACTADHERIN	96.7%	3.4	1	1	1	4	2,728,173	2,768,440	2,628,010	2,985,845	132,588	111,095	141,933	107,032	10.9	9.0	12.1	8.0	1.0	0.8	-1.0	0.6	1.1	0.2	-1.1	0.5	1.1	0.2	1.1	0.08
				NLFETPILARYVR	3	96.7%	1																									
IPI00002255	LRBA	isoform 1 of Lipopolysaccharide-responsive and beige-like anchor protein	99.9%	0.9	2	2	2	3	1,666,540	1,642,931	1,633,501	1,888,442	134,385	70,265	108,947	153,786	18.0	9.6	14.9	18.2	-1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.2	1.2	0.2
IPI00945818	LRBA	isoform 2 of Lipopolysaccharide-responsive and beige-like anchor protein	99.9%	1.0	2	2	2	3	1,666,540	1,642,931	1,633,501	1,888,442	134,385	70,265	108,947	153,786	18.0	9.6	14.9	18.2	-1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.2	1.2	0.2
IPI00967340	LRBA	Uncharacterized protein	99.9%	1.1	2	2	2	3	1,666,540	1,642,931	1,633,501	1,888,442	134,385	70,265	108,947	153,786	18.0	9.6	14.9	18.2	-1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.2	1.2	0.2
				ATDAQLCLESSPK	2	89.7%	1																									
				NAGLAFIELVNEGR	2	99.7%	1																									
IPI00002270	C6orf211	UPF0364 protein C6orf211	99.9%	9.1	2	2	2	2	1,373,930	1,500,661	1,603,057	1,624,563	102,287	108,730	134,646	48,961	16.7	16.2	18.8	6.7	1.1	0.4	1.2	0.2	1.2	0.06	1.1	0.6	1.1	0.3	1.0	0.9
IPI01014584	C6orf211	37 kDa protein	99.9%	12.4	2	2	2	2	1,373,930	1,500,661	1,603,057	1,624,563	102,287	108,730	134,646	48,961	16.7	16.2	18.8	6.7	1.1	0.4	1.2	0.2	1.2	0.06	1.1	0.6	1.1	0.3	1.0	0.9
				IHEAIIQSPPIDYFDVFK	3	83.3%	1																									
				TIPWFVSDTTIHDFNWLIEQVK	3	99.1%	1																									
IPI00002324	MAT2B	isoform 1 of Methionine adenosyltransferase 2 subunit beta	100.0%	21.6	4	4	4	4	4,134,722	4,424,692	4,447,036	4,857,578	437,893	236,875	364,385	221,777	23.7	12.0	18.3	10.2	1.1	0.6	1.1	0.6	1.2	0.2	1.0	1	1.1	0.2	1.1	0.4
IPI00181717	MAT2B	isoform 2 of Methionine adenosyltransferase 2 subunit beta	100.0%	22.3	4	4	4	4	4,134,722	4,424,692	4,447,036	4,857,578	437,893	236,875	364,385	221,777	23.7	12.0	18.3	10.2	1.1	0.6	1.1	0.6	1.2	0.2	1.0	1	1.1	0.2	1.1	0.4
IPI00845294	MAT2B	isoform 3 of Methionine adenosyltransferase 2 subunit beta	100.0%	27.8	4	4	4	4	4,134,722	4,424,692	4,447,036	4,857,578	437,893	236,875	364,385	221,777	23.7	12.0	18.3	10.2	1.1	0.6	1.1	0.6	1.2	0.2	1.0	1	1.1	0.2	1.1	0.4
IPI00845510	MAT2B	isoform 4 of Methionine adenosyltransferase 2 subunit beta	100.0%	23.5	4	4	4	4	4,134,722	4,424,692	4,447,036	4,857,578	437,893	236,875	364,385	221,777	23.7	12.0	18.3	10.2	1.1	0.6	1.1	0.6	1.2	0.2	1.0	1	1.1	0.2	1.1	0.4
				AVLENNLGAAVLR	2	100.0%	1																									
				IPILYGEVEKLEESAVTVMFDK	3	100.0%	1																									
				RPDVVENQPDAASQLNVDASGNLAK	3	99.9%	1																									
				VLVTGATGLLGR	2	99.9%	1																									
IPI00002349	NUFIP2	Nuclear fragile X mental retardation-interacting protein 2	100.0%	3.9	2	2	2	1	7,268,140	7,335,920	8,417,360	8,631,250	353,903	266,392	721,288	433,078	10.9	8.1	19.2	11.2	1.0	0.9	1.2	0.2	1.2	0.04	1.1	0.2	1.2	0.03	1.0	0.8

				ADTSSQGALVFLSK	2	99.3%	1																									
				NLSSDEATNPISR	2	95.0%	1																									
IPI00002372	ABCD3	isoform 1 of ATP-binding cassette sub-family D member 3	100.0%	8.5	3	3	3	3	1,423,724	1,280,754	1,567,707	1,586,967	222,234	105,381	179,888	77,863	34.9	18.4	25.7	11.0	-1.1	0.6	1.1	0.6	1.1	0.5	1.2	0.2	1.2	0.05	1.0	0.9
IPI00185503	ABCD3	isoform 2 of ATP-binding cassette sub-family D member 3	100.0%	10.2	3	3	3	3	1,423,724	1,280,754	1,567,707	1,586,967	222,234	105,381	179,888	77,863	34.9	18.4	25.7	11.0	-1.1	0.6	1.1	0.6	1.1	0.5	1.2	0.2	1.2	0.05	1.0	0.9
IPI01015425	ABCD3	67 kDa protein	100.0%	9.6	3	3	3	3	1,423,724	1,280,754	1,567,707	1,586,967	222,234	105,381	179,888	77,863	34.9	18.4	25.7	11.0	-1.1	0.6	1.1	0.6	1.1	0.5	1.2	0.2	1.2	0.05	1.0	0.9
				EGGWDSVQDWMDVLSGGEK	2	100.0%	1																									
				GIEGVQVIPLIPGAGEIIIADNIIK	3	100.0%	1																									
				VLGELWPLFGGR	2	99.8%	1																									
IPI00002406	BCAM	Basal cell adhesion molecule	98.0%	2.1	1	1	1	2	2,333,705	2,099,755	1,931,075	2,387,015	371,834	133,099	225,617	128,145	35.6	14.2	26.1	12.0	-1.1	0.6	-1.2	0.4	1.0	0.9	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00554618	BCAM	basal cell adhesion molecule isoform 2 precursor	98.0%	2.2	1	1	1	2	2,333,705	2,099,755	1,931,075	2,387,015	371,834	133,099	225,617	128,145	35.6	14.2	26.1	12.0	-1.1	0.6	-1.2	0.4	1.0	0.9	-1.1	0.5	1.1	0.2	1.2	0.1
				VAYLDPLELSEGK	2	98.0%	1																									
IPI00002460	ANXA7	isoform 1 of Annexin A7	100.0%	13.3	5	5	5	4	3,612,469	3,569,452	3,657,696	3,950,118	337,476	137,272	227,346	130,530	20.9	8.6	13.9	7.4	-1.0	0.9	1.0	0.9	1.1	0.4	1.0	0.7	1.1	0.08	1.1	0.3
IPI00021771	ANXA7	isoform 2 of Annexin A7	100.0%	14.0	5	5	5	4	3,612,469	3,569,452	3,657,696	3,950,118	337,476	137,272	227,346	130,530	20.9	8.6	13.9	7.4	-1.0	0.9	1.0	0.9	1.1	0.4	1.0	0.7	1.1	0.08	1.1	0.3
IPI00953297	ANXA7	cDNA FLJ55060, highly similar to Annexin A7	100.0%	15.0	5	5	5	4	3,612,469	3,569,452	3,657,696	3,950,118	337,476	137,272	227,346	130,530	20.9	8.6	13.9	7.4	-1.0	0.9	1.0	0.9	1.1	0.4	1.0	0.7	1.1	0.08	1.1	0.3
IPI01011531	ANXA7	cDNA FLJ54149, highly similar to Annexin A7	100.0%	19.4	5	5	5	4	3,612,469	3,569,452	3,657,696	3,950,118	337,476	137,272	227,346	130,530	20.9	8.6	13.9	7.4	-1.0	0.9	1.0	0.9	1.1	0.4	1.0	0.7	1.1	0.08	1.1	0.3
				ATMEAYSR	2	96.7%	1																									
				EFSGYVESGLK	2	98.9%	1																									
				GFGTDEQAIVDVVANR	2	100.0%	1																									
				LGTDESCFNMILATR	2	100.0%	1																									
				TLGTMIAGDTSGDYR	2	99.8%	1																									
IPI00002519	SHMT1	isoform 1 of Serine hydroxymethyltransferase, cytosolic	100.0%	5.4	2	2	3	3	1,970,012	1,816,276	1,721,289	2,030,820	306,931	86,401	86,451	145,364	34.8	10.6	11.2	16.0	-1.1	0.7	-1.1	0.5	1.0	0.9	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00220668	SHMT1	isoform 2 of Serine hydroxymethyltransferase, cytosolic	100.0%	5.9	2	2	3	3	1,970,012	1,816,276	1,721,289	2,030,820	306,931	86,401	86,451	145,364	34.8	10.6	11.2	16.0	-1.1	0.7	-1.1	0.5	1.0	0.9	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00793862	SHMT1	Serine hydroxymethyltransferase	100.0%	5.8	2	2	3	3	1,970,012	1,816,276	1,721,289	2,030,820	306,931	86,401	86,451	145,364	34.8	10.6	11.2	16.0	-1.1	0.7	-1.1	0.5	1.0	0.9	-1.1	0.5	1.1	0.2	1.2	0.1
				ALSEALTELGYK	2	99.1%	1																									
				ISATSIFFESMPYK	2	100.0%	2																									
IPI00002520	SHMT2	Serine hydroxymethyltransferase, mitochondrial	100.0%	28.0	9	9	12	1	6,531,607	6,389,324	7,178,224	7,589,432	613,101	231,818	523,158	420,378	21.0	8.1	16.3	12.4	-1.0	0.8	1.1	0.4	1.2	0.2	1.1	0.2	1.2	0.04	1.1	0.6
				AALEALGSCLNNK	2	100.0%	2																									
				AMADALLER	2	90.9%	1																									
				CGQLVRMAIRAQHSNAAQTQTGEANR	3	93.4%	1																									
				GLELIASENFCSR	2	96.9%	1																									
				IMGLDLPDGGHLTHGYMSDVKR	3	95.8%	1																									
				ISATSIFFESMPYK	2	100.0%	2																									
				VLELVSITANK	2	100.0%	2																									
				VVDFIDEGVNIGLEVK	2	100.0%	1																									
				YYGGAEVVDEIELLCQR	2	100.0%	1																									
IPI00002521	ATP5J	ATP synthase-coupling factor 6, mitochondrial	99.5%	13.9	1	1	1	3	1,316,903	1,392,963	1,309,580	1,357,837	232,524	92,712	75,976	67,338	39.5	14.9	13.0	11.1	1.1	0.8	-1.0	1	1.0	0.9	-1.1	0.5	-1.0	0.8	1.0	0.6
IPI00456008	ATP5J	ATP synthase-coupling factor 6, mitochondrial isoform b precursor	99.5%	12.9	1	1	1	3	1,316,903	1,392,963	1,309,580	1,357,837	232,524	92,712	75,976	67,338	39.5	14.9	13.0	11.1	1.1	0.8	-1.0	1	1.0	0.9	-1.1	0.5	-1.0	0.8	1.0	0.6
IPI00794158	ATP5J	ATP synthase-coupling factor 6, mitochondrial	99.5%	12.6	1	1	1	3	1,316,903	1,392,963	1,309,580	1,357,837	232,524	92,712	75,976	67,338	39.5	14.9	13.0	11.1	1.1	0.8	-1.0	1	1.0	0.9	-1.1	0.5	-1.0	0.8	1.0	0.6
				QMFGNADMNTFPTFK	2	99.5%	1																									
IPI00002525	NENF	Neudesin	99.9%	19.2	2	2	2	1	6,966,140	6,276,700	7,087,540	6,892,250	698,301	382,090	173,025	434,628	22.4	13.6	5.5	14.1	-1.1	0.4	1.0	0.9	-1.0	0.9	1.1	0.09	1.1	0.3	-1.0	0.7
				MSLDPADLTHDTTGLTAK	3	95.2%	1																									
				YGGEEEDQPIYLAVK	2	97.6%	1																									
IPI00002535	FKBP2	Peptidyl-prolyl cis-trans isomerase FKBP2	100.0%	28.9	3	3	5	1	12,485,745	12,999,340	13,407,945	14,719,335	962,398	647,921	852,564	501,908	17.2	11.2	14.2	7.6	1.0	0.7	1.1	0.5	1.2	0.07	1.0	0.7	1.1	0.07	1.1	0.2
				GWDQGLLGMCEGEK	2	100.0%	1																									
				IPGGATLVFEVELLK	2	100.0%	2																									
				LVIPSELGYGER	2	99.6%	2																									
IPI00002552	AP1M2	isoform 1 of AP-1 complex subunit mu-2	100.0%	8.3	3	3	3	2	6,839,178	6,963,350	6,876,502	7,732,810	1,084,887	736,973	516,025	520,876	35.5	23.7	16.8	15.1	1.0	0.9	1.0	1	1.1	0.5	-1.0	0.9	1.1	0.4	1.1	0.3
IPI00219794	AP1M2	isoform 2 of AP-1 complex subunit mu-2	100.0%	8.2	3	3	3	2	6,839,178	6,963,350	6,876,502	7,732,810	1,084,887	736,973	516,025	520,876	35.5	23.7	16.8	15.1	1.0	0.9	1.0	1	1.1	0.5	-1.0	0.9	1.1	0.4	1.1	0.3
				FEIPYFTVSGIQVR	2	94.3%	1																									
				SGYQALPWVR	2	99.6%	1																									
				YITQSGDYQLR	2	99.8%	1																									
IPI00002557	COPG2	Coatomer subunit gamma-2	100.0%	1.4	1	1	2	1	618,661	568,647	600,910	649,725	84,269	50,733	78,909	76,092	30.5	20.0	29.4	26.2	-1.1	0.6	-1.0	0.9	1.1	0.8	1.1	0.7	1.1	0.4	1.1	0.7
				SIATLAITTLLK	2	100.0%	2																									
IPI00002606	SCIN	isoform 1 of Adseverin	100.0%	7.0	4	4	4	1	27,009,550	28,071,210	26,363,610	30,399,430	1,904,314	1,456,540	1,933,863	1,114,922	15.8	11.6	16.4	8.2	1.0	0.7	-1.0	0.8	1.1	0.2	-1.1	0.5	1.1	0.2	1.2	0.1
				ELQGYESNDFVSYFK	2	99.8%	1																									
				LPQNSGYIWVGK	2	98.5%	1																									
				MYLETDPSGR	2	99.4%	1																									
				TAEEFLQQMNYSK	2	99.9%	1																									
IPI00002618	ABCD2	ATP-binding cassette sub-family D member 2	98.8%	2.8	1	1	1	1	4,681,540	5,954,940	4,378,090	5,941,030	502,651	323,340	303,585	256,653	24.0	12.1	15.5	9.7	1.3	0.07	-1.1	0.6	1.3	0.06	-1.4	0.007	-1.0	1	1.4	0.004
				AACLVAAAYALKTLYPIIGKR	3	98.8%	1																									
IPI00002647	WASF4	Putative Wiskott-Aldrich syndrome protein family member 4	100.0%	5.9	3	3	3	1	7,105,878	8,245,991	5,966,900	8,442,408	1,378,762	1,156,703	578,164	725,046	43.4	31.4	21.7	19.2	1.2	0.5	-1.2	0.5	1.2	0.4	-1.4	0.1	1.0	0.9	1.4	0.03
				FYTDPSYFFDLWK	2	100.0%	1																									
				MGQEFVESK	2	95.2%	1																									
				WDVVGNDVATILSRR	2	80.6%	1																									
IPI00002649	PNN	isoform 2 of Pinin	100.0%	8.1	3	3	3	1	4,410,543	4,574,489	5,200,153	5,331,074	669,666	337,025	441,571	343,800	34.0	16.5	19.0	14.4	1.0	0.8	1.2	0.4	1.2	0.3	1.1	0.3	1.2	0.2	1.0	0.8
				IFGLLMGTLQK	2	100.0%	1																									
				QQDSQPEEVMDVLEMVENVK	3	93.7%	1																									
				VELAQLQEEWNEHNAK	3	83.0%	1																									
IPI00219171	POU2F1	isoform 2 of POU domain, class 2, transcription factor 1	97.6%	1.7	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00555623	POU2F1	isoform 4 of POU domain, class 2, transcription factor 1	97.6%	2.0	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00555806	POU2F1	isoform 3 of POU domain, class 2, transcription factor 1	97.6%	1.8	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00640177	POU2F1	POU domain, class 2, transcription factor 1 isoform 3	97.6%	1.9	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI01011031	POU2F1	POU domain, class 2, transcription factor 1 isoform 1	97.6%	1.7	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00002666	POU2F2	POU domain, class 2, transcription factor 2	97.6%	2.8	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00012533	POU2F2	isoform 1 of POU domain, class 2, transcription factor 2	97.6%	2.7	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00221055	POU2F2	isoform 2 of POU domain, class 2, transcription factor 2	97.6%	2.8	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00335926	POU2F2	isoform 4 of POU domain, class 2, transcription factor 2	97.6%	3.3	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00888702	POU2F2	isoform 5 of POU domain, class 2, transcription factor 2	97.6%	2.2	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00953226	POU2F2	Uncharacterized protein	97.6%	2.2	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00980009	POU2F2	Uncharacterized protein	97.6%	2.2	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00982384	POU2F2	51 kDa protein	97.6%	2.7	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00748827	POU2F3	POU domain, class 2, transcription factor 3	97.6%	3.0	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00981679	POU2F3	Uncharacterized protein	97.6%	5.9	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI00984752	POU2F3	Uncharacterized protein	97.6%	3.3	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
IPI01009181	POU2F3	48 kDa protein	97.6%	3.0	1	1	1	17	185,220	226,871	205,272	220,415	10,129	17,301	18,297	5,992	12.2	17.1	19.9	6.1	1.2	0.07	1.1	0.4	1.2	0.02	-1.1	0.4	-1.0	0.7	1.1	0.5
				LYGNDFSQTTISR	2	97.6%	1																									
IPI00002745	CTSZ	Cathepsin Z	100.0%	10.6	3	3	3	1	70,448,260	66,654,940	66,598,540	71,984,690	6,815,478	2,582,413	3,024,492	2,087,231	21.6	8.7	10.2	6.5	-1.1	0.6	-1.1	0.6	1.0	0.8	-1.0	1	1.1	0.1	1.1	0.2
				NSWGEPWGER	2	98.7%	1																									
				NVDGVNYASITR	2	99.7%	1																									
				VGDYGSLSGR	2	100.0%	1																									
IPI00002857	MAPK14	isoform CSBP2 of Mitogen-activated protein kinase 14	99.5%	12.2	2	2	2	3	609,020	704,100	857,883	910,667	60,754	84,022	86,120	74,960	22.3	26.7	22.5	18.4	1.2	0.4	1.4	0.05	1.5	0.01	1.2	0.2	1.3	0.1	1.1	0.7
IPI00221141	MAPK14	isoform CSBP1 of Mitogen-activated protein kinase 14	99.5%	12.2	2	2	2	3	609,020	704,100	857,883	910,667	60,754	84,022	86,120	74,960	22.3	26.7	22.5	18.4	1.2	0.4	1.4	0.05	1.5	0.01	1.2	0.2	1.3	0.1	1.1	0.7
IPI00945296	MAPK14	cDNA FLJ58214, highly similar to Mitogen-activated protein kinase 14	99.5%	15.6	2	2	2	3	609,020	704,100	857,883	910,667	60,754	84,022	86,120	74,960	22.3	26.7	22.5	18.4	1.2	0.4	1.4	0.05	1.5	0.01	1.2	0.2	1.3	0.1	1.1	0.7
				MNFANVFIGANPLAVDLLEK	2	99.5%	1																									
				SLEEFNDVYLVTHLMGADLNNIVK	3	94.2%	1																									
IPI00002922	TBL1XR1	F-box-like/WD repeat-containing protein TBL1XR1	100.0%	4.5	2	2	2	4	792,416	902,604	825,236	1,002,567	72,517	60,605	89,519	46,488	20.5	15.0	24.3	10.4	1.1	0.3	1.0	0.8	1.3	0.04	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00922336	TBL1XR1	cDNA FLJ55712, highly similar to F-box-like/WD repeat protein TBL1XR1	100.0%	6.1	2	2	2	4	792,416	902,604	825,236	1,002,567	72,517	60,605	89,519	46,488	20.5	15.0	24.3	10.4	1.1	0.3	1.0	0.8	1.3	0.04	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00218132	TBL1X	isoform 2 of F-box-like/WD repeat-containing protein TBL1X	100.0%	4.4	2	2	2	4	792,416	902,604	825,236	1,002,567	72,517	60,605	89,519	46,488	20.5	15.0	24.3	10.4	1.1	0.3	1.0	0.8	1.3	0.04	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00640917	TBL1X	isoform 1 of F-box-like/WD repeat-containing protein TBL1X	100.0%	4.0	2	2	2	4	792,416	902,604	825,236	1,002,567	72,517	60,605	89,519	46,488	20.5	15.0	24.3	10.4	1.1	0.3	1.0	0.8	1.3	0.04	-1.1	0.5	1.1	0.2	1.2	0.1
				GPIFALK	2	97.3%	1																									
				VGASASDGSVCVLDLR	2	99.9%	1																									
IPI00002926	VPS37B	Vacuolar protein sorting-associated protein 37B	98.8%	6.3	1	1	1	3	890,973	803,657	981,070	973,080	151,492	137,929	141,788	97,006	38.0	38.4	32.3	22.3	-1.1	0.7	1.1	0.7	1.1	0.7	1.2	0.4	1.2	0.3	-1.0	1
IPI01014380	VPS37B	21 kDa protein	98.8%	9.8	1	1	1	3	890,973	803,657	981,070	973,080	151,492	137,929	141,788	97,006	38.0	38.4	32.3	22.3	-1.1	0.7	1.1	0.7	1.1	0.7	1.2	0.4	1.2	0.3	-1.0	1
IPI01014913	VPS37B	30 kDa protein	98.8%	6.6	1	1	1	3	890,973	803,657	981,070	973,080	151,492	137,929	141,788	97,006	38.0	38.4	32.3	22.3	-1.1	0.7	1.1	0.7	1.1	0.7	1.2	0.4	1.2	0.3	-1.0	1
				FLDGELPLDSFIDVYQSK	2	98.8%	1																									
IPI00002957	TBC1D17	TBC1 domain family member 17	95.8%	1.2	1	1	1	2	1,929,690	1,952,845	2,052,535	2,280,240	123,252	148,017	148,786	164,651	14.3	17.0	16.2	16.2	1.0	0.9	1.1	0.5	1.2	0.1	1.1	0.6	1.2	0.2	1.1	0.3
IPI00954884	TBC1D17	TBC1 domain family member 17 isoform 2	95.8%	1.3	1	1	1	2	1,929,690	1,952,845	2,052,535	2,280,240	123,252	148,017	148,786	164,651	14.3	17.0	16.2	16.2	1.0	0.9	1.1	0.5	1.2	0.1	1.1	0.6	1.2	0.2	1.1	0.3
				WLLIWFKR	2	95.8%	1																									
IPI00002966	HSPA4	Heat shock 70 kDa protein 4	100.0%	37.3	24	25	34	1	115,544,839	116,695,850	117,103,413	130,162,229	########	4,680,647	7,103,578	4,603,553	19.4	9.0	13.6	7.9	1.0	0.9	1.0	0.9	1.1	0.2	1.0	1	1.1	0.07	1.1	0.2
				AFSDPFVEAEK	2	100.0%	2																									
				AFSDPFVEAEKSNLAYDIVQLPTGLTGIK	3	95.6%	1																									
				AGGIETIANEYSDR	2	100.0%	2																									
				EDIYAVEIVGGATR	2	100.0%	2																									
				EFSITDVVPYPISLR	2	100.0%	2																									
				ELSTTLNADEAVTR	2	100.0%	2																									
				EMLNLYIENEGK	2	100.0%	1																									
				FLEMCNDLLAR	2	99.1%	1																									
				GCALQCAILSPAFK	2	81.4%	1																									
				KFDEVLVNHFCEEFGK	3	99.6%	1																									
				LEDTENWLYEDGEDQPK	2	100.0%	1																									
				LKETAESVLK	2	90.5%	1																									
				LKVLATAFDTTLGGRK	3	86.8%	1																									
				NFTTEQVTAMLLSK	2	100.0%	2																									
				NKEDQYDHLDAADMTK	3	100.0%	2																									
				QSLTMDPVVK	2	97.9%	1																									
				SIGAAAKSQVISNAKNTVQGFK	3	93.6%	1																									
				SNLAYDIVQLPTGLTGIK	2	100.0%	2																									
				STNEAMEWMNNK	2	100.0%	1																									
				SVMDATQIAGLNCLR	2	100.0%	1																									
				TSTVDLPIENQLLWQIDR	2	100.0%	1																									
				TSTVDLPIENQLLWQIDR	3	99.8%	1																									
				VLATAFDTTLGGR	2	100.0%	2																									
				VTYMEEER	2	99.7%	1																									
				WNSPAEEGSSDCEVFSK	2	100.0%	1																									
IPI00003031	ISOC2	isoform 2 of Isochorismatase domain-containing protein 2, mitochondrial	99.6%	22.2	2	2	2	3	3,059,079	2,939,412	3,205,788	3,434,827	231,745	82,028	224,222	60,524	16.9	6.2	15.6	3.9	-1.0	0.6	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.001	1.1	0.4
IPI00442223	ISOC2	isoform 3 of Isochorismatase domain-containing protein 2, mitochondrial	99.6%	36.3	2	2	2	3	3,059,079	2,939,412	3,205,788	3,434,827	231,745	82,028	224,222	60,524	16.9	6.2	15.6	3.9	-1.0	0.6	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.001	1.1	0.4
IPI00551022	ISOC2	isoform 1 of Isochorismatase domain-containing protein 2, mitochondrial	99.6%	23.9	2	2	2	3	3,059,079	2,939,412	3,205,788	3,434,827	231,745	82,028	224,222	60,524	16.9	6.2	15.6	3.9	-1.0	0.6	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.001	1.1	0.4
				LIKEPAPDSGLLGLFQGQNSLLH	3	99.6%	1																									
				QSGAFLSTSEGLILQLVGDAVHPQFK	3	95.2%	1																									
IPI00003035	C15orf29	Uncharacterized protein C15orf29	97.1%	10.9	2	2	2	1	7,192,260	7,648,370	7,641,000	9,304,600	837,058	664,190	802,493	258,102	26.0	19.4	23.5	6.2	1.1	0.7	1.1	0.7	1.3	0.06	-1.0	1	1.2	0.07	1.2	0.1
				IEDLGVVVDCLPVLTNCLQEEK	3	83.2%	1																									
				VHHPFPNPCYR	2	83.3%	1																									
IPI00003081	PTGER1	Prostaglandin E2 receptor EP1 subtype	95.8%	5.5	1	1	1	1	5,847,390	5,915,340	6,084,970	6,966,150	261,642	384,712	491,469	531,652	10.0	14.5	18.1	17.1	1.0	0.9	1.0	0.7	1.2	0.1	1.0	0.8	1.2	0.1	1.1	0.3
				GGPAGLGLTPSAWEASSLRSSR	3	95.8%	1																									
IPI00003084	DRAP1	isoform 1 of Dr1-associated corepressor	97.6%	9.3	2	2	2	2	7,403,805	7,339,720	6,676,745	8,643,395	526,408	343,736	402,253	245,162	15.9	10.5	13.5	6.3	-1.0	0.9	-1.1	0.3	1.2	0.07	-1.1	0.2	1.2	0.01	1.3	0.003
IPI00477494	DRAP1	Uncharacterized protein	97.6%	9.0	2	2	2	2	7,403,805	7,339,720	6,676,745	8,643,395	526,408	343,736	402,253	245,162	15.9	10.5	13.5	6.3	-1.0	0.9	-1.1	0.3	1.2	0.07	-1.1	0.2	1.2	0.01	1.3	0.003
				IMQTDEEIGK	2	86.5%	1																									

				KACQVTQSR	2	83.8%	1																									
IPI00003128	P4HA2	isoform IIb of Prolyl 4-hydroxylase subunit alpha-2	100.0%	15.7	6	6	6	1	14,703,465	16,583,963	16,865,503	18,454,958	959,354	914,588	637,991	782,877	14.6	12.3	8.5	9.5	1.1	0.2	1.1	0.1	1.3	0.02	1.0	0.8	1.1	0.2	1.1	0.2
				QFFPTDEDEIGAAK	2	99.7%	1																									
				SQVLDYLSYAVFQLGDLHR	3	93.8%	1																									
				SSWLEEDDDPVVAR	2	100.0%	1																									
				TGVLTVASYR	2	99.2%	1																									
				YQAMLSVDDCFGMGR	2	97.7%	1																									
				YYDVMSDEEIER	2	100.0%	1																									
IPI00003217	PSMB7	Proteasome subunit beta type-7	100.0%	10.8	3	3	3	1	14,902,447	15,458,477	13,901,633	17,158,263	982,093	638,377	1,420,601	490,426	14.7	9.2	22.9	6.4	1.0	0.6	-1.1	0.6	1.2	0.07	-1.1	0.3	1.1	0.07	1.2	0.08
				DGIVLGADTR	2	91.8%	1																									
				FRPDMEEEEAK	2	99.7%	1																									
				GTTAVLTEK	2	99.4%	1																									
IPI00003309	POLR2H	DNA-directed RNA polymerases I, II, and III subunit RPABC3	98.7%	7.3	1	1	1	4	2,391,353	2,432,238	2,362,173	2,576,753	126,381	116,588	95,760	103,325	11.8	10.7	9.1	9.0	1.0	0.8	-1.0	0.9	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
IPI00924545	POLR2H	Uncharacterized protein	98.7%	9.7	1	1	1	4	2,391,353	2,432,238	2,362,173	2,576,753	126,381	116,588	95,760	103,325	11.8	10.7	9.1	9.0	1.0	0.8	-1.0	0.9	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
IPI00927044	POLR2H	Uncharacterized protein	98.7%	6.3	1	1	1	4	2,391,353	2,432,238	2,362,173	2,576,753	126,381	116,588	95,760	103,325	11.8	10.7	9.1	9.0	1.0	0.8	-1.0	0.9	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
IPI00927876	POLR2H	Uncharacterized protein	98.7%	7.4	1	1	1	4	2,391,353	2,432,238	2,362,173	2,576,753	126,381	116,588	95,760	103,325	11.8	10.7	9.1	9.0	1.0	0.8	-1.0	0.9	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
				ADQFEYVMYGK	2	98.7%	1																									
IPI00003327	ARL3	ADP-ribosylation factor-like protein 3	99.6%	12.1	1	1	1	1	7,438,900	7,332,760	7,134,450	8,643,990	311,649	467,927	507,352	447,664	9.4	14.3	15.9	11.6	-1.0	0.9	-1.0	0.6	1.2	0.06	-1.0	0.8	1.2	0.08	1.2	0.06
				QDLLTAAPASEIAEGLNLHTIR	3	99.6%	1																									
IPI00003348	GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	100.0%	40.3	8	9	12	1	24,595,298	24,267,468	23,599,656	27,049,394	1,734,993	1,138,114	1,628,972	809,387	15.8	10.5	15.4	6.7	-1.0	0.9	-1.0	0.7	1.1	0.2	-1.0	0.7	1.1	0.08	1.1	0.09
				AGVLAGHDNR	2	100.0%	1																									
				IYAMHWGTDSR	2	100.0%	1																									
				KACGDSTLTQITAGLDPVGR	3	99.8%	1																									
				LIIWDSYTTNK	2	100.0%	2																									
				LLLAGYDDFNCNIWDAMK	2	100.0%	2																									
				QTFIGHESDINAVAFFPNGYAFTTGSDDATCR	3	100.0%	1																									
				TFVSGACDASIK	2	100.0%	1																									
				VSCLGVTDDGMAVATGSWDSFLK	2	100.0%	2																									
				VSCLGVTDDGMAVATGSWDSFLK	3	100.0%	1																									
IPI00003362	HSPA5	78 kDa glucose-regulated protein	100.0%	49.2	34	43	58	1	360,400,779	375,391,067	365,213,021	417,703,757	########	########	########	6,174,987	18.3	8.6	13.6	3.3	1.0	0.7	1.0	0.9	1.2	0.1	-1.0	0.7	1.1	0.03	1.1	0.08
				AKFEELNMDLFR	2	100.0%	2																									
				AKFEELNMDLFR	3	100.0%	1																									
				AVEEKIEWLESHQDADIEDFK	3	99.8%	1																									
				DAGTIAGLNVMR	2	100.0%	2																									
				DNHLLGTFDLTGIPPAPR	2	100.0%	2																									
				DNHLLGTFDLTGIPPAPR	3	100.0%	2																									
				EFFNGKEPSR	2	99.7%	2																									
				ELEEIVQPIISK	2	100.0%	2																									
				ETAEAYLGKK	2	98.8%	1																									
				FEELNMDLFR	2	100.0%	2																									
				IEIESFYEGEDFSETLTR	3	99.6%	1																									
				IEWLESHQDADIEDFK	2	100.0%	1																									
				IEWLESHQDADIEDFK	3	100.0%	1																									
				IEWLESHQDADIEDFKAK	3	100.0%	1																									
				ITITNDQNR	2	99.9%	2																									
				ITPSYVAFTPEGER	2	99.7%	1																									
				KKELEEIVQPIISK	3	100.0%	1																									
				KSDIDEIVLVGGSTR	2	100.0%	1																									
				KSDIDEIVLVGGSTR	3	99.9%	1																									
				KVTHAVVTVPAYFNDAQR	3	99.6%	1																									
				LYGSAGPPPTGEEDTAEK	2	84.6%	1																									
				LYGSAGPPPTGEEDTAEKDEL	2	100.0%	2																									
				MKETAEAYLGK	2	98.6%	1																									
				MKETAEAYLGK	3	100.0%	1																									
				MKETAEAYLGKK	2	92.0%	1																									
				MKETAEAYLGKK	3	95.7%	1																									
				MVNDAEKFAEEDKK	3	98.4%	1																									
				NGRVEIIANDQGNR	2	99.3%	1																									
				NQLTSNPENTVFDAK	2	100.0%	2																									
				NQLTSNPENTVFDAKR	3	99.7%	1																									
				SDIDEIVLVGGSTR	2	100.0%	1																									
				SQIFSTASDNQPTVTIK	2	100.0%	2																									
				SQIFSTASDNQPTVTIK	3	100.0%	1																									
				TFAPEEISAMVLTK	2	100.0%	2																									
				TKPYIQVDIGGGQTK	2	100.0%	2																									
				TKPYIQVDIGGGQTK	3	100.0%	1																									
				TWNDPSVQQDIK	2	100.0%	2																									
				VLEDSDLKK	2	99.9%	1																									
				VLEDSDLKKSDIDEIVLVGGSTR	3	100.0%	1																									
				VMEHFIK	2	98.0%	1																									
				VTHAVVTVPAYFNDAQR	2	100.0%	1																									
				VTHAVVTVPAYFNDAQR	3	100.0%	1																									
				VYEGERPLTK	2	100.0%	2																									
IPI00003363	PPP1R1B	isoform 1 of Protein phosphatase 1 regulatory subunit 1B	99.6%	13.7	1	1	1	3	574,251	803,177	603,110	679,290	84,239	69,954	48,534	48,461	32.8	19.5	18.0	16.0	1.4	0.07	1.1	0.8	1.2	0.3	-1.3	0.05	-1.2	0.2	1.1	0.3
IPI00220698	PPP1R1B	isoform 2 of Protein phosphatase 1 regulatory subunit 1B	99.6%	16.7	1	1	1	3	574,251	803,177	603,110	679,290	84,239	69,954	48,534	48,461	32.8	19.5	18.0	16.0	1.4	0.07	1.1	0.8	1.2	0.3	-1.3	0.05	-1.2	0.2	1.1	0.3
IPI00795211	PPP1R1B	Uncharacterized protein	99.6%	13.0	1	1	1	3	574,251	803,177	603,110	679,290	84,239	69,954	48,534	48,461	32.8	19.5	18.0	16.0	1.4	0.07	1.1	0.8	1.2	0.3	-1.3	0.05	-1.2	0.2	1.1	0.3
				IAESHLQSISNLNENQASEEEDELGELR	3	99.6%	1																									
IPI00975938	LOC100510742	occludin-like	97.3%	4.5	1	1	1	9	542,130	565,768	474,190	675,460	102,371	60,235	76,664	70,992	42.2	23.8	36.2	23.5	1.0	0.8	-1.1	0.6	1.2	0.3	-1.2	0.4	1.2	0.3	1.4	0.09
IPI00976572	LOC100510742	occludin-like	97.3%	4.0	1	1	1	9	542,130	565,768	474,190	675,460	102,371	60,235	76,664	70,992	42.2	23.8	36.2	23.5	1.0	0.8	-1.1	0.6	1.2	0.3	-1.2	0.4	1.2	0.3	1.4	0.09
IPI00977990	LOC100510742	occludin-like	97.3%	7.8	1	1	1	9	542,130	565,768	474,190	675,460	102,371	60,235	76,664	70,992	42.2	23.8	36.2	23.5	1.0	0.8	-1.1	0.6	1.2	0.3	-1.2	0.4	1.2	0.3	1.4	0.09
IPI01015715	LOC100510742	23 kDa protein	97.3%	10.5	1	1	1	9	542,130	565,768	474,190	675,460	102,371	60,235	76,664	70,992	42.2	23.8	36.2	23.5	1.0	0.8	-1.1	0.6	1.2	0.3	-1.2	0.4	1.2	0.3	1.4	0.09
IPI00978650	OCLN	Occludin variant	97.3%	4.4	1	1	1	9	542,130	565,768	474,190	675,460	102,371	60,235	76,664	70,992	42.2	23.8	36.2	23.5	1.0	0.8	-1.1	0.6	1.2	0.3	-1.2	0.4	1.2	0.3	1.4	0.09
IPI00003373	OCLN	Occludin	97.3%	4.0	1	1	1	9	542,130	565,768	474,190	675,460	102,371	60,235	76,664	70,992	42.2	23.8	36.2	23.5	1.0	0.8	-1.1	0.6	1.2	0.3	-1.2	0.4	1.2	0.3	1.4	0.09
IPI00479078	OCLN	Tight junction protein occludin TM4 minus	97.3%	4.5	1	1	1	9	542,130	565,768	474,190	675,460	102,371	60,235	76,664	70,992	42.2	23.8	36.2	23.5	1.0	0.8	-1.1	0.6	1.2	0.3	-1.2	0.4	1.2	0.3	1.4	0.09
IPI00965141	OCLN	OCLN	97.3%	10.5	1	1	1	9	542,130	565,768	474,190	675,460	102,371	60,235	76,664	70,992	42.2	23.8	36.2	23.5	1.0	0.8	-1.1	0.6	1.2	0.3	-1.2	0.4	1.2	0.3	1.4	0.09
IPI00978567	OCLN	occludin isoform b	97.3%	7.8	1	1	1	9	542,130	565,768	474,190	675,460	102,371	60,235	76,664	70,992	42.2	23.8	36.2	23.5	1.0	0.8	-1.1	0.6	1.2	0.3	-1.2	0.4	1.2	0.3	1.4	0.09
				STPVPEVVQELPLTSPVDDFR	3	97.3%	1																									
IPI00003377	SRSF7	isoform 1 of Serine/arginine-rich splicing factor 7	100.0%	13.9	3	3	4	5	4,039,017	4,045,462	4,081,788	4,555,236	310,858	150,376	165,621	159,708	17.2	8.3	9.1	7.8	1.0	1	1.0	0.9	1.1	0.2	1.0	0.9	1.1	0.05	1.1	0.07
IPI00744364	SRSF7	Uncharacterized protein	100.0%	20.0	3	3	4	5	4,039,017	4,045,462	4,081,788	4,555,236	310,858	150,376	165,621	159,708	17.2	8.3	9.1	7.8	1.0	1	1.0	0.9	1.1	0.2	1.0	0.9	1.1	0.05	1.1	0.07
IPI00916448	SRSF7	Uncharacterized protein	100.0%	14.0	3	3	4	5	4,039,017	4,045,462	4,081,788	4,555,236	310,858	150,376	165,621	159,708	17.2	8.3	9.1	7.8	1.0	1	1.0	0.9	1.1	0.2	1.0	0.9	1.1	0.05	1.1	0.07
IPI00917346	SRSF7	serine/arginine-rich splicing factor 7 isoform 2	100.0%	14.6	3	3	4	5	4,039,017	4,045,462	4,081,788	4,555,236	310,858	150,376	165,621	159,708	17.2	8.3	9.1	7.8	1.0	1	1.0	0.9	1.1	0.2	1.0	0.9	1.1	0.05	1.1	0.07
IPI00939530	SRSF7	cDNA FLJ34106 fis, clone FCBBF3008073, highly similar to SPLICING FACTOR, A	100.0%	24.1	3	3	4	5	4,039,017	4,045,462	4,081,788	4,555,236	310,858	150,376	165,621	159,708	17.2	8.3	9.1	7.8	1.0	1	1.0	0.9	1.1	0.2	1.0	0.9	1.1	0.05	1.1	0.07
				NPPGFAFVEFEDPR	2	99.9%	1																									
				NPPGFAFVEFEDPRDAEDAVR	3	99.6%	1																									
				VYVGNLGTGAGK	2	100.0%	2																									
IPI00003406	DBN1	isoform 1 of Drebrin	99.5%	8.5	3	3	3	3	2,394,112	2,449,178	2,488,536	2,830,678	284,353	185,564	206,806	128,445	26.6	16.9	18.6	10.2	1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.9	1.2	0.1	1.1	0.2
IPI00295624	DBN1	isoform 2 of Drebrin	99.5%	8.5	3	3	3	3	2,394,112	2,449,178	2,488,536	2,830,678	284,353	185,564	206,806	128,445	26.6	16.9	18.6	10.2	1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.9	1.2	0.1	1.1	0.2
IPI00794221	DBN1	Uncharacterized protein	99.5%	7.9	3	3	3	3	2,394,112	2,449,178	2,488,536	2,830,678	284,353	185,564	206,806	128,445	26.6	16.9	18.6	10.2	1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.9	1.2	0.1	1.1	0.2
				LAASGEGGLQELSGHFENQK	3	95.7%	1																									
				SESEVEEAAAIIAQRPDNPR	3	93.4%	1																									
				YVLINWVGEDVPDAR	2	99.5%	1																									
IPI00003419	C11orf58	Small acidic protein	100.0%	12.6	2	2	2	4	1,242,113	1,390,560	1,282,471	1,507,103	138,912	157,968	203,532	148,281	25.0	25.4	35.5	22.0	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.7	1.1	0.6	1.2	0.4
IPI00917641	C11orf58	Uncharacterized protein	100.0%	16.6	2	2	2	4	1,242,113	1,390,560	1,282,471	1,507,103	138,912	157,968	203,532	148,281	25.0	25.4	35.5	22.0	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.7	1.1	0.6	1.2	0.4
IPI00977975	C11orf58	Uncharacterized protein	100.0%	25.6	2	2	2	4	1,242,113	1,390,560	1,282,471	1,507,103	138,912	157,968	203,532	148,281	25.0	25.4	35.5	22.0	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.7	1.1	0.6	1.2	0.4
IPI00982700	C11orf58	Uncharacterized protein	100.0%	14.7	2	2	2	4	1,242,113	1,390,560	1,282,471	1,507,103	138,912	157,968	203,532	148,281	25.0	25.4	35.5	22.0	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.7	1.1	0.6	1.2	0.4
				INEELESQYQQSMDSK	2	100.0%	1																									
				TGEEDKKINEELESQYQQSMDSK	3	100.0%	1																									
IPI00003479	MAPK1	Mitogen-activated protein kinase 1	98.4%	2.5	1	1	1	6	2,400,318	2,528,927	2,393,082	2,773,455	276,651	178,528	170,472	136,693	25.8	15.8	15.9	11.0	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.6	1.1	0.3	1.2	0.1
IPI00874012	MAPK1	Extracellular signal-regulated kinase-2 splice variant	98.4%	2.9	1	1	1	6	2,400,318	2,528,927	2,393,082	2,773,455	276,651	178,528	170,472	136,693	25.8	15.8	15.9	11.0	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.6	1.1	0.3	1.2	0.1
IPI01015278	MAPK1	cDNA FLJ58314, highly similar to Mitogen-activated protein kinase 1	98.4%	2.6	1	1	1	6	2,400,318	2,528,927	2,393,082	2,773,455	276,651	178,528	170,472	136,693	25.8	15.8	15.9	11.0	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.6	1.1	0.3	1.2	0.1
IPI00982169	MAPK3	Protein	98.4%	4.4	1	1	1	6	2,400,318	2,528,927	2,393,082	2,773,455	276,651	178,528	170,472	136,693	25.8	15.8	15.9	11.0	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.6	1.1	0.3	1.2	0.1
IPI00982739	MAPK3	cDNA FLJ33690 fis, clone BRAWH2002967, highly similar to Mitogen-activated prot	98.4%	3.4	1	1	1	6	2,400,318	2,528,927	2,393,082	2,773,455	276,651	178,528	170,472	136,693	25.8	15.8	15.9	11.0	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.6	1.1	0.3	1.2	0.1
IPI00985374	MAPK3	Protein	98.4%	3.0	1	1	1	6	2,400,318	2,528,927	2,393,082	2,773,455	276,651	178,528	170,472	136,693	25.8	15.8	15.9	11.0	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.6	1.1	0.3	1.2	0.1
				APEIMLNSK	2	98.4%	1																									
IPI00003482	DECR1	2,4-dienoyl-CoA reductase, mitochondrial	99.9%	15.8	4	4	4	2	6,538,405	7,495,352	6,693,259	7,663,142	357,501	570,408	340,087	620,937	12.2	17.0	11.4	18.1	1.1	0.2	1.0	0.8	1.2	0.2	-1.1	0.3	1.0	0.8	1.1	0.2
IPI00980553	DECR1	cDNA FLJ50204, highly similar to 2,4-dienoyl-CoA reductase, mitochondrial	99.9%	16.3	4	4	4	2	6,538,405	7,495,352	6,693,259	7,663,142	357,501	570,408	340,087	620,937	12.2	17.0	11.4	18.1	1.1	0.2	1.0	0.8	1.2	0.2	-1.1	0.3	1.0	0.8	1.1	0.2
				AGVEAMSK	2	80.9%	1																									
				ATAEQISSQTGNK	2	99.8%	1																									
				TITDIVLNGTAFVTLEIGK	2	94.7%	1																									
				VAFITGGGTGLGK	2	99.1%	1																									
IPI00003519	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component	100.0%	16.6	12	14	16	3	16,322,878	16,148,211	15,945,182	18,379,059	1,576,733	816,750	1,224,198	598,897	21.6	11.3	17.2	7.3	-1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.06	1.2	0.1
IPI00917777	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component isoform b	100.0%	17.2	12	14	16	3	16,322,878	16,148,211	15,945,182	18,379,059	1,576,733	816,750	1,224,198	598,897	21.6	11.3	17.2	7.3	-1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.06	1.2	0.1
IPI01012385	EFTUD2	cDNA FLJ44500 fis, clone UTERU3000828, highly similar to 116 kDa U5 small nucl	100.0%	16.7	12	14	16	3	16,322,878	16,148,211	15,945,182	18,379,059	1,576,733	816,750	1,224,198	598,897	21.6	11.3	17.2	7.3	-1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.06	1.2	0.1
				AFIPAIDSFGFETDLR	2	100.0%	1																									
				DSIVQGFQWGTR	2	99.7%	1																									
				FFDDPMLLELAK	2	100.0%	2																									
				GGGQIIPTAR	2	94.6%	1																									
				GLAEDIENEVVQITWNR	2	99.9%	1																									
				GLAEDIENEVVQITWNR	3	99.9%	1																									
				IAVEPVNPSELPK	2	100.0%	1																									
				ILAQVVGDVDTSLPR	2	100.0%	2																									
				ITMIAEPLEK	2	99.1%	1																									
				LGEFFQTK	2	99.7%	1																									
				SFVEFILEPLYK	2	100.0%	1																									
				SFVEFILEPLYK	3	94.5%	1																									
				STPVTVVLPDTK	2	92.2%	1																									
				SYLFNIMDTPGHVNFSDEVTAGLR	3	99.9%	1																									
IPI00003527	SLC9A3R1	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	100.0%	39.1	9	11	14	1	52,723,180	53,540,853	53,240,715	60,721,775	3,752,261	2,197,887	3,813,915	2,330,252	15.9	9.2	16.0	8.6	1.0	0.9	1.0	0.9	1.2	0.1	-1.0	0.9	1.1	0.06	1.1	0.1
				AQEAPGQAEPPAAAEVQGAGNENEPR	3	100.0%	1																									
				EALAEAALESPRPALVR	2	90.9%	1																									
				EALAEAALESPRPALVR	3	100.0%	1																									
				IVEVNGVCMEGK	2	100.0%	2																									
				KGPSGYGFNLHSDK	2	90.6%	1																									
				KGPSGYGFNLHSDK	3	100.0%	1																									
				LLVVDPETDEQLQK	2	100.0%	2																									
				LVEVNGENVEK	2	99.9%	1																									
				LVEVNGENVEKETHQQVVSR	3	100.0%	1																									

				SVDPDSPAEASGLR	2	100.0%	2																									
				VIPSQEHLNGPLPVPFTNGEIQK	3	99.9%	1																									
IPI00003565	PSMD10	26S proteasome non-ATPase regulatory subunit 10	98.7%	15.5	2	2	2	3	1,954,647	1,899,537	2,055,080	2,002,353	155,842	81,356	80,657	56,026	17.8	9.6	8.8	6.3	-1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.2	1.1	0.3	-1.0	0.6
IPI00027699	PSMD10	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10	98.7%	18.1	2	2	2	3	1,954,647	1,899,537	2,055,080	2,002,353	155,842	81,356	80,657	56,026	17.8	9.6	8.8	6.3	-1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.2	1.1	0.3	-1.0	0.6
IPI00552190	PSMD10	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10	98.7%	18.9	2	2	2	3	1,954,647	1,899,537	2,055,080	2,002,353	155,842	81,356	80,657	56,026	17.8	9.6	8.8	6.3	-1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.2	1.1	0.3	-1.0	0.6
				LLVSQGASIYIENKEEK	3	90.3%	1																									
				MEGCVSNLMVCNLAYSGK	2	86.5%	1																									
IPI00003588	EEF1E1	Eukaryotic translation elongation factor 1 epsilon-1	99.4%	5.8	1	1	1	6	1,273,673	1,202,692	1,203,447	1,253,397	81,465	43,852	109,469	83,166	14.3	8.2	20.3	14.8	-1.1	0.5	-1.1	0.6	-1.0	0.9	1.0	1	1.0	0.6	1.0	0.7
IPI00646720	EEF1E1	Uncharacterized protein	99.4%	6.6	1	1	1	6	1,273,673	1,202,692	1,203,447	1,253,397	81,465	43,852	109,469	83,166	14.3	8.2	20.3	14.8	-1.1	0.5	-1.1	0.6	-1.0	0.9	1.0	1	1.0	0.6	1.0	0.7
IPI00913838	EEF1E1	eukaryotic translation elongation factor 1 epsilon-1 isoform 2	99.4%	7.2	1	1	1	6	1,273,673	1,202,692	1,203,447	1,253,397	81,465	43,852	109,469	83,166	14.3	8.2	20.3	14.8	-1.1	0.5	-1.1	0.6	-1.0	0.9	1.0	1	1.0	0.6	1.0	0.7
IPI00963998	EEF1E1	Protein	99.4%	7.4	1	1	1	6	1,273,673	1,202,692	1,203,447	1,253,397	81,465	43,852	109,469	83,166	14.3	8.2	20.3	14.8	-1.1	0.5	-1.1	0.6	-1.0	0.9	1.0	1	1.0	0.6	1.0	0.7
IPI00964364	EEF1E1	Uncharacterized protein	99.4%	6.7	1	1	1	6	1,273,673	1,202,692	1,203,447	1,253,397	81,465	43,852	109,469	83,166	14.3	8.2	20.3	14.8	-1.1	0.5	-1.1	0.6	-1.0	0.9	1.0	1	1.0	0.6	1.0	0.7
IPI00964664	EEF1E1	Uncharacterized protein	99.4%	10.6	1	1	1	6	1,273,673	1,202,692	1,203,447	1,253,397	81,465	43,852	109,469	83,166	14.3	8.2	20.3	14.8	-1.1	0.5	-1.1	0.6	-1.0	0.9	1.0	1	1.0	0.6	1.0	0.7
				AIVQQWLEYR	2	99.4%	1																									
IPI00003590	QSOX1	isoform 1 of Sulfhydryl oxidase 1	100.0%	11.0	6	7	8	2	12,261,386	12,115,007	12,001,718	13,312,326	766,449	433,455	640,179	291,692	14.0	8.0	11.9	4.9	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.05	1.1	0.1
IPI00465016	QSOX1	isoform 2 of Sulfhydryl oxidase 1	100.0%	13.6	6	7	8	2	12,261,386	12,115,007	12,001,718	13,312,326	766,449	433,455	640,179	291,692	14.0	8.0	11.9	4.9	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.05	1.1	0.1
				DCASHFEQMAAASMHR	3	92.2%	1																									
				EVALDLSQHK	2	96.4%	1																									
				LAGAPSEDPQFPK	2	100.0%	2																									
				LDVPVWDVEATLNFLK	2	100.0%	1																									
				LDVPVWDVEATLNFLK	3	99.4%	1																									
				SALYSPSDPLTLLQADTVR	2	100.0%	1																									
				VPVLMESR	2	99.2%	1																									
IPI00003627	ACTL6A	isoform 1 of Actin-like protein 6A	100.0%	14.2	4	4	4	2	7,291,814	8,116,164	7,197,558	7,932,663	631,964	306,586	286,615	466,186	19.4	8.5	8.9	13.1	1.1	0.3	-1.0	0.9	1.1	0.4	-1.1	0.06	-1.0	0.8	1.1	0.2
IPI00216622	ACTL6A	isoform 2 of Actin-like protein 6A	100.0%	15.8	4	4	4	2	7,291,814	8,116,164	7,197,558	7,932,663	631,964	306,586	286,615	466,186	19.4	8.5	8.9	13.1	1.1	0.3	-1.0	0.9	1.1	0.4	-1.1	0.06	-1.0	0.8	1.1	0.2
				LIANNTTVER	2	93.5%	1																									
				NGMVEDWDSFQAILDHTYK	3	98.6%	1																									
				QGGPTYYIDTNALR	2	99.9%	1																									
				SEASLHPVLMSEAPWNTR	3	100.0%	1																									
IPI00003635	ERGIC1	cDNA FLJ56280, highly similar to Endoplasmic reticulum-Golgi intermediate compar	100.0%	14.5	2	2	2	2	5,211,660	5,675,777	5,134,707	5,151,012	317,151	227,224	371,932	324,865	13.6	9.0	16.2	14.1	1.1	0.3	-1.0	0.9	-1.0	0.9	-1.1	0.2	-1.1	0.2	1.0	1
IPI00022887	ERGIC1	isoform 1 of Endoplasmic reticulum-Golgi intermediate compartment protein 1	100.0%	11.7	2	2	2	2	5,211,660	5,675,777	5,134,707	5,151,012	317,151	227,224	371,932	324,865	13.6	9.0	16.2	14.1	1.1	0.3	-1.0	0.9	-1.0	0.9	-1.1	0.2	-1.1	0.2	1.0	1
				LSFGDTLQVQNIHGAFNALGGADR	3	99.9%	1																									
				YSYQYTVANK	2	99.3%	1																									
IPI00003704	RBM4	isoform 1 of RNA-binding protein 4	100.0%	17.6	4	4	4	1	4,294,609	4,404,626	3,933,803	4,777,241	275,650	265,831	227,233	477,090	14.4	13.5	12.9	22.3	1.0	0.8	-1.1	0.3	1.1	0.4	-1.1	0.2	1.1	0.5	1.2	0.1
				ATAPVPTVGEGYGYGHESELSQASAAAR	3	99.9%	1																									
				GLDNTEFQGK	2	99.9%	1																									
				NYGFVHIEDK	2	99.2%	1																									
				VADLTEQYNEQYGAVR	2	99.6%	1																									
IPI00003766	ETHE1	Protein ETHE1, mitochondrial	100.0%	16.1	3	3	3	1	68,714,000	66,248,120	64,062,920	74,793,890	4,963,167	2,603,106	4,253,688	2,357,545	16.2	8.8	14.9	7.1	-1.0	0.7	-1.1	0.5	1.1	0.3	-1.0	0.7	1.1	0.04	1.2	0.06
				EAVLIDPVLETAPR	2	100.0%	1																									
				LSGAQADLHIEDGDSIR	3	99.9%	1																									
				LTLSCEEFVK	2	99.8%	1																									
IPI00003783	MAP2K2	Dual specificity mitogen-activated protein kinase kinase 2	100.0%	9.0	2	3	3	1	5,671,005	5,718,539	5,212,192	6,372,093	337,858	291,043	238,130	314,874	13.3	11.4	10.2	11.1	1.0	0.9	-1.1	0.3	1.1	0.2	-1.1	0.2	1.1	0.2	1.2	0.02
				ISELGAGNGGVVTK	2	93.1%	1																									
				LCDFGVSGQLIDSMANSFVGTR	2	100.0%	1																									
				LCDFGVSGQLIDSMANSFVGTR	3	99.6%	1																									
IPI00003799	HEBP2	isoform 2 of Heme-binding protein 2	100.0%	12.0	2	2	2	1	4,916,285	5,094,580	4,845,145	5,782,070	259,481	220,312	458,275	175,183	11.8	9.7	21.2	6.8	1.0	0.6	-1.0	0.9	1.2	0.02	-1.1	0.6	1.1	0.04	1.2	0.1
				NNEVWLIQK	2	99.6%	1																									
				NQEQLLTLASILR	2	100.0%	1																									
IPI00003802	MAN2A1	Alpha-mannosidase 2	92.2%	1.0	1	1	1	1	2,336,970	2,323,600	2,552,290	2,464,460	416,084	142,140	152,584	139,015	39.8	13.7	13.4	12.6	-1.0	1	1.1	0.6	1.1	0.8	1.1	0.3	1.1	0.5	-1.0	0.7
				FIWSEISYLSK	2	92.2%	1																									
IPI00003815	ARHGDIA	Rho GDP-dissociation inhibitor 1	100.0%	29.4	6	7	8	3	6,443,837	6,651,228	6,772,743	7,285,267	614,142	372,732	578,675	292,031	21.3	12.5	19.1	9.0	1.0	0.8	1.1	0.7	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.5
IPI00794402	ARHGDIA	28 kDa protein	100.0%	24.1	6	7	8	3	6,443,837	6,651,228	6,772,743	7,285,267	614,142	372,732	578,675	292,031	21.3	12.5	19.1	9.0	1.0	0.8	1.1	0.7	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.5
IPI00796541	ARHGDIA	26 kDa protein	100.0%	25.5	6	7	8	3	6,443,837	6,651,228	6,772,743	7,285,267	614,142	372,732	578,675	292,031	21.3	12.5	19.1	9.0	1.0	0.8	1.1	0.7	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.5
				AEEYEFLTPVEEAPK	2	100.0%	2																									
				EIVSGMK	1	98.7%	1																									
				IDKTDYMVGSYGPR	2	100.0%	1																									
				IDKTDYMVGSYGPR	3	100.0%	1																									
				SIQEIQELDKDDESLRK	3	100.0%	1																									
				TDYMVGSYGPR	2	100.0%	1																									
				YIQHTYR	2	99.4%	1																									
IPI00003843	TJP2	isoform A1 of Tight junction protein ZO-2	100.0%	7.1	6	6	6	3	8,146,611	8,599,628	7,385,509	9,346,157	662,210	265,999	622,486	496,250	18.2	6.9	18.9	11.9	1.1	0.5	-1.1	0.4	1.1	0.2	-1.2	0.1	1.1	0.2	1.3	0.04
IPI00955022	TJP2	tight junction protein ZO-2 isoform 3	100.0%	7.0	6	6	6	3	8,146,611	8,599,628	7,385,509	9,346,157	662,210	265,999	622,486	496,250	18.2	6.9	18.9	11.9	1.1	0.5	-1.1	0.4	1.1	0.2	-1.2	0.1	1.1	0.2	1.3	0.04
IPI00955040	TJP2	tight junction protein ZO-2 isoform 4	100.0%	7.4	6	6	6	3	8,146,611	8,599,628	7,385,509	9,346,157	662,210	265,999	622,486	496,250	18.2	6.9	18.9	11.9	1.1	0.5	-1.1	0.4	1.1	0.2	-1.2	0.1	1.1	0.2	1.3	0.04
				AEQMASVQNAQR	2	99.9%	1																									
				AFEVMDEFDGR	2	100.0%	1																									
				GEMVTILAQSR	2	99.9%	1																									
				MSYLTAMGADYLSCDSR	2	99.9%	1																									
				RPVVLFGPIADIAMEK	2	85.0%	1																									
				TFLRPSPEDEAIYGPNTK	3	100.0%	1																									
IPI00003856	ATP6V1E1	V-type proton ATPase subunit E 1	93.1%	4.9	1	1	1	4	1,528,220	1,668,525	1,512,678	1,755,138	87,153	142,251	145,029	128,656	12.8	19.1	21.4	16.4	1.1	0.4	-1.0	0.9	1.1	0.2	-1.1	0.5	1.1	0.7	1.2	0.2
IPI00719366	ATP6V1E1	V-type proton ATPase subunit E 1 isoform c	93.1%	5.6	1	1	1	4	1,528,220	1,668,525	1,512,678	1,755,138	87,153	142,251	145,029	128,656	12.8	19.1	21.4	16.4	1.1	0.4	-1.0	0.9	1.1	0.2	-1.1	0.5	1.1	0.7	1.2	0.2
IPI00719806	ATP6V1E1	V-type proton ATPase subunit E 1 isoform b	93.1%	5.4	1	1	1	4	1,528,220	1,668,525	1,512,678	1,755,138	87,153	142,251	145,029	128,656	12.8	19.1	21.4	16.4	1.1	0.4	-1.0	0.9	1.1	0.2	-1.1	0.5	1.1	0.7	1.2	0.2
IPI00853433	ATP6V1E1	Uncharacterized protein	93.1%	5.4	1	1	1	4	1,528,220	1,668,525	1,512,678	1,755,138	87,153	142,251	145,029	128,656	12.8	19.1	21.4	16.4	1.1	0.4	-1.0	0.9	1.1	0.2	-1.1	0.5	1.1	0.7	1.2	0.2
				IQMSNLMNQAR	2	93.1%	1																									
IPI00003865	HSPA8	isoform 1 of Heat shock cognate 71 kDa protein	100.0%	48.6	28	39	60	1	317,471,595	328,850,054	311,674,489	364,827,004	########	########	########	8,900,877	18.1	8.1	17.3	5.5	1.0	0.7	-1.0	0.9	1.1	0.1	-1.1	0.5	1.1	0.04	1.2	0.09
				ARFEELNADLFR	2	99.5%	2																									
				CNEIINWLDK	2	99.8%	2																									
				DAGTIAGLNVLR	2	100.0%	2																									
				DAGTIAGLNVLR	3	99.9%	1																									
				DNNLLGK	1	100.0%	2																									
				DNNLLGK	2	81.4%	1																									
				FDDAVVQSDMK	2	100.0%	2																									
				FEELNADLFR	2	100.0%	2																									
				GPAVGIDLGTTYSCVGVFQHGK	3	99.1%	1																									
				GTLDPVEK	1	93.3%	1																									
				GTLDPVEK	2	92.5%	1																									
				HWPFMVVNDAGRPK	3	100.0%	1																									
				IINEPTAAAIAYGLDKK	3	100.0%	2																									
				LDKSQIHDIVLVGGSTR	3	100.0%	1																									
				LLQDFFNGK	2	100.0%	2																									
				LSKEDIER	1	88.8%	1																									
				LSKEDIER	2	93.8%	1																									
				MKEIAEAYLGK	2	100.0%	2																									
				MKEIAEAYLGK	3	100.0%	1																									
				MVNHFIAEFK	2	100.0%	2																									
				MVNHFIAEFK	3	100.0%	1																									
				NQVAMNPTNTVFDAK	2	100.0%	2																									
				NQVAMNPTNTVFDAKR	3	99.4%	2																									
				NSLESYAFNMK	2	100.0%	2																									
				QTQTFTTYSDNQPGVLIQVYEGER	2	100.0%	1																									
				RFDDAVVQSDMK	2	100.0%	2																									
				RFDDAVVQSDMK	3	91.2%	1																									
				SFYPEEVSSMVLTK	2	100.0%	2																									
				SINPDEAVAYGAAVQAAILSGDK	2	100.0%	2																									
				SINPDEAVAYGAAVQAAILSGDK	3	100.0%	1																									
				SQIHDIVLVGGSTR	2	100.0%	2																									
				SQIHDIVLVGGSTR	3	97.0%	1																									
				STAGDTHLGGEDFDNR	2	100.0%	2																									
				STAGDTHLGGEDFDNR	3	100.0%	2																									
				TTPSYVAFTDTER	2	100.0%	1																									
				TVTNAVVTVPAYFNDSQR	2	100.0%	2																									
				TVTNAVVTVPAYFNDSQR	3	100.0%	1																									
				VQVEYK	1	99.0%	1																									
				VQVEYKGETK	2	99.6%	2																									
IPI00003881	HNRNPF	Heterogeneous nuclear ribonucleoprotein F	100.0%	51.1	12	15	20	1	75,686,525	75,832,916	72,863,596	84,295,153	6,437,354	1,328,135	4,425,116	2,760,527	19.0	3.9	13.6	7.3	1.0	1	-1.0	0.7	1.1	0.3	-1.0	0.6	1.1	0.02	1.2	0.06
				ATENDIYNFFSPLNPVR	2	100.0%	1																									
				ATENDIYNFFSPLNPVR	3	100.0%	1																									
				DLSYCLSGMYDHR	2	99.9%	1																									
				EEIVQFFSGLEIVPNGITLPVDPEGK	2	100.0%	1																									
				FMSVQRPGPYDRPGTAR	3	92.6%	1																									
				HSGPNSADSANDGFVR	2	100.0%	2																									
				HSGPNSADSANDGFVR	3	100.0%	1																									
				ITGEAFVQFASQELAEK	2	100.0%	1																									
				ITGEAFVQFASQELAEK	3	100.0%	1																									
				MRPGAYSTGYGGYEEYSGLSDGYGFTTDLFGR	3	100.0%	2																									
				QSGEAFVELGSEDDVK	2	100.0%	2																									
				TEMDWVLK	2	99.7%	2																									
				VHIEIGPDGR	2	100.0%	2																									
				VTGEADVEFATHEEAVAAMSK	2	100.0%	1																									
				YGDSEFTVQSTTGHCVHMR	3	100.0%	1																									
IPI00003909	SLC2A3	Solute carrier family 2, facilitated glucose transporter member 3	100.0%	10.7	6	6	6	3	5,411,123	5,625,306	5,859,962	6,314,134	517,973	279,122	435,748	217,798	21.4	11.1	16.6	7.7	1.0	0.7	1.1	0.5	1.2	0.1	1.0	0.7	1.1	0.09	1.1	0.4
IPI00816836	SLC2A3	Solute carrier family 2 (Facilitated glucose transporter), member 3 variant (Fragment	100.0%	18.3	6	6	6	3	5,411,123	5,625,306	5,859,962	6,314,134	517,973	279,122	435,748	217,798	21.4	11.1	16.6	7.7	1.0	0.7	1.1	0.5	1.2	0.1	1.0	0.7	1.1	0.09	1.1	0.4
IPI01011292	SLC2A3	46 kDa protein	100.0%	12.6	6	6	6	3	5,411,123	5,625,306	5,859,962	6,314,134	517,973	279,122	435,748	217,798	21.4	11.1	16.6	7.7	1.0	0.7	1.1	0.5	1.2	0.1	1.0	0.7	1.1	0.09	1.1	0.4
				AFEGQAHGADR	2	98.8%	1																									
				DGVMEMNSIEPAK	2	100.0%	1																									
				DGVMEMNSIEPAKETTTNV	2	100.0%	1																									
				LWGTQDVSQDIQEMK	2	100.0%	1																									
				LWGTQDVSQDIQEMKDESAR	3	100.0%	1																									
				SGKDGVMEMNSIEPAKETTTNV	3	99.9%	1																									
IPI00003918	RPL4	60S ribosomal protein L4	100.0%	14.1	4	4	5	2	6,262,035	6,192,493	6,500,591	7,325,909	556,037	297,675	364,757	400,372	19.9	10.8	12.6	12.2	-1.0	0.9	1.0	0.7	1.2	0.2	1.0	0.5	1.2	0.05	1.1	0.2
IPI00795303	RPL4	cDNA FLJ50996, highly similar to 60S ribosomal protein L4	100.0%	14.5	4	4	5	2	6,262,035	6,192,493	6,500,591	7,325,909	556,037	297,675	364,757	400,372	19.9	10.8	12.6	12.2	-1.0	0.9	1.0	0.7	1.2	0.2	1.0	0.5	1.2	0.05	1.1	0.2
				AAAAAAALQAK	2	99.9%	2																									
				APIRPDIVNFVHTNLR	3	100.0%	1																									
				QPYAVSELAGHQTSAESWGTGR	3	99.9%	1																									
				SGQGAFGNMCR	2	84.4%	1																									
IPI00003923	UMPS	isoform 1 of Uridine 5'-monophosphate synthase	99.2%	7.1	2	2	2	2	1,066,684	1,089,453	1,049,243	1,294,428	106,949	52,917	120,425	83,198	22.4	10.9	25.7	14.4	1.0	0.9	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.07	1.2	0.1

IPI00947553	UMPS	Uncharacterized protein	99.2%	9.9	2	2	2	2	1,066,684	1,089,453	1,049,243	1,294,428	106,949	52,917	120,425	83,198	22.4	10.9	25.7	14.4	1.0	0.9	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.07	1.2	0.1
				AALGPLVTGLYDVQAFK	2	99.2%	1																									
				ELLQLADALGPSICMLK	2	96.9%	1																									
IPI00003925	PDHB	isoform 1 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	100.0%	33.4	8	9	10	3	15,799,619	16,878,651	15,213,874	18,858,342	1,755,911	854,754	973,666	604,070	24.9	11.3	14.3	7.2	1.1	0.6	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.1	1.2	0.01
IPI00549885	PDHB	isoform 2 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	100.0%	35.2	8	9	10	3	15,799,619	16,878,651	15,213,874	18,858,342	1,755,911	854,754	973,666	604,070	24.9	11.3	14.3	7.2	1.1	0.6	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.1	1.2	0.01
IPI00946404	PDHB	pyruvate dehydrogenase E1 component subunit beta, mitochondrial isoform 2 precu	100.0%	35.2	8	9	10	3	15,799,619	16,878,651	15,213,874	18,858,342	1,755,911	854,754	973,666	604,070	24.9	11.3	14.3	7.2	1.1	0.6	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.1	1.2	0.01
				DNNPVVVLENELMYGVPFEFPPEAQSK	3	97.1%	1																									
				EGVECEVINMR	2	99.4%	1																									
				ILEDNSIPQVK	2	99.8%	1																									
				IMEGPAFNFLDAPAVR	2	100.0%	2																									
				TIRPMDMETIEASVMK	2	100.0%	1																									
				TIRPMDMETIEASVMK	3	99.1%	1																									
				VFLLGEEVAQYDGAYK	2	95.3%	1																									
				VTGADVPMPYAK	2	99.7%	1																									
				VVSPWNSEDAK	2	98.6%	1																									
IPI00003927	PPID	Peptidyl-prolyl cis-trans isomerase D	94.6%	3.2	1	1	1	1	867,627	834,720	991,953	1,022,861	22,765	79,874	116,435	34,243	5.9	21.4	26.3	7.5	-1.0	0.7	1.1	0.3	1.2	0.005	1.2	0.3	1.2	0.06	1.0	0.8
				IVLELFADIVPK	2	94.6%	1																									
IPI00003929	GSTA3	Glutathione S-transferase A3	100.0%	9.9	2	2	2	1	4,677,130	5,344,900	5,001,428	5,641,560	1,240,978	918,709	746,550	559,291	59.3	38.4	33.4	22.2	1.1	0.7	1.1	0.8	1.2	0.5	-1.1	0.8	1.1	0.8	1.1	0.5
				AILNYIASK	2	100.0%	1																									
				WLLAAAGVEFEEK	2	100.0%	1																									
IPI00220403	HIST1H2BB	Histone H2B type 1-B	100.0%	24.6	3	5	8	4	3,824,112	3,600,489	3,983,699	4,755,146	165,537	162,467	136,392	196,709	9.7	10.1	7.7	9.3	-1.1	0.4	1.0	0.5	1.2	0.007	1.1	0.1	1.3	0.002	1.2	0.01
IPI00515061	HIST1H2BJ	Histone H2B type 1-J	100.0%	24.6	3	5	8	4	3,824,112	3,600,489	3,983,699	4,755,146	165,537	162,467	136,392	196,709	9.7	10.1	7.7	9.3	-1.1	0.4	1.0	0.5	1.2	0.007	1.1	0.1	1.3	0.002	1.2	0.01
IPI00152785	HIST1H2BO	Histone H2B type 1-O	100.0%	24.6	3	5	8	4	3,824,112	3,600,489	3,983,699	4,755,146	165,537	162,467	136,392	196,709	9.7	10.1	7.7	9.3	-1.1	0.4	1.0	0.5	1.2	0.007	1.1	0.1	1.3	0.002	1.2	0.01
IPI00003935	HIST2H2BE	Histone H2B type 2-E	100.0%	24.6	3	5	8	4	3,824,112	3,600,489	3,983,699	4,755,146	165,537	162,467	136,392	196,709	9.7	10.1	7.7	9.3	-1.1	0.4	1.0	0.5	1.2	0.007	1.1	0.1	1.3	0.002	1.2	0.01
				AMGIMNSFVNDIFER	2	100.0%	4																									
				AMGIMNSFVNDIFER	3	100.0%	1																									
				EIQTAVR	1	87.0%	1																									
				EIQTAVR	2	94.1%	1																									
				LLLPGELAK	1	84.1%	1																									
IPI00003949	UBE2N	Ubiquitin-conjugating enzyme E2 N	100.0%	42.1	5	5	7	1	39,390,695	38,007,100	41,389,925	41,744,405	2,069,343	1,562,701	2,060,309	682,007	11.8	9.2	11.1	3.7	-1.0	0.6	1.1	0.5	1.1	0.3	1.1	0.2	1.1	0.06	1.0	0.9
				LELFLPEEYPMAAPK	2	100.0%	1																									
				LLAEPVPGIK	2	98.4%	1																									
				TNEAQAIETAR	2	100.0%	2																									
				WSPALQIR	2	99.8%	1																									
				YFHVVIAGPQDSPFEGGTFK	3	100.0%	2																									
IPI00003964	USP9X	isoform 2 of Probable ubiquitin carboxyl-terminal hydrolase FAF-X	99.8%	0.4	1	1	2	2	4,072,145	3,855,150	3,750,310	4,146,750	318,814	100,696	361,779	132,907	17.5	5.8	21.6	7.2	-1.1	0.5	-1.1	0.5	1.0	0.8	-1.0	0.8	1.1	0.1	1.1	0.4
IPI00221012	USP9X	isoform 1 of Probable ubiquitin carboxyl-terminal hydrolase FAF-X	99.8%	0.4	1	1	2	2	4,072,145	3,855,150	3,750,310	4,146,750	318,814	100,696	361,779	132,907	17.5	5.8	21.6	7.2	-1.1	0.5	-1.1	0.5	1.0	0.8	-1.0	0.8	1.1	0.1	1.1	0.4
				LAQQISDEASR	2	99.7%	2																									
IPI00003965	USP7	Ubiquitin carboxyl-terminal hydrolase 7	100.0%	2.8	2	2	2	4	1,645,902	1,706,390	1,700,671	2,006,001	159,061	60,616	138,916	75,544	21.6	7.9	18.3	8.4	1.0	0.7	1.0	0.8	1.2	0.08	-1.0	1	1.2	0.01	1.2	0.09
IPI00646721	USP7	Ubiquitin carboxyl-terminal hydrolase	100.0%	2.9	2	2	2	4	1,645,902	1,706,390	1,700,671	2,006,001	159,061	60,616	138,916	75,544	21.6	7.9	18.3	8.4	1.0	0.7	1.0	0.8	1.2	0.08	-1.0	1	1.2	0.01	1.2	0.09
IPI01009317	USP7	cDNA FLJ50426, highly similar to Ubiquitin carboxyl-terminal hydrolase 7	100.0%	3.9	2	2	2	4	1,645,902	1,706,390	1,700,671	2,006,001	159,061	60,616	138,916	75,544	21.6	7.9	18.3	8.4	1.0	0.7	1.0	0.8	1.2	0.08	-1.0	1	1.2	0.01	1.2	0.09
IPI01011924	USP7	117 kDa protein	100.0%	3.1	2	2	2	4	1,645,902	1,706,390	1,700,671	2,006,001	159,061	60,616	138,916	75,544	21.6	7.9	18.3	8.4	1.0	0.7	1.0	0.8	1.2	0.08	-1.0	1	1.2	0.01	1.2	0.09
				NSSLAEFVQSLSQTMGFPQDQIR	3	99.6%	1																									
				VDVIFCDK	2	99.7%	1																									
IPI00003966	CA9	Carbonic anhydrase 9	100.0%	17.9	5	5	5	1	19,121,351	19,264,324	18,617,312	20,559,154	1,156,318	615,078	753,449	788,025	13.5	7.1	9.1	8.6	1.0	0.9	-1.0	0.7	1.1	0.3	-1.0	0.5	1.1	0.2	1.1	0.1
				FPAEIHVVHLSTAFAR	3	100.0%	1																									
				GGVSYRPAEVAETGA	2	99.9%	1																									
				PGGLAVLAAFLEEGPEENSAYEQLLSR	3	98.8%	1																									
				VIEASFPAGVDSSPR	2	99.6%	1																									
				YGGDPPWPR	2	100.0%	1																									
IPI00003990	BPHL	isoform 2 of Valacyclovir hydrolase	99.4%	6.9	1	1	1	4	210,615	210,188	212,420	261,142	23,024	9,919	24,823	19,143	24.4	10.6	26.1	16.4	-1.0	1	1.0	1	1.2	0.1	1.0	0.9	1.2	0.05	1.2	0.2
IPI00384428	BPHL	isoform 1 of Valacyclovir hydrolase	99.4%	6.5	1	1	1	4	210,615	210,188	212,420	261,142	23,024	9,919	24,823	19,143	24.4	10.6	26.1	16.4	-1.0	1	1.0	1	1.2	0.1	1.0	0.9	1.2	0.05	1.2	0.2
IPI00844403	BPHL	Biphenyl hydrolase-like (Serine hydrolase	99.4%	9.8	1	1	1	4	210,615	210,188	212,420	261,142	23,024	9,919	24,823	19,143	24.4	10.6	26.1	16.4	-1.0	1	1.0	1	1.2	0.1	1.0	0.9	1.2	0.05	1.2	0.2
IPI00909698	BPHL	cDNA FLJ58913, highly similar to Valacyclovir hydrolase	99.4%	9.0	1	1	1	4	210,615	210,188	212,420	261,142	23,024	9,919	24,823	19,143	24.4	10.6	26.1	16.4	-1.0	1	1.0	1	1.2	0.1	1.0	0.9	1.2	0.05	1.2	0.2
				VSLLGWSDGGITALIAAAK	2	99.4%	1																									
IPI00004233	MKI67	isoform Long of Antigen KI-67	99.8%	0.8	2	2	2	3	12,996,460	13,053,817	12,618,140	15,049,393	870,920	556,041	1,057,686	687,457	15.0	9.5	18.7	10.2	1.0	1	-1.0	0.8	1.2	0.1	-1.0	0.7	1.2	0.05	1.2	0.09
IPI00413173	MKI67	isoform Short of Antigen KI-67	99.8%	0.9	2	2	2	3	12,996,460	13,053,817	12,618,140	15,049,393	870,920	556,041	1,057,686	687,457	15.0	9.5	18.7	10.2	1.0	1	-1.0	0.8	1.2	0.1	-1.0	0.7	1.2	0.05	1.2	0.09
IPI01011955	MKI67	359 kDa protein	99.8%	0.8	2	2	2	3	12,996,460	13,053,817	12,618,140	15,049,393	870,920	556,041	1,057,686	687,457	15.0	9.5	18.7	10.2	1.0	1	-1.0	0.8	1.2	0.1	-1.0	0.7	1.2	0.05	1.2	0.09
				QESGSEIHVEVK	2	95.0%	1																									
				QMLDPANYGTGMER	3	93.7%	1																									
IPI00004273	RBM25	isoform 1 of RNA-binding protein 25	99.5%	3.0	1	1	1	1	266,802	249,715	358,476	348,349	38,358	46,150	66,951	48,147	32.2	41.3	41.8	30.9	-1.1	0.8	1.3	0.3	1.3	0.2	1.4	0.2	1.4	0.2	-1.0	0.9
				IPTAKPELFAYPLDWSIVDSILMER	3	99.5%	1																									
IPI00004324	TRAPPC3	Trafficking protein particle complex subunit 3	99.5%	7.2	1	1	1	2	4,085,940	3,542,820	4,267,855	3,750,650	291,974	203,261	212,472	677,832	16.0	12.8	11.1	40.4	-1.2	0.2	1.0	0.6	-1.1	0.7	1.2	0.04	1.1	0.8	-1.1	0.5
IPI00640089	TRAPPC3	Uncharacterized protein	99.5%	9.7	1	1	1	2	4,085,940	3,542,820	4,267,855	3,750,650	291,974	203,261	212,472	677,832	16.0	12.8	11.1	40.4	-1.2	0.2	1.0	0.6	-1.1	0.7	1.2	0.04	1.1	0.8	-1.1	0.5
				GALEMVQMAVEAK	2	99.5%	1																									
IPI00004358	PYGB	Glycogen phosphorylase, brain form	100.0%	44.5	30	33	45	1	170,486,484	177,547,024	174,776,437	197,860,827	########	7,141,323	########	6,711,789	20.8	9.0	15.4	7.6	1.0	0.7	1.0	0.8	1.2	0.2	-1.0	0.8	1.1	0.07	1.1	0.1
				ARPEYMLPVHFYGR	3	100.0%	2																									
				EIWGVEPSDLQIPPPNIPR	2	95.0%	1																									
				EIWGVEPSDLQIPPPNIPRD	2	99.8%	1																									
				EYYDHLPELK	2	99.0%	1																									
				FSAFLEK	2	99.0%	1																									
				GLAGLGDVAEVR	2	100.0%	1																									
				HLDHVAALFPGDVDR	3	86.1%	1																									
				IGEEFLTDLSQLK	2	100.0%	2																									
				IGEEFLTDLSQLKK	2	100.0%	1																									
				IGEEFLTDLSQLKK	3	100.0%	1																									
				ILVDVEK	2	98.0%	1																									
				LAACFLDSMATLGLAAYGYGIR	2	100.0%	2																									
				LKQEYFVVAATLQDIIR	3	100.0%	1																									
				LLPLVSDEVFIR	2	100.0%	2																									
				LQDFNVGDYIEAVLDR	2	100.0%	2																									
				LQDFNVGDYIEAVLDR	3	100.0%	1																									
				LVTSIGDVVNHDPVVGDR	3	100.0%	1																									
				MSVIEEGDCKR	2	99.8%	1																									
				QAVDQISSGFFSPK	2	100.0%	2																									
				QISVRGLAGLGDVAEVR	3	94.4%	1																									
				RWLLLCNPGLADTIVEK	3	100.0%	1																									
				TCFETFPDKVAIQLNDTHPALSIPELMR	3	100.0%	1																									
				VEDVEALDR	2	99.9%	1																									
				VFADYEAYMQCQAQVDQLYR	3	99.9%	1																									
				VIPAADLSQQISTAGTEASGTGNMK	2	99.8%	2																									
				VLYPNDNFFEGK	2	100.0%	2																									
				VSLAEK	1	91.7%	2																									
				WLDTQVVLAMPYDTPVPGYK	2	100.0%	2																									
				WLDTQVVLAMPYDTPVPGYK	3	100.0%	1																									
				WLLLCNPGLADTIVEK	2	100.0%	1																									
				WPVSMFEK	2	99.8%	2																									
				YEFGIFNQK	2	100.0%	2																									
				YGNPWEK	2	98.6%	1																									
IPI00004363	STK39	STE20/SPS1-related proline-alanine-rich protein kinase	100.0%	7.1	2	2	2	1	1,244,240	1,170,497	1,022,071	1,191,747	113,434	76,208	76,918	52,734	20.4	14.6	16.8	9.9	-1.1	0.6	-1.2	0.1	-1.0	0.7	-1.1	0.2	1.0	0.8	1.2	0.1
				DAYELQEVIGSGATAVVQAALCKPR	3	99.5%	1																									
				NGVLEEAIIATILK	2	99.1%	1																									
IPI00927929	RALA	Uncharacterized protein	100.0%	19.8	1	1	1	5	86,665	82,704	106,489	76,349	9,340	6,957	14,774	4,385	24.1	18.8	31.0	12.8	-1.0	0.7	1.2	0.3	-1.1	0.3	1.3	0.2	-1.1	0.5	-1.4	0.1
IPI00004397	RALB	cDNA FLJ55177, highly similar to Ras-related protein Ral-B	100.0%	8.8	1	1	1	5	86,665	82,704	106,489	76,349	9,340	6,957	14,774	4,385	24.1	18.8	31.0	12.8	-1.0	0.7	1.2	0.3	-1.1	0.3	1.3	0.2	-1.1	0.5	-1.4	0.1
IPI00925885	RALB	Uncharacterized protein	100.0%	17.9	1	1	1	5	86,665	82,704	106,489	76,349	9,340	6,957	14,774	4,385	24.1	18.8	31.0	12.8	-1.0	0.7	1.2	0.3	-1.1	0.3	1.3	0.2	-1.1	0.5	-1.4	0.1
IPI00926453	RALB	Uncharacterized protein	100.0%	12.0	1	1	1	5	86,665	82,704	106,489	76,349	9,340	6,957	14,774	4,385	24.1	18.8	31.0	12.8	-1.0	0.7	1.2	0.3	-1.1	0.3	1.3	0.2	-1.1	0.5	-1.4	0.1
IPI01015571	RALB	Ras-related protein Ral-B	100.0%	9.7	1	1	1	5	86,665	82,704	106,489	76,349	9,340	6,957	14,774	4,385	24.1	18.8	31.0	12.8	-1.0	0.7	1.2	0.3	-1.1	0.3	1.3	0.2	-1.1	0.5	-1.4	0.1
				SALTLQFMYDEFVEDYEPTK	2	100.0%	1																									
IPI00004408	ADD3	isoform 2 of Gamma-adducin	99.5%	5.4	3	3	3	2	8,570,050	9,038,085	7,460,020	9,018,810	503,597	533,045	565,297	372,004	13.1	13.2	16.9	9.2	1.1	0.5	-1.1	0.2	1.1	0.5	-1.2	0.08	-1.0	1	1.2	0.05
IPI00220754	ADD3	isoform 1 of Gamma-adducin	99.5%	5.6	3	3	3	2	8,570,050	9,038,085	7,460,020	9,018,810	503,597	533,045	565,297	372,004	13.1	13.2	16.9	9.2	1.1	0.5	-1.1	0.2	1.1	0.5	-1.2	0.08	-1.0	1	1.2	0.05
				KRVTQILQSPAFR	2	91.3%	1																									
				QDFNMMEQR	2	88.9%	1																									
				VNIIGEVVDQGSTNLK	2	95.0%	1																									
IPI00004416	CHMP2A	Charged multivesicular body protein 2a	99.3%	4.5	1	1	1	1	1,328,171	1,440,040	1,462,214	1,854,652	139,639	210,684	101,170	67,682	23.5	32.7	15.5	8.2	1.1	0.7	1.1	0.5	1.4	0.009	1.0	0.9	1.3	0.1	1.3	0.01
				SNNSMAQAMK	2	99.3%	1																									
IPI00004450	RBMXL2	RNA-binding motif protein, X-linked-like-2	100.0%	3.6	1	1	2	3	1,296,315	1,426,700	1,409,800	1,571,297	147,722	69,063	116,862	51,667	25.5	10.8	18.5	7.4	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00975815	RBMXL2	Conserved hypothetical protein	100.0%	4.3	1	1	2	3	1,296,315	1,426,700	1,409,800	1,571,297	147,722	69,063	116,862	51,667	25.5	10.8	18.5	7.4	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00167369	RBMXL3	RNA-binding motif protein, X-linked-like-3	100.0%	1.3	1	1	2	3	1,296,315	1,426,700	1,409,800	1,571,297	147,722	69,063	116,862	51,667	25.5	10.8	18.5	7.4	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.9	1.1	0.1	1.1	0.2
				GFAFVTFESPADAK	2	100.0%	2																									
IPI00004488	ATP6V1F	V-type proton ATPase subunit F	100.0%	20.2	1	2	2	2	728,966	672,412	805,923	853,569	135,248	67,370	110,870	64,447	41.5	22.4	30.8	16.9	-1.1	0.7	1.1	0.7	1.2	0.4	1.2	0.3	1.3	0.09	1.1	0.7
IPI00946714	ATP6V1F	V-type proton ATPase subunit F isoform 2	100.0%	16.3	1	2	2	2	728,966	672,412	805,923	853,569	135,248	67,370	110,870	64,447	41.5	22.4	30.8	16.9	-1.1	0.7	1.1	0.7	1.2	0.4	1.2	0.3	1.3	0.09	1.1	0.7
				LIAVIGDEDTVTGFLLGGIGELNK	2	100.0%	1																									
				LIAVIGDEDTVTGFLLGGIGELNK	3	100.0%	1																									
IPI00004534	PFAS	Phosphoribosylformylglycinamidine synthase	100.0%	2.0	2	2	2	1	10,455,798	10,396,210	9,578,947	12,877,304	1,858,607	526,372	1,073,131	729,603	39.8	11.3	25.1	12.7	-1.0	1	-1.1	0.7	1.2	0.3	-1.1	0.5	1.2	0.02	1.3	0.03
				FGEPVLAGFAR	2	93.3%	1																									
				LMWLFGCPLLLDDVAR	2	100.0%	1																									
IPI00004656	B2M	Beta-2-microglobulin	100.0%	26.9	2	2	2	2	2,232,417	2,611,522	2,647,535	2,764,255	192,591	65,512	365,416	240,555	19.3	5.6	30.9	19.5	1.2	0.1	1.2	0.3	1.2	0.1	1.0	0.9	1.1	0.6	1.0	0.8
IPI00796379	B2M	cDNA FLJ57067, highly similar to Beta-2-microglobulin	100.0%	26.2	2	2	2	2	2,232,417	2,611,522	2,647,535	2,764,255	192,591	65,512	365,416	240,555	19.3	5.6	30.9	19.5	1.2	0.1	1.2	0.3	1.2	0.1	1.0	0.9	1.1	0.6	1.0	0.8
				SNFLNCYVSGFHPSDIEVDLLK	3	99.8%	1																									
				VNHVTLSQPK	2	99.4%	1																									
IPI00976108	-	Conserved hypothetical protein	98.5%	14.5	1	1	1	4	861,755	853,683	790,620	874,068	54,253	30,580	47,363	45,560	14.1	8.0	13.4	11.7	-1.0	0.9	-1.1	0.4	1.0	0.9	-1.1	0.3	1.0	0.7	1.1	0.2
IPI00004669	GALNT2	Polypeptide N-acetylgalactosaminyltransferase 2	98.5%	1.9	1	1	1	4	861,755	853,683	790,620	874,068	54,253	30,580	47,363	45,560	14.1	8.0	13.4	11.7	-1.0	0.9	-1.1	0.4	1.0	0.9	-1.1	0.3	1.0	0.7	1.1	0.2
IPI00922793	GALNT2	cDNA FLJ58016, highly similar to Polypeptide N-acetylgalactosaminyltransferase2	98.5%	3.1	1	1	1	4	861,755	853,683	790,620	874,068	54,253	30,580	47,363	45,560	14.1	8.0	13.4	11.7	-1.0	0.9	-1.1	0.4	1.0	0.9	-1.1	0.3	1.0	0.7	1.1	0.2
IPI01012012	GALNT2	61 kDa protein	98.5%	2.1	1	1	1	4	861,755	853,683	790,620	874,068	54,253	30,580	47,363	45,560	14.1	8.0	13.4	11.7	-1.0	0.9	-1.1	0.4	1.0	0.9	-1.1	0.3	1.0	0.7	1.1	0.2
				WYLENVYPELR	2	98.5%	1																									
IPI00004670	GALNT3	isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 3	99.5%	2.1	1	1	1	4	590,260	594,888	525,830	606,245	68,449	38,450	27,129	23,140	25.9	14.5	11.5	8.5	1.0	1	-1.1	0.4	1.0	0.8	-1.1	0.2	1.0	0.8	1.2	0.05
IPI00456483	GALNT3	isoform 2 of Polypeptide N-acetylgalactosaminyltransferase 3	99.5%	6.8	1	1	1	4	590,260	594,888	525,830	606,245	68,449	38,450	27,129	23,140	25.9	14.5	11.5	8.5	1.0	1	-1.1	0.4	1.0	0.8	-1.1	0.2	1.0	0.8	1.2	0.05
IPI00915831	GALNT3	Uncharacterized protein	99.5%	2.8	1	1	1	4	590,260	594,888	525,830	606,245	68,449	38,450	27,129	23,140	25.9	14.5	11.5	8.5	1.0	1	-1.1	0.4	1.0	0.8	-1.1	0.2	1.0	0.8	1.2	0.05
IPI00953363	GALNT3	Uncharacterized protein	99.5%	14.4	1	1	1	4	590,260	594,888	525,830	606,245	68,449	38,450	27,129	23,140	25.9	14.5	11.5	8.5	1.0	1	-1.1	0.4	1.0	0.8	-1.1	0.2	1.0	0.8	1.2	0.05
				MLDLMLEAVNNIK	2	99.5%	1																									
IPI00004671	GOLGB1	Golgin subfamily B member 1	99.7%	0.8	2	2	2	2	2,174,375	2,587,103	2,779,438	2,183,449	238,302	202,617	255,520	135,524	24.5	17.5	20.6	13.9	1.2	0.2	1.3	0.1	1.0	1	1.1	0.6	-1.2	0.1	-1.3	0.07
IPI00796891	GOLGB1	Golgin B1	99.7%	0.8	2	2	2	2	2,174,375	2,587,103	2,779,438	2,183,449	238,302	202,617	255,520	135,524	24.5	17.5	20.6	13.9	1.2	0.2	1.3	0.1	1.0	1	1.1	0.6	-1.2	0.1	-1.3	0.07
				AQTEVQLQQK	2	92.6%	1																									
				AQVVDLLQQELTAAEQR	2	96.6%	1																									
IPI00976078	-	HLA class I histocompatibility antigen, Cw-15 alpha chain-like isoform 15, partial	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976426	-	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like isoform 5	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976613	-	HLA class I histocompatibility antigen, Cw-15 alpha chain-like isoform 5	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4

IPI00976715	-	HLA class I histocompatibility antigen, Cw-15 alpha chain-like isoform 6	98.0%	6.9	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977138	-	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like isoform 10	98.0%	7.7	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977355	-	HLA class I histocompatibility antigen, Cw-15 alpha chain-like isoform 11	98.0%	7.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977814	-	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like isoform 11	98.0%	7.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00978215	-	HLA class I histocompatibility antigen, Cw-15 alpha chain-like isoform 4, partial	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00978866	-	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like isoform 6, partial	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00979573	-	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like isoform 7	98.0%	6.9	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980123	-	HLA class I histocompatibility antigen, Cw-15 alpha chain-like isoform 7	98.0%	7.0	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00981275	-	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like isoform 13	98.0%	8.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00982511	-	HLA class I histocompatibility antigen, Cw-15 alpha chain-like isoform 10	98.0%	7.7	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00983562	-	HLA class I histocompatibility antigen, Cw-15 alpha chain-like isoform 12	98.0%	8.2	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984851	-	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like isoform 14, partial	98.0%	7.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472943	HLA-B	HLA class I histocompatibility antigen, B-73 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00471951	HLA-C	HLA class I histocompatibility antigen, Cw-15 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472035	HLA-C	isoform 2 of HLA class I histocompatibility antigen, Cw-16 alpha chain	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472605	HLA-C	HLA class I histocompatibility antigen, Cw-2 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472903	HLA-C	HLA class I histocompatibility antigen, Cw-8 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00473006	HLA-C	HLA class I histocompatibility antigen, Cw-17 alpha chain	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00642409	HLA-C	HLA class I histocompatibility antigen, Cw-7 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00657976	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00743716	HLA-C	HLA class I histocompatibility antigen, Cw-12 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00744964	HLA-C	HLA class I histocompatibility antigen, Cw-6 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00745649	HLA-C	isoform 1 of HLA class I histocompatibility antigen, Cw-16 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00788914	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00789567	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00789627	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00790240	HLA-C	Uncharacterized protein	98.0%	6.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00790450	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00796489	HLA-C	Uncharacterized protein	98.0%	6.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00797121	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00797359	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00892834	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00892868	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00893004	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00893894	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00894106	HLA-C	Major histocompatibility complex, class I, C	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00914567	HLA-C	Uncharacterized protein	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00922944	HLA-C	Uncharacterized protein	98.0%	6.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00940896	HLA-C	cDNA FLJ54183, highly similar to HLA class I histocompatibility antigen, Cw-7 alpha	98.0%	6.0	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976792	HLA-C	HLA class I histocompatibility antigen, Cw-15 alpha chain-like isoform 9, partial	98.0%	7.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980419	HLA-C	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like isoform 12	98.0%	8.2	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00981933	HLA-C	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like isoform 3	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI01008908	HLA-C	HLA class I histocompatibility antigen, Cw-15 alpha chain-like isoform 14	98.0%	9.9	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI01009434	HLA-C	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like isoform 8	98.0%	7.0	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00004672	HLA-H	Putative HLA class I histocompatibility antigen, alpha chain H	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472921	;LOC100507703;HLA	HLA class I histocompatibility antigen, A-29 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00743359	;LOC100507703;HLA	HLA class I histocompatibility antigen, A-26 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976393	;LOC100507703;HLA	HLA class I histocompatibility antigen, A-32 alpha chain-like isoform 5	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00985070	;LOC100507703;HLA	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 14	98.0%	9.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00975557	LOC100507680	HLA class I histocompatibility antigen, A-74 alpha chain-like isoform 3	98.0%	7.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00975790	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 18	98.0%	9.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00975864	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 16, partial	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976139	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 6	98.0%	6.3	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976221	LOC100507680	HLA class I histocompatibility antigen, A-74 alpha chain-like isoform 4	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976413	LOC100507680	HLA class I histocompatibility antigen, A-32 alpha chain-like isoform 11	98.0%	7.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976450	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 17	98.0%	7.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976530	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 19	98.0%	8.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976731	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 7	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976759	LOC100507680	HLA class I histocompatibility antigen, A-74 alpha chain-like isoform 9	98.0%	9.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977061	LOC100507680	HLA class I histocompatibility antigen, A-32 alpha chain-like isoform 8	98.0%	6.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977093	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 16	98.0%	7.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977359	LOC100507680	HLA class I histocompatibility antigen, A-74 alpha chain-like isoform 10	98.0%	7.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977441	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 4	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977789	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 6	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977869	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 17	98.0%	8.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00978281	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 15	98.0%	7.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00978828	LOC100507680	HLA class I histocompatibility antigen, A-32 alpha chain-like isoform 4	98.0%	7.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00978900	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 12	98.0%	6.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00979178	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 2	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00979662	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 18	98.0%	8.2	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00979794	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 3	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980229	LOC100507680	HLA class I histocompatibility antigen, A-32 alpha chain-like isoform 10	98.0%	9.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980259	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 19	98.0%	6.9	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980692	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 11	98.0%	6.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980786	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 9	98.0%	6.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980959	LOC100507680	HLA class I histocompatibility antigen, A-74 alpha chain-like isoform 11	98.0%	8.2	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00981276	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 8	98.0%	6.2	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00981387	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 14	98.0%	8.9	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00981501	LOC100507680	HLA class I histocompatibility antigen, A-74 alpha chain-like isoform 12	98.0%	7.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00982001	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 9	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00982542	LOC100507680	HLA class I histocompatibility antigen, A-32 alpha chain-like isoform 6	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00982574	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 14, partial	98.0%	6.7	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00983187	LOC100507680	HLA class I histocompatibility antigen, A-32 alpha chain-like isoform 14	98.0%	8.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00983622	LOC100507680	HLA class I histocompatibility antigen, A-74 alpha chain-like isoform 7	98.0%	6.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00983641	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 7	98.0%	6.3	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00983646	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 20, partial	98.0%	6.7	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00983719	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 10	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984238	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 4	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984305	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 11	98.0%	8.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984336	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 20	98.0%	7.3	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984386	LOC100507680	HLA class I histocompatibility antigen, A-32 alpha chain-like isoform 12	98.0%	8.3	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984787	LOC100507680	HLA class I histocompatibility antigen, A-74 alpha chain-like isoform 13	98.0%	8.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984956	LOC100507680	HLA class I histocompatibility antigen, A-32 alpha chain-like isoform 13	98.0%	7.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984981	LOC100507680	HLA class I histocompatibility antigen, A-43 alpha chain-like isoform 21	98.0%	8.2	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00985177	LOC100507680	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 8	98.0%	6.9	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472825	HLA-A	HLA class I histocompatibility antigen, A-32 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00745699	HLA-A	Major histocompatibility complex, class I, A	98.0%	8.0	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00785070	HLA-A	Major histocompatibility complex, class I, A	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00885217	HLA-A	MHC class I antigen	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00892768	HLA-A	Major histocompatibility complex, class I, A	98.0%	8.0	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976023	HLA-A	MHC class I HLA-A	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977260	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 13	98.0%	7.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980076	HLA-A	Major histocompatibility complex, class I, A	98.0%	8.0	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00026569	HLA-A	HLA class I histocompatibility antigen, A-1 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472013	HLA-A	HLA class I histocompatibility antigen, A-33 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472112	HLA-A	isoform 2 of HLA class I histocompatibility antigen, A-11 alpha chain	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472151	HLA-A	HLA class I histocompatibility antigen, A-23 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472222	HLA-A	HLA class I histocompatibility antigen, A-74 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472448	HLA-A	isoform 1 of HLA class I histocompatibility antigen, A-11 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472736	HLA-A	HLA class I histocompatibility antigen, A-80 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472855	HLA-A	HLA class I histocompatibility antigen, A-30 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00472882	HLA-A	HLA class I histocompatibility antigen, A-68 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00644748	HLA-A	HLA class I histocompatibility antigen, A-36 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00646225	HLA-A	HLA class I histocompatibility antigen, A-31 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00647457	HLA-A	Major histocompatibility complex, class I, A	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00647634	HLA-A	HLA class I histocompatibility antigen, A-3 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00742968	HLA-A	HLA class I histocompatibility antigen, A-24 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00743503	HLA-A	HLA class I histocompatibility antigen, A-34 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00760554	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00794678	HLA-A	MHC class I antigen	98.0%	7.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00816779	HLA-A	Leukocyte antigen	98.0%	7.0	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00876963	HLA-A	HLA class I histocompatibility antigen, A-2 alpha chain	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00893131	HLA-A	Major histocompatibility complex, class I, A	98.0%	8.0	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00893949	HLA-A	Major histocompatibility complex, class I, A	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00894325	HLA-A	Major histocompatibility complex, class I, A	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00970871	HLA-A	MHC class I antigen	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00971191	HLA-A	cDNA FLJ43620 fis, clone SPLEN2021701, highly similar to HLA CLASS I HISTOC	98.0%	8.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00975972	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 7	98.0%	6.2	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976053	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 4	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976392	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 12	98.0%	6.9	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976552	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 5	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976618	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 12, partial	98.0%	6.7	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977204	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 1	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977325	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 10	98.0%	6.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977708	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 3	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00978158	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 9	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00978768	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 19	98.0%	7.7	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00979058	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 8	98.0%	6.9	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00979570	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 7	98.0%	6.2	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00979770	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 9	98.0%	6.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980153	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 6	98.0%	6.3	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980405	HLA-A	MHC class I antigen	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980578	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 20	98.0%	8.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980743	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 15	98.0%	7.7	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980805	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 4	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00980915	HLA-A	MHC class I antigen	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00983097	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 11	98.0%	6.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4

IPI00983570	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 17	98.0%	9.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00983762	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 16	98.0%	7.3	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984171	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 16	98.0%	7.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984415	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 17	98.0%	8.1	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00984895	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 15, partial	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00985446	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 14, partial	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI01014229	HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain-like isoform 18	98.0%	8.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI01014905	HLA-A	cDNA FLJ59905, highly similar to HLA class I histocompatibility antigen, A-34alpha c	98.0%	15.7	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00975553	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 13, partial	98.0%	6.7	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00975726	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 5	98.0%	6.2	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976095	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 12	98.0%	7.7	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976331	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 4	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976872	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 11	98.0%	8.0	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00976897	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 3	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977384	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 10	98.0%	8.8	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00977477	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 2	98.0%	6.5	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00978503	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 9	98.0%	6.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00979096	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 1	98.0%	6.6	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00979118	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 8	98.0%	6.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00979905	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 7	98.0%	7.4	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00985195	LOC100510327	HLA class I histocompatibility antigen, A-30 alpha chain-like isoform 14	98.0%	7.0	1	1	1	171	4,181	4,329	4,216	4,669	451	349	470	244	24.1	18.0	24.9	11.7	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.4
				DGEDQTQDTELVETRPAGDGTFQK	3	98.9%	1																									
IPI00004795	CLNS1A	Methylosome subunit pICln	99.6%	23.6	2	2	2	3	1,075,676	1,224,067	1,425,251	1,237,537	141,803	95,320	136,573	134,572	29.5	17.4	21.4	24.3	1.1	0.4	1.3	0.1	1.2	0.4	1.2	0.3	1.0	0.9	-1.2	0.4
IPI00979926	CLNS1A	PRO1478	99.6%	27.6	2	2	2	3	1,075,676	1,224,067	1,425,251	1,237,537	141,803	95,320	136,573	134,572	29.5	17.4	21.4	24.3	1.1	0.4	1.3	0.1	1.2	0.4	1.2	0.3	1.0	0.9	-1.2	0.4
IPI00980681	CLNS1A	Uncharacterized protein	99.6%	33.5	2	2	2	3	1,075,676	1,224,067	1,425,251	1,237,537	141,803	95,320	136,573	134,572	29.5	17.4	21.4	24.3	1.1	0.4	1.3	0.1	1.2	0.4	1.2	0.3	1.0	0.9	-1.2	0.4
				LSWLDGSGLGFSLEYPTISLHALSR	3	99.6%	1																									
				TEDSIRDYEDGMEVDTTPTVAGQFEDADVDH	3	99.6%	1																									
IPI00004838	CRK	isoform Crk-II of Adapter molecule crk	100.0%	9.2	2	2	3	1	2,112,969	2,170,780	2,123,860	2,465,540	169,059	106,160	204,499	47,556	17.9	10.9	21.5	4.3	1.0	0.8	1.0	1	1.2	0.1	-1.0	0.8	1.1	0.04	1.2	0.2
				IGDQEFDSLPALLEFYK	2	100.0%	2																									
				QEAVALLQGQR	2	99.7%	1																									
IPI00004839	CRKL	Crk-like protein	100.0%	21.1	5	5	6	1	36,601,946	36,874,811	35,784,720	42,886,740	3,630,394	1,022,430	2,752,716	2,164,367	22.2	6.2	17.2	11.3	1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.7	1.2	0.04	1.2	0.08
				IGDQEFDHLPALLEFYK	3	100.0%	1																									
				MNINGQWEGEVNGR	2	99.4%	1																									
				SAWYMGPVSR	2	99.4%	1																									
				TALALEVGDIVK	2	100.0%	2																									
				VGMIPVPYVEK	2	99.3%	1																									
IPI00004860	RARS	isoform Complexed of Arginyl-tRNA synthetase, cytoplasmic	100.0%	22.0	10	10	11	2	17,835,074	17,554,781	16,739,703	19,121,408	1,961,657	687,730	1,443,632	636,851	24.6	8.8	19.3	7.5	-1.0	0.9	-1.1	0.7	1.1	0.6	-1.0	0.6	1.1	0.1	1.1	0.2
IPI00759723	RARS	isoform Monomeric of Arginyl-tRNA synthetase, cytoplasmic	100.0%	24.7	10	10	11	2	17,835,074	17,554,781	16,739,703	19,121,408	1,961,657	687,730	1,443,632	636,851	24.6	8.8	19.3	7.5	-1.0	0.9	-1.1	0.7	1.1	0.6	-1.0	0.6	1.1	0.1	1.1	0.2
				AAYPDLENPPLLVTPSQQAK	3	82.6%	1																									
				AYQCVVLLQGK	2	99.9%	1																									
				DFVSEQLTSLLVNGVQLPALGENKK	3	100.0%	1																									
				FGDYQCNSAMGISQMLK	3	83.2%	1																									
				IVFVPGCSIPLTIVK	2	100.0%	1																									
				LANIDEEMLQK	2	97.0%	1																									
				LFEFAGYDVLR	2	100.0%	1																									
				LNDYIFSFDK	2	99.7%	1																									
				MLLCEAVAAVMAK	2	99.8%	1																									
				VIVDFSSPNIAK	2	99.9%	2																									
IPI00004902	ETFB	isoform 1 of Electron transfer flavoprotein subunit beta	100.0%	33.7	7	7	7	2	15,473,643	16,957,485	15,336,890	18,006,924	1,197,787	423,416	1,066,998	693,153	17.3	5.6	15.6	8.6	1.1	0.3	-1.0	0.9	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.07
IPI00556451	ETFB	isoform 2 of Electron transfer flavoprotein subunit beta	100.0%	24.9	7	7	7	2	15,473,643	16,957,485	15,336,890	18,006,924	1,197,787	423,416	1,066,998	693,153	17.3	5.6	15.6	8.6	1.1	0.3	-1.0	0.9	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.07
				EIDGGLETLR	2	100.0%	1																									
				EVIAVSCGPAQCQETIR	2	100.0%	1																									
				HSMNPFCEIAVEEAVR	2	99.2%	1																									
				IEVIKPGDLGVDLTSK	2	99.8%	1																									
				LPAVVTADLR	2	100.0%	1																									
				TALAMGADR	2	96.4%	1																									
				VDLVLLGK	2	98.3%	1																									
IPI00004968	PRPF19	Pre-mRNA-processing factor 19	100.0%	9.5	4	4	5	1	30,877,930	30,198,660	28,427,480	34,753,730	2,086,124	1,146,163	1,909,277	1,070,996	15.1	8.5	15.0	6.9	-1.0	0.8	-1.1	0.4	1.1	0.1	-1.1	0.4	1.2	0.02	1.2	0.02
				ATVLTTER	2	96.1%	1																									
				ILTGGADKNVVVFDK	2	88.7%	1																									
				IWSVPNASCVQVVR	2	95.9%	1																									
				TLQLDNNFEVK	2	99.9%	2																									
IPI00965271	LOC653877	small subunit processome component 20 homolog	98.7%	0.4	1	1	1	2	1,940,765	1,978,960	2,142,410	2,181,015	273,961	92,373	67,664	119,538	31.6	10.4	7.1	12.3	1.0	0.9	1.1	0.5	1.1	0.4	1.1	0.2	1.1	0.2	1.0	0.8
IPI00004970	UTP20	Small subunit processome component 20 homolog	98.7%	0.4	1	1	1	2	1,940,765	1,978,960	2,142,410	2,181,015	273,961	92,373	67,664	119,538	31.6	10.4	7.1	12.3	1.0	0.9	1.1	0.5	1.1	0.4	1.1	0.2	1.1	0.2	1.0	0.8
				LEAAYSPRNPLK	2	98.3%	1																									
IPI00004977	VAV2	isoform 3 of Guanine nucleotide exchange factor VAV2	92.5%	1.4	1	1	1	4	604,273	675,595	652,565	698,150	55,439	50,803	48,110	40,961	20.5	16.8	16.5	13.1	1.1	0.4	1.1	0.5	1.2	0.2	-1.0	0.8	1.0	0.7	1.1	0.5
IPI00472451	VAV2	isoform 1 of Guanine nucleotide exchange factor VAV2	92.5%	1.4	1	1	1	4	604,273	675,595	652,565	698,150	55,439	50,803	48,110	40,961	20.5	16.8	16.5	13.1	1.1	0.4	1.1	0.5	1.2	0.2	-1.0	0.8	1.0	0.7	1.1	0.5
IPI00872160	VAV2	isoform 2 of Guanine nucleotide exchange factor VAV2	92.5%	1.4	1	1	1	4	604,273	675,595	652,565	698,150	55,439	50,803	48,110	40,961	20.5	16.8	16.5	13.1	1.1	0.4	1.1	0.5	1.2	0.2	-1.0	0.8	1.0	0.7	1.1	0.5
IPI00935955	VAV2	100 kDa protein	92.5%	1.4	1	1	1	4	604,273	675,595	652,565	698,150	55,439	50,803	48,110	40,961	20.5	16.8	16.5	13.1	1.1	0.4	1.1	0.5	1.2	0.2	-1.0	0.8	1.0	0.7	1.1	0.5
				VEECTLKVQDGK	2	87.6%	1																									
IPI00005038	HRSP12	Ribonuclease UK114	99.6%	11.7	1	1	1	2	1,551,040	1,781,570	1,849,415	1,638,150	95,470	84,906	81,483	163,454	13.8	10.7	9.9	22.3	1.1	0.1	1.2	0.04	1.1	0.7	1.0	0.6	-1.1	0.5	-1.1	0.3
IPI00974387	HRSP12	Uncharacterized protein	99.6%	14.0	1	1	1	2	1,551,040	1,781,570	1,849,415	1,638,150	95,470	84,906	81,483	163,454	13.8	10.7	9.9	22.3	1.1	0.1	1.2	0.04	1.1	0.7	1.0	0.6	-1.1	0.5	-1.1	0.3
				APGAIGPYSQAVLVDR	2	99.6%	1																									
IPI00005040	ACADM	isoform 1 of Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	99.9%	5.7	2	2	2	4	1,891,692	1,991,894	1,763,613	2,056,109	232,897	90,130	147,989	156,022	27.5	10.1	18.8	17.0	1.1	0.7	-1.1	0.7	1.1	0.6	-1.1	0.2	1.0	0.7	1.2	0.2
IPI00513827	ACADM	Putative uncharacterized protein DKFZp686M24262	99.9%	5.3	2	2	2	4	1,891,692	1,991,894	1,763,613	2,056,109	232,897	90,130	147,989	156,022	27.5	10.1	18.8	17.0	1.1	0.7	-1.1	0.7	1.1	0.6	-1.1	0.2	1.0	0.7	1.2	0.2
IPI00895801	ACADM	isoform 2 of Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	99.9%	5.7	2	2	2	4	1,891,692	1,991,894	1,763,613	2,056,109	232,897	90,130	147,989	156,022	27.5	10.1	18.8	17.0	1.1	0.7	-1.1	0.7	1.1	0.6	-1.1	0.2	1.0	0.7	1.2	0.2
IPI01015888	ACADM	cDNA, FLJ78845, highly similar to Medium-chain specific acyl-CoA dehydrogenase,	99.9%	6.2	2	2	2	4	1,891,692	1,991,894	1,763,613	2,056,109	232,897	90,130	147,989	156,022	27.5	10.1	18.8	17.0	1.1	0.7	-1.1	0.7	1.1	0.6	-1.1	0.2	1.0	0.7	1.2	0.2
				IYQIYEGTSQIQR	2	99.8%	1																									
				KGDEYIINGQK	2	98.3%	1																									
IPI00005087	TMOD3	Tropomodulin-3	100.0%	21.0	4	4	5	1	18,089,020	19,492,190	18,789,170	21,104,970	2,022,717	724,375	958,985	706,749	25.0	8.3	11.4	7.5	1.1	0.5	1.0	0.8	1.2	0.2	-1.0	0.6	1.1	0.1	1.1	0.09
				FCNIMGSSNGVDQEHFSNVVK	3	95.3%	1																									
				QLETVLDDLDPENALLPAGFR	2	100.0%	2																									
				QQLGTAVELEMAK	2	100.0%	1																									
				YKDLDEDELLGNLSETELK	3	100.0%	1																									
IPI00005102	SMS	isoform 1 of Spermine synthase	100.0%	18.6	4	5	5	1	12,640,478	12,169,204	11,951,692	13,679,300	1,042,360	461,080	1,541,200	1,043,696	18.4	8.5	28.8	17.1	-1.0	0.7	-1.1	0.7	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.4
				HSTLDFMLGAK	2	100.0%	1																									
				MKELSQDSTGR	3	99.9%	1																									
				QFGNILILSGDVNLAESDLAYTR	2	99.6%	1																									
				YFTQGNCVNLTEALSLYEEQLGR	2	99.6%	1																									
				YFTQGNCVNLTEALSLYEEQLGR	3	99.7%	1																									
IPI00005154	SSRP1	FACT complex subunit SSRP1	97.4%	2.5	1	1	1	1	8,730,640	9,139,750	5,554,840	7,725,460	1,089,633	1,038,711	798,026	504,360	27.9	25.4	32.1	14.6	1.0	0.8	-1.6	0.05	-1.1	0.4	-1.6	0.03	-1.2	0.3	1.4	0.05
				DEDISLTLNMNEEEVEKR	3	84.6%	1																									
IPI00005158	LONP1	Lon protease homolog, mitochondrial	96.2%	1.3	1	1	1	3	748,997	730,403	708,707	758,553	174,902	61,047	54,292	57,558	52.2	18.7	17.1	17.0	-1.0	0.9	-1.1	0.8	1.0	1	-1.0	0.8	1.0	0.7	1.1	0.5
IPI00334291	LONP1	cDNA FLJ45970 fis, clone PLACE7016526, highly similar to Lon protease homolog,	96.2%	1.3	1	1	1	3	748,997	730,403	708,707	758,553	174,902	61,047	54,292	57,558	52.2	18.7	17.1	17.0	-1.0	0.9	-1.1	0.8	1.0	1	-1.0	0.8	1.0	0.7	1.1	0.5
IPI00642982	LONP1	LONP1 protein	96.2%	1.6	1	1	1	3	748,997	730,403	708,707	758,553	174,902	61,047	54,292	57,558	52.2	18.7	17.1	17.0	-1.0	0.9	-1.1	0.8	1.0	1	-1.0	0.8	1.0	0.7	1.1	0.5
				HVMDVVDEELSK	2	94.8%	1																									
IPI00005159	ACTR2	Actin-related protein 2	100.0%	17.0	5	5	6	1	9,780,910	10,254,640	9,781,795	10,402,215	366,506	318,160	363,628	192,333	8.4	6.9	8.3	4.1	1.0	0.4	1.0	1	1.1	0.2	-1.0	0.4	1.0	0.7	1.1	0.2
				GYAFNHSADFETVR	3	100.0%	1																									
				HIVLSGGSTMYPGLPSR	3	85.0%	1																									
				HLWDYTFGPEK	2	100.0%	1																									
				ILLTEPPMNPTK	2	100.0%	2																									
				LCYVGYNIEQEQK	2	100.0%	1																									
IPI00005162	ARPC3	Actin-related protein 2/3 complex subunit 3	95.5%	6.2	1	1	1	1	3,300,460	2,888,844	3,324,000	3,788,780	150,300	189,591	558,265	282,671	10.2	14.7	37.6	16.7	-1.1	0.1	1.0	1	1.1	0.2	1.2	0.5	1.3	0.03	1.1	0.5
				VFDPQNDKPSK	2	95.5%	1																									
IPI00005179	POLR1C	isoform 1 of DNA-directed RNA polymerases I and III subunit RPAC1	99.6%	6.1	1	1	1	2	911,068	793,715	779,985	1,007,020	118,116	94,755	65,300	48,434	29.0	26.7	18.7	10.8	-1.1	0.5	-1.2	0.4	1.1	0.5	-1.0	0.9	1.3	0.08	1.3	0.02
IPI00217386	POLR1C	isoform 2 of DNA-directed RNA polymerases I and III subunit RPAC1	99.6%	6.1	1	1	1	2	911,068	793,715	779,985	1,007,020	118,116	94,755	65,300	48,434	29.0	26.7	18.7	10.8	-1.1	0.5	-1.2	0.4	1.1	0.5	-1.0	0.9	1.3	0.08	1.3	0.02
				LLPDITLLEPVEGEAAEELSR	2	99.6%	1																									
IPI00005194	UBFD1	Ubiquitin domain-containing protein UBFD1	95.8%	3.6	1	1	1	3	1,871,440	1,431,637	1,573,507	1,867,397	467,171	140,115	105,969	104,752	55.8	21.9	15.1	12.5	-1.3	0.4	-1.2	0.6	-1.0	1	1.1	0.4	1.3	0.04	1.2	0.08
IPI00643653	UBFD1	cDNA FLJ42145 fis, clone TESTI4000228, highly similar to Mus musculus ubiquitin f	95.8%	3.7	1	1	1	3	1,871,440	1,431,637	1,573,507	1,867,397	467,171	140,115	105,969	104,752	55.8	21.9	15.1	12.5	-1.3	0.4	-1.2	0.6	-1.0	1	1.1	0.4	1.3	0.04	1.2	0.08
IPI01008762	UBFD1	57 kDa protein	95.8%	2.1	1	1	1	3	1,871,440	1,431,637	1,573,507	1,867,397	467,171	140,115	105,969	104,752	55.8	21.9	15.1	12.5	-1.3	0.4	-1.2	0.6	-1.0	1	1.1	0.4	1.3	0.04	1.2	0.08
				LEQDQLWIGTK	2	95.8%	1																									
IPI00005198	ILF2	Interleukin enhancer-binding factor 2	100.0%	9.2	3	3	3	1	14,524,760	16,100,925	14,883,365	17,876,855	2,301,759	1,184,807	854,477	767,325	35.4	16.5	12.8	9.6	1.1	0.6	1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.2	1.2	0.03
				ILPTLEAVAALGNK	2	100.0%	1																									
				VLQSALAAIR	2	99.9%	1																									
				WFEENASQSTVK	2	100.0%	1																									
IPI00005264	PKP2	isoform 2 of Plakophilin-2	99.8%	2.8	2	2	2	2	2,524,837	2,573,958	2,707,808	3,022,307	130,800	202,555	119,901	166,667	11.6	17.6	9.9	12.3	1.0	0.8	1.1	0.3	1.2	0.05	1.1	0.6	1.2	0.1	1.1	0.2
IPI00219688	PKP2	isoform 1 of Plakophilin-2	99.8%	3.0	2	2	2	2	2,524,837	2,573,958	2,707,808	3,022,307	130,800	202,555	119,901	166,667	11.6	17.6	9.9	12.3	1.0	0.8	1.1	0.3	1.2	0.05	1.1	0.6	1.2	0.1	1.1	0.2
				IMAISAGDAYASNK	2	94.8%	1																									
				IQEQVQQTLAR	2	99.7%	1																									
IPI00005416	UBAP2L	NICE-4 protein	100.0%	2.3	1	1	1	2	275,503	288,353	265,390	320,666	40,195	19,504	7,085	28,875	32.6	15.1	6.0	20.1	1.0	0.8	-1.0	0.8	1.2	0.4	-1.1	0.3	1.1	0.4	1.2	0.1
IPI00977741	UBAP2L	Ubiquitin associated protein 2-like	100.0%	2.5	1	1	1	2	275,503	288,353	265,390	320,666	40,195	19,504	7,085	28,875	32.6	15.1	6.0	20.1	1.0	0.8	-1.0	0.8	1.2	0.4	-1.1	0.3	1.1	0.4	1.2	0.1
				DGSLASNPYSGDLTK	2	100.0%	1																									
IPI00005474	LHPP	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	99.9%	7.8	1	2	2	1	2,486,040	2,418,148	2,806,710	3,100,733	262,876	306,547	277,879	124,022	23.6	28.4	22.1	8.9	-1.0	0.9	1.1	0.4	1.2	0.07	1.2	0.4	1.3	0.07	1.1	0.4
				ADGYVDNLAEAVDLLLQHADK	2	95.7%	1																									
				ADGYVDNLAEAVDLLLQHADK	3	99.9%	1																									
IPI00005490	GOLPH3	Golgi phosphoprotein 3	100.0%	13.4	2	2	4	2	324,087	317,019	416,896	362,562	50,531	31,160	51,643	17,262	34.9	22.0	27.7	10.7	-1.0	0.9	1.3	0.2	1.1	0.5	1.3	0.1	1.1	0.2	-1.1	0.4
IPI01010778	GOLPH3	cDNA FLJ55806, highly similar to Golgi phosphoprotein 3	100.0%	13.9	2	2	4	2	324,087	317,019	416,896	362,562	50,531	31,160	51,643	17,262	34.9	22.0	27.7	10.7	-1.0	0.9	1.3	0.2	1.1	0.5	1.3	0.1	1.1	0.2	-1.1	0.4
				ANTNEVLWAVVAAFTK	2	100.0%	2																									
				ETQPPETVQNWIELLSGETWNPLK	2	100.0%	2																									
IPI01015060	MRPL12	39S ribosomal protein L12, mitochondrial	100.0%	6.1	1	1	1	2	2,939,155	3,169,190	3,161,785	3,522,575	288,442	156,154	267,124	158,398	21.9	11.0	18.9	10.1	1.1	0.5	1.1	0.6	1.2	0.1	-1.0	1	1.1	0.2	1.1	0.3
IPI00005537	SLC25A10	cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier	100.0%	2.7	1	1	1	2	2,939,155	3,169,190	3,161,785	3,522,575	288,442	156,154	267,124	158,398	21.9	11.0	18.9	10.1	1.1	0.5	1.1	0.6	1.2	0.1	-1.0	1	1.1	0.2	1.1	0.3
				NYIQGINLVQAK	2	100.0%	1																									
IPI00005824	LIN7A	Protein lin-7 homolog A	96.8%	4.3	1	1	1	2	5,225,625	5,515,550	5,019,750	6,425,975	711,336	296,732	538,393	220,564	30.4	12.0	24.0	7.7	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.4	1.2	0.04	1.3	0.04
IPI00005566	LIN7B	Protein lin-7 homolog B	96.8%	4.8	1	1	1	2	5,225,625	5,515,550	5,019,750	6,425,975	711,336	296,732	538,393	220,564	30.4	12.0	24.0	7.7	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.4	1.2	0.04	1.3	0.04
				EQNSPIYISR	2	96.8%	1																									
IPI00005573	NT5C	isoform 1 of 5'(3')-deoxyribonucleotidase, cytosolic type	100.0%	15.4	2	3	4	2	3,163,036	2,802,216	2,853,324	3,169,611	418,911	86,845	240,205	164,727	29.6	6.9	18.8	11.6	-1.1	0.4	-1.1	0.5	1.0	1	1.0	0.8	1.1	0.08	1.1	0.3
IPI00790117	NT5C	20 kDa protein	100.0%	17.0	2	3	4	2	3,163,036	2,802,216	2,853,324	3,169,611	418,911	86,845	240,205	164,727	29.6	6.9	18.8	11.6	-1.1	0.4	-1.1	0.5	1.0	1	1.0	0.8	1.1	0.08	1.1	0.3
				VLVDMDGVLADFEAGLLR	2	100.0%	2																									
				VLVDMDGVLADFEAGLLR	3	100.0%	1																									
				WVEQHLGPQFVER	3	99.4%	1																									
IPI00005578	EHD4	EH domain-containing protein 4	100.0%	19.6	9	9	9	1	90,014,470	94,543,620	89,224,700	103,577,940	8,402,287	3,568,846	5,160,853	3,113,358	20.9	8.4	12.9	6.7	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.09	1.2	0.04
				ADQVDTQQLMR	2	100.0%	1																									
				AGGADAVQTVTGGLR	2	99.9%	1																									
				EYQISAGDFPEVK	2	99.0%	1																									
				FGNAFLNR	2	98.0%	1																									
				FMCSQLPNQVLK	2	93.7%	1																									
				LFEAEAQDLFR	2	99.5%	1																									

				LPEIYIQLQR	2	81.8%	1																									
				SISVIDSPGILSGEK	2	99.8%	1																									
				YLLEQDFPGMR	2	100.0%	1																									
IPI00005585	TAX1BP3	Tax1-binding protein 3	100.0%	28.2	2	2	3	1	7,023,620	6,800,100	6,553,360	7,423,160	1,064,713	382,500	481,898	257,747	33.9	12.6	16.4	7.8	-1.0	0.9	-1.1	0.7	1.1	0.7	-1.0	0.7	1.1	0.2	1.1	0.2
				IMQVNGWDMTMVTHDQAR	3	99.5%	1																									
				VSEGGPAEIAGLQIGDK	2	100.0%	2																									
IPI00005613	U2AF1	Splicing factor U2AF 35 kDa subunit	100.0%	10.8	2	3	3	1	8,807,503	8,938,473	7,450,015	9,208,150	924,918	640,357	695,480	416,403	23.5	16.0	20.9	10.1	1.0	0.9	-1.2	0.3	1.0	0.7	-1.2	0.2	1.0	0.7	1.2	0.06
				AVIDLNNR	2	89.5%	1																									
				WFNGQPIHAELSPVTDFR	2	99.5%	1																									
				WFNGQPIHAELSPVTDFR	3	100.0%	1																									
IPI00005614	SPTBN1	isoform Long of Spectrin beta chain, brain 1	100.0%	37.7	63	69	85	1	262,820,743	265,233,701	259,177,070	301,798,105	########	9,517,166	########	########	17.7	8.0	13.2	8.7	1.0	0.9	-1.0	0.9	1.1	0.1	-1.0	0.7	1.1	0.04	1.2	0.06
				AFEDEMSGR	2	99.9%	1																									
				AKDEQSAVSMLK	2	99.6%	1																									
				AQQYYFDAAEAEAWMSEQELYMMSEEK	3	80.0%	1																									
				AQTLPTSVVTITSESSPGKR	3	94.0%	1																									
				DALLLWCQMK	2	100.0%	1																									
				DASVAEAWLLGQEPYLSSR	2	100.0%	1																									
				DASVAEAWLLGQEPYLSSR	3	100.0%	1																									
				DGMAFNALIHK	2	99.1%	1																									
				DGMAFNALIHK	3	99.5%	1																									
				DLMLWMEDVIR	2	100.0%	2																									
				DVEDEILWVGER	2	100.0%	2																									
				DVSSVELLMNNHQGIK	2	100.0%	1																									
				EAEKLESEHPDQAQAILSR	3	100.0%	1																									
				EAVCEVALDYK	2	99.7%	1																									
				EGMQLISEKPETEAVVK	3	99.3%	1																									
				EIEELQSQAQALSQEGK	2	100.0%	1																									
				EQWANLEQLSAIR	2	95.4%	1																									
				ETASELLMR	2	86.7%	1																									
				EVDDLEQWIAER	2	100.0%	1																									
				EVVAGSHELGQDYEHVTMLQER	3	100.0%	1																									
				FANSLVGVQQQLQAFNTYR	2	100.0%	1																									
				FANSLVGVQQQLQAFNTYR	3	95.6%	1																									
				FATDGEGYKPCDPQVIR	3	99.3%	1																									
				FESLEPEMNNQASR	2	100.0%	1																									
				FFWEMAEEEGWIR	2	100.0%	2																									
				FMELLEPLNER	2	100.0%	2																									
				FQIQDISVETEDNKEK	3	99.9%	1																									
				HLLGVEDLLQK	2	100.0%	2																									
				HQILEQAVEDYAETVHQLSK	3	100.0%	1																									
				HRPDLIDFDK	3	98.3%	1																									
				ITDLYTDLR	2	99.8%	1																									
				KQEDFMTTMDANEEK	3	99.1%	1																									
				LAEISDVWEEMK	2	100.0%	2																									
				LILEVHQFSR	2	97.9%	1																									
				LLDPEDISVDHPDEK	2	97.9%	1																									
				LLEVLSGER	2	100.0%	2																									
				LLTQHENIKNEIDNYEEDYQK	3	100.0%	1																									
				LPEELGRDQNTVETLQR	3	97.5%	1																									
				LQAAYAGDK	2	99.6%	1																									
				LQAAYAGDKADDIQKR	3	98.0%	1																									
				LQALDTGWNELHK	2	100.0%	1																									
				LQALDTGWNELHK	3	99.9%	1																									
				LSGIEER	2	89.6%	1																									
				LTTLELLEVR	2	100.0%	2																									
				LVDTGDKFR	2	96.4%	1																									
				LVDTGDKFR	3	94.4%	1																									
				LVSDGNINSDR	2	100.0%	2																									
				LVSQDNFGFDLPAVEAATK	2	100.0%	2																									
				MHTTFEHDIQALGTQVR	3	100.0%	1																									
				MLTAQDMSYDEAR	2	100.0%	2																									
				MWEVLESTTQTK	2	100.0%	2																									
				NDSFTTCIELGK	2	99.9%	2																									
				QAEAFLNNQEYVLAHTEMPTTLEGAEAAIK	3	100.0%	1																									
				QALQDTLALYK	2	93.2%	1																									
				QNLLSQSHAYQQFLR	3	100.0%	1																									
				SNAHYNLQNAFNLAEQHLGLTK	3	99.3%	1																									
				SQNIVTDSSSLSAEAIR	2	100.0%	2																									
				SQNIVTDSSSLSAEAIR	3	99.8%	1																									
				TAGYPNVNIHNFTTSWR	3	94.1%	1																									
				TALPAQSAATLPAR	2	100.0%	2																									
				TQILAASYELHK	3	99.9%	1																									
				TQTAIASEDMPNTLTEAEK	2	100.0%	2																									
				VAVVNQIAR	2	100.0%	1																									
				VDTVNHLADELINSGHSDAATIAEWK	3	100.0%	1																									
				VHLENMGSHDIVDGNHR	3	99.8%	1																									
				VLDNAIETEK	2	100.0%	1																									
				VLVLSQDYGK	2	100.0%	1																									
				VQAVVAVAR	2	99.9%	1																									
				YKEVAELTR	2	99.6%	1																									
IPI00005615	TIAL1	Nucleolysin TIAR	100.0%	28.3	8	8	9	2	12,940,852	12,715,677	12,410,011	14,297,253	1,166,968	445,601	932,929	544,020	20.2	7.8	16.8	8.5	-1.0	0.9	-1.0	0.7	1.1	0.3	-1.0	0.8	1.1	0.05	1.2	0.1
IPI00647436	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1, isoform CRA_a	100.0%	40.0	8	8	9	2	12,940,852	12,715,677	12,410,011	14,297,253	1,166,968	445,601	932,929	544,020	20.2	7.8	16.8	8.5	-1.0	0.9	-1.0	0.7	1.1	0.3	-1.0	0.8	1.1	0.05	1.2	0.1
				DAAAALAAMNGR	2	92.8%	1																									
				DTSNHFHVFVGDLSPEITTEDIK	3	94.8%	1																									
				FEDVVNQSSPK	2	100.0%	1																									
				GYGFVSFYNK	2	83.3%	1																									
				LDAENAIVHMGGQWLGGR	3	100.0%	1																									
				QTFSPFGQIMEIR	2	100.0%	2																									
				SAFAPFGK	2	99.9%	1																									
				VNWATTPSSQK	2	98.8%	1																									
IPI00005648	SAFB2	Scaffold attachment factor B2	100.0%	3.9	2	2	2	1	2,630,831	2,623,051	2,127,542	2,750,476	173,045	148,394	279,655	142,048	14.7	12.7	29.4	11.6	-1.0	1	-1.2	0.2	1.0	0.6	-1.2	0.2	1.0	0.6	1.3	0.08
				NTLETSSLNFK	2	98.9%	1																									
				SEPVKEESSELEQPFAQDTSSVGPDR	3	100.0%	1																									
IPI00005657	PFDN6	Prefoldin subunit 6	99.5%	9.3	1	1	1	1	3,300,420	3,217,190	3,371,670	3,836,980	253,846	195,815	171,567	359,559	17.2	13.6	11.4	21.0	-1.0	0.8	1.0	0.8	1.2	0.3	1.0	0.6	1.2	0.2	1.1	0.3
				ETLAQLQQEFQR	2	99.5%	1																									
IPI00005668	AKR1C2	Aldo-keto reductase family 1 member C2	100.0%	19.5	4	4	5	1	3,527,976	3,500,745	3,472,598	3,892,602	425,178	97,465	300,095	149,109	27.0	6.2	19.3	8.6	-1.0	1	-1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.06	1.1	0.2
				ILFDTVDLCATWEAMEK	2	99.4%	1																									
				LNDGHFMPVLGFGTYAPAEVPK	3	100.0%	1																									
				QNVQVFEFQLTSEEMK	2	98.0%	1																									
				TPALIALR	2	99.8%	2																									
IPI00005677	GNPAT	Dihydroxyacetone phosphate acyltransferase	99.5%	1.9	1	1	1	3	146,757	172,390	138,160	145,412	22,336	15,790	5,647	26,248	34.0	20.5	9.1	40.4	1.2	0.4	-1.1	0.7	-1.0	1	-1.2	0.1	-1.2	0.4	1.1	0.8
IPI00514057	GNPAT	cDNA FLJ53146, highly similar to Dihydroxyacetone phosphate acyltransferase	99.5%	2.1	1	1	1	3	146,757	172,390	138,160	145,412	22,336	15,790	5,647	26,248	34.0	20.5	9.1	40.4	1.2	0.4	-1.1	0.7	-1.0	1	-1.2	0.1	-1.2	0.4	1.1	0.8
IPI00640892	GNPAT	Glyceronephosphate O-acyltransferase	99.5%	2.2	1	1	1	3	146,757	172,390	138,160	145,412	22,336	15,790	5,647	26,248	34.0	20.5	9.1	40.4	1.2	0.4	-1.1	0.7	-1.0	1	-1.2	0.1	-1.2	0.4	1.1	0.8
				FGLLNIVMEPFFK	2	99.5%	1																									
IPI00005705	PPP1CC	isoform Gamma-1 of Serine/threonine-protein phosphatase PP1-gamma catalytic su	100.0%	26.6	7	7	9	2	5,656,548	5,789,828	5,853,025	6,697,524	528,423	108,072	512,572	155,316	20.9	4.2	19.6	5.2	1.0	0.8	1.0	0.8	1.2	0.1	1.0	0.9	1.2	0.001	1.1	0.2
IPI00218187	PPP1CC	isoform Gamma-2 of Serine/threonine-protein phosphatase PP1-gamma catalytic su	100.0%	25.5	7	7	9	2	5,656,548	5,789,828	5,853,025	6,697,524	528,423	108,072	512,572	155,316	20.9	4.2	19.6	5.2	1.0	0.8	1.0	0.8	1.2	0.1	1.0	0.9	1.2	0.001	1.1	0.2
				EIFLSQPILLELEAPLK	2	100.0%	2																									
				HDLDLICR	2	99.9%	2																									
				IYGFYDECK	2	99.2%	1																									
				LFEYGGFPPESNYLFLGDYVDR	2	90.7%	1																									
				NVQLQENEIR	2	99.7%	1																									
				SREIFLSQPILLELEAPLK	3	98.3%	1																									
				TFTDCFNCLPIAAIVDEK	2	100.0%	1																									
IPI00005719	RAB1A	isoform 1 of Ras-related protein Rab-1A	100.0%	33.7	5	7	9	1	10,359,938	10,960,718	11,421,854	12,643,885	1,054,656	580,334	844,632	342,051	22.8	11.8	16.5	6.1	1.1	0.6	1.1	0.5	1.2	0.1	1.0	0.7	1.2	0.04	1.1	0.2
				EFADSLGIPFLETSAK	2	100.0%	2																									
				FADDTYTESYISTIGVDFK	2	100.0%	2																									
				FADDTYTESYISTIGVDFK	3	100.0%	1																									
				KVVDYTTAK	2	97.5%	1																									
				NATNVEQSFMTMAAEIK	2	100.0%	1																									
				NATNVEQSFMTMAAEIK	3	100.0%	1																									
				QWLQEIDR	2	95.3%	1																									
IPI00005760	TRAF5	TNF receptor-associated factor 5, isoform CRA_a	95.6%	3.9	1	1	1	2	136,287	156,508	220,462	158,366	14,970	16,968	53,785	15,174	24.6	24.2	54.6	21.4	1.1	0.4	1.6	0.2	1.2	0.3	1.4	0.3	1.0	0.9	-1.4	0.3
IPI00982254	TRAF5	cDNA FLJ60573, highly similar to TNF receptor-associated factor 5	95.6%	5.3	1	1	1	2	136,287	156,508	220,462	158,366	14,970	16,968	53,785	15,174	24.6	24.2	54.6	21.4	1.1	0.4	1.6	0.2	1.2	0.3	1.4	0.3	1.0	0.9	-1.4	0.3
				REAVDGHTVSIFSQSFYTSRCGYR	3	95.6%	1																									
IPI00977968	BCL2L2-PABPN1	BCL2L2-PABPN1 protein	100.0%	9.3	3	3	3	3	5,051,733	5,057,803	4,703,360	5,666,597	924,765	293,197	334,905	133,863	40.9	13.0	15.9	5.3	1.0	1	-1.1	0.7	1.1	0.5	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00005792	PABPN1	isoform 1 of Polyadenylate-binding protein 2	100.0%	10.1	3	3	3	3	5,051,733	5,057,803	4,703,360	5,666,597	924,765	293,197	334,905	133,863	40.9	13.0	15.9	5.3	1.0	1	-1.1	0.7	1.1	0.5	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00414963	PABPN1	isoform 2 of Polyadenylate-binding protein 2	100.0%	10.5	3	3	3	3	5,051,733	5,057,803	4,703,360	5,666,597	924,765	293,197	334,905	133,863	40.9	13.0	15.9	5.3	1.0	1	-1.1	0.7	1.1	0.5	-1.1	0.4	1.1	0.1	1.2	0.03
				FSGHPKGFAYIEFSDKESVR	3	93.4%	1																									
				GFAYIEFSDK	2	88.7%	1																									
				TSLALDESLFR	2	100.0%	1																									
IPI00005826	HERC2	E3 ubiquitin-protein ligase HERC2	97.3%	0.6	1	1	1	1	2,082,698	2,422,867	2,430,930	2,244,300	656,805	656,228	385,173	439,912	70.5	60.6	35.4	43.8	1.2	0.7	1.2	0.7	1.1	0.8	1.0	1	-1.1	0.8	-1.1	0.8
				LYPGESIGQTSDISSPELMGVGSLLKK	2	97.3%	1																									
IPI00005969	CAPZA1	F-actin-capping protein subunit alpha-1	100.0%	35.3	7	7	9	1	22,125,686	22,563,458	22,631,286	24,631,818	1,419,474	488,668	1,652,717	588,599	14.4	4.8	16.3	5.3	1.0	0.8	1.0	0.8	1.1	0.1	1.0	1	1.1	0.03	1.1	0.3
				DVQDSLTVSNEAQTAK	2	100.0%	1																									
				EASDPQPEEADGGLK	2	99.9%	1																									
				FITHAPPGEFNEVFNDVR	3	100.0%	1																									
				FTITPPTAQVVGVLK	2	100.0%	2																									
				IEGYEDQVLITEHGDLGNSR	3	99.3%	1																									
				LLLNNDNLLR	2	100.0%	2																									
				RQLPVTR	2	99.9%	1																									
IPI00005978	SRSF2	Serine/arginine-rich splicing factor 2	100.0%	11.3	2	2	4	5	3,926,554	3,903,570	4,180,660	4,469,142	268,328	79,860	227,942	205,555	15.3	4.6	12.2	10.3	-1.0	0.9	1.1	0.5	1.1	0.1	1.1	0.3	1.1	0.05	1.1	0.4
IPI00385786	SRSF2	cDNA FLJ35170 fis, clone PLACE6012942, highly similar to SPLICING FACTOR, AI	100.0%	12.4	2	2	4	5	3,926,554	3,903,570	4,180,660	4,469,142	268,328	79,860	227,942	205,555	15.3	4.6	12.2	10.3	-1.0	0.9	1.1	0.5	1.1	0.1	1.1	0.3	1.1	0.05	1.1	0.4
IPI00796848	SRSF2	cDNA FLJ52570, highly similar to Splicing factor, arginine/serine-rich 2	100.0%	12.0	2	2	4	5	3,926,554	3,903,570	4,180,660	4,469,142	268,328	79,860	227,942	205,555	15.3	4.6	12.2	10.3	-1.0	0.9	1.1	0.5	1.1	0.1	1.1	0.3	1.1	0.05	1.1	0.4
IPI01009595	SRSF2	25 kDa protein	100.0%	11.3	2	2	4	5	3,926,554	3,903,570	4,180,660	4,469,142	268,328	79,860	227,942	205,555	15.3	4.6	12.2	10.3	-1.0	0.9	1.1	0.5	1.1	0.1	1.1	0.3	1.1	0.05	1.1	0.4
IPI01011463	SRSF2	cDNA FLJ40890 fis, clone UTERU2001024, highly similar to SPLICING FACTOR, A	100.0%	12.0	2	2	4	5	3,926,554	3,903,570	4,180,660	4,469,142	268,328	79,860	227,942	205,555	15.3	4.6	12.2	10.3	-1.0	0.9	1.1	0.5	1.1	0.1	1.1	0.3	1.1	0.05	1.1	0.4
				DAEDAMDAMDGAVLDGR	2	100.0%	2																									
				VGDVYIPR	2	99.9%	2																									

IPI00006025	SART3	isoform 1 of Squamous cell carcinoma antigen recognized by T-cells 3	99.4%	1.5	1	1	1	4	762,808	708,490	684,855	869,643	59,663	72,043	43,971	40,087	17.5	22.7	14.4	10.3	-1.1	0.6	-1.1	0.3	1.1	0.2	-1.0	0.8	1.2	0.09	1.3	0.01
IPI00719256	SART3	SART3 protein	99.4%	1.5	1	1	1	4	762,808	708,490	684,855	869,643	59,663	72,043	43,971	40,087	17.5	22.7	14.4	10.3	-1.1	0.6	-1.1	0.3	1.1	0.2	-1.0	0.8	1.2	0.09	1.3	0.01
IPI00790281	SART3	cDNA FLJ51777, highly similar to Squamous cell carcinoma antigen recognized byT	99.4%	2.0	1	1	1	4	762,808	708,490	684,855	869,643	59,663	72,043	43,971	40,087	17.5	22.7	14.4	10.3	-1.1	0.6	-1.1	0.3	1.1	0.2	-1.0	0.8	1.2	0.09	1.3	0.01
IPI01012420	SART3	60 kDa protein	99.4%	2.7	1	1	1	4	762,808	708,490	684,855	869,643	59,663	72,043	43,971	40,087	17.5	22.7	14.4	10.3	-1.1	0.6	-1.1	0.3	1.1	0.2	-1.0	0.8	1.2	0.09	1.3	0.01
				TEGSLEDWDIAVQK	2	99.4%	1																									
IPI00006034	CRIP2	Cysteine-rich protein 2	100.0%	23.1	2	2	3	1	3,301,609	3,805,506	3,604,196	4,320,110	337,700	292,953	420,136	200,752	22.9	17.2	26.1	10.4	1.2	0.3	1.1	0.6	1.3	0.03	-1.1	0.7	1.1	0.2	1.2	0.2
				ASSVTTFTGEPNTCPR	2	100.0%	1																									
				GVNIGGAGSYIYEKPLAEGPQVTGPIEVPAAR	3	100.0%	2																									
IPI00006052	PFDN2	Prefoldin subunit 2	100.0%	16.9	2	2	2	1	31,106,480	28,315,550	30,092,160	31,985,020	2,057,189	1,126,389	1,102,922	1,614,759	14.8	8.9	8.2	11.3	-1.1	0.3	-1.0	0.7	1.0	0.7	1.1	0.3	1.1	0.1	1.1	0.4
				GAVSAEQVIAGFNR	2	100.0%	1																									
				IIETLTQQLQAK	2	85.7%	1																									
IPI00006079	BCLAF1	isoform 1 of Bcl-2-associated transcription factor 1	94.6%	1.4	1	1	1	9	602,734	656,531	539,433	733,972	86,145	56,084	67,400	65,719	32.0	19.1	27.9	20.0	1.1	0.6	-1.1	0.6	1.2	0.3	-1.2	0.2	1.1	0.4	1.4	0.07
IPI00413671	BCLAF1	isoform 2 of Bcl-2-associated transcription factor 1	94.6%	1.4	1	1	1	9	602,734	656,531	539,433	733,972	86,145	56,084	67,400	65,719	32.0	19.1	27.9	20.0	1.1	0.6	-1.1	0.6	1.2	0.3	-1.2	0.2	1.1	0.4	1.4	0.07
IPI00413672	BCLAF1	isoform 3 of Bcl-2-associated transcription factor 1	94.6%	1.5	1	1	1	9	602,734	656,531	539,433	733,972	86,145	56,084	67,400	65,719	32.0	19.1	27.9	20.0	1.1	0.6	-1.1	0.6	1.2	0.3	-1.2	0.2	1.1	0.4	1.4	0.07
IPI00976642	BCLAF1	Uncharacterized protein	94.6%	1.7	1	1	1	9	602,734	656,531	539,433	733,972	86,145	56,084	67,400	65,719	32.0	19.1	27.9	20.0	1.1	0.6	-1.1	0.6	1.2	0.3	-1.2	0.2	1.1	0.4	1.4	0.07
IPI00977358	BCLAF1	Uncharacterized protein	94.6%	1.5	1	1	1	9	602,734	656,531	539,433	733,972	86,145	56,084	67,400	65,719	32.0	19.1	27.9	20.0	1.1	0.6	-1.1	0.6	1.2	0.3	-1.2	0.2	1.1	0.4	1.4	0.07
IPI00978390	BCLAF1	Uncharacterized protein	94.6%	1.7	1	1	1	9	602,734	656,531	539,433	733,972	86,145	56,084	67,400	65,719	32.0	19.1	27.9	20.0	1.1	0.6	-1.1	0.6	1.2	0.3	-1.2	0.2	1.1	0.4	1.4	0.07
IPI00980443	BCLAF1	Uncharacterized protein	94.6%	1.8	1	1	1	9	602,734	656,531	539,433	733,972	86,145	56,084	67,400	65,719	32.0	19.1	27.9	20.0	1.1	0.6	-1.1	0.6	1.2	0.3	-1.2	0.2	1.1	0.4	1.4	0.07
IPI00886854	LOC731605	bcl-2-associated transcription factor 1-like isoform 2, partial	94.6%	1.5	1	1	1	9	602,734	656,531	539,433	733,972	86,145	56,084	67,400	65,719	32.0	19.1	27.9	20.0	1.1	0.6	-1.1	0.6	1.2	0.3	-1.2	0.2	1.1	0.4	1.4	0.07
IPI00886987	LOC731605	bcl-2-associated transcription factor 1-like, partial	94.6%	1.5	1	1	1	9	602,734	656,531	539,433	733,972	86,145	56,084	67,400	65,719	32.0	19.1	27.9	20.0	1.1	0.6	-1.1	0.6	1.2	0.3	-1.2	0.2	1.1	0.4	1.4	0.07
				ETGYVVERPSTTK	2	94.6%	1																									
IPI00006084	CNNM2	isoform 1 of Metal transporter CNNM2	93.8%	3.0	1	1	1	4	749,720	657,723	822,085	724,275	27,724	18,931	63,098	29,759	8.3	6.4	17.2	9.2	-1.1	0.03	1.1	0.3	-1.0	0.5	1.2	0.06	1.1	0.1	-1.1	0.2
IPI00396142	CNNM2	isoform 2 of Metal transporter CNNM2	93.8%	3.0	1	1	1	4	749,720	657,723	822,085	724,275	27,724	18,931	63,098	29,759	8.3	6.4	17.2	9.2	-1.1	0.03	1.1	0.3	-1.0	0.5	1.2	0.06	1.1	0.1	-1.1	0.2
IPI00401870	CNNM2	isoform 3 of Metal transporter CNNM2	93.8%	4.5	1	1	1	4	749,720	657,723	822,085	724,275	27,724	18,931	63,098	29,759	8.3	6.4	17.2	9.2	-1.1	0.03	1.1	0.3	-1.0	0.5	1.2	0.06	1.1	0.1	-1.1	0.2
IPI01012840	CNNM2	metal transporter CNNM2 isoform 3	93.8%	4.7	1	1	1	4	749,720	657,723	822,085	724,275	27,724	18,931	63,098	29,759	8.3	6.4	17.2	9.2	-1.1	0.03	1.1	0.3	-1.0	0.5	1.2	0.06	1.1	0.1	-1.1	0.2
				DCFMITGEAILDFNTMSEIMESGYTR	3	93.8%	1																									
IPI00006092	PMM2	Phosphomannomutase 2	100.0%	8.9	2	2	2	1	7,390,237	7,455,753	7,456,163	7,949,633	597,840	495,987	462,398	298,629	18.1	14.9	13.9	8.4	1.0	0.9	1.0	0.9	1.1	0.4	1.0	1	1.1	0.4	1.1	0.4
				IGVVGGSDFEK	2	99.8%	1																									
				NGMLNVSPIGR	2	96.5%	1																									
IPI00006103	CD2BP2	CD2 antigen cytoplasmic tail-binding protein 2	99.9%	3.2	1	1	1	1	3,608,940	3,455,390	3,550,050	3,656,140	195,279	261,149	403,600	140,557	12.1	16.9	25.4	8.6	-1.0	0.7	-1.0	0.9	1.0	0.8	1.0	0.8	1.1	0.5	1.0	0.8
				DSWLDNIDWVK	2	99.9%	1																									
IPI00006167	PPM1G	Protein phosphatase 1G	100.0%	9.7	4	4	5	1	28,446,837	29,037,693	27,591,533	33,260,607	2,181,760	1,662,156	1,935,244	1,996,458	17.2	12.8	15.7	13.4	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.6	1.1	0.1	1.2	0.08
				ALEDAFLAIDAK	2	99.5%	1																									
				LPLPYGFSAMQGWR	2	99.5%	2																									
				NLPPEEQMISALPDIK	2	100.0%	1																									
				QLIVANAGDSR	2	99.7%	1																									
IPI00006176	HGS	isoform 1 of Hepatocyte growth factor-regulated tyrosine kinase substrate	94.2%	1.3	1	1	1	4	641,265	599,710	534,820	737,833	46,434	35,938	51,892	38,948	16.2	13.4	21.7	11.8	-1.1	0.5	-1.2	0.2	1.2	0.1	-1.1	0.3	1.2	0.03	1.4	0.01
IPI00916785	HGS	isoform 2 of Hepatocyte growth factor-regulated tyrosine kinase substrate	94.2%	1.5	1	1	1	4	641,265	599,710	534,820	737,833	46,434	35,938	51,892	38,948	16.2	13.4	21.7	11.8	-1.1	0.5	-1.2	0.2	1.2	0.1	-1.1	0.3	1.2	0.03	1.4	0.01
IPI00939822	HGS	Uncharacterized protein	94.2%	1.5	1	1	1	4	641,265	599,710	534,820	737,833	46,434	35,938	51,892	38,948	16.2	13.4	21.7	11.8	-1.1	0.5	-1.2	0.2	1.2	0.1	-1.1	0.3	1.2	0.03	1.4	0.01
IPI01013257	HGS	cDNA FLJ61530, highly similar to Hepatocyte growth factor-regulated tyrosine kinas	94.2%	1.5	1	1	1	4	641,265	599,710	534,820	737,833	46,434	35,938	51,892	38,948	16.2	13.4	21.7	11.8	-1.1	0.5	-1.2	0.2	1.2	0.1	-1.1	0.3	1.2	0.03	1.4	0.01
				VEGHVFPEFK	3	94.2%	1																									
IPI00006181	EIF3D	Eukaryotic translation initiation factor 3 subunit D	99.5%	2.9	1	1	1	4	1,707,593	1,978,148	1,701,450	1,946,530	234,595	288,990	227,071	251,635	30.7	32.7	29.8	28.9	1.2	0.5	-1.0	1	1.1	0.5	-1.2	0.5	-1.0	0.9	1.1	0.5
IPI00789582	EIF3D	cDNA FLJ51552, highly similar to Eukaryotic translation initiation factor 3 subunit 7	99.5%	3.2	1	1	1	4	1,707,593	1,978,148	1,701,450	1,946,530	234,595	288,990	227,071	251,635	30.7	32.7	29.8	28.9	1.2	0.5	-1.0	1	1.1	0.5	-1.2	0.5	-1.0	0.9	1.1	0.5
IPI00791086	EIF3D	cDNA FLJ53917, highly similar to Eukaryotic translation initiation factor 3 subunit 7	99.5%	3.0	1	1	1	4	1,707,593	1,978,148	1,701,450	1,946,530	234,595	288,990	227,071	251,635	30.7	32.7	29.8	28.9	1.2	0.5	-1.0	1	1.1	0.5	-1.2	0.5	-1.0	0.9	1.1	0.5
IPI00903191	EIF3D	Eukaryotic translation initiation factor 3, subunit D	99.5%	6.0	1	1	1	4	1,707,593	1,978,148	1,701,450	1,946,530	234,595	288,990	227,071	251,635	30.7	32.7	29.8	28.9	1.2	0.5	-1.0	1	1.1	0.5	-1.2	0.5	-1.0	0.9	1.1	0.5
				SDWEVKEEMDFPQLMK	3	99.5%	1																									
IPI00006196	NUMA1	isoform 2 of Nuclear mitotic apparatus protein 1	100.0%	13.0	17	17	20	1	30,277,592	31,857,865	31,579,992	35,475,457	1,993,016	1,212,695	2,285,812	1,145,212	14.7	8.5	16.2	7.2	1.1	0.5	1.0	0.7	1.2	0.05	-1.0	0.9	1.1	0.06	1.1	0.2
				AQELGHSQSALASAQR	3	99.9%	1																									
				DAQIAMMQQR	2	98.9%	1																									
				DSALETLQGQLEEK	2	100.0%	1																									
				HQVEQLSSSLK	2	98.5%	1																									
				INQLSEENGDLSFK	2	100.0%	2																									
				LADDLSTLQEK	2	100.0%	1																									
				LDFVCSFLQK	2	88.6%	1																									
				LEILQQQLQVANEAR	2	100.0%	2																									
				LGHELQQAGLK	2	82.8%	1																									
				LQAQLNELQAQLSQK	2	100.0%	2																									
				LTAQVASLTSELTTLNATIQQQDQELAGLK	3	99.9%	1																									
				NSLISSLEEEVSILNR	2	100.0%	1																									
				QEATRQDHAQQLATAAEEREASLR	3	94.9%	1																									
				SLEAQVAHADQQLR	2	94.6%	1																									
				SQAPLESSLDSLGDVFLDSGR	2	100.0%	1																									
				VASENLRQELTSQAERAEELGQELK	3	90.1%	1																									
				VEFATLQEALAHALTEK	3	100.0%	1																									
IPI00006207	LRRFIP1	isoform 2 of Leucine-rich repeat flightless-interacting protein 1	100.0%	6.8	4	4	5	3	1,964,859	2,081,191	2,402,051	2,350,525	71,370	140,993	111,181	147,570	8.1	15.2	10.4	14.0	1.1	0.5	1.2	0.01	1.2	0.05	1.2	0.1	1.1	0.2	-1.0	0.8
IPI00382733	LRRFIP1	isoform 3 of Leucine-rich repeat flightless-interacting protein 1	100.0%	7.1	4	4	5	3	1,964,859	2,081,191	2,402,051	2,350,525	71,370	140,993	111,181	147,570	8.1	15.2	10.4	14.0	1.1	0.5	1.2	0.01	1.2	0.05	1.2	0.1	1.1	0.2	-1.0	0.8
IPI00785113	LRRFIP1	isoform 1 of Leucine-rich repeat flightless-interacting protein 1	100.0%	6.6	4	4	5	3	1,964,859	2,081,191	2,402,051	2,350,525	71,370	140,993	111,181	147,570	8.1	15.2	10.4	14.0	1.1	0.5	1.2	0.01	1.2	0.05	1.2	0.1	1.1	0.2	-1.0	0.8
				CEMSEHPSQTVR	2	97.5%	1																									
				DMLLELEEQLAESR	2	90.2%	1																									
				IDGATQSSPAEPK	2	99.9%	2																									
				SAVEAQNEVTENPK	2	100.0%	1																									
IPI00006211	VAPB	isoform 1 of Vesicle-associated membrane protein-associated protein B/C	100.0%	13.2	2	2	3	1	2,316,372	2,620,341	2,422,747	2,790,004	137,529	133,075	177,680	152,543	13.3	11.4	16.4	12.2	1.1	0.2	1.0	0.6	1.2	0.05	-1.1	0.4	1.1	0.4	1.2	0.2
				FMVQSMFAPTDTSDMEAVWK	2	100.0%	2																									
				GPFTDVVTTNLK	2	99.9%	1																									
IPI00006252	AIMP1	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	100.0%	20.8	4	4	4	2	13,080,996	13,900,343	13,964,611	15,420,620	1,121,655	637,980	791,861	511,386	19.2	10.3	12.7	7.4	1.1	0.5	1.1	0.5	1.2	0.09	1.0	1	1.1	0.1	1.1	0.2
IPI00793201	AIMP1	aminoacyl tRNA synthase complex-interacting multifunctional protein 1 isoform b pre	100.0%	19.4	4	4	4	2	13,080,996	13,900,343	13,964,611	15,420,620	1,121,655	637,980	791,861	511,386	19.2	10.3	12.7	7.4	1.1	0.5	1.1	0.5	1.2	0.09	1.0	1	1.1	0.1	1.1	0.2
				EIEELKQELIQAEIQNGVK	3	100.0%	1																									
				IGCIITAR	2	96.7%	1																									
				IWEQIQPDLHTNDECVATYK	3	97.9%	1																									
				KQQSIAGSADSKPIDVSR	3	96.8%	1																									
IPI00006298	PPIG	isoform 1 of Peptidyl-prolyl cis-trans isomerase G	94.4%	2.0	1	1	1	4	230,121	212,134	209,099	235,601	16,860	23,036	34,149	24,122	16.4	24.3	36.5	22.9	-1.1	0.5	-1.1	0.6	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.5
IPI00409624	PPIG	isoform 2 of Peptidyl-prolyl cis-trans isomerase G	94.4%	4.2	1	1	1	4	230,121	212,134	209,099	235,601	16,860	23,036	34,149	24,122	16.4	24.3	36.5	22.9	-1.1	0.5	-1.1	0.6	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.5
IPI00917609	PPIG	Uncharacterized protein	94.4%	3.1	1	1	1	4	230,121	212,134	209,099	235,601	16,860	23,036	34,149	24,122	16.4	24.3	36.5	22.9	-1.1	0.5	-1.1	0.6	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.5
IPI01014703	PPIG	PPIG protein (Fragment)	94.4%	3.4	1	1	1	4	230,121	212,134	209,099	235,601	16,860	23,036	34,149	24,122	16.4	24.3	36.5	22.9	-1.1	0.5	-1.1	0.6	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.5
				DFMVQGGDFSEGNGR	2	94.4%	1																									
IPI00006377	POMP	Proteasome maturation protein	99.3%	10.6	1	1	2	1	6,246,290	6,010,570	6,661,000	6,502,050	719,224	650,296	388,309	644,803	25.8	24.2	13.0	22.2	-1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.4	1.1	0.6	-1.0	0.8
				LPFLSSSNLSLDVLR	2	99.3%	2																									
IPI00006379	NOP58	Nucleolar protein 58	100.0%	8.9	3	3	3	1	6,031,990	5,735,459	7,631,802	6,908,018	526,150	501,176	506,251	430,881	19.5	19.5	14.8	14.0	-1.1	0.7	1.3	0.06	1.1	0.2	1.3	0.03	1.2	0.1	-1.1	0.3
				FQDTAEALAAFTALMEGK	2	100.0%	1																									
				MMAIAPNVTVMVGELVGAR	2	100.0%	1																									
				TQLYEYLQNR	2	99.3%	1																									
IPI00977991	LOC100507699	vesicle-fusing ATPase-like	98.0%	2.1	1	1	1	4	1,298,655	1,673,813	1,312,195	1,987,000	263,649	141,085	195,517	70,424	45.4	18.9	33.3	7.9	1.3	0.2	1.0	1	1.5	0.06	-1.3	0.2	1.2	0.08	1.5	0.02
IPI00006451	NSF	Vesicle-fusing ATPase	98.0%	1.6	1	1	1	4	1,298,655	1,673,813	1,312,195	1,987,000	263,649	141,085	195,517	70,424	45.4	18.9	33.3	7.9	1.3	0.2	1.0	1	1.5	0.06	-1.3	0.2	1.2	0.08	1.5	0.02
IPI00985110	NSF	cDNA FLJ59316, highly similar to Vesicle-fusing ATPase	98.0%	1.9	1	1	1	4	1,298,655	1,673,813	1,312,195	1,987,000	263,649	141,085	195,517	70,424	45.4	18.9	33.3	7.9	1.3	0.2	1.0	1	1.5	0.06	-1.3	0.2	1.2	0.08	1.5	0.02
IPI01013355	NSF	cDNA FLJ54349, highly similar to Vesicle-fusing ATPase	98.0%	1.7	1	1	1	4	1,298,655	1,673,813	1,312,195	1,987,000	263,649	141,085	195,517	70,424	45.4	18.9	33.3	7.9	1.3	0.2	1.0	1	1.5	0.06	-1.3	0.2	1.2	0.08	1.5	0.02
				NFSGAELEGLVR	2	98.0%	1																									
IPI00006482	ATP1A1	isoform Long of Sodium/potassium-transporting ATPase subunit alpha-1	100.0%	27.0	20	20	26	1	40,770,868	42,958,971	43,954,521	46,853,198	3,401,270	2,212,261	2,799,036	1,533,017	18.7	11.5	14.2	7.3	1.1	0.6	1.1	0.5	1.1	0.1	1.0	0.8	1.1	0.2	1.1	0.4
				ADIGVAMGIAGSDVSK	2	100.0%	2																									
				AVAGDASESALLK	2	100.0%	1																									
				AVFQANQENLPILK	2	100.0%	2																									
				DGPNALTPPPTTPEWIK	2	97.7%	1																									
				DMTSEQLDDILK	2	100.0%	1																									
				EQPLDEELKDAFQNAYLELGGLGER	3	100.0%	1																									
				GIVVYTGDR	2	100.0%	1																									
				GVGRDKYEPAAVSEQGDK	3	99.7%	1																									
				IAGLCNR	2	95.9%	1																									
				IVEIPFNSTNK	2	99.9%	2																									
				LNIPVSQVNPR	2	99.9%	2																									
				LSLDELHR	2	99.6%	1																									
				MSINAEEVVVGDLVEVK	2	100.0%	1																									
				NPNTSEPQHLLVMK	3	99.9%	1																									
				QAADMILLDDNFASIVTGVEEGR	2	100.0%	2																									
				QGAIVAVTGDGVNDSPALK	2	100.0%	1																									
				SPDFTNENPLETR	2	100.0%	2																									
				VIMVTGDHPITAK	2	99.7%	1																									
				YGTDLSR	2	97.7%	1																									
				YHTEIVFAR	3	82.4%	1																									
IPI00006558	SH3GLB1	isoform 1 of Endophilin-B1	97.9%	3.0	1	1	1	2	2,620,680	2,943,640	2,681,105	3,100,335	218,926	251,031	346,755	249,924	18.7	19.1	28.9	18.0	1.1	0.4	1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.7	1.2	0.4
IPI00022824	SH3GLB1	isoform 2 of Endophilin-B1	97.9%	2.9	1	1	1	2	2,620,680	2,943,640	2,681,105	3,100,335	218,926	251,031	346,755	249,924	18.7	19.1	28.9	18.0	1.1	0.4	1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.7	1.2	0.4
				LAADAGTFLSR	2	97.9%	1																									
IPI00006579	COX4I1	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	92.9%	6.5	1	1	1	2	4,516,360	3,970,905	3,715,150	4,570,630	395,577	230,664	255,946	377,827	19.6	13.0	15.4	18.5	-1.1	0.3	-1.2	0.1	1.0	0.9	-1.1	0.5	1.2	0.2	1.2	0.1
IPI00645361	COX4I1	COX4I1 protein	92.9%	13.3	1	1	1	2	4,516,360	3,970,905	3,715,150	4,570,630	395,577	230,664	255,946	377,827	19.6	13.0	15.4	18.5	-1.1	0.3	-1.2	0.1	1.0	0.9	-1.1	0.5	1.2	0.2	1.2	0.1
				DHPLPEVAHVK	3	92.9%	1																									
IPI00006658	PIN4	isoform 2 of Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	100.0%	33.3	3	3	3	2	6,898,430	7,326,215	6,702,205	8,115,265	1,136,089	645,000	916,056	415,371	36.8	19.7	30.6	11.5	1.1	0.8	-1.0	0.9	1.2	0.4	-1.1	0.6	1.1	0.3	1.2	0.2
IPI00941201	PIN4	isoform 1 of Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	100.0%	39.7	3	3	3	2	6,898,430	7,326,215	6,702,205	8,115,265	1,136,089	645,000	916,056	415,371	36.8	19.7	30.6	11.5	1.1	0.8	-1.0	0.9	1.2	0.4	-1.1	0.6	1.1	0.3	1.2	0.2
				FNEVAAQYSEDK	2	96.6%	1																									
				GSMVGPFQEAAFALPVSGMDKPVFTDPPVK	3	100.0%	1																									
				QGGDLGWMTR	2	98.8%	1																									
IPI00006663	ALDH2	Aldehyde dehydrogenase, mitochondrial	100.0%	20.7	8	8	11	1	22,789,920	22,926,640	20,867,730	25,711,930	1,985,491	1,217,899	1,628,464	966,635	19.5	11.9	17.5	8.4	1.0	1	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.03
				ANNSTYGLAAAVFTK	2	99.4%	1																									
				ELGEYGLQAYTEVK	2	100.0%	2																									
				GYFIQPTVFGDVQDGMTIAK	2	100.0%	1																									
				LADLIER	2	91.9%	1																									
				LGPALATGNVVVMK	2	99.9%	2																									
				LLCGGGIAADR	2	95.4%	1																									
				TFVQEDIYDEFVER	2	100.0%	2																									
				VIQVAAGSSNLK	2	96.6%	1																									
IPI00006702	PELP1	cDNA FLJ56414, highly similar to Homo sapiens proline-, glutamic acid-, leucine-rich	98.6%	1.1	1	1	1	4	741,500	731,840	800,453	795,033	47,496	68,060	92,000	80,607	14.3	20.8	25.7	22.7	-1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.6	1.1	0.6	-1.0	1
IPI00178047	PELP1	Uncharacterized protein	98.6%	1.3	1	1	1	4	741,500	731,840	800,453	795,033	47,496	68,060	92,000	80,607	14.3	20.8	25.7	22.7	-1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.6	1.1	0.6	-1.0	1
IPI00787089	PELP1	isoform 2 of Proline-, glutamic acid- and leucine-rich protein 1	98.6%	1.0	1	1	1	4	741,500	731,840	800,453	795,033	47,496	68,060	92,000	80,607	14.3	20.8	25.7	22.7	-1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.6	1.1	0.6	-1.0	1
IPI00953543	PELP1	Uncharacterized protein	98.6%	1.0	1	1	1	4	741,500	731,840	800,453	795,033	47,496	68,060	92,000	80,607	14.3	20.8	25.7	22.7	-1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.6	1.1	0.6	-1.0	1
				LPSLGAGFSQGLK	2	93.3%	1																									
IPI00006713	DNAJC3	DnaJ homolog subfamily C member 3	99.6%	14.5	4	4	4	1	22,234,666	24,351,938	23,443,520	24,583,490	2,535,161	1,694,736	1,391,597	1,287,996	25.5	15.6	13.3	11.7	1.1	0.5	1.1	0.7	1.1	0.4	-1.0	0.7	1.0	0.9	1.0	0.6
				ILEVCVWDAELR	2	99.4%	1																									
				LIESAEELIR	2	92.5%	1																									
				LLAAGQLADALSQFHAAVDGDPDNYIAYYR	3	98.0%	1																									
				SQALNAFGSGDYTAAIAFLDK	2	99.6%	1																									

IPI00006715	RAD21	Double-strand-break repair protein rad21 homolog	96.9%	2.1	1	1	1	1	2,400,030	3,005,130	2,346,110	3,095,100	480,539	436,216	210,538	170,413	44.8	32.5	20.1	12.3	1.3	0.4	-1.0	0.9	1.3	0.2	-1.3	0.2	1.0	0.9	1.3	0.02
				DVIDEPIIEEPSR	2	96.9%	1																									
IPI00006723	SNRNP40	cDNA FLJ56825, highly similar to WD repeat protein 57	92.9%	2.4	1	1	1	3	1,840,827	1,782,230	1,733,053	2,030,293	116,125	192,456	78,009	126,956	14.1	24.2	10.1	14.0	-1.0	0.8	-1.1	0.5	1.1	0.3	-1.0	0.8	1.1	0.3	1.2	0.08
IPI00385642	SNRNP40	WD repeat domain 57 (U5 snRNP specific), isoform CRA_b	92.9%	7.9	1	1	1	3	1,840,827	1,782,230	1,733,053	2,030,293	116,125	192,456	78,009	126,956	14.1	24.2	10.1	14.0	-1.0	0.8	-1.1	0.5	1.1	0.3	-1.0	0.8	1.1	0.3	1.2	0.08
IPI00940685	SNRNP40	U5 small nuclear ribonucleoprotein 40 kDa protein	92.9%	2.8	1	1	1	3	1,840,827	1,782,230	1,733,053	2,030,293	116,125	192,456	78,009	126,956	14.1	24.2	10.1	14.0	-1.0	0.8	-1.1	0.5	1.1	0.3	-1.0	0.8	1.1	0.3	1.2	0.08
				FVYVWDTTSR	2	92.9%	1																									
IPI00006725	DDX23	Probable ATP-dependent RNA helicase DDX23	98.1%	1.3	1	1	1	2	5,395,230	5,588,730	5,130,365	6,297,600	403,457	271,531	388,046	364,483	16.7	10.9	16.9	12.9	1.0	0.7	-1.1	0.6	1.2	0.1	-1.1	0.4	1.1	0.2	1.2	0.06
IPI00903057	DDX23	cDNA FLJ46571 fis, clone THYMU3041428, highly similar to Probable ATP-depende	98.1%	1.4	1	1	1	2	5,395,230	5,588,730	5,130,365	6,297,600	403,457	271,531	388,046	364,483	16.7	10.9	16.9	12.9	1.0	0.7	-1.1	0.6	1.2	0.1	-1.1	0.4	1.1	0.2	1.2	0.06
				DILVATDVAGR	2	98.1%	1																									
IPI00006754	DCAF7	DDB1- and CUL4-associated factor 7	98.9%	3.8	1	1	1	3	2,140,273	2,335,567	2,057,733	2,423,697	231,055	65,564	216,543	156,861	24.1	6.3	23.5	14.5	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.3	1.0	0.6	1.2	0.2
IPI00908632	DCAF7	cDNA FLJ54214, highly similar to WD repeat protein 68	98.9%	9.2	1	1	1	3	2,140,273	2,335,567	2,057,733	2,423,697	231,055	65,564	216,543	156,861	24.1	6.3	23.5	14.5	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.3	1.0	0.6	1.2	0.2
IPI00910594	DCAF7	Uncharacterized protein	98.9%	7.9	1	1	1	3	2,140,273	2,335,567	2,057,733	2,423,697	231,055	65,564	216,543	156,861	24.1	6.3	23.5	14.5	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.3	1.0	0.6	1.2	0.2
				LALGSFVEEYNNK	2	98.9%	1																									
IPI00006854	RASAL2	Ras GTPase-activating protein nGAP	94.4%	0.8	1	1	1	2	3,425,440	3,676,765	4,117,080	4,138,360	253,485	295,073	449,602	245,885	16.6	18.0	24.4	13.3	1.1	0.5	1.2	0.2	1.2	0.08	1.1	0.4	1.1	0.3	1.0	1
IPI00946817	RASAL2	ras GTPase-activating protein nGAP isoform 2	94.4%	0.7	1	1	1	2	3,425,440	3,676,765	4,117,080	4,138,360	253,485	295,073	449,602	245,885	16.6	18.0	24.4	13.3	1.1	0.5	1.2	0.2	1.2	0.08	1.1	0.4	1.1	0.3	1.0	1
				LMSALTQVK	2	81.9%	1																									
IPI00006865	SEC22B	Vesicle-trafficking protein SEC22b	100.0%	16.7	3	3	3	1	22,376,070	23,121,350	21,403,120	24,840,870	1,364,903	888,509	1,716,696	687,083	13.6	8.6	17.9	6.2	1.0	0.7	-1.0	0.7	1.1	0.1	-1.1	0.4	1.1	0.2	1.2	0.1
				DLQQYQSQAK	2	99.3%	1																									
				IMVANIEEVLQR	2	99.5%	1																									
				NLGSINTELQDVQR	2	100.0%	1																									
IPI00006907	C12orf5	Probable fructose-2,6-bisphosphatase TIGAR	99.4%	6.3	1	1	1	1	1,705,390	1,780,970	1,519,832	1,875,470	77,517	225,307	124,252	120,593	10.2	28.3	18.3	14.4	1.0	0.8	-1.1	0.2	1.1	0.3	-1.2	0.3	1.1	0.7	1.2	0.07
				IIQGQGVDEPLSETGFK	2	99.4%	1																									
IPI00006932	LUC7L2	cDNA FLJ55988, highly similar to RNA-binding protein Luc7-like 2	100.0%	11.4	4	4	5	3	1,777,646	1,835,187	1,710,596	1,986,550	123,976	80,151	152,650	89,579	15.6	9.8	20.0	10.1	1.0	0.7	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.2	1.2	0.2
IPI00893216	LUC7L2	cDNA FLJ55994, highly similar to RNA-binding protein Luc7-like 2	100.0%	13.4	4	4	5	3	1,777,646	1,835,187	1,710,596	1,986,550	123,976	80,151	152,650	89,579	15.6	9.8	20.0	10.1	1.0	0.7	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.2	1.2	0.2
IPI01008748	LUC7L2	isoform 2 of Putative RNA-binding protein Luc7-like 2	100.0%	13.3	4	4	5	3	1,777,646	1,835,187	1,710,596	1,986,550	123,976	80,151	152,650	89,579	15.6	9.8	20.0	10.1	1.0	0.7	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.2	1.2	0.2
				LAETQEEISAEVAAK	2	100.0%	1																									
				NSMPASSFQQQK	2	99.9%	1																									
				VEQLGAEGNVEESQK	2	100.0%	2																									
				VHELNEEIGK	2	99.4%	1																									
IPI00006962	LPAR5	cDNA FLJ51160, highly similar to Probable G-protein coupled receptor 92	94.8%	6.1	1	1	1	1	16,952,120	23,435,200	21,027,800	25,163,500	3,685,150	2,793,501	4,055,380	2,671,514	48.6	26.7	43.1	23.7	1.4	0.2	1.2	0.5	1.5	0.1	-1.1	0.6	1.1	0.7	1.2	0.4
				VYTQEGGLGTWTFGWQFQLSNAEEYK	3	94.8%	1																									
IPI00006980	C14orf166	UPF0568 protein C14orf166	100.0%	31.6	6	6	6	2	6,776,530	6,630,226	7,310,611	7,871,547	416,847	329,309	631,768	367,144	13.8	11.1	19.3	10.4	-1.0	0.8	1.1	0.5	1.2	0.08	1.1	0.4	1.2	0.04	1.1	0.5
IPI00792100	C14orf166	CLE	100.0%	31.6	6	6	6	2	6,776,530	6,630,226	7,310,611	7,871,547	416,847	329,309	631,768	367,144	13.8	11.1	19.3	10.4	-1.0	0.8	1.1	0.5	1.2	0.08	1.1	0.4	1.2	0.04	1.1	0.5
				HDDYLVMLK	2	100.0%	1																									
				HILGFDTGDAVLNEAAQILR	3	100.0%	1																									
				IQDRQEAIDWLLGLAVR	3	98.3%	1																									
				LTALDYHNPAGFNCKDETEFR	3	95.6%	1																									
				NFIVWLEDQK	2	99.8%	1																									
				QEAIDWLLGLAVR	2	100.0%	1																									
IPI00007001	MRPL11	isoform 1 of 39S ribosomal protein L11, mitochondrial	95.0%	6.3	1	1	1	2	3,143,900	3,513,225	3,787,625	4,435,610	344,062	353,665	454,489	434,641	24.5	22.5	26.8	21.9	1.1	0.5	1.2	0.3	1.4	0.05	1.1	0.6	1.3	0.1	1.2	0.3
IPI00377233	MRPL11	isoform 2 of 39S ribosomal protein L11, mitochondrial	95.0%	7.2	1	1	1	2	3,143,900	3,513,225	3,787,625	4,435,610	344,062	353,665	454,489	434,641	24.5	22.5	26.8	21.9	1.1	0.5	1.2	0.3	1.4	0.05	1.1	0.6	1.3	0.1	1.2	0.3
				DLSSEELAAFQK	2	95.0%	1																									
IPI00007024	FAM96B	Mitotic spindle-associated MMXD complex subunit MIP18	100.0%	26.4	2	2	2	1	4,191,249	4,213,189	4,292,006	5,369,463	285,126	190,634	304,749	426,401	15.2	10.1	15.9	17.8	1.0	1	1.0	0.8	1.3	0.05	1.0	0.8	1.3	0.04	1.3	0.07
				SGERPVTAGEEDEQVPDSIDAR	3	99.9%	1																									
				VAAALENTHLLEVVNQCLSAR	3	98.2%	1																									
IPI00007052	FIS1	Mitochondrial fission 1 protein	100.0%	15.8	2	2	2	1	5,572,930	5,954,993	5,848,026	6,564,764	326,577	485,822	291,215	414,828	13.1	18.2	11.1	14.1	1.1	0.5	1.0	0.5	1.2	0.1	-1.0	0.9	1.1	0.4	1.1	0.2
				GIVLLEELLPK	2	99.8%	1																									
				GLLQTEPQNNQAK	2	99.9%	1																									
IPI00007058	CORO1B	Coronin-1B	100.0%	13.1	4	4	6	1	8,698,660	8,906,098	9,593,568	10,772,453	609,059	410,938	1,321,619	849,748	15.7	10.3	30.8	17.6	1.0	0.8	1.1	0.6	1.2	0.08	1.1	0.6	1.2	0.08	1.1	0.5
				AGEAGKLEEVMQELR	2	100.0%	2																									
				KSDLFQDDLYPDTAGPEAALEAEEWVSGR	3	100.0%	1																									
				NDQCYEDIR	2	93.7%	1																									
				VGIIAWHPTAR	3	100.0%	2																									
IPI00007068	ACTR3B	isoform 1 of Actin-related protein 3B	100.0%	4.8	2	2	3	2	763,676	875,515	865,898	932,083	60,329	80,683	39,221	69,310	17.7	20.6	10.1	16.6	1.1	0.3	1.1	0.2	1.2	0.1	-1.0	0.9	1.1	0.6	1.1	0.4
IPI00892652	ACTR3B	isoform 2 of Actin-related protein 3B	100.0%	6.1	2	2	3	2	763,676	875,515	865,898	932,083	60,329	80,683	39,221	69,310	17.7	20.6	10.1	16.6	1.1	0.3	1.1	0.2	1.2	0.1	-1.0	0.9	1.1	0.6	1.1	0.4
				DITYFIQQLLR	2	100.0%	2																									
				LSEELSGGR	2	99.2%	1																									
IPI00007074	YARS	Tyrosyl-tRNA synthetase, cytoplasmic	100.0%	24.6	10	10	10	1	66,187,520	71,421,260	68,556,150	71,861,140	5,112,503	3,411,986	4,707,680	2,657,571	17.3	10.7	15.4	8.3	1.1	0.4	1.0	0.7	1.1	0.4	-1.0	0.6	1.0	0.9	1.0	0.6
				GVESQGMLLCASIEGINR	2	99.9%	1																									
				HPDADSLYVEK	2	81.5%	1																									
				HVLFPLK	2	99.5%	1																									
				IDVGEAEPR	2	99.3%	1																									
				ISEECIAQWK	2	100.0%	1																									
				NLQEVLGEEK	2	99.7%	1																									
				NSEPEEVIPSR	2	100.0%	1																									
				QVEPLDPPAGSAPGEHVFVK	3	99.9%	1																									
				TYTAYVDLEKDFAAEVVHPGDLK	3	100.0%	1																									
				VDAQFGGIDQR	2	99.7%	1																									
IPI00007084	SLC25A13	Calcium-binding mitochondrial carrier protein Aralar2	99.1%	3.9	2	2	2	2	9,279,445	10,894,060	9,920,165	13,269,330	1,376,237	628,546	1,147,552	1,133,455	33.2	12.9	25.9	19.1	1.2	0.3	1.1	0.7	1.4	0.06	-1.1	0.5	1.2	0.1	1.3	0.07
IPI00930710	SLC25A13	calcium-binding mitochondrial carrier protein Aralar2 isoform 1	99.1%	3.9	2	2	2	2	9,279,445	10,894,060	9,920,165	13,269,330	1,376,237	628,546	1,147,552	1,133,455	33.2	12.9	25.9	19.1	1.2	0.3	1.1	0.7	1.4	0.06	-1.1	0.5	1.2	0.1	1.3	0.07
				TVELLSGVVDQTK	2	91.8%	1																									
				YLNIFGESQPNPK	2	99.1%	1																									
IPI00007102	GLOD4	Uncharacterized protein C17orf25	100.0%	23.8	8	8	10	4	12,562,436	13,378,477	12,857,832	14,839,643	1,282,792	575,525	1,119,708	500,041	22.8	9.6	19.5	7.5	1.1	0.6	1.0	0.9	1.2	0.2	-1.0	0.7	1.1	0.09	1.2	0.1
IPI00032575	GLOD4	isoform 1 of Glyoxalase domain-containing protein 4	100.0%	38.3	8	8	10	4	12,562,436	13,378,477	12,857,832	14,839,643	1,282,792	575,525	1,119,708	500,041	22.8	9.6	19.5	7.5	1.1	0.6	1.0	0.9	1.2	0.2	-1.0	0.7	1.1	0.09	1.2	0.1
IPI00745272	GLOD4	isoform 2 of Glyoxalase domain-containing protein 4	100.0%	40.3	8	8	10	4	12,562,436	13,378,477	12,857,832	14,839,643	1,282,792	575,525	1,119,708	500,041	22.8	9.6	19.5	7.5	1.1	0.6	1.0	0.9	1.2	0.2	-1.0	0.7	1.1	0.09	1.2	0.1
IPI00922891	GLOD4	cDNA FLJ55095	100.0%	41.5	8	8	10	4	12,562,436	13,378,477	12,857,832	14,839,643	1,282,792	575,525	1,119,708	500,041	22.8	9.6	19.5	7.5	1.1	0.6	1.0	0.9	1.2	0.2	-1.0	0.7	1.1	0.09	1.2	0.1
				ALLGYADNQCK	2	100.0%	2																									
				GGVDHAAAFGR	3	87.5%	1																									
				ILTPLVSLDTPGK	2	100.0%	1																									
				LGNDFMGITLASSQAVSNAR	3	100.0%	1																									
				LLDDAMAADKSDEWFAK	3	99.9%	1																									
				SLNYWCNLLGMK	2	100.0%	1																									
				TMVGFGPEDDHFVAELTYNYGVGDYK	3	100.0%	1																									
				VTLAVSDLQK	2	99.9%	2																									
IPI00007163	LSM7	U6 snRNA-associated Sm-like protein LSm7	95.1%	24.3	1	1	1	2	517,964	542,892	883,931	760,079	60,455	127,570	222,937	90,809	26.1	52.5	56.4	26.7	1.0	0.9	1.7	0.2	1.5	0.06	1.6	0.2	1.4	0.2	-1.2	0.6
IPI00942405	LSM7	R30783_1	95.1%	17.2	1	1	1	2	517,964	542,892	883,931	760,079	60,455	127,570	222,937	90,809	26.1	52.5	56.4	26.7	1.0	0.9	1.7	0.2	1.5	0.06	1.6	0.2	1.4	0.2	-1.2	0.6
				GFDPLLNLVLDGTIEYMRDPDDQYK	3	95.1%	1																									
IPI00007188	SLC25A5	ADP/ATP translocase 2	100.0%	20.8	6	6	8	1	24,484,242	25,439,025	25,214,400	28,433,165	1,741,003	1,444,106	1,457,865	1,625,277	15.9	12.7	12.9	12.8	1.0	0.7	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.2	1.1	0.2
				AAYFGIYDTAK	2	96.3%	1																									
				DFLAGGVAAAISK	2	100.0%	2																									
				EQGVLSFWR	2	99.7%	1																									
				LLLQVQHASK	2	95.3%	1																									
				MMMQSGR	2	98.9%	1																									
				YFPTQALNFAFK	2	100.0%	2																									
IPI00007189	CDC42	isoform 1 of Cell division control protein 42 homolog	100.0%	6.8	1	1	2	2	708,542	693,700	783,574	804,858	43,125	65,612	95,538	73,638	13.6	21.2	27.3	20.5	-1.0	0.9	1.1	0.5	1.1	0.3	1.1	0.5	1.2	0.3	1.0	0.9
IPI00642590	CDC42	Cell division cycle 42	100.0%	9.6	1	1	2	2	708,542	693,700	783,574	804,858	43,125	65,612	95,538	73,638	13.6	21.2	27.3	20.5	-1.0	0.9	1.1	0.5	1.1	0.3	1.1	0.5	1.2	0.3	1.0	0.9
				TPFLLVGTQIDLR	2	100.0%	2																									
IPI00007242	LGALS2	Galectin-2	100.0%	48.5	5	7	7	1	38,354,600	39,216,610	37,135,990	41,857,770	1,937,312	1,141,908	2,052,238	1,382,952	11.3	6.5	12.4	7.4	1.0	0.7	-1.0	0.7	1.1	0.2	-1.1	0.4	1.1	0.2	1.1	0.09
				FSESTIVCNSLDGSNWGQEQR	3	99.9%	1																									
				FTVTFESDKFK	2	99.5%	1																									
				FTVTFESDKFK	3	97.0%	1																									
				GGFNMSSFK	2	96.8%	1																									
				LPDGHELTFPNR	2	100.0%	1																									
				LPDGHELTFPNR	3	100.0%	1																									
				NMDMKPGSTLK	2	93.0%	1																									
IPI00007247	PCCB	Propionyl-CoA carboxylase beta chain, mitochondrial	95.5%	2.2	1	1	1	9	571,200	648,184	729,717	712,469	89,735	47,253	123,511	66,777	35.1	16.3	37.9	21.0	1.1	0.5	1.3	0.3	1.2	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
IPI00921904	PCCB	propionyl-CoA carboxylase beta chain, mitochondrial isoform 2 precursor	95.5%	2.2	1	1	1	9	571,200	648,184	729,717	712,469	89,735	47,253	123,511	66,777	35.1	16.3	37.9	21.0	1.1	0.5	1.3	0.3	1.2	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
IPI00945117	PCCB	Uncharacterized protein	95.5%	2.2	1	1	1	9	571,200	648,184	729,717	712,469	89,735	47,253	123,511	66,777	35.1	16.3	37.9	21.0	1.1	0.5	1.3	0.3	1.2	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
IPI00945130	PCCB	Uncharacterized protein	95.5%	2.5	1	1	1	9	571,200	648,184	729,717	712,469	89,735	47,253	123,511	66,777	35.1	16.3	37.9	21.0	1.1	0.5	1.3	0.3	1.2	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
IPI00945862	PCCB	cDNA FLJ53115, highly similar to Propionyl-CoA carboxylase beta chain, mitochond	95.5%	2.8	1	1	1	9	571,200	648,184	729,717	712,469	89,735	47,253	123,511	66,777	35.1	16.3	37.9	21.0	1.1	0.5	1.3	0.3	1.2	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
IPI00946409	PCCB	Uncharacterized protein	95.5%	2.3	1	1	1	9	571,200	648,184	729,717	712,469	89,735	47,253	123,511	66,777	35.1	16.3	37.9	21.0	1.1	0.5	1.3	0.3	1.2	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
IPI00946553	PCCB	Uncharacterized protein	95.5%	2.3	1	1	1	9	571,200	648,184	729,717	712,469	89,735	47,253	123,511	66,777	35.1	16.3	37.9	21.0	1.1	0.5	1.3	0.3	1.2	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
IPI00946876	PCCB	Uncharacterized protein	95.5%	2.2	1	1	1	9	571,200	648,184	729,717	712,469	89,735	47,253	123,511	66,777	35.1	16.3	37.9	21.0	1.1	0.5	1.3	0.3	1.2	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
IPI00947502	PCCB	Uncharacterized protein	95.5%	2.1	1	1	1	9	571,200	648,184	729,717	712,469	89,735	47,253	123,511	66,777	35.1	16.3	37.9	21.0	1.1	0.5	1.3	0.3	1.2	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
				LLYAFAEATVPK	2	95.5%	1																									
IPI00007262	USP21	isoform 1 of Ubiquitin carboxyl-terminal hydrolase 21	95.5%	1.8	1	1	1	3	2,051,247	1,932,947	1,971,797	2,263,233	183,098	81,640	132,306	98,439	20.0	9.4	15.0	9.7	-1.1	0.6	-1.0	0.7	1.1	0.3	1.0	0.8	1.2	0.03	1.1	0.1
IPI00182036	USP21	Uncharacterized protein	95.5%	1.8	1	1	1	3	2,051,247	1,932,947	1,971,797	2,263,233	183,098	81,640	132,306	98,439	20.0	9.4	15.0	9.7	-1.1	0.6	-1.0	0.7	1.1	0.3	1.0	0.8	1.2	0.03	1.1	0.1
IPI00376946	USP21	isoform 3 of Ubiquitin carboxyl-terminal hydrolase 21	95.5%	1.8	1	1	1	3	2,051,247	1,932,947	1,971,797	2,263,233	183,098	81,640	132,306	98,439	20.0	9.4	15.0	9.7	-1.1	0.6	-1.0	0.7	1.1	0.3	1.0	0.8	1.2	0.03	1.1	0.1
				LSLGDFASDK	2	93.4%	1																									
IPI00007277	LRRFIP2	isoform 1 of Leucine-rich repeat flightless-interacting protein 2	98.3%	3.7	2	2	2	4	1,196,383	1,227,100	1,128,548	1,402,327	129,074	92,157	109,323	28,372	24.1	16.8	21.7	4.5	1.0	0.9	-1.1	0.7	1.2	0.2	-1.1	0.5	1.1	0.1	1.2	0.06
IPI00015103	LRRFIP2	isoform 2 of Leucine-rich repeat flightless-interacting protein 2	98.3%	6.8	2	2	2	4	1,196,383	1,227,100	1,128,548	1,402,327	129,074	92,157	109,323	28,372	24.1	16.8	21.7	4.5	1.0	0.9	-1.1	0.7	1.2	0.2	-1.1	0.5	1.1	0.1	1.2	0.06
IPI00789379	LRRFIP2	isoform 4 of Leucine-rich repeat flightless-interacting protein 2	98.3%	6.4	2	2	2	4	1,196,383	1,227,100	1,128,548	1,402,327	129,074	92,157	109,323	28,372	24.1	16.8	21.7	4.5	1.0	0.9	-1.1	0.7	1.2	0.2	-1.1	0.5	1.1	0.1	1.2	0.06
IPI00910490	LRRFIP2	cDNA FLJ58304, moderately similar to Leucine-rich repeat flightless-interacting prot	98.3%	5.4	2	2	2	4	1,196,383	1,227,100	1,128,548	1,402,327	129,074	92,157	109,323	28,372	24.1	16.8	21.7	4.5	1.0	0.9	-1.1	0.7	1.2	0.2	-1.1	0.5	1.1	0.1	1.2	0.06
				AEQDITTLEQSISR	2	95.1%	1																									
				FSAEDEALSNIAR	2	98.3%	1																									
IPI00007280	ARPC5	isoform 2 of Actin-related protein 2/3 complex subunit 5	100.0%	7.8	1	1	1	1	9,286,450	9,230,750	8,524,650	11,139,800	1,231,399	548,006	757,641	504,147	29.7	13.3	19.9	10.1	-1.0	1	-1.1	0.6	1.2	0.2	-1.1	0.5	1.2	0.03	1.3	0.02
				ALAAGGVGSIVR	2	99.9%	1																									
IPI00007306	CFDP1	isoform 1 of Craniofacial development protein 1	98.4%	3.3	1	1	1	2	2,588,270	2,311,210	2,407,615	2,861,225	190,033	146,760	146,191	194,849	16.4	14.2	13.6	15.2	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.7	1.2	0.05	1.2	0.1
IPI00646794	CFDP1	isoform 2 of Craniofacial development protein 1	98.4%	4.6	1	1	1	2	2,588,270	2,311,210	2,407,615	2,861,225	190,033	146,760	146,191	194,849	16.4	14.2	13.6	15.2	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.7	1.2	0.05	1.2	0.1
				VFDFAGEEVR	2	98.4%	1																									
IPI00007321	LYPLA1	cDNA FLJ60607, highly similar to Acyl-protein thioesterase 1	100.0%	16.4	3	3	4	3	2,661,737	2,543,629	2,685,081	2,978,339	199,126	176,130	193,535	230,831	16.7	15.5	16.1	17.3	-1.0	0.7	1.0	0.9	1.1	0.3	1.1	0.6	1.2	0.2	1.1	0.4
IPI00398727	LYPLA1	isoform 2 of Acyl-protein thioesterase 1	100.0%	20.1	3	3	4	3	2,661,737	2,543,629	2,685,081	2,978,339	199,126	176,130	193,535	230,831	16.7	15.5	16.1	17.3	-1.0	0.7	1.0	0.9	1.1	0.3	1.1	0.6	1.2	0.2	1.1	0.4
IPI00984941	LYPLA1	Uncharacterized protein	100.0%	30.9	3	3	4	3	2,661,737	2,543,629	2,685,081	2,978,339	199,126	176,130	193,535	230,831	16.7	15.5	16.1	17.3	-1.0	0.7	1.0	0.9	1.1	0.3	1.1	0.6	1.2	0.2	1.1	0.4
				LAGVTALSCWLPLR	2	100.0%	2																									
				TLVNPANVTFK	2	99.4%	1																									
				TYEGMMHSSCQQEMMDVK	3	99.9%	1																									
IPI00007334	ACIN1	isoform 1 of Apoptotic chromatin condensation inducer in the nucleus	100.0%	5.4	7	7	8	3	19,939,559	20,374,113	18,430,987	22,034,891	1,840,148	1,135,126	1,359,571	1,152,525	20.6	12.5	16.5	11.7	1.0	0.8	-1.1	0.5	1.1	0.4	-1.1	0.3	1.1	0.3	1.2	0.08
IPI00911038	ACIN1	apoptotic chromatin condensation inducer in the nucleus isoform 3	100.0%	5.6	7	7	8	3	19,939,559	20,374,113	18,430,987	22,034,891	1,840,148	1,135,126	1,359,571	1,152,525	20.6	12.5	16.5	11.7	1.0	0.8	-1.1	0.5	1.1	0.4	-1.1	0.3	1.1	0.3	1.2	0.08
IPI00946415	ACIN1	apoptotic chromatin condensation inducer in the nucleus isoform 2	100.0%	5.5	7	7	8	3	19,939,559	20,374,113	18,430,987	22,034,891	1,840,148	1,135,126	1,359,571	1,152,525	20.6	12.5	16.5	11.7	1.0	0.8	-1.1	0.5	1.1	0.4	-1.1	0.3	1.1	0.3	1.2	0.08
				AAPCIYWLPLTDSQIVQK	2	96.2%	1																									
				GLLVDRPSETK	2	96.8%	1																									
				KVTLGDTLTR	2	88.8%	1																									
				SGVSITIDDPVR	2	98.0%	2																									
				SQEQEVLER	2	81.2%	1																									
				TGTLVEEAFWIDK	2	99.9%	1																									
				VTLGDTLTR	2	87.0%	1																									
IPI00007401	IPO8	Importin-8	100.0%	1.0	1	1	1	3	1,497,658	1,538,455	1,419,380	1,489,190	118,356	52,790	69,455	40,980	17.7	7.7	10.9	6.2	1.0	0.8	-1.1	0.6	-1.0	0.9	-1.1	0.2	-1.0	0.5	1.0	0.4

IPI00793997	IPO8	importin-8 isoform 2	100.0%	1.2	1	1	1	3	1,497,658	1,538,455	1,419,380	1,489,190	118,356	52,790	69,455	40,980	17.7	7.7	10.9	6.2	1.0	0.8	-1.1	0.6	-1.0	0.9	-1.1	0.2	-1.0	0.5	1.0	0.4
IPI01011377	IPO8	59 kDa protein	100.0%	2.0	1	1	1	3	1,497,658	1,538,455	1,419,380	1,489,190	118,356	52,790	69,455	40,980	17.7	7.7	10.9	6.2	1.0	0.8	-1.1	0.6	-1.0	0.9	-1.1	0.2	-1.0	0.5	1.0	0.4
				LLEVIILQCK	2	99.9%	1																									
IPI00007402	IPO7	Importin-7	100.0%	12.2	9	11	11	1	33,129,136	34,319,820	33,675,168	36,624,653	2,743,652	859,979	1,594,882	766,584	18.5	5.6	10.6	4.7	1.0	0.7	1.0	0.9	1.1	0.3	-1.0	0.7	1.1	0.08	1.1	0.1
				AFAVGVQQVLLK	2	100.0%	1																									
				DGALHMIGSLAEILLK	2	81.4%	1																									
				DGALHMIGSLAEILLK	3	100.0%	1																									
				LFERYGSPGNVSK	2	90.2%	1																									
				LLEVIILQCK	2	99.9%	1																									
				QLQDIATLADQR	2	99.5%	1																									
				SPLVAAMQHFLPVLK	2	89.0%	1																									
				SPLVAAMQHFLPVLK	3	98.4%	1																									
				TMGFCYQILTEPNADPR	2	82.1%	1																									
				VEAAIALQVLISNQEK	2	89.3%	1																									
				VLTGVAGEDAECHAAK	2	95.8%	1																									
IPI00007423	ANP32B	isoform 1 of Acidic leucine-rich nuclear phosphoprotein 32 family member B	100.0%	11.6	2	3	4	2	4,054,730	3,218,222	3,994,975	3,997,505	247,632	200,707	292,695	270,717	13.7	14.0	16.4	15.1	-1.3	0.03	-1.0	0.9	-1.0	0.9	1.2	0.06	1.2	0.05	1.0	1
IPI00759824	ANP32B	isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member B	100.0%	14.9	2	3	4	2	4,054,730	3,218,222	3,994,975	3,997,505	247,632	200,707	292,695	270,717	13.7	14.0	16.4	15.1	-1.3	0.03	-1.0	0.9	-1.0	0.9	1.2	0.06	1.2	0.05	1.0	1
				LPNLTHLNLSGNK	2	100.0%	1																									
				SLDLFNCEVTNLNDYR	2	100.0%	2																									
				SLDLFNCEVTNLNDYR	3	100.0%	1																									
IPI00007426	ARL6IP5	PRA1 family protein 3	100.0%	16.0	2	2	2	2	4,351,757	4,271,081	4,178,193	5,158,735	455,540	303,503	320,737	308,337	23.4	15.9	17.2	13.4	-1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.8	1.2	0.07	1.2	0.06
IPI00908696	ARL6IP5	Uncharacterized protein	100.0%	18.1	2	2	2	2	4,351,757	4,271,081	4,178,193	5,158,735	455,540	303,503	320,737	308,337	23.4	15.9	17.2	13.4	-1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.8	1.2	0.07	1.2	0.06
				AWDDFFPGSDR	2	99.9%	1																									
				TPMGIVLDALEQQEEGINR	2	100.0%	1																									
IPI00007427	AGR2	AGR2	100.0%	47.2	9	14	26	2	99,646,896	91,150,880	94,589,700	112,862,392	8,658,123	3,825,908	7,842,096	6,337,779	19.4	9.4	18.5	12.6	-1.1	0.4	-1.1	0.7	1.1	0.3	1.0	0.7	1.2	0.02	1.2	0.1
IPI00942032	AGR2	Anterior gradient protein 2 homolog	100.0%	52.6	9	14	26	2	99,646,896	91,150,880	94,589,700	112,862,392	8,658,123	3,825,908	7,842,096	6,337,779	19.4	9.4	18.5	12.6	-1.1	0.4	-1.1	0.7	1.1	0.3	1.0	0.7	1.2	0.02	1.2	0.1
				GWGDQLIWTQTYEEALYK	2	100.0%	4																									
				GWGDQLIWTQTYEEALYK	3	100.0%	2																									
				HLSPDGQYVPR	2	100.0%	1																									
				IMFVDPSLTVR	1	94.8%	1																									
				IMFVDPSLTVR	2	100.0%	2																									
				LAEQFVLLNLVYETTDK	2	100.0%	2																									
				LAEQFVLLNLVYETTDK	3	100.0%	2																									
				LAEQFVLLNLVYETTDKHLSPDGQYVPR	3	100.0%	2																									
				LPQTLSR	1	99.2%	1																									
				LPQTLSR	2	93.6%	1																									
				LYAYEPADTALLLDNMK	3	100.0%	2																									
				LYAYEPADTALLLDNMKK	2	100.0%	2																									
				LYAYEPADTALLLDNMKK	3	100.0%	2																									
				VFAENKEIQK	2	99.9%	2																									
IPI00007611	ATP5O	ATP synthase subunit O, mitochondrial	100.0%	23.5	4	5	5	1	22,322,048	22,565,445	22,412,415	25,819,129	1,644,360	477,942	1,651,920	939,749	16.5	4.7	16.5	8.1	1.0	0.9	1.0	1	1.2	0.1	-1.0	0.9	1.1	0.01	1.2	0.1
				FSPLTTNLINLLAENGR	2	100.0%	1																									
				FSPLTTNLINLLAENGR	3	99.9%	1																									
				SFLSQGQVLK	2	85.3%	1																									
				TDPSILGGMIVR	2	100.0%	1																									
				VAASVLNPYVK	2	97.7%	1																									
IPI00007673	CHCHD2	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial	100.0%	33.8	3	3	3	1	20,199,179	21,217,316	19,595,078	23,380,539	1,122,253	1,011,253	1,070,515	1,273,483	12.4	10.7	12.2	12.2	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.2	1.2	0.05
				AAPRPAPVAQPPAAAPPSAVGSSAAAPR	3	100.0%	1																									
				LCEGFNEVLK	2	81.2%	1																									
				QFLECAQNQGDIK	2	95.3%	1																									
IPI00007676	HSD17B12	Estradiol 17-beta-dehydrogenase 12	93.9%	4.8	1	1	1	1	1,355,470	1,552,055	1,611,000	1,608,460	137,044	285,602	212,082	166,533	22.6	41.2	29.4	23.2	1.1	0.6	1.2	0.3	1.2	0.3	1.0	0.9	1.0	0.9	-1.0	1
				TFVDFFSQCLHEEYR	2	93.9%	1																									
IPI00007682	ATP6V1A	V-type proton ATPase catalytic subunit A	100.0%	6.8	4	4	5	2	3,994,579	4,456,217	4,512,711	4,507,140	230,714	192,194	386,696	132,734	12.9	9.6	19.2	6.6	1.1	0.2	1.1	0.3	1.1	0.09	1.0	0.9	1.0	0.8	-1.0	1
IPI00946636	ATP6V1A	cDNA FLJ51804, highly similar to Vacuolar ATP synthase catalytic subunit A, ubiqui	100.0%	7.2	4	4	5	2	3,994,579	4,456,217	4,512,711	4,507,140	230,714	192,194	386,696	132,734	12.9	9.6	19.2	6.6	1.1	0.2	1.1	0.3	1.1	0.09	1.0	0.9	1.0	0.8	-1.0	1
				FTMVQVWPVR	2	100.0%	2																									
				IKSDYAQLLEDMQNAFR	3	100.0%	1																									
				SDYAQLLEDMQNAFR	2	100.0%	1																									
				TALVANTSNMPVAAR	2	100.0%	1																									
IPI00007731	BAG5	isoform 1 of BAG family molecular chaperone regulator 5	99.2%	2.7	1	1	1	2	2,513,390	2,426,935	2,548,475	2,549,975	534,169	594,389	221,628	267,536	47.5	54.8	19.5	23.5	-1.0	0.9	1.0	1	1.0	1	1.1	0.9	1.1	0.9	1.0	1
IPI00556027	BAG5	isoform 2 of BAG family molecular chaperone regulator 5	99.2%	2.5	1	1	1	2	2,513,390	2,426,935	2,548,475	2,549,975	534,169	594,389	221,628	267,536	47.5	54.8	19.5	23.5	-1.0	0.9	1.0	1	1.0	1	1.1	0.9	1.1	0.9	1.0	1
				LAQNILSYLDLK	2	99.2%	1																									
IPI00007750	TUBA4A	Tubulin alpha-4A chain	100.0%	50.9	15	19	30	2	78,539,918	80,681,225	78,986,800	94,692,847	9,069,745	3,803,874	7,266,452	2,519,706	25.8	10.5	20.6	6.0	1.0	0.8	1.0	1	1.2	0.2	-1.0	0.8	1.2	0.02	1.2	0.1
IPI00794663	TUBA4A	cDNA FLJ58687, highly similar to Tubulin alpha-4 chain	100.0%	52.7	15	19	30	2	78,539,918	80,681,225	78,986,800	94,692,847	9,069,745	3,803,874	7,266,452	2,519,706	25.8	10.5	20.6	6.0	1.0	0.8	1.0	1	1.2	0.2	-1.0	0.8	1.2	0.02	1.2	0.1
				AFVHWYVGEGMEEGEFSEAREDMAALEK	3	99.9%	1																									
				AVCMLSNTTAIAEAWAR	2	100.0%	1																									
				AVCMLSNTTAIAEAWAR	3	100.0%	1																									
				AVFVDLEPTVIDEIR	2	99.7%	2																									
				AYHEQLSVAEITNACFEPANQMVK	3	98.3%	1																									
				DVNAAIAAIK	2	98.9%	1																									
				FDGALNVDLTEFQTNLVPYPR	2	100.0%	2																									
				FDLMYAK	2	99.9%	2																									
				IHFPLATYAPVISAEK	2	100.0%	3																									
				IHFPLATYAPVISAEK	3	100.0%	1																									
				LISQIVSSITASLR	2	100.0%	2																									
				LISQIVSSITASLR	3	100.0%	2																									
				NLDIERPTYTNLNR	2	99.2%	2																									
				NLDIERPTYTNLNR	3	100.0%	1																									
				QLFHPEQLITGKEDAANNYAR	3	100.0%	2																									
				RNLDIERPTYTNLNR	3	99.6%	1																									
				SIQFVDWCPTGFK	2	100.0%	1																									
				VGINYQPPTVVPGGDLAK	2	100.0%	2																									
				YMACCLLYR	2	100.0%	2																									
IPI00007752	TUBB2C	Tubulin beta-2C chain	100.0%	53.0	19	24	37	1	244,214,660	238,396,470	229,774,414	277,120,699	########	7,616,033	########	########	20.1	7.1	15.9	9.3	-1.0	0.8	-1.1	0.6	1.1	0.2	-1.0	0.6	1.2	0.02	1.2	0.05
				ALTVPELTQQMFDAK	2	100.0%	3																									
				AVLVDLEPGTMDSVR	2	100.0%	2																									
				EVDEQMLNVQNK	2	100.0%	2																									
				FPGQLNADLR	2	100.0%	2																									
				FPGQLNADLRK	2	96.7%	2																									
				FPGQLNADLRK	3	99.3%	1																									
				FWEVISDEHGIDPTGTYHGDSDLQLER	3	100.0%	2																									
				GHYTEGAELVDSVLDVVR	3	100.0%	2																									
				IMNTFSVVPSPK	2	100.0%	2																									
				INVYYNEATGGK	2	100.0%	2																									
				ISEQFTAMFR	2	100.0%	1																									
				LAVNMVPFPR	2	100.0%	2																									
				LHFFMPGFAPLTSR	2	100.0%	1																									
				LHFFMPGFAPLTSR	3	100.0%	1																									
				MSATFIGNSTAIQELFK	2	99.2%	1																									
				MSATFIGNSTAIQELFK	3	90.7%	1																									
				MSMKEVDEQMLNVQNK	2	99.6%	1																									
				MSMKEVDEQMLNVQNK	3	99.9%	1																									
				NMMAACDPR	2	99.7%	1																									
				NSSYFVEWIPNNVK	2	100.0%	1																									
				RISEQFTAMFR	2	97.8%	1																									
				SGPFGQIFRPDNFVFGQSGAGNNWAK	2	100.0%	2																									
				SGPFGQIFRPDNFVFGQSGAGNNWAK	3	100.0%	2																									
				YLTVAAVFR	2	100.0%	1																									
IPI00007755	RAB21	Ras-related protein Rab-21	99.1%	4.4	1	1	1	2	7,136,250	7,102,300	6,450,010	8,232,400	531,561	453,411	464,318	459,190	16.7	14.3	16.1	12.5	-1.0	1	-1.1	0.4	1.2	0.2	-1.1	0.3	1.2	0.1	1.3	0.03
IPI01010993	RAB21	19 kDa protein	99.1%	5.7	1	1	1	2	7,136,250	7,102,300	6,450,010	8,232,400	531,561	453,411	464,318	459,190	16.7	14.3	16.1	12.5	-1.0	1	-1.1	0.4	1.2	0.2	-1.1	0.3	1.2	0.1	1.3	0.03
				MIETAQVDER	2	99.1%	1																									
IPI00007764	HN1	isoform 1 of Hematological and neurological expressed 1 protein	99.5%	11.7	1	1	1	5	715,764	662,366	731,878	851,656	135,547	71,909	65,880	77,850	42.4	24.3	20.1	20.4	-1.1	0.7	1.0	0.9	1.2	0.4	1.1	0.5	1.3	0.1	1.2	0.3
IPI00384857	HN1	isoform 2 of Hematological and neurological expressed 1 protein	99.5%	9.9	1	1	1	5	715,764	662,366	731,878	851,656	135,547	71,909	65,880	77,850	42.4	24.3	20.1	20.4	-1.1	0.7	1.0	0.9	1.2	0.4	1.1	0.5	1.3	0.1	1.2	0.3
IPI00447316	HN1	isoform 3 of Hematological and neurological expressed 1 protein	99.5%	16.7	1	1	1	5	715,764	662,366	731,878	851,656	135,547	71,909	65,880	77,850	42.4	24.3	20.1	20.4	-1.1	0.7	1.0	0.9	1.2	0.4	1.1	0.5	1.3	0.1	1.2	0.3
IPI00917313	HN1	Uncharacterized protein	99.5%	16.8	1	1	1	5	715,764	662,366	731,878	851,656	135,547	71,909	65,880	77,850	42.4	24.3	20.1	20.4	-1.1	0.7	1.0	0.9	1.2	0.4	1.1	0.5	1.3	0.1	1.2	0.3
IPI01016073	HN1	Conserved hypothetical protein	99.5%	16.7	1	1	1	5	715,764	662,366	731,878	851,656	135,547	71,909	65,880	77,850	42.4	24.3	20.1	20.4	-1.1	0.7	1.0	0.9	1.2	0.4	1.1	0.5	1.3	0.1	1.2	0.3
				MASNIFGTPEENQASWAK	2	99.5%	1																									
IPI00007765	HSPA9	Stress-70 protein, mitochondrial	100.0%	30.5	16	17	26	2	36,523,475	37,498,243	34,815,071	41,176,645	3,088,768	1,765,331	2,411,190	1,205,383	18.9	10.5	15.5	6.6	1.0	0.8	-1.0	0.7	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.05
IPI00966238	HSPA9	cDNA FLJ51907, highly similar to Stress-70 protein, mitochondrial	100.0%	31.1	16	17	26	2	36,523,475	37,498,243	34,815,071	41,176,645	3,088,768	1,765,331	2,411,190	1,205,383	18.9	10.5	15.5	6.6	1.0	0.8	-1.0	0.7	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.05
				AQFEGIVTDLIR	2	100.0%	2																									
				ASNGDAWVEAHGK	2	99.6%	1																									
				DAGQISGLNVLR	2	100.0%	2																									
				ERVEAVNMAEGIIHDTETK	3	99.2%	1																									
				ETAENYLGHTAK	2	95.0%	1																									
				LFEMAYK	2	99.7%	1																									
				LYSPSQIGAFVLMK	2	99.9%	2																									
				MKETAENYLGHTAK	3	98.1%	1																									
				NAVITVPAYFNDSQR	2	99.9%	1																									
				QAASSLQQASLK	2	99.6%	1																									
				QAVTNPNNTFYATK	2	100.0%	2																									
				SDIGEVILVGGMTR	2	100.0%	2																									
				SQVFSTAADGQTQVEIK	2	100.0%	1																									
				STNGDTFLGGEDFDQALLR	2	100.0%	3																									
				STNGDTFLGGEDFDQALLR	3	100.0%	1																									
				TTPSVVAFTADGER	2	100.0%	2																									
				VQQTVQDLFGR	2	100.0%	2																									
IPI00737213	-	15 kDa protein	99.9%	14.8	2	2	2	2	3,649,720	4,059,922	3,680,657	4,087,647	339,550	148,622	301,472	200,402	20.8	8.2	18.3	11.0	1.1	0.3	1.0	0.9	1.1	0.3	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00007797	FABP5	Fatty acid-binding protein, epidermal	99.9%	14.8	2	2	2	2	3,649,720	4,059,922	3,680,657	4,087,647	339,550	148,622	301,472	200,402	20.8	8.2	18.3	11.0	1.1	0.3	1.0	0.9	1.1	0.3	-1.1	0.3	1.0	0.9	1.1	0.3
				ELGVGIALR	2	93.3%	1																									
				TTQFSCTLGEK	2	99.6%	1																									
IPI00007812	ATP6V1B2	V-type proton ATPase subunit B, brain isoform	100.0%	16.1	5	6	6	1	3,093,122	3,409,495	3,503,639	3,653,195	286,984	171,571	287,352	222,559	20.8	11.3	18.3	13.6	1.1	0.4	1.1	0.3	1.2	0.2	1.0	0.8	1.1	0.4	1.0	0.7
				AVVGEEALTSDDLLYLEFLQK	2	98.6%	1																									
				AVVQVFEGTSGIDAK	2	99.4%	1																									
				IYPEEMIQTGISAIDGMNSIAR	2	98.1%	1																									
				IYPEEMIQTGISAIDGMNSIAR	3	99.9%	1																									
				TPVSEDMLGR	2	98.5%	1																									
				TVFETLDIGWQLLR	2	99.8%	1																									
IPI00007836	TRPC5	Short transient receptor potential channel 5	99.1%	2.3	1	1	1	1	2,070,810	2,105,780	2,318,380	2,639,540	201,114	213,343	242,313	58,166	21.7	22.7	23.4	4.9	1.0	0.9	1.1	0.5	1.3	0.05	1.1	0.5	1.3	0.07	1.1	0.3

				AEYEELSQQCKLFAKDLLDQAR	3	99.1%	1																									
IPI00007847	UBE2V1	isoform 4 of Ubiquitin-conjugating enzyme E2 variant 1	100.0%	24.3	2	2	3	2	3,214,022	3,127,163	3,115,507	3,656,212	225,528	174,046	152,120	100,792	15.7	12.5	10.9	6.2	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	1	1.2	0.03	1.2	0.02
IPI00872898	UBE2V1	Uncharacterized protein	100.0%	24.3	2	2	3	2	3,214,022	3,127,163	3,115,507	3,656,212	225,528	174,046	152,120	100,792	15.7	12.5	10.9	6.2	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	1	1.2	0.03	1.2	0.02
				INMNGVNSSNGVVDPR	2	100.0%	2																									
				YPEAPPFVR	2	98.2%	1																									
IPI00007856	MYH2	Myosin-2	99.0%	2.7	3	3	3	1	7,487,280	7,821,133	8,397,683	8,339,605	550,667	248,132	610,761	299,086	16.5	7.1	16.3	8.0	1.0	0.6	1.1	0.3	1.1	0.2	1.1	0.4	1.1	0.2	-1.0	0.9
				EEITSGKIQGTLEDQIISANPLLEAFGNAK	3	92.7%	1																									
				EMATMK	1	88.6%	1																									
				VQLLHTQNTSLINTKKK	3	96.4%	1																									
IPI00007879	SRF	Serum response factor	91.8%	7.5	1	1	1	2	312,887	387,821	393,242	404,842	67,528	28,138	58,582	51,925	48.3	16.2	33.3	28.7	1.2	0.3	1.3	0.4	1.3	0.3	1.0	0.9	1.0	0.8	1.0	0.9
IPI00556557	SRF	Serum response factor (C-fos serum response element-binding transcription factor)	91.8%	12.9	1	1	1	2	312,887	387,821	393,242	404,842	67,528	28,138	58,582	51,925	48.3	16.2	33.3	28.7	1.2	0.3	1.3	0.4	1.3	0.3	1.0	0.9	1.0	0.8	1.0	0.9
				SLSEMEIGMVVGGPEASAAATGGYGPVSGAVSGAKPG	3	91.8%	1																									
IPI00007926	C6orf108	isoform 1 of Deoxyribonucleoside 5'-monophosphate N-glycosidase	100.0%	9.8	1	1	2	1	1,751,695	1,466,245	1,920,455	1,916,260	186,606	92,577	242,366	172,898	23.8	14.1	28.2	20.2	-1.2	0.2	1.1	0.6	1.1	0.5	1.3	0.1	1.3	0.05	-1.0	1
				FQVWDYEEGEVEALLDR	2	100.0%	2																									
IPI00007928	PRPF8	Pre-mRNA-processing-splicing factor 8	100.0%	1.2	2	2	2	1	2,369,272	2,206,668	2,692,300	2,398,358	227,949	198,599	347,890	166,453	21.5	20.1	28.9	15.5	-1.1	0.6	1.1	0.5	1.0	0.9	1.2	0.3	1.1	0.5	-1.1	0.5
				EAVVNTQELLDLLVK	2	97.7%	1																									
				GTYFPTWEGLFWEK	2	99.6%	1																									
IPI00007935	PDLIM5	isoform 1 of PDZ and LIM domain protein 5	100.0%	3.5	2	2	2	4	4,846,642	4,458,863	4,764,475	4,156,000	118,826	148,287	180,703	111,635	5.5	7.4	8.5	6.0	-1.1	0.08	-1.0	0.7	-1.2	0.003	1.1	0.2	-1.1	0.1	-1.1	0.02
IPI00553102	PDLIM5	isoform 4 of PDZ and LIM domain protein 5	100.0%	4.3	2	2	2	4	4,846,642	4,458,863	4,764,475	4,156,000	118,826	148,287	180,703	111,635	5.5	7.4	8.5	6.0	-1.1	0.08	-1.0	0.7	-1.2	0.003	1.1	0.2	-1.1	0.1	-1.1	0.02
IPI00966347	PDLIM5	Uncharacterized protein	100.0%	4.4	2	2	2	4	4,846,642	4,458,863	4,764,475	4,156,000	118,826	148,287	180,703	111,635	5.5	7.4	8.5	6.0	-1.1	0.08	-1.0	0.7	-1.2	0.003	1.1	0.2	-1.1	0.1	-1.1	0.02
IPI00966603	PDLIM5	Uncharacterized protein	100.0%	3.4	2	2	2	4	4,846,642	4,458,863	4,764,475	4,156,000	118,826	148,287	180,703	111,635	5.5	7.4	8.5	6.0	-1.1	0.08	-1.0	0.7	-1.2	0.003	1.1	0.2	-1.1	0.1	-1.1	0.02
				DFNMPLTISSLK	2	99.9%	1																									
				GPFLVALGK	2	97.6%	1																									
IPI00007940	ERLIN1	erlin-1	94.3%	3.5	1	1	1	3	1,562,678	1,761,108	1,692,524	1,811,786	133,120	127,223	58,942	87,378	19.1	16.2	7.8	10.8	1.1	0.3	1.1	0.4	1.2	0.2	-1.0	0.6	1.0	0.8	1.1	0.3
IPI00879747	ERLIN1	ER lipid raft associated 1	94.3%	4.4	1	1	1	3	1,562,678	1,761,108	1,692,524	1,811,786	133,120	127,223	58,942	87,378	19.1	16.2	7.8	10.8	1.1	0.3	1.1	0.4	1.2	0.2	-1.0	0.6	1.0	0.8	1.1	0.3
IPI00936931	ERLIN1	cDNA FLJ57553, highly similar to SPFH domain-containing protein 1	94.3%	5.2	1	1	1	3	1,562,678	1,761,108	1,692,524	1,811,786	133,120	127,223	58,942	87,378	19.1	16.2	7.8	10.8	1.1	0.3	1.1	0.4	1.2	0.2	-1.0	0.6	1.0	0.8	1.1	0.3
				ISEIEDAAFLAR	2	94.3%	1																									
IPI00007948	POLR3C	DNA-directed RNA polymerase III subunit RPC3	94.4%	3.6	1	1	1	2	549,405	499,409	533,153	603,685	29,850	7,210	47,123	31,882	12.2	3.2	19.8	11.8	-1.1	0.2	-1.0	0.8	1.1	0.2	1.1	0.5	1.2	0.03	1.1	0.3
IPI00642130	POLR3C	Uncharacterized protein	94.4%	4.6	1	1	1	2	549,405	499,409	533,153	603,685	29,850	7,210	47,123	31,882	12.2	3.2	19.8	11.8	-1.1	0.2	-1.0	0.8	1.1	0.2	1.1	0.5	1.2	0.03	1.1	0.3
				TLYSDTGELIVEELLLNGK	3	94.4%	1																									
IPI00917269	-	Uncharacterized protein	99.3%	8.3	1	1	1	8	598,269	626,484	587,930	686,310	94,280	65,284	50,390	47,516	35.2	23.3	19.2	15.5	1.0	0.8	-1.0	0.9	1.1	0.4	-1.1	0.7	1.1	0.5	1.2	0.2
IPI00917419	-	Protein	99.3%	7.8	1	1	1	8	598,269	626,484	587,930	686,310	94,280	65,284	50,390	47,516	35.2	23.3	19.2	15.5	1.0	0.8	-1.0	0.9	1.1	0.4	-1.1	0.7	1.1	0.5	1.2	0.2
IPI00972953	-	35 kDa protein	99.3%	3.4	1	1	1	8	598,269	626,484	587,930	686,310	94,280	65,284	50,390	47,516	35.2	23.3	19.2	15.5	1.0	0.8	-1.0	0.9	1.1	0.4	-1.1	0.7	1.1	0.5	1.2	0.2
IPI00007983	PDLIM2	isoform 3 of PDZ and LIM domain protein 2	99.3%	3.0	1	1	1	8	598,269	626,484	587,930	686,310	94,280	65,284	50,390	47,516	35.2	23.3	19.2	15.5	1.0	0.8	-1.0	0.9	1.1	0.4	-1.1	0.7	1.1	0.5	1.2	0.2
IPI00386717	PDLIM2	isoform 4 of PDZ and LIM domain protein 2	99.3%	4.0	1	1	1	8	598,269	626,484	587,930	686,310	94,280	65,284	50,390	47,516	35.2	23.3	19.2	15.5	1.0	0.8	-1.0	0.9	1.1	0.4	-1.1	0.7	1.1	0.5	1.2	0.2
IPI00396593	PDLIM2	isoform 1 of PDZ and LIM domain protein 2	99.3%	3.1	1	1	1	8	598,269	626,484	587,930	686,310	94,280	65,284	50,390	47,516	35.2	23.3	19.2	15.5	1.0	0.8	-1.0	0.9	1.1	0.4	-1.1	0.7	1.1	0.5	1.2	0.2
IPI00916064	PDLIM2	Uncharacterized protein	99.3%	4.3	1	1	1	8	598,269	626,484	587,930	686,310	94,280	65,284	50,390	47,516	35.2	23.3	19.2	15.5	1.0	0.8	-1.0	0.9	1.1	0.4	-1.1	0.7	1.1	0.5	1.2	0.2
IPI01010772	PDLIM2	PDZ and LIM domain protein 2 isoform 2	99.3%	1.8	1	1	1	8	598,269	626,484	587,930	686,310	94,280	65,284	50,390	47,516	35.2	23.3	19.2	15.5	1.0	0.8	-1.0	0.9	1.1	0.4	-1.1	0.7	1.1	0.5	1.2	0.2
				LLQEALEAEER	2	99.3%	1																									
IPI00008037	ACSL5	isoform 1 of Long-chain-fatty-acid--CoA ligase 5	100.0%	14.4	6	6	6	3	10,526,877	11,363,488	11,082,339	12,112,670	786,047	582,535	579,268	441,794	16.7	11.5	11.7	8.2	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.3	1.1	0.2
IPI00401990	ACSL5	isoform 2 of Long-chain-fatty-acid--CoA ligase 5	100.0%	13.3	6	6	6	3	10,526,877	11,363,488	11,082,339	12,112,670	786,047	582,535	579,268	441,794	16.7	11.5	11.7	8.2	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.3	1.1	0.2
IPI00854706	ACSL5	isoform 3 of Long-chain-fatty-acid--CoA ligase 5	100.0%	14.9	6	6	6	3	10,526,877	11,363,488	11,082,339	12,112,670	786,047	582,535	579,268	441,794	16.7	11.5	11.7	8.2	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.3	1.1	0.2
				AIFLHPEPFSIENGLLTPTLK	3	93.7%	1																									
				GLAVSDNGPCLGYR	2	83.0%	1																									
				SGIEILSLYDAENLGK	2	100.0%	1																									
				SSLVGVVVPDTDVLPSFAAK	2	100.0%	1																									
				TQIDSLYEHIQD	2	100.0%	1																									
				VIILMDPFDDDLKQR	3	97.0%	1																									
IPI00008164	PREP	Prolyl endopeptidase	100.0%	8.5	4	4	5	1	17,004,750	17,877,960	16,811,620	20,926,540	3,261,480	926,920	1,784,392	820,146	42.9	11.6	23.7	8.8	1.1	0.8	-1.0	1	1.2	0.3	-1.1	0.6	1.2	0.04	1.2	0.07
				LWYCDLQQESSGIAGILK	2	100.0%	1																									
				VFLDPNILSDDGTVALR	2	99.9%	2																									
				VLYVQDSLEGEAR	2	92.3%	1																									
				WMGGAELSDDGR	2	98.3%	1																									
IPI00008167	ATP1B3	Sodium/potassium-transporting ATPase subunit beta-3	95.3%	3.9	1	1	1	3	1,028,973	1,014,950	1,139,217	1,329,440	50,874	48,965	78,191	62,594	11.1	10.8	15.4	10.5	-1.0	0.8	1.1	0.3	1.3	0.006	1.1	0.2	1.3	0.004	1.2	0.09
IPI00787965	ATP1B3	cDNA FLJ50753, highly similar to Sodium/potassium-transporting ATPase subunit b	95.3%	5.7	1	1	1	3	1,028,973	1,014,950	1,139,217	1,329,440	50,874	48,965	78,191	62,594	11.1	10.8	15.4	10.5	-1.0	0.8	1.1	0.3	1.3	0.006	1.1	0.2	1.3	0.004	1.2	0.09
IPI00946024	ATP1B3	3 kDa protein	95.3%	40.7	1	1	1	3	1,028,973	1,014,950	1,139,217	1,329,440	50,874	48,965	78,191	62,594	11.1	10.8	15.4	10.5	-1.0	0.8	1.1	0.3	1.3	0.006	1.1	0.2	1.3	0.004	1.2	0.09
				IIGLKPEGVPR	2	95.3%	1																									
IPI00008207	MAN1B1	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase	99.9%	1.7	1	1	1	4	180,825	162,214	145,344	169,980	17,655	19,602	12,679	13,557	21.8	27.0	19.5	17.8	-1.1	0.5	-1.2	0.1	-1.1	0.6	-1.1	0.5	1.0	0.8	1.2	0.2
IPI00383856	MAN1B1	cDNA FLJ58473, highly similar to Endoplasmic reticulummannosyl-oligosaccharide	99.9%	1.7	1	1	1	4	180,825	162,214	145,344	169,980	17,655	19,602	12,679	13,557	21.8	27.0	19.5	17.8	-1.1	0.5	-1.2	0.1	-1.1	0.6	-1.1	0.5	1.0	0.8	1.2	0.2
IPI00470859	MAN1B1	Putative uncharacterized protein DKFZp686C04126	99.9%	1.3	1	1	1	4	180,825	162,214	145,344	169,980	17,655	19,602	12,679	13,557	21.8	27.0	19.5	17.8	-1.1	0.5	-1.2	0.1	-1.1	0.6	-1.1	0.5	1.0	0.8	1.2	0.2
IPI00854698	MAN1B1	Uncharacterized protein	99.9%	1.4	1	1	1	4	180,825	162,214	145,344	169,980	17,655	19,602	12,679	13,557	21.8	27.0	19.5	17.8	-1.1	0.5	-1.2	0.1	-1.1	0.6	-1.1	0.5	1.0	0.8	1.2	0.2
				DVDVNLFESTIR	2	91.9%	1																									
IPI00008215	ME1	NADP-dependent malic enzyme	100.0%	6.8	2	2	3	1	295,452	272,715	362,074	337,987	38,414	11,243	50,795	19,448	29.1	9.2	31.4	12.9	-1.1	0.6	1.2	0.3	1.1	0.4	1.3	0.2	1.2	0.02	-1.1	0.7
				GSEYDDFLDEFMEAVSSK	2	100.0%	2																									
				QITDNIFLTTAEVIAQQVSDK	2	99.5%	1																									
IPI00008219	RAD23A	UV excision repair protein RAD23 homolog A	99.6%	8.3	1	1	1	2	863,630	1,115,715	980,275	993,055	114,898	159,461	116,241	137,926	29.8	32.0	26.5	31.1	1.3	0.2	1.1	0.5	1.1	0.5	-1.1	0.5	-1.1	0.6	1.0	0.9
IPI01011338	RAD23A	cDNA FLJ51789, highly similar to UV excision repair protein RAD23 homolog A	99.6%	15.2	1	1	1	2	863,630	1,115,715	980,275	993,055	114,898	159,461	116,241	137,926	29.8	32.0	26.5	31.1	1.3	0.2	1.1	0.5	1.1	0.5	-1.1	0.5	-1.1	0.6	1.0	0.9
				QVIQQNPALLPALLQQLGQENPQLLQQISR	3	99.6%	1																									
IPI00008223	RAD23B	UV excision repair protein RAD23 homolog B	100.0%	25.9	9	10	11	1	20,647,575	20,246,728	20,604,015	22,799,218	1,414,260	512,561	1,043,612	906,334	15.3	5.7	11.3	8.9	-1.0	0.8	-1.0	1	1.1	0.2	1.0	0.8	1.1	0.04	1.1	0.2
				ASFNNPDR	2	93.1%	1																									
				AVEYLLMGIPGDR	2	99.5%	1																									
				GKDAFPVAGQK	2	98.6%	1																									
				IDIDPEETVK	2	99.8%	1																									
				NENLAANFLLQQNFDED	2	91.7%	1																									
				NFVVVMVTKPK	2	99.8%	1																									
				NQPQFQQMR	2	99.9%	1																									
				QIIQQNPSLLPALLQQIGR	2	100.0%	2																									
				QIIQQNPSLLPALLQQIGR	3	100.0%	1																									
				TLQQQTFK	2	97.2%	1																									
IPI00008240	MARS	Methionyl-tRNA synthetase, cytoplasmic	100.0%	8.7	6	6	7	1	12,252,673	12,271,448	11,166,716	13,153,149	618,599	679,805	337,324	787,768	11.3	12.4	6.8	13.4	1.0	1	-1.1	0.2	1.1	0.4	-1.1	0.2	1.1	0.4	1.2	0.05
				AGMFVSK	2	83.4%	1																									
				FFGGYVPEMVLTPDDQR	2	99.8%	1																									
				GFVLQDTVEQLR	2	95.7%	1																									
				GVGVFGDMAQDTGIPADIWR	2	100.0%	1																									
				ITQDIFQQLLK	2	99.9%	2																									
				WFNISFDIFGR	2	87.4%	1																									
IPI00008247	ANAPC5	isoform 1 of Anaphase-promoting complex subunit 5	96.5%	2.1	1	1	1	4	671,798	724,423	708,610	837,500	83,613	35,114	51,668	36,670	27.8	10.8	16.3	9.8	1.1	0.6	1.1	0.7	1.2	0.1	-1.0	0.8	1.2	0.06	1.2	0.08
IPI00788662	ANAPC5	anaphase-promoting complex subunit 5 isoform b	96.5%	2.5	1	1	1	4	671,798	724,423	708,610	837,500	83,613	35,114	51,668	36,670	27.8	10.8	16.3	9.8	1.1	0.6	1.1	0.7	1.2	0.1	-1.0	0.8	1.2	0.06	1.2	0.08
IPI00798336	ANAPC5	cDNA FLJ58697, highly similar to Anaphase-promoting complex subunit 5	96.5%	3.8	1	1	1	4	671,798	724,423	708,610	837,500	83,613	35,114	51,668	36,670	27.8	10.8	16.3	9.8	1.1	0.6	1.1	0.7	1.2	0.1	-1.0	0.8	1.2	0.06	1.2	0.08
IPI01010709	ANAPC5	84 kDa protein	96.5%	2.2	1	1	1	4	671,798	724,423	708,610	837,500	83,613	35,114	51,668	36,670	27.8	10.8	16.3	9.8	1.1	0.6	1.1	0.7	1.2	0.1	-1.0	0.8	1.2	0.06	1.2	0.08
				KAEALEAAIENLNEAK	2	84.3%	1																									
IPI00008253	HS1BP3	Uncharacterized protein	98.9%	5.6	1	1	1	2	8,124,100	7,431,450	7,731,150	8,695,000	750,497	366,986	759,620	331,719	20.7	11.0	22.0	8.5	-1.1	0.4	-1.1	0.7	1.1	0.5	1.0	0.7	1.2	0.03	1.1	0.3
IPI00328868	HS1BP3	HCLS1-binding protein 3	98.9%	4.3	1	1	1	2	8,124,100	7,431,450	7,731,150	8,695,000	750,497	366,986	759,620	331,719	20.7	11.0	22.0	8.5	-1.1	0.4	-1.1	0.7	1.1	0.5	1.0	0.7	1.2	0.03	1.1	0.3
				DAELAGSPELLEFLGTR	2	98.9%	1																									
IPI00008274	CAP1	isoform 1 of Adenylyl cyclase-associated protein 1	100.0%	28.8	11	14	18	2	17,142,496	17,879,626	18,489,005	20,305,295	769,302	145,615	1,043,318	610,479	10.0	1.8	12.6	6.7	1.0	0.4	1.1	0.3	1.2	0.01	1.0	0.6	1.1	0.01	1.1	0.2
IPI01009563	CAP1	49 kDa protein	100.0%	30.3	11	14	18	2	17,142,496	17,879,626	18,489,005	20,305,295	769,302	145,615	1,043,318	610,479	10.0	1.8	12.6	6.7	1.0	0.4	1.1	0.3	1.2	0.01	1.0	0.6	1.1	0.01	1.1	0.2
				AGAAPYVQAFDSLLAGPVAEYLK	2	100.0%	2																									
				AGAAPYVQAFDSLLAGPVAEYLK	3	99.9%	1																									
				ALLVTASQCQQPAENK	2	100.0%	1																									
				GAAPYVQAFDSLLAGPVAEYLK	2	99.9%	2																									
				HAEMVHTGLK	2	99.5%	1																									
				HVDWVK	2	99.7%	1																									
				KEPAVLELEGK	2	99.9%	1																									
				KEPAVLELEGK	3	99.2%	1																									
				LSDLLAPISEQIKEVITFR	3	99.8%	1																									
				SSLFAQINQGESITHALK	3	95.2%	1																									
				TDGCHAYLSK	2	100.0%	2																									
				VENQENVSNLVIEDTELK	2	100.0%	2																									
				VENQENVSNLVIEDTELK	3	96.5%	1																									
				VQVMGK	1	95.6%	1																									
IPI00008367	CES1P1	Similar to Inactive carboxylesterase 4 precursor	100.0%	5.2	1	1	2	2	5,445,643	5,690,829	6,063,386	5,884,657	371,815	580,488	805,537	684,894	15.3	22.8	29.7	26.0	1.0	0.7	1.1	0.5	1.1	0.6	1.1	0.7	1.0	0.8	-1.0	0.9
IPI00963992	CES1P1	isoform 2 of Putative inactive carboxylesterase 4	100.0%	9.9	1	1	2	2	5,445,643	5,690,829	6,063,386	5,884,657	371,815	580,488	805,537	684,894	15.3	22.8	29.7	26.0	1.0	0.7	1.1	0.5	1.1	0.6	1.1	0.7	1.0	0.8	-1.0	0.9
				AISESGVALTSVLVK	2	100.0%	2																									
IPI00008380	PPP2CA	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	100.0%	39.5	8	8	8	1	23,689,955	24,133,469	23,188,044	26,348,552	1,168,324	791,974	1,286,186	943,310	11.0	7.3	12.4	8.0	1.0	0.8	-1.0	0.8	1.1	0.1	-1.0	0.5	1.1	0.1	1.1	0.08
				CGNQAAIMELDDTLK	2	99.9%	1																									
				ELDQWIEQLNECK	2	100.0%	1																									
				GAGYTFGQDISETFNHANGLTLVSR	3	100.0%	1																									
				LQEVPHEGPMCDLLWSDPDDR	3	99.2%	1																									
				QITQVYGFYDECLR	2	100.0%	1																									
				SPDTNYLFMGDYVDR	2	100.0%	1																									
				YGNANVWK	2	99.3%	1																									
				YSFLQFDPAPR	2	100.0%	1																									
IPI00008418	DIABLO	Diablo homolog, mitochondrial precursor	98.7%	3.2	1	1	1	5	979,504	1,131,128	1,031,454	1,222,620	149,232	95,420	107,545	135,396	34.1	18.9	23.3	24.8	1.2	0.4	1.1	0.8	1.2	0.3	-1.1	0.5	1.1	0.6	1.2	0.3
IPI00148255	DIABLO	diablo homolog, mitochondrial isoform 3 precursor	98.7%	5.1	1	1	1	5	979,504	1,131,128	1,031,454	1,222,620	149,232	95,420	107,545	135,396	34.1	18.9	23.3	24.8	1.2	0.4	1.1	0.8	1.2	0.3	-1.1	0.5	1.1	0.6	1.2	0.3
IPI00219865	DIABLO	isoform 2 of Diablo homolog, mitochondrial	98.7%	5.4	1	1	1	5	979,504	1,131,128	1,031,454	1,222,620	149,232	95,420	107,545	135,396	34.1	18.9	23.3	24.8	1.2	0.4	1.1	0.8	1.2	0.3	-1.1	0.5	1.1	0.6	1.2	0.3
IPI00794003	DIABLO	18 kDa protein	98.7%	6.4	1	1	1	5	979,504	1,131,128	1,031,454	1,222,620	149,232	95,420	107,545	135,396	34.1	18.9	23.3	24.8	1.2	0.4	1.1	0.8	1.2	0.3	-1.1	0.5	1.1	0.6	1.2	0.3
IPI01010768	DIABLO	15 kDa protein	98.7%	7.5	1	1	1	5	979,504	1,131,128	1,031,454	1,222,620	149,232	95,420	107,545	135,396	34.1	18.9	23.3	24.8	1.2	0.4	1.1	0.8	1.2	0.3	-1.1	0.5	1.1	0.6	1.2	0.3
				LAEAQIEELR	2	98.7%	1																									
IPI00008433	RPS5	40S ribosomal protein S5	100.0%	23.0	4	5	5	1	17,716,290	18,828,940	18,634,635	19,901,180	411,599	659,519	582,752	1,113,813	5.2	7.8	7.0	12.5	1.1	0.2	1.1	0.2	1.1	0.1	-1.0	0.8	1.1	0.4	1.1	0.3
				AQCPIVER	2	91.0%	1																									
				GSSNSYAIK	2	99.1%	1																									
				LTNSMMMHGR	2	100.0%	1																									
				WSTDDVQINDISLQDYIAVK	2	100.0%	1																									
				WSTDDVQINDISLQDYIAVK	3	99.7%	1																									
IPI00008438	RPS10	40S ribosomal protein S10	100.0%	14.6	2	2	2	3	3,738,323	3,980,436	3,804,498	4,598,683	424,920	349,449	344,079	359,137	25.4	19.6	20.2	17.5	1.1	0.7	1.0	0.9	1.2	0.2	-1.0	0.7	1.2	0.3	1.2	0.1
IPI00478810	RPS10	Ribosomal protein S10	100.0%	14.0	2	2	2	3	3,738,323	3,980,436	3,804,498	4,598,683	424,920	349,449	344,079	359,137	25.4	19.6	20.2	17.5	1.1	0.7	1.0	0.9	1.2	0.2	-1.0	0.7	1.2	0.3	1.2	0.1
IPI00749512	RPS10	Ribosomal protein S10 variant (Fragment)	100.0%	13.8	2	2	2	3	3,738,323	3,980,436	3,804,498	4,598,683	424,920	349,449	344,079	359,137	25.4	19.6	20.2	17.5	1.1	0.7	1.0	0.9	1.2	0.2	-1.0	0.7	1.2	0.3	1.2	0.1
				HFYWYLTNEGIQYLR	3	100.0%	1																									
				IAIYELLFK	2	100.0%	1																									
IPI00008445	URM1	isoform 1 of Ubiquitin-related modifier 1 homolog	98.2%	12.9	1	1	1	3	1,428,487	1,677,437	1,607,960	1,849,677	124,212	59,975	179,447	59,000	19.4	8.0	25.0	7.1	1.2	0.1	1.1	0.4	1.3	0.02	-1.0	0.7	1.1	0.07	1.2	0.3
IPI00642486	URM1	7 kDa protein	98.2%	20.6	1	1	1	3	1,428,487	1,677,437	1,607,960	1,849,677	124,212	59,975	179,447	59,000	19.4	8.0	25.0	7.1	1.2	0.1	1.1	0.4	1.3	0.02	-1.0	0.7	1.1	0.07	1.2	0.3
IPI00910850	URM1	isoform 2 of Ubiquitin-related modifier 1 homolog	98.2%	8.9	1	1	1	3	1,428,487	1,677,437	1,607,960	1,849,677	124,212	59,975	179,447	59,000	19.4	8.0	25.0	7.1	1.2	0.1	1.1	0.4	1.3	0.02	-1.0	0.7	1.1	0.07	1.2	0.3
				VTLPGQEEPWDIR	2	98.2%	1																									
IPI00910500	-	cDNA FLJ61400, highly similar to Pre-mRNA 3'-end-processing factor FIP1	93.9%	6.3	1	1	1	5	706,317	788,895	837,440	868,852	77,425	49,919	77,813	63,435	24.5	14.2	20.8	16.3	1.1	0.4	1.2	0.3	1.2	0.1	1.1	0.6	1.1	0.4	1.0	0.8
IPI00008449	FIP1L1	isoform 3 of Pre-mRNA 3'-end-processing factor FIP1	93.9%	2.7	1	1	1	5	706,317	788,895	837,440	868,852	77,425	49,919	77,813	63,435	24.5	14.2	20.8	16.3	1.1	0.4	1.2	0.3	1.2	0.1	1.1	0.6	1.1	0.4	1.0	0.8
IPI00395337	FIP1L1	isoform 1 of Pre-mRNA 3'-end-processing factor FIP1	93.9%	2.4	1	1	1	5	706,317	788,895	837,440	868,852	77,425	49,919	77,813	63,435	24.5	14.2	20.8	16.3	1.1	0.4	1.2	0.3	1.2	0.1	1.1	0.6	1.1	0.4	1.0	0.8
IPI00658114	FIP1L1	pre-mRNA 3'-end-processing factor FIP1 isoform 2	93.9%	2.4	1	1	1	5	706,317	788,895	837,440	868,852	77,425	49,919	77,813	63,435	24.5	14.2	20.8	16.3	1.1	0.4	1.2	0.3	1.2	0.1	1.1	0.6	1.1	0.4	1.0	0.8

IPI00965581	FIP1L1	isoform 4 of Pre-mRNA 3'-end-processing factor FIP1	93.9%	3.7	1	1	1	5	706,317	788,895	837,440	868,852	77,425	49,919	77,813	63,435	24.5	14.2	20.8	16.3	1.1	0.4	1.2	0.3	1.2	0.1	1.1	0.6	1.1	0.4	1.0	0.8
				MGLEVIPVTSTTNK	2	93.9%	1																									
IPI00008454	DNAJB11	DnaJ homolog subfamily B member 11	100.0%	7.8	2	2	2	1	6,819,000	7,057,080	6,842,455	8,236,245	402,858	256,362	269,666	535,000	13.2	8.1	8.8	14.5	1.0	0.6	1.0	1	1.2	0.07	-1.0	0.6	1.2	0.08	1.2	0.05
				FQDLGAAYEVLSDSEKR	3	88.8%	1																									
				TLEVEIEPGVR	2	99.9%	1																									
IPI00008455	MYO6	isoform 2 of Myosin-VI	100.0%	6.2	7	7	7	5	7,403,807	7,534,370	7,606,467	8,412,150	623,186	292,677	319,127	338,170	18.8	8.7	9.4	9.0	1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.9	1.1	0.09	1.1	0.1
IPI00069126	MYO6	isoform 1 of Myosin-VI	100.0%	6.1	7	7	7	5	7,403,807	7,534,370	7,606,467	8,412,150	623,186	292,677	319,127	338,170	18.8	8.7	9.4	9.0	1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.9	1.1	0.09	1.1	0.1
IPI00642722	MYO6	isoform 5 of Myosin-VI	100.0%	6.2	7	7	7	5	7,403,807	7,534,370	7,606,467	8,412,150	623,186	292,677	319,127	338,170	18.8	8.7	9.4	9.0	1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.9	1.1	0.09	1.1	0.1
IPI00816452	MYO6	isoform 3 of Myosin-VI	100.0%	6.0	7	7	7	5	7,403,807	7,534,370	7,606,467	8,412,150	623,186	292,677	319,127	338,170	18.8	8.7	9.4	9.0	1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.9	1.1	0.09	1.1	0.1
IPI00816461	MYO6	isoform 4 of Myosin-VI	100.0%	6.1	7	7	7	5	7,403,807	7,534,370	7,606,467	8,412,150	623,186	292,677	319,127	338,170	18.8	8.7	9.4	9.0	1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.9	1.1	0.09	1.1	0.1
				FNEVVSVLK	2	95.8%	1																									
				IQAEVEAQLAR	2	100.0%	1																									
				IVEANPLLEAFGNAK	2	98.0%	1																									
				NLEISIDTLMAK	2	96.7%	1																									
				SSEELLSALQK	2	99.9%	1																									
				STMMTQEQIQK	2	97.9%	1																									
				TQLNLLLDK	2	91.2%	1																									
IPI00008475	HMGCS1	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	100.0%	27.1	9	9	10	2	19,145,045	20,508,617	19,692,580	21,854,415	841,178	463,719	1,085,711	822,278	9.8	5.1	12.3	8.4	1.1	0.2	1.0	0.7	1.1	0.05	-1.0	0.5	1.1	0.2	1.1	0.2
IPI00963899	HMGCS1	cDNA FLJ38173 fis, clone FCBBF1000053, highly similar to HYDROXYMETHYLGL	100.0%	27.7	9	9	10	2	19,145,045	20,508,617	19,692,580	21,854,415	841,178	463,719	1,085,711	822,278	9.8	5.1	12.3	8.4	1.1	0.2	1.0	0.7	1.1	0.05	-1.0	0.5	1.1	0.2	1.1	0.2
				DVGIVALEIYFPSQYVDQAELEKYDGVDAGK	3	99.9%	1																									
				LEVGTETIIDK	2	100.0%	2																									
				LPATAAEPEAAVISNGEH	2	100.0%	1																									
				LSIQCYLSALDR	2	100.0%	1																									
				MLLNDFLNDQNR	2	100.0%	1																									
				PTGGVGAVALLIGPNAPLIFER	2	99.7%	1																									
				TGVAPDVFAENMK	2	100.0%	1																									
				VTQDATPGSALDK	2	99.9%	1																									
				YTIGLGQAK	2	100.0%	1																									
IPI00008485	ACO1	Cytoplasmic aconitate hydratase	100.0%	15.5	9	9	10	1	17,687,807	17,740,477	19,093,507	21,258,378	1,490,440	552,063	1,732,168	605,932	18.8	7.0	20.3	6.4	1.0	1	1.1	0.6	1.2	0.06	1.1	0.5	1.2	0.003	1.1	0.3
				AVDAGLNVMPYIK	2	91.3%	1																									
				DFNDPSQDPDFTQVVELDLK	2	100.0%	1																									
				FVEFFGPGVAQLSIADR	2	100.0%	2																									
				NQDLEFER	2	93.0%	1																									
				QAPQTIHLPSGEILDVFDAAER	3	99.4%	1																									
				SPPFFENLTLDLQPPK	2	91.4%	1																									
				VILQDFTGVPAVVDFAAMR	2	100.0%	1																									
				YLQAVGMFR	2	99.9%	1																									
				YQQAGLPLIVLAGK	2	100.0%	1																									
IPI00008524	PABPC1	isoform 1 of Polyadenylate-binding protein 1	100.0%	17.1	9	9	11	5	15,456,586	15,713,465	14,430,934	17,174,349	1,038,152	370,520	1,183,794	703,200	15.0	5.3	18.3	9.2	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.08
IPI00410017	PABPC1	isoform 2 of Polyadenylate-binding protein 1	100.0%	19.9	9	9	11	5	15,456,586	15,713,465	14,430,934	17,174,349	1,038,152	370,520	1,183,794	703,200	15.0	5.3	18.3	9.2	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.08
IPI00796945	PABPC1	cDNA FLJ37875 fis, clone BRSSN2018771, highly similar to Poly(A)-binding protein	100.0%	17.1	9	9	11	5	15,456,586	15,713,465	14,430,934	17,174,349	1,038,152	370,520	1,183,794	703,200	15.0	5.3	18.3	9.2	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.08
IPI00909378	PABPC1	cDNA FLJ59219, highly similar to Poly(A)-binding protein 1	100.0%	18.1	9	9	11	5	15,456,586	15,713,465	14,430,934	17,174,349	1,038,152	370,520	1,183,794	703,200	15.0	5.3	18.3	9.2	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.08
IPI00977833	PABPC1	Uncharacterized protein	100.0%	18.4	9	9	11	5	15,456,586	15,713,465	14,430,934	17,174,349	1,038,152	370,520	1,183,794	703,200	15.0	5.3	18.3	9.2	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.08
				AKEFTNVYIK	3	99.9%	1																									
				ALDTMNFDVIK	2	100.0%	2																									
				EFSPFGTITSAK	2	98.8%	1																									
				GFGFVSFER	2	99.9%	1																									
				ITGMLLEIDNSELLHMLESPESLR	3	100.0%	1																									
				KEFSPFGTITSAK	2	99.8%	1																									
				MNGMLLNDR	2	95.6%	1																									
				SKVDEAVAVLQAHQAK	3	100.0%	1																									
				SLGYAYVNFQQPADAER	2	100.0%	2																									
IPI00008527	RPLP1	60S acidic ribosomal protein P1	100.0%	29.0	2	2	3	1	18,497,061	18,945,090	19,936,875	21,362,400	1,400,209	730,788	1,688,334	769,128	16.9	8.6	18.9	8.1	1.0	0.8	1.1	0.5	1.2	0.1	1.1	0.6	1.1	0.05	1.1	0.5
				AAGVNVEPFWPGLFAK	2	99.9%	2																									
				KEESEESDDDMGFGLFD	2	100.0%	1																									
IPI00008529	RPLP2	60S acidic ribosomal protein P2	100.0%	85.2	7	10	14	1	91,319,984	92,919,735	91,289,972	99,401,124	6,110,724	3,298,578	4,410,973	3,663,684	15.0	7.9	10.8	8.2	1.0	0.8	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.2	1.1	0.2
				ILDSVGIEADDDR	2	100.0%	1																									
				ILDSVGIEADDDRLNK	2	100.0%	2																									
				ILDSVGIEADDDRLNK	3	99.9%	1																									
				KEESEESDDDMGFGLFD	2	100.0%	1																									
				KILDSVGIEADDDRLNK	3	100.0%	2																									
				LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	2	100.0%	2																									
				LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	3	100.0%	1																									
				NIEDVIAQGIGK	2	100.0%	2																									
				YVASYLLAALGGNSSPSAK	2	100.0%	1																									
				YVASYLLAALGGNSSPSAK	3	100.0%	1																									
IPI00008530	RPLP0	60S acidic ribosomal protein P0	100.0%	51.7	12	12	18	1	54,955,248	55,780,904	52,077,656	62,925,681	3,546,095	1,118,630	2,833,126	1,411,992	14.4	4.5	12.2	5.0	1.0	0.8	-1.1	0.5	1.1	0.07	-1.1	0.3	1.1	0.004	1.2	0.009
				AFLADPSAFVAAAPVAAATTAAPAAAAAPAK	2	100.0%	1																									
				AGAIAPCEVTVPAQNTGLGPEK	2	100.0%	2																									
				AVVLMGK	2	95.9%	1																									
				CFIVGADNVGSK	2	100.0%	2																									
				GHLENNPALEK	2	100.0%	2																									
				GHLENNPALEKLLPHIR	3	81.2%	1																									
				GNVGFVFTK	2	100.0%	2																									
				GNVGFVFTKEDLTEIRDMLLANK	3	99.7%	1																									
				GTIEILSDVQLIK	2	100.0%	2																									
				IIQLLDDYPK	2	100.0%	1																									
				TSFFQALGITTK	2	100.0%	2																									
				VLALSVETDYTFPLAEK	2	100.0%	1																									
IPI00008552	GLRX3	Glutaredoxin-3	100.0%	11.3	3	3	3	1	15,150,830	13,671,070	15,852,060	16,738,130	1,953,234	969,865	1,252,576	536,642	28.8	15.9	17.7	7.2	-1.1	0.5	1.0	0.8	1.1	0.5	1.2	0.2	1.2	0.02	1.1	0.5
				AYSNWPTYPQLYVK	2	99.9%	1																									
				GELVGGLDIVK	2	98.4%	1																									
				YEISSVPTFLFFK	2	100.0%	1																									
IPI00008557	IGF2BP1	Insulin-like growth factor 2 mRNA-binding protein 1	100.0%	20.1	9	9	11	1	45,008,157	48,091,893	42,918,667	54,354,158	7,852,014	2,791,836	4,158,534	3,593,918	39.0	13.0	21.7	14.8	1.1	0.7	-1.0	0.8	1.2	0.3	-1.1	0.3	1.1	0.2	1.3	0.07
				DQTPDENDQVIVK	2	100.0%	2																									
				GQSNQAQAR	2	85.3%	1																									
				ISYSGQFLVK	2	96.7%	1																									
				LYIGNLNESVTPADLEK	2	100.0%	1																									
				MVIITGPPEAQFK	2	100.0%	2																									
				QGSPVAAGAPAK	2	95.5%	1																									
				QQQVDIPLR	2	99.5%	1																									
				SGYAFVDCPDEHWAMK	3	82.7%	1																									
				TVNELQNLTAAEVVVPR	2	99.9%	1																									
IPI00008575	KHDRBS1	isoform 1 of KH domain-containing, RNA-binding, signal transduction-associated pro	100.0%	11.3	4	4	4	3	6,527,473	7,582,314	6,806,392	8,091,277	844,852	604,608	740,942	241,782	28.9	17.8	24.3	6.7	1.2	0.3	1.0	0.8	1.2	0.1	-1.1	0.4	1.1	0.5	1.2	0.2
IPI00385834	KHDRBS1	isoform 2 of KH domain-containing, RNA-binding, signal transduction-associated pro	100.0%	12.0	4	4	4	3	6,527,473	7,582,314	6,806,392	8,091,277	844,852	604,608	740,942	241,782	28.9	17.8	24.3	6.7	1.2	0.3	1.0	0.8	1.2	0.1	-1.1	0.4	1.1	0.5	1.2	0.2
IPI00479209	KHDRBS1	cDNA FLJ54590, highly similar to KH domain-containing, RNA-binding, signaltransd	100.0%	11.8	4	4	4	3	6,527,473	7,582,314	6,806,392	8,091,277	844,852	604,608	740,942	241,782	28.9	17.8	24.3	6.7	1.2	0.3	1.0	0.8	1.2	0.1	-1.1	0.4	1.1	0.5	1.2	0.2
				DSLDPSFTHAMQLLTAEIEK	3	100.0%	1																									
				FNFVGK	2	92.8%	1																									
				ILGPQGNTIK	2	85.5%	1																									
				KDDEENYLDLFSHK	3	100.0%	1																									
IPI00008673	TLR4	isoform 1 of Toll-like receptor 4	92.8%	2.0	1	1	1	4	6,545,700	7,374,575	5,975,175	8,126,550	605,745	626,773	677,427	655,952	20.7	19.0	25.4	18.1	1.1	0.4	-1.1	0.5	1.2	0.1	-1.2	0.2	1.1	0.4	1.4	0.05
IPI00374265	TLR4	isoform 2 of Toll-like receptor 4	92.8%	2.1	1	1	1	4	6,545,700	7,374,575	5,975,175	8,126,550	605,745	626,773	677,427	655,952	20.7	19.0	25.4	18.1	1.1	0.4	-1.1	0.5	1.2	0.1	-1.2	0.2	1.1	0.4	1.4	0.05
IPI00914904	TLR4	isoform 3 of Toll-like receptor 4	92.8%	2.7	1	1	1	4	6,545,700	7,374,575	5,975,175	8,126,550	605,745	626,773	677,427	655,952	20.7	19.0	25.4	18.1	1.1	0.4	-1.1	0.5	1.2	0.1	-1.2	0.2	1.1	0.4	1.4	0.05
IPI00954813	TLR4	Toll-like receptor 4 (Fragment)	92.8%	13.7	1	1	1	4	6,545,700	7,374,575	5,975,175	8,126,550	605,745	626,773	677,427	655,952	20.7	19.0	25.4	18.1	1.1	0.4	-1.1	0.5	1.2	0.1	-1.2	0.2	1.1	0.4	1.4	0.05
				VAFNGIFNGLSSLEVLK	2	92.8%	1																									
IPI00008708	RSL1D1	Ribosomal L1 domain-containing protein 1	98.4%	1.8	1	1	1	2	5,139,650	5,661,000	5,458,835	6,057,775	449,756	212,635	334,771	200,435	19.6	8.4	13.7	7.4	1.1	0.3	1.1	0.6	1.2	0.1	-1.0	0.6	1.1	0.2	1.1	0.2
IPI00642046	RSL1D1	Uncharacterized protein	98.4%	1.8	1	1	1	2	5,139,650	5,661,000	5,458,835	6,057,775	449,756	212,635	334,771	200,435	19.6	8.4	13.7	7.4	1.1	0.3	1.1	0.6	1.2	0.1	-1.0	0.6	1.1	0.2	1.1	0.2
				RLLPSLIGR	2	98.4%	1																									
IPI00008726	IREB2	Iron-responsive element-binding protein 2	100.0%	5.5	3	3	3	2	11,147,837	12,766,815	11,846,405	14,028,365	1,213,754	665,840	1,120,589	624,132	24.4	11.7	21.2	10.0	1.1	0.3	1.1	0.7	1.3	0.07	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00853333	IREB2	99 kDa protein	100.0%	5.9	3	3	3	2	11,147,837	12,766,815	11,846,405	14,028,365	1,213,754	665,840	1,120,589	624,132	24.4	11.7	21.2	10.0	1.1	0.3	1.1	0.7	1.3	0.07	-1.1	0.5	1.1	0.2	1.2	0.1
				EGIPLIILAGKKYGSGNSR	3	96.6%	1																									
				FVEFFGSGVSQLSIVDR	3	97.9%	1																									
				WNSLEAPDSVLFPWDLK	2	99.1%	1																									
IPI00008779	TM4SF4	Transmembrane 4 L6 family member 4	99.4%	12.9	1	1	1	1	2,473,780	2,434,310	2,766,810	2,882,450	222,454	147,527	501,652	224,014	20.1	13.6	40.5	17.4	-1.0	0.9	1.1	0.6	1.2	0.2	1.1	0.6	1.2	0.1	1.0	0.8
				CLMANSTWGYPFHDGDYLNDEALWNK	3	99.4%	1																									
IPI00008787	NAGLU	Alpha-N-acetylglucosaminidase	99.5%	2.4	1	1	1	3	441,325	419,813	427,312	492,589	19,959	43,647	31,134	44,265	10.1	23.3	16.3	20.1	-1.1	0.7	-1.0	0.7	1.1	0.3	1.0	0.9	1.2	0.3	1.2	0.3
IPI00555656	NAGLU	Huntingtin interacting protein-1-related (Fragment)	99.5%	4.0	1	1	1	3	441,325	419,813	427,312	492,589	19,959	43,647	31,134	44,265	10.1	23.3	16.3	20.1	-1.1	0.7	-1.0	0.7	1.1	0.3	1.0	0.9	1.2	0.3	1.2	0.3
IPI00746033	NAGLU	47 kDa protein	99.5%	4.3	1	1	1	3	441,325	419,813	427,312	492,589	19,959	43,647	31,134	44,265	10.1	23.3	16.3	20.1	-1.1	0.7	-1.0	0.7	1.1	0.3	1.0	0.9	1.2	0.3	1.2	0.3
				YQLTLWGPEGNILDYANK	2	99.5%	1																									
IPI00008918	LIMA1	isoform Beta of LIM domain and actin-binding protein 1	100.0%	17.7	9	10	12	1	14,893,340	15,643,444	16,791,333	17,416,467	707,393	727,932	1,149,980	574,695	10.6	10.4	15.3	7.4	1.1	0.5	1.1	0.2	1.2	0.02	1.1	0.4	1.1	0.09	1.0	0.6
				IAWPPPTELGSSGSALEEGIK	2	99.9%	1																									
				ISANENSLAVR	2	100.0%	2																									
				NENEEILERPAQLANAR	3	100.0%	1																									
				QSSSTNYTNELK	2	99.9%	1																									
				SEVQQPVHPKPLSPDSR	3	87.4%	1																									
				SLNWSSFVDNTFAEEFTTQNQK	2	83.9%	1																									
				SLNWSSFVDNTFAEEFTTQNQK	3	100.0%	1																									
				SNTENLSQHFR	2	94.4%	1																									
				SPPEALVQGR	2	99.9%	1																									
				SQDVELWEGEVVK	2	100.0%	2																									
IPI00008934	HMGCS2	Hydroxymethylglutaryl-CoA synthase, mitochondrial	100.0%	6.7	2	2	2	1	14,378,995	14,389,070	14,339,290	17,498,765	1,120,069	443,611	1,282,883	594,010	17.4	6.9	20.0	7.6	1.0	1	-1.0	1	1.2	0.04	-1.0	1	1.2	0.003	1.2	0.06
				LMFNDFLSASSDTQTSLYK	2	100.0%	1																									
				PTGGAGAVAMLIGPK	2	99.2%	1																									
IPI00019918	DDX19A	ATP-dependent RNA helicase DDX19A	100.0%	6.7	3	3	3	5	3,358,629	3,335,837	3,291,870	3,654,985	354,766	112,368	218,536	205,502	23.6	7.5	14.8	12.6	-1.0	1	-1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00155054	DDX19A	cDNA FLJ50635, highly similar to ATP-dependent RNA helicase DDX19A	100.0%	7.2	3	3	3	5	3,358,629	3,335,837	3,291,870	3,654,985	354,766	112,368	218,536	205,502	23.6	7.5	14.8	12.6	-1.0	1	-1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00008943	DDX19B	isoform 1 of ATP-dependent RNA helicase DDX19B	100.0%	6.7	3	3	3	5	3,358,629	3,335,837	3,291,870	3,654,985	354,766	112,368	218,536	205,502	23.6	7.5	14.8	12.6	-1.0	1	-1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00027599	DDX19B	cDNA FLJ52357, highly similar to ATP-dependent RNA helicase DDX19B	100.0%	7.1	3	3	3	5	3,358,629	3,335,837	3,291,870	3,654,985	354,766	112,368	218,536	205,502	23.6	7.5	14.8	12.6	-1.0	1	-1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00939593	DDX19B	isoform 2 of ATP-dependent RNA helicase DDX19B	100.0%	7.1	3	3	3	5	3,358,629	3,335,837	3,291,870	3,654,985	354,766	112,368	218,536	205,502	23.6	7.5	14.8	12.6	-1.0	1	-1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.3
				DPNSPLYSVK	2	99.7%	1																									
				LDTDDLDEIEK	2	98.4%	1																									
				TASWLAAELSK	2	86.9%	1																									
IPI00008964	RAB1B	Ras-related protein Rab-1B	100.0%	47.8	6	7	10	1	13,405,136	14,062,183	14,169,456	16,110,585	1,333,790	600,699	872,725	381,289	22.3	9.6	13.8	5.3	1.0	0.7	1.1	0.6	1.2	0.1	1.0	0.9	1.1	0.02	1.1	0.08
				EFADSLGIPFLETSAK	2	100.0%	2																									
				FADDTYTESYISTIGVDFK	2	100.0%	2																									
				FADDTYTESYISTIGVDFK	3	100.0%	1																									
				GAHGIIVVYDVTDQESYANVK	3	99.1%	1																									
				MGPGAASGGERPNLK	2	100.0%	1																									

				NATNVEQAFMTMAAEIK	2	100.0%	2																									
				QWLQEIDR	2	95.3%	1																									
IPI00008982	ALDH18A1	isoform Long of Delta-1-pyrroline-5-carboxylate synthase	100.0%	15.2	10	10	12	2	64,304,648	66,987,972	68,484,189	76,304,542	6,071,546	2,884,116	5,499,216	2,945,763	21.1	9.6	18.0	8.6	1.0	0.7	1.1	0.6	1.2	0.1	1.0	0.8	1.1	0.05	1.1	0.2
IPI00218547	ALDH18A1	isoform Short of Delta-1-pyrroline-5-carboxylate synthase	100.0%	15.3	10	10	12	2	64,304,648	66,987,972	68,484,189	76,304,542	6,071,546	2,884,116	5,499,216	2,945,763	21.1	9.6	18.0	8.6	1.0	0.7	1.1	0.6	1.2	0.1	1.0	0.8	1.1	0.05	1.1	0.2
				FASYLTFSPSEVK	2	100.0%	2																									
				GDECGLALGR	2	99.3%	1																									
				ILHLLTQEALSIHGVK	3	95.3%	1																									
				LASIVEQVSVLQNQGR	2	100.0%	1																									
				MIDLIIPR	2	99.9%	1																									
				MLATLEPEQR	2	98.3%	1																									
				NLNGTLHELLR	2	88.0%	1																									
				QIAASSQDSVGR	2	100.0%	1																									
				TPLFDQIIDMLR	2	100.0%	2																									
				VSGHVITDIVEGK	2	100.0%	1																									
IPI00008991	DR1	Protein Dr1	99.2%	21.0	2	2	2	1	3,016,755	2,863,785	3,351,199	3,847,939	290,821	203,705	433,264	229,842	21.6	15.9	28.9	13.4	-1.1	0.7	1.1	0.5	1.3	0.06	1.2	0.3	1.3	0.01	1.1	0.3
				LENLGIPEEELLR	2	97.6%	1																									
				TISPEHVIQALESLGFGSYISEVK	3	97.7%	1																									
IPI00938044	LOC100291405	3-hydroxyacyl-CoA dehydratase 3-like isoform 1	97.9%	11.5	1	1	1	3	614,059	601,989	783,293	568,767	79,577	62,497	55,435	23,904	29.0	23.2	15.8	9.4	-1.0	0.9	1.3	0.1	-1.1	0.6	1.3	0.06	-1.1	0.6	-1.4	0.007
IPI00008998	PTPLAD1	3-hydroxyacyl-CoA dehydratase 3	97.9%	5.8	1	1	1	3	614,059	601,989	783,293	568,767	79,577	62,497	55,435	23,904	29.0	23.2	15.8	9.4	-1.0	0.9	1.3	0.1	-1.1	0.6	1.3	0.06	-1.1	0.6	-1.4	0.007
IPI00787433	PTPLAD1	cDNA FLJ54138, highly similar to Homo sapiens butyrate-induced transcript 1 (HSP	97.9%	6.8	1	1	1	3	614,059	601,989	783,293	568,767	79,577	62,497	55,435	23,904	29.0	23.2	15.8	9.4	-1.0	0.9	1.3	0.1	-1.1	0.6	1.3	0.06	-1.1	0.6	-1.4	0.007
				VELSDVQNPAISITENVLHFK	3	97.9%	1																									
IPI00009010	TRMT112	tRNA methyltransferase 112 homolog	100.0%	21.6	2	2	2	2	4,390,935	4,189,888	4,337,430	4,999,547	349,590	215,083	255,041	195,433	17.8	11.5	13.2	8.7	-1.0	0.6	-1.0	0.9	1.1	0.2	1.0	0.7	1.2	0.02	1.2	0.07
IPI01014610	TRMT112	12 kDa protein	100.0%	25.5	2	2	2	2	4,390,935	4,189,888	4,337,430	4,999,547	349,590	215,083	255,041	195,433	17.8	11.5	13.2	8.7	-1.0	0.6	-1.0	0.9	1.1	0.2	1.0	0.7	1.2	0.02	1.2	0.07
				ICPVEFNPNFVAR	2	100.0%	1																									
				VEWSAFLEAADNLR	2	99.9%	1																									
IPI00009030	LAMP2	isoform LAMP-2A of Lysosome-associated membrane glycoprotein 2	98.7%	2.0	1	1	1	5	726,506	691,798	641,842	847,614	51,988	51,967	86,524	39,784	16.0	16.8	30.1	10.5	-1.1	0.6	-1.1	0.4	1.2	0.1	-1.1	0.6	1.2	0.04	1.3	0.06
IPI00216172	LAMP2	lysosome-associated membrane glycoprotein 2 isoform C precursor	98.7%	2.0	1	1	1	5	726,506	691,798	641,842	847,614	51,988	51,967	86,524	39,784	16.0	16.8	30.1	10.5	-1.1	0.6	-1.1	0.4	1.2	0.1	-1.1	0.6	1.2	0.04	1.3	0.06
IPI00739827	LAMP2	isoform LAMP-2B of Lysosome-associated membrane glycoprotein 2	98.7%	2.0	1	1	1	5	726,506	691,798	641,842	847,614	51,988	51,967	86,524	39,784	16.0	16.8	30.1	10.5	-1.1	0.6	-1.1	0.4	1.2	0.1	-1.1	0.6	1.2	0.04	1.3	0.06
IPI00922445	LAMP2	cDNA FLJ52540, highly similar to Lysosome-associated membrane glycoprotein 2	98.7%	2.7	1	1	1	5	726,506	691,798	641,842	847,614	51,988	51,967	86,524	39,784	16.0	16.8	30.1	10.5	-1.1	0.6	-1.1	0.4	1.2	0.1	-1.1	0.6	1.2	0.04	1.3	0.06
IPI00980890	LAMP2	cDNA FLJ58780, highly similar to Homo sapiens lysosomal-associated membrane p	98.7%	2.2	1	1	1	5	726,506	691,798	641,842	847,614	51,988	51,967	86,524	39,784	16.0	16.8	30.1	10.5	-1.1	0.6	-1.1	0.4	1.2	0.1	-1.1	0.6	1.2	0.04	1.3	0.06
				IPLNDLFR	2	98.7%	1																									
IPI00009032	SSB	Lupus La protein	100.0%	25.7	9	11	15	2	23,235,051	23,227,449	23,927,414	25,454,820	2,009,002	1,669,718	2,013,607	704,370	19.3	16.1	18.8	6.2	-1.0	1	1.0	0.8	1.1	0.3	1.0	0.8	1.1	0.3	1.1	0.5
IPI00916802	SSB	Uncharacterized protein	100.0%	29.1	9	11	15	2	23,235,051	23,227,449	23,927,414	25,454,820	2,009,002	1,669,718	2,013,607	704,370	19.3	16.1	18.8	6.2	-1.0	1	1.0	0.8	1.1	0.3	1.0	0.8	1.1	0.3	1.1	0.5
				EQIKLDEGWVPLEIMIK	2	98.9%	1																									
				EQIKLDEGWVPLEIMIK	3	99.4%	1																									
				GQVLNIQMR	2	88.2%	1																									
				GSIFVVFDSIESAK	2	100.0%	2																									
				ICHQIEYYFGDFNLPR	2	100.0%	1																									
				ICHQIEYYFGDFNLPR	3	99.6%	1																									
				IIEDQQESLNK	2	100.0%	2																									
				LDEGWVPLEIMIK	2	100.0%	2																									
				LTTDFNVIVEALSK	2	100.0%	2																									
				SPSKPLPEVTDEYKNDVK	3	100.0%	1																									
				WIDFVR	2	93.0%	1																									
IPI00009054	BMP1	isoform BMP1-3 of Bone morphogenetic protein 1	91.6%	0.6	1	1	1	8	826,865	822,574	731,611	797,943	55,589	50,333	54,135	45,841	15.0	13.7	16.6	12.9	-1.0	1	-1.1	0.3	-1.0	0.7	-1.1	0.3	-1.0	0.7	1.1	0.4
IPI00014021	BMP1	isoform BMP1-1 of Bone morphogenetic protein 1	91.6%	0.8	1	1	1	8	826,865	822,574	731,611	797,943	55,589	50,333	54,135	45,841	15.0	13.7	16.6	12.9	-1.0	1	-1.1	0.3	-1.0	0.7	-1.1	0.3	-1.0	0.7	1.1	0.4
IPI00218040	BMP1	isoform BMP1-4 of Bone morphogenetic protein 1	91.6%	2.0	1	1	1	8	826,865	822,574	731,611	797,943	55,589	50,333	54,135	45,841	15.0	13.7	16.6	12.9	-1.0	1	-1.1	0.3	-1.0	0.7	-1.1	0.3	-1.0	0.7	1.1	0.4
IPI00218042	BMP1	isoform BMP1-5 of Bone morphogenetic protein 1	91.6%	1.0	1	1	1	8	826,865	822,574	731,611	797,943	55,589	50,333	54,135	45,841	15.0	13.7	16.6	12.9	-1.0	1	-1.1	0.3	-1.0	0.7	-1.1	0.3	-1.0	0.7	1.1	0.4
IPI00218044	BMP1	isoform BMP1-6 of Bone morphogenetic protein 1	91.6%	0.8	1	1	1	8	826,865	822,574	731,611	797,943	55,589	50,333	54,135	45,841	15.0	13.7	16.6	12.9	-1.0	1	-1.1	0.3	-1.0	0.7	-1.1	0.3	-1.0	0.7	1.1	0.4
IPI00218045	BMP1	isoform BMP1-7 of Bone morphogenetic protein 1	91.6%	0.7	1	1	1	8	826,865	822,574	731,611	797,943	55,589	50,333	54,135	45,841	15.0	13.7	16.6	12.9	-1.0	1	-1.1	0.3	-1.0	0.7	-1.1	0.3	-1.0	0.7	1.1	0.4
IPI00719138	BMP1	BMP1 protein	91.6%	2.0	1	1	1	8	826,865	822,574	731,611	797,943	55,589	50,333	54,135	45,841	15.0	13.7	16.6	12.9	-1.0	1	-1.1	0.3	-1.0	0.7	-1.1	0.3	-1.0	0.7	1.1	0.4
IPI00923496	BMP1	Bone morphogenetic protein 1 isoform 1, variant (Fragment)	91.6%	0.8	1	1	1	8	826,865	822,574	731,611	797,943	55,589	50,333	54,135	45,841	15.0	13.7	16.6	12.9	-1.0	1	-1.1	0.3	-1.0	0.7	-1.1	0.3	-1.0	0.7	1.1	0.4
				HVSIVR	2	91.6%	1																									
IPI00009057	G3BP2	isoform A of Ras GTPase-activating protein-binding protein 2	99.4%	6.2	2	2	2	3	3,008,262	2,892,130	3,084,453	3,334,063	181,313	138,274	268,926	41,618	13.5	10.7	19.5	2.8	-1.0	0.6	1.0	0.8	1.1	0.1	1.1	0.5	1.2	0.03	1.1	0.4
IPI00179890	G3BP2	isoform B of Ras GTPase-activating protein-binding protein 2	99.4%	6.7	2	2	2	3	3,008,262	2,892,130	3,084,453	3,334,063	181,313	138,274	268,926	41,618	13.5	10.7	19.5	2.8	-1.0	0.6	1.0	0.8	1.1	0.1	1.1	0.5	1.2	0.03	1.1	0.4
IPI00965308	G3BP2	Uncharacterized protein	99.4%	7.1	2	2	2	3	3,008,262	2,892,130	3,084,453	3,334,063	181,313	138,274	268,926	41,618	13.5	10.7	19.5	2.8	-1.0	0.6	1.0	0.8	1.1	0.1	1.1	0.5	1.2	0.03	1.1	0.4
				LPNFGFVVFDDSEPVQR	2	99.4%	1																									
				VEAKPEVQSQPPR	3	98.0%	1																									
IPI00009063	CAPN9	isoform 1 of Calpain-9	91.9%	1.9	1	1	1	3	1,027,897	1,182,243	1,211,827	1,615,850	105,111	112,627	188,161	107,540	22.9	21.3	34.7	14.9	1.2	0.3	1.2	0.4	1.6	0.004	1.0	0.9	1.4	0.02	1.3	0.1
IPI00016919	CAPN9	isoform 2 of Calpain-9	91.9%	2.0	1	1	1	3	1,027,897	1,182,243	1,211,827	1,615,850	105,111	112,627	188,161	107,540	22.9	21.3	34.7	14.9	1.2	0.3	1.2	0.4	1.6	0.004	1.0	0.9	1.4	0.02	1.3	0.1
IPI00448880	CAPN9	cDNA FLJ52338, highly similar to Calpain-9	91.9%	2.1	1	1	1	3	1,027,897	1,182,243	1,211,827	1,615,850	105,111	112,627	188,161	107,540	22.9	21.3	34.7	14.9	1.2	0.3	1.2	0.4	1.6	0.004	1.0	0.9	1.4	0.02	1.3	0.1
				NFLDTFWTNPQIK	2	91.9%	1																									
IPI00009070	HBS1L	isoform 1 of HBS1-like protein	93.0%	1.6	1	1	1	6	983,120	1,176,688	1,018,053	1,219,047	148,699	109,882	71,259	90,748	33.8	20.9	15.7	16.7	1.2	0.3	1.0	0.8	1.2	0.2	-1.2	0.3	1.0	0.8	1.2	0.1
IPI00550360	HBS1L	cDNA FLJ52343, highly similar to HBS1-like protein	93.0%	2.1	1	1	1	6	983,120	1,176,688	1,018,053	1,219,047	148,699	109,882	71,259	90,748	33.8	20.9	15.7	16.7	1.2	0.3	1.0	0.8	1.2	0.2	-1.2	0.3	1.0	0.8	1.2	0.1
IPI00922255	HBS1L	Uncharacterized protein	93.0%	1.8	1	1	1	6	983,120	1,176,688	1,018,053	1,219,047	148,699	109,882	71,259	90,748	33.8	20.9	15.7	16.7	1.2	0.3	1.0	0.8	1.2	0.2	-1.2	0.3	1.0	0.8	1.2	0.1
IPI00974576	HBS1L	isoform 3 of HBS1-like protein	93.0%	1.7	1	1	1	6	983,120	1,176,688	1,018,053	1,219,047	148,699	109,882	71,259	90,748	33.8	20.9	15.7	16.7	1.2	0.3	1.0	0.8	1.2	0.2	-1.2	0.3	1.0	0.8	1.2	0.1
IPI00983593	HBS1L	61 kDa protein	93.0%	2.0	1	1	1	6	983,120	1,176,688	1,018,053	1,219,047	148,699	109,882	71,259	90,748	33.8	20.9	15.7	16.7	1.2	0.3	1.0	0.8	1.2	0.2	-1.2	0.3	1.0	0.8	1.2	0.1
IPI00984269	HBS1L	cDNA FLJ59477, highly similar to HBS1-like protein	93.0%	2.7	1	1	1	6	983,120	1,176,688	1,018,053	1,219,047	148,699	109,882	71,259	90,748	33.8	20.9	15.7	16.7	1.2	0.3	1.0	0.8	1.2	0.2	-1.2	0.3	1.0	0.8	1.2	0.1
				INVGCIFCGPK	2	89.8%	1																									
IPI00074587	SRSF10	isoform 1 of Serine/arginine-rich splicing factor 10	100.0%	14.5	3	3	3	8	2,246,486	2,040,012	2,112,402	2,470,467	179,967	97,559	84,848	72,419	17.9	10.7	9.0	6.6	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.6	1.2	0.008	1.2	0.01
IPI00386662	SRSF10	isoform 4 of Serine/arginine-rich splicing factor 10	100.0%	22.0	3	3	3	8	2,246,486	2,040,012	2,112,402	2,470,467	179,967	97,559	84,848	72,419	17.9	10.7	9.0	6.6	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.6	1.2	0.008	1.2	0.01
IPI00983630	LOC653884	serine/arginine-rich splicing factor 10-like, partial	100.0%	21.0	3	3	3	8	2,246,486	2,040,012	2,112,402	2,470,467	179,967	97,559	84,848	72,419	17.9	10.7	9.0	6.6	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.6	1.2	0.008	1.2	0.01
IPI00009071	SRSF10	isoform 3 of Serine/arginine-rich splicing factor 10	100.0%	20.8	3	3	3	8	2,246,486	2,040,012	2,112,402	2,470,467	179,967	97,559	84,848	72,419	17.9	10.7	9.0	6.6	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.6	1.2	0.008	1.2	0.01
IPI00979506	SRSF10	serine/arginine-rich splicing factor 10 isoform 6	100.0%	23.0	3	3	3	8	2,246,486	2,040,012	2,112,402	2,470,467	179,967	97,559	84,848	72,419	17.9	10.7	9.0	6.6	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.6	1.2	0.008	1.2	0.01
IPI00412643	SRSF10	isoform 2 of Serine/arginine-rich splicing factor 10	100.0%	14.6	3	3	3	8	2,246,486	2,040,012	2,112,402	2,470,467	179,967	97,559	84,848	72,419	17.9	10.7	9.0	6.6	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.6	1.2	0.008	1.2	0.01
IPI00645384	SRSF10	FUS interacting protein (Serine/arginine-rich) 1	100.0%	22.1	3	3	3	8	2,246,486	2,040,012	2,112,402	2,470,467	179,967	97,559	84,848	72,419	17.9	10.7	9.0	6.6	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.6	1.2	0.008	1.2	0.01
IPI00646643	SRSF10	serine/arginine-rich splicing factor 10 isoform 5	100.0%	20.9	3	3	3	8	2,246,486	2,040,012	2,112,402	2,470,467	179,967	97,559	84,848	72,419	17.9	10.7	9.0	6.6	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.6	1.2	0.008	1.2	0.01
				GFAYVQFEDVR	2	100.0%	1																									
				QIEIQFAQGDR	2	99.8%	1																									
				YGPIVDVYVPLDFYTR	2	99.4%	1																									
IPI00009104	RUVBL2	RuvB-like 2	100.0%	30.2	11	11	13	1	28,689,316	29,501,061	28,303,036	33,078,756	2,911,508	810,679	2,023,637	1,043,279	22.7	6.1	16.0	7.1	1.0	0.8	-1.0	0.9	1.2	0.2	-1.0	0.6	1.1	0.03	1.2	0.07
				AAGVVLEMIR	2	99.3%	1																									
				ALESDMAPVLIMATNR	2	100.0%	1																									
				AVLIAGQPGTGK	2	100.0%	1																									
				DYDAMGSQTK	2	99.9%	1																									
				EYQDAFLFNELKGETMDTS	2	100.0%	1																									
				FVQCPDGELQK	2	99.9%	1																									
				GLGLDDALEPR	2	99.9%	1																									
				GTSYQSPHGIPIDLLDR	3	100.0%	1																									
				IGLETSLR	2	95.8%	1																									
				QASQGMVGQLAAR	2	100.0%	2																									
				TTEMETIYDLGTK	2	100.0%	2																									
IPI00009123	NUCB2	isoform 1 of Nucleobindin-2	98.2%	3.8	1	1	1	4	324,096	319,844	322,145	352,622	59,400	22,303	25,913	70,824	41.0	15.6	18.0	44.9	-1.0	0.9	-1.0	1	1.1	0.8	1.0	0.9	1.1	0.7	1.1	0.7
IPI00922708	NUCB2	isoform 2 of Nucleobindin-2	98.2%	3.8	1	1	1	4	324,096	319,844	322,145	352,622	59,400	22,303	25,913	70,824	41.0	15.6	18.0	44.9	-1.0	0.9	-1.0	1	1.1	0.8	1.0	0.9	1.1	0.7	1.1	0.7
IPI00979363	NUCB2	Uncharacterized protein	98.2%	4.1	1	1	1	4	324,096	319,844	322,145	352,622	59,400	22,303	25,913	70,824	41.0	15.6	18.0	44.9	-1.0	0.9	-1.0	1	1.1	0.8	1.0	0.9	1.1	0.7	1.1	0.7
IPI00980065	NUCB2	Protein	98.2%	8.1	1	1	1	4	324,096	319,844	322,145	352,622	59,400	22,303	25,913	70,824	41.0	15.6	18.0	44.9	-1.0	0.9	-1.0	1	1.1	0.8	1.0	0.9	1.1	0.7	1.1	0.7
				EYENIIALQENELKKK	3	98.2%	1																									
IPI00009213	BCL11B	isoform 1 of B-cell lymphoma/leukemia 11B	99.4%	5.2	2	2	2	2	4,137,885	4,111,130	4,213,235	4,910,490	419,150	215,480	263,269	246,059	22.7	11.7	14.0	11.2	-1.0	1	1.0	0.9	1.2	0.2	1.0	0.8	1.2	0.04	1.2	0.09
IPI00009646	BCL11B	isoform 2 of B-cell lymphoma/leukemia 11B	99.4%	5.6	2	2	2	2	4,137,885	4,111,130	4,213,235	4,910,490	419,150	215,480	263,269	246,059	22.7	11.7	14.0	11.2	-1.0	1	1.0	0.9	1.2	0.2	1.0	0.8	1.2	0.04	1.2	0.09
				GGGFAPGTEPFPGLFPR	2	87.1%	1																									
				VSEPVEIGIQVTPDEDDHLLSPTKGICPK	3	95.2%	1																									
IPI00009235	SSR3	Translocon-associated protein subunit gamma	99.6%	7.6	1	1	1	3	1,148,773	1,270,380	1,176,097	1,122,030	122,332	113,954	118,294	65,816	23.8	20.1	22.5	13.1	1.1	0.5	1.0	0.9	-1.0	0.9	-1.1	0.6	-1.1	0.3	-1.0	0.7
IPI00945960	SSR3	Uncharacterized protein	99.6%	8.1	1	1	1	3	1,148,773	1,270,380	1,176,097	1,122,030	122,332	113,954	118,294	65,816	23.8	20.1	22.5	13.1	1.1	0.5	1.0	0.9	-1.0	0.9	-1.1	0.6	-1.1	0.3	-1.0	0.7
IPI00946150	SSR3	cDNA FLJ52061, highly similar to Translocon-associated protein subunit gamma	99.6%	7.1	1	1	1	3	1,148,773	1,270,380	1,176,097	1,122,030	122,332	113,954	118,294	65,816	23.8	20.1	22.5	13.1	1.1	0.5	1.0	0.9	-1.0	0.9	-1.1	0.6	-1.1	0.3	-1.0	0.7
				QQSEEDLLLQDFSR	2	99.6%	1																									
IPI00909244	-	cDNA FLJ60015, highly similar to Adapter-related protein complex 1 sigma- 1B subu	99.8%	7.7	1	1	1	6	2,232,667	2,153,011	2,302,089	2,797,978	146,959	190,053	237,363	84,285	14.7	19.7	23.1	6.7	-1.0	0.7	1.0	0.8	1.3	0.01	1.1	0.6	1.3	0.01	1.2	0.1
IPI01015114	-	18 kDa protein	99.8%	10.5	1	1	1	6	2,232,667	2,153,011	2,302,089	2,797,978	146,959	190,053	237,363	84,285	14.7	19.7	23.1	6.7	-1.0	0.7	1.0	0.8	1.3	0.01	1.1	0.6	1.3	0.01	1.2	0.1
IPI00009244	AP1S2	cDNA FLJ52741, highly similar to Mus musculus adaptor-related protein complex 1,	99.8%	7.9	1	1	1	6	2,232,667	2,153,011	2,302,089	2,797,978	146,959	190,053	237,363	84,285	14.7	19.7	23.1	6.7	-1.0	0.7	1.0	0.8	1.3	0.01	1.1	0.6	1.3	0.01	1.2	0.1
IPI00385342	AP1S2	Uncharacterized protein	99.8%	10.5	1	1	1	6	2,232,667	2,153,011	2,302,089	2,797,978	146,959	190,053	237,363	84,285	14.7	19.7	23.1	6.7	-1.0	0.7	1.0	0.8	1.3	0.01	1.1	0.6	1.3	0.01	1.2	0.1
IPI00646398	AP1S2	cDNA FLJ53621, highly similar to Adapter-relatedprotein complex 1 sigma- 1B subu	99.8%	8.2	1	1	1	6	2,232,667	2,153,011	2,302,089	2,797,978	146,959	190,053	237,363	84,285	14.7	19.7	23.1	6.7	-1.0	0.7	1.0	0.8	1.3	0.01	1.1	0.6	1.3	0.01	1.2	0.1
IPI00922006	AP1S2	AP-1 complex subunit sigma-2	99.8%	10.2	1	1	1	6	2,232,667	2,153,011	2,302,089	2,797,978	146,959	190,053	237,363	84,285	14.7	19.7	23.1	6.7	-1.0	0.7	1.0	0.8	1.3	0.01	1.1	0.6	1.3	0.01	1.2	0.1
				YFGSVCELDIIFNFEK	2	98.9%	1																									
IPI00009253	NAPA	Alpha-soluble NSF attachment protein	100.0%	27.1	6	6	8	1	28,648,482	32,844,796	30,143,276	34,995,462	1,198,071	769,301	2,221,814	1,449,309	9.4	5.2	16.5	9.3	1.1	0.02	1.1	0.6	1.2	0.01	-1.1	0.3	1.1	0.2	1.2	0.1
				AIDIYEQVGTNAMDSPLLK	2	100.0%	1																									
				AIEIYTDMGR	2	99.8%	1																									
				LDQWLTTMLLR	2	100.0%	1																									
				NSQSFFSGLFGGSSK	2	100.0%	1																									
				VAGYAALLEQYQK	2	100.0%	2																									
				YEELFPAFSDSR	2	99.9%	2																									
IPI00009268	ACY1	cDNA FLJ60317, highly similar to Aminoacylase-1	100.0%	15.5	6	7	7	3	11,498,007	11,800,822	12,328,254	13,133,855	1,061,322	838,491	943,242	673,336	20.6	15.9	17.1	11.5	1.0	0.8	1.1	0.6	1.1	0.2	1.0	0.7	1.1	0.3	1.1	0.5
IPI00791053	ACY1	aminoacylase-1 isoform b	100.0%	22.9	6	7	7	3	11,498,007	11,800,822	12,328,254	13,133,855	1,061,322	838,491	943,242	673,336	20.6	15.9	17.1	11.5	1.0	0.8	1.1	0.6	1.1	0.2	1.0	0.7	1.1	0.3	1.1	0.5
IPI00940464	ACY1	Aminoacylase-1	100.0%	18.9	6	7	7	3	11,498,007	11,800,822	12,328,254	13,133,855	1,061,322	838,491	943,242	673,336	20.6	15.9	17.1	11.5	1.0	0.8	1.1	0.6	1.1	0.2	1.0	0.7	1.1	0.3	1.1	0.5
				DMNLTLEPEIMPAATDNR	2	100.0%	1																									
				EGSVTSVNLTK	2	98.8%	1																									
				GPEEEHPSVTLFR	3	99.3%	1																									
				LLPALASVPALPSDS	2	93.1%	1																									
				PDYGAAVAFFEETAR	2	90.9%	1																									
				TVQPKPDYGAAVAFFEETAR	2	100.0%	1																									
				TVQPKPDYGAAVAFFEETAR	3	100.0%	1																									
IPI00009286	MLL	isoform 1 of Histone-lysine N-methyltransferase MLL	93.5%	0.8	1	1	1	2	289,564	377,325	501,707	605,315	54,352	47,435	115,588	62,726	42.0	28.1	51.5	23.2	1.3	0.3	1.7	0.1	2.1	0.005	1.3	0.3	1.6	0.02	1.2	0.5
IPI00218500	MLL	isoform 14P-18B of Histone-lysine N-methyltransferase MLL	93.5%	0.8	1	1	1	2	289,564	377,325	501,707	605,315	54,352	47,435	115,588	62,726	42.0	28.1	51.5	23.2	1.3	0.3	1.7	0.1	2.1	0.005	1.3	0.3	1.6	0.02	1.2	0.5
				IMSPMRTGNTYSRNNVSSVSTTGTATDLESSAK	3	91.9%	1																									
IPI00009303	RFX5	DNA-binding protein RFX5	95.3%	4.2	1	1	1	3	3,559,850	3,322,560	3,557,983	3,491,980	204,332	217,819	169,063	170,846	12.8	14.7	10.6	10.9	-1.1	0.4	-1.0	1	-1.0	0.8	1.1	0.4	1.1	0.6	-1.0	0.8
IPI00658131	RFX5	Regulatory factor X, 5	95.3%	4.4	1	1	1	3	3,559,850	3,322,560	3,557,983	3,491,980	204,332	217,819	169,063	170,846	12.8	14.7	10.6	10.9	-1.1	0.4	-1.0	1	-1.0	0.8	1.1	0.4	1.1	0.6	-1.0	0.8
IPI00894289	RFX5	cDNA FLJ52375, highly similar to DNA-binding protein RFX5	95.3%	4.5	1	1	1	3	3,559,850	3,322,560	3,557,983	3,491,980	204,332	217,819	169,063	170,846	12.8	14.7	10.6	10.9	-1.1	0.4	-1.0	1	-1.0	0.8	1.1	0.4	1.1	0.6	-1.0	0.8
				LPLLLPRAPRSLIPPIPVSPPILAPR	3	95.3%	1																									
IPI00009305	GNPDA1	Glucosamine-6-phosphate isomerase 1	98.0%	10.0	2	2	2	5	2,736,413	2,726,948	2,936,677	2,837,349	257,444	154,045	173,447	101,962	21.0	12.6	13.2	8.0	-1.0	1	1.1	0.5	1.0	0.7	1.1	0.4	1.0	0.6	-1.0	0.6
IPI00963913	GNPDA1	Uncharacterized protein	98.0%	10.6	2	2	2	5	2,736,413	2,726,948	2,936,677	2,837,349	257,444	154,045	173,447	101,962	21.0	12.6	13.2	8.0	-1.0	1	1.1	0.5	1.0	0.7	1.1	0.4	1.0	0.6	-1.0	0.6
IPI00965994	GNPDA1	Uncharacterized protein	98.0%	21.0	2	2	2	5	2,736,413	2,726,948	2,936,677	2,837,349	257,444	154,045	173,447	101,962	21.0	12.6	13.2	8.0	-1.0	1	1.1	0.5	1.0	0.7	1.1	0.4	1.0	0.6	-1.0	0.6
IPI00967259	GNPDA1	Uncharacterized protein	98.0%	12.2	2	2	2	5	2,736,413	2,726,948	2,936,677	2,837,349	257,444	154,045	173,447	101,962	21.0	12.6	13.2	8.0	-1.0	1	1.1	0.5	1.0	0.7	1.1	0.4	1.0	0.6	-1.0	0.6
IPI00967567	GNPDA1	Uncharacterized protein	98.0%	18.0	2	2	2	5	2,736,413	2,726,948	2,936,677	2,837,349	257,444	154,045	173,447	101,962	21.0	12.6	13.2	8.0	-1.0	1	1.1	0.5	1.0	0.7	1.1	0.4	1.0	0.6	-1.0	0.6
				TFNMDEYVGLPR	2	98.0%	1																									
				YFTLGLPTGSTPLGCYK	2	94.5%	1																									
IPI00009315	ACBD3	Golgi resident protein GCP60	100.0%	13.5	4	4	4	1	6,636,299	6,265,111	6,429,600	7,355,130	589,004	524,334	571,565	377,113	19.9	18.7	19.9	11.5	-1.1	0.7	-1.0	0.8	1.1	0.3	1.0	0.8	1.2	0.1	1.1	0.2
				IQQDADSVITVGR	2	99.9%	1																									
				QLQEQHYQQYMQQLYQVQLAQQQAALQK	3	99.2%	1																									
				QQEVVVAGSSLPTSSK	2	100.0%	1																									

				WGFGLEELYGLALR	2	100.0%	1																									
IPI00009326	YAP1	Yes-associated protein beta	100.0%	6.0	2	2	2	4	599,007	623,806	739,961	621,884	82,376	60,669	86,908	53,764	30.8	21.8	26.3	19.3	1.0	0.8	1.2	0.3	1.0	0.8	1.2	0.3	-1.0	1	-1.2	0.3
IPI00216919	YAP1	isoform 1 of Yorkie homolog	100.0%	5.6	2	2	2	4	599,007	623,806	739,961	621,884	82,376	60,669	86,908	53,764	30.8	21.8	26.3	19.3	1.0	0.8	1.2	0.3	1.0	0.8	1.2	0.3	-1.0	1	-1.2	0.3
IPI00956212	YAP1	isoform 2 of Yorkie homolog	100.0%	5.7	2	2	2	4	599,007	623,806	739,961	621,884	82,376	60,669	86,908	53,764	30.8	21.8	26.3	19.3	1.0	0.8	1.2	0.3	1.0	0.8	1.2	0.3	-1.0	1	-1.2	0.3
IPI01009979	YAP1	53 kDa protein	100.0%	5.7	2	2	2	4	599,007	623,806	739,961	621,884	82,376	60,669	86,908	53,764	30.8	21.8	26.3	19.3	1.0	0.8	1.2	0.3	1.0	0.8	1.2	0.3	-1.0	1	-1.2	0.3
				GDSETDLEALFNAVMNPK	2	94.4%	1																									
				LDKESFLTWL	2	99.1%	1																									
IPI00009328	EIF4A3	Eukaryotic initiation factor 4A-III	100.0%	23.6	7	7	8	1	40,481,828	42,624,357	42,935,777	48,917,400	4,790,018	1,756,063	3,551,315	1,617,640	26.5	9.2	18.5	7.4	1.1	0.7	1.1	0.7	1.2	0.2	1.0	0.9	1.1	0.03	1.1	0.2
				DIEQYYSTQIDEMPMNVADLI	2	95.3%	1																									
				ETQALILAPTR	2	100.0%	1																									
				GIYAYGFEKPSAIQQR	3	99.8%	1																									
				GLDVPQVSLIINYDLPNNR	2	100.0%	2																									
				MLVLDEADEMLNK	2	100.0%	1																									
				VDWLTEK	2	95.2%	1																									
				VLISTDVWAR	2	99.6%	1																									
IPI00009329	UTRN	Utrophin	99.7%	0.8	2	2	2	1	4,475,875	4,498,550	4,928,030	4,862,900	305,385	384,577	355,323	234,968	15.3	19.1	16.1	10.8	1.0	1	1.1	0.4	1.1	0.3	1.1	0.4	1.1	0.4	-1.0	0.9
				QLLEQPESDSR	2	98.4%	1																									
				STSEGLLGDLDTEISWAK	2	93.5%	1																									
IPI00009342	IQGAP1	Ras GTPase-activating-like protein IQGAP1	100.0%	24.4	30	31	37	1	176,403,995	180,907,191	176,528,519	200,748,600	########	4,476,411	########	4,972,520	16.0	5.5	15.0	5.5	1.0	0.7	1.0	1	1.1	0.1	-1.0	0.7	1.1	0.02	1.1	0.1
				ALQSPALGLR	2	80.1%	1																									
				ATFYGEQVDYYK	2	100.0%	2																									
				DHINDIIK	2	99.8%	1																									
				DSLHEKFPDAGEDELLK	3	99.9%	1																									
				EEIQSSISGVTAAYNR	2	100.0%	1																									
				EQLWLANEGLITR	2	100.0%	2																									
				FALGIFAINEAVESGDVGK	2	100.0%	2																									
				FDVPGDENAEMDAR	2	88.1%	1																									
				FVHLLDQSDQDFQEELDLMK	3	100.0%	1																									
				GLQQQNSDWYLK	2	99.9%	1																									
				GVLLEIEDLQVNQFK	2	100.0%	1																									
				HTDNVIQWLNAMDEIGLPK	3	100.0%	1																									
				ILAIGLINEALDEGDAQK	2	100.0%	1																									
				ITLQDVVSHSK	2	99.7%	1																									
				LAAVALINAAIQK	2	99.3%	1																									
				LEGVLAEVAQHYQDTLIR	2	96.4%	1																									
				LEGVLAEVAQHYQDTLIR	3	100.0%	2																									
				LGNFFSPK	2	99.4%	1																									
				LIFQMPQNK	2	99.7%	1																									
				LIVDVIR	2	90.7%	1																									
				LPYDVTPEQALAHEEVK	3	99.9%	1																									
				MFLGDNAHLSIINEYLSQSYQK	3	100.0%	1																									
				NVIFEISPTEEVGDFEVK	2	100.0%	2																									
				RLIVDVIR	2	91.2%	1																									
				SNQQLENDLNLMDIK	2	100.0%	1																									
				TLINAEDPPMVVVR	2	100.0%	1																									
				TLQALQIPAAK	2	99.9%	2																									
				VDQIQEIVTGNPTVIK	2	100.0%	1																									
				VNVNLLIFLLNK	2	85.0%	1																									
				YGIQMPAFSK	2	99.9%	1																									
				YQELINDIAR	2	99.9%	1																									
IPI00009368	SFXN1	Sideroflexin-1	100.0%	39.8	8	9	10	1	24,444,397	25,217,289	26,066,566	27,527,483	1,723,094	1,048,554	2,332,755	825,918	15.8	9.3	20.0	6.7	1.0	0.7	1.1	0.6	1.1	0.1	1.0	0.7	1.1	0.1	1.1	0.6
				ILMAAPGMAIPPFIMNTLEK	2	98.8%	1																									
				ILMAAPGMAIPPFIMNTLEK	3	85.5%	1																									
				IQESHPELR	2	90.8%	1																									
				NILLTNEQLESAR	2	100.0%	2																									
				QAITQVVVSR	2	99.2%	1																									
				QGIVPPGLTENELWR	2	100.0%	1																									
				SGDAPLTVNELGTAYVSATTGAVATALGLNALTK	3	100.0%	1																									
				SSMSVTSLEAELQAK	2	99.9%	1																									
				VGIPVTDENGNR	2	97.3%	1																									
IPI00009375	HAAO	isoform 1 of 3-hydroxyanthranilate 3,4-dioxygenase	100.0%	11.5	2	2	2	2	1,414,875	1,273,286	1,398,561	1,434,491	135,737	48,300	142,745	100,497	21.5	8.5	22.8	15.7	-1.1	0.4	-1.0	0.9	1.0	0.9	1.1	0.4	1.1	0.2	1.0	0.8
IPI00894425	HAAO	Uncharacterized protein	100.0%	18.6	2	2	2	2	1,414,875	1,273,286	1,398,561	1,434,491	135,737	48,300	142,745	100,497	21.5	8.5	22.8	15.7	-1.1	0.4	-1.0	0.9	1.0	0.9	1.1	0.4	1.1	0.2	1.0	0.8
				DLGTQLAPIIQEFFSSEQYR	3	100.0%	1																									
				YYVGDTMDVLFEK	2	99.8%	1																									
IPI00009456	NT5E	5'-nucleotidase	95.5%	4.5	2	2	2	2	4,592,177	4,901,708	5,409,863	5,353,040	268,396	312,124	212,312	150,886	13.1	14.2	8.8	6.3	1.1	0.5	1.2	0.04	1.2	0.04	1.1	0.2	1.1	0.2	-1.0	0.8
IPI00552302	NT5E	5'-nucleotidase isoform 2 preproprotein	95.5%	5.0	2	2	2	2	4,592,177	4,901,708	5,409,863	5,353,040	268,396	312,124	212,312	150,886	13.1	14.2	8.8	6.3	1.1	0.5	1.2	0.04	1.2	0.04	1.1	0.2	1.1	0.2	-1.0	0.8
				GPLASQISGLYLPYK	2	92.6%	1																									
				YPFIVTSDDGR	2	83.6%	1																									
IPI00009480	COPS8	COP9 signalosome complex subunit 8	100.0%	12.9	2	2	2	4	1,202,439	1,075,382	1,168,643	1,335,253	130,362	107,370	149,125	61,851	24.2	22.3	28.5	10.4	-1.1	0.5	-1.0	0.9	1.1	0.4	1.1	0.6	1.2	0.07	1.1	0.3
IPI00377080	COPS8	COP9 signalosome complex subunit 8 isoform 2	100.0%	16.9	2	2	2	4	1,202,439	1,075,382	1,168,643	1,335,253	130,362	107,370	149,125	61,851	24.2	22.3	28.5	10.4	-1.1	0.5	-1.0	0.9	1.1	0.4	1.1	0.6	1.2	0.07	1.1	0.3
IPI00915801	COPS8	Protein	100.0%	32.5	2	2	2	4	1,202,439	1,075,382	1,168,643	1,335,253	130,362	107,370	149,125	61,851	24.2	22.3	28.5	10.4	-1.1	0.5	-1.0	0.9	1.1	0.4	1.1	0.6	1.2	0.07	1.1	0.3
IPI00916489	COPS8	Uncharacterized protein	100.0%	15.6	2	2	2	4	1,202,439	1,075,382	1,168,643	1,335,253	130,362	107,370	149,125	61,851	24.2	22.3	28.5	10.4	-1.1	0.5	-1.0	0.9	1.1	0.4	1.1	0.6	1.2	0.07	1.1	0.3
				GILEQGWQADSTTR	2	100.0%	1																									
				KPVAGALDVSFNK	2	98.4%	1																									
IPI00009490	C17orf59	PRO2472	93.6%	13.5	1	1	1	1	2,298,800	2,117,300	2,198,760	2,240,180	87,148	82,642	145,675	73,919	8.5	8.7	14.8	7.4	-1.1	0.2	-1.0	0.6	-1.0	0.6	1.0	0.6	1.1	0.3	1.0	0.8
				MQPTLSAVSSCTAPPRPR	2	93.6%	1																									
IPI00019346	RAP2A	Ras-related protein Rap-2a	97.4%	13.1	1	1	1	4	835,663	945,733	780,033	819,555	70,521	96,346	63,851	85,363	18.9	22.8	18.3	23.3	1.1	0.4	-1.1	0.6	-1.0	0.9	-1.2	0.2	-1.2	0.4	1.1	0.7
IPI00980330	RAP2A	12 kDa protein	97.4%	22.2	1	1	1	4	835,663	945,733	780,033	819,555	70,521	96,346	63,851	85,363	18.9	22.8	18.3	23.3	1.1	0.4	-1.1	0.6	-1.0	0.9	-1.2	0.2	-1.2	0.4	1.1	0.7
IPI00018364	RAP2B	Ras-related protein Rap-2b	97.4%	13.1	1	1	1	4	835,663	945,733	780,033	819,555	70,521	96,346	63,851	85,363	18.9	22.8	18.3	23.3	1.1	0.4	-1.1	0.6	-1.0	0.9	-1.2	0.2	-1.2	0.4	1.1	0.7
IPI00009607	RAP2C	Ras-related protein Rap-2c	97.4%	13.1	1	1	1	4	835,663	945,733	780,033	819,555	70,521	96,346	63,851	85,363	18.9	22.8	18.3	23.3	1.1	0.4	-1.1	0.6	-1.0	0.9	-1.2	0.2	-1.2	0.4	1.1	0.7
				NGQGFILVYSLVNQQSFQDIKPMR	3	97.4%	1																									
IPI00009629	ST3GAL1	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 1	93.4%	6.2	1	1	1	1	4,860,770	5,521,550	4,542,090	5,476,530	211,949	427,629	327,998	187,138	9.8	17.3	16.2	7.6	1.1	0.2	-1.1	0.4	1.1	0.06	-1.2	0.1	-1.0	0.9	1.2	0.04
				TGVHDADFESNVTATLASINK	2	93.4%	1																									
IPI00009631	ST3GAL4	isoform 1 of CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransfera	95.0%	3.9	1	1	1	8	330,119	326,728	436,059	385,279	18,978	30,394	47,536	24,435	12.9	20.8	24.4	14.2	-1.0	0.9	1.3	0.07	1.2	0.1	1.3	0.09	1.2	0.2	-1.1	0.4
IPI00216273	ST3GAL4	isoform 2 of CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransfera	95.0%	3.9	1	1	1	8	330,119	326,728	436,059	385,279	18,978	30,394	47,536	24,435	12.9	20.8	24.4	14.2	-1.0	0.9	1.3	0.07	1.2	0.1	1.3	0.09	1.2	0.2	-1.1	0.4
IPI00216274	ST3GAL4	isoform 3 of CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransfera	95.0%	4.0	1	1	1	8	330,119	326,728	436,059	385,279	18,978	30,394	47,536	24,435	12.9	20.8	24.4	14.2	-1.0	0.9	1.3	0.07	1.2	0.1	1.3	0.09	1.2	0.2	-1.1	0.4
IPI00216275	ST3GAL4	isoform 4 of CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransfera	95.0%	3.8	1	1	1	8	330,119	326,728	436,059	385,279	18,978	30,394	47,536	24,435	12.9	20.8	24.4	14.2	-1.0	0.9	1.3	0.07	1.2	0.1	1.3	0.09	1.2	0.2	-1.1	0.4
IPI00306884	ST3GAL4	Uncharacterized protein	95.0%	3.7	1	1	1	8	330,119	326,728	436,059	385,279	18,978	30,394	47,536	24,435	12.9	20.8	24.4	14.2	-1.0	0.9	1.3	0.07	1.2	0.1	1.3	0.09	1.2	0.2	-1.1	0.4
IPI00795122	ST3GAL4	isoform 5 of CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransfera	95.0%	4.0	1	1	1	8	330,119	326,728	436,059	385,279	18,978	30,394	47,536	24,435	12.9	20.8	24.4	14.2	-1.0	0.9	1.3	0.07	1.2	0.1	1.3	0.09	1.2	0.2	-1.1	0.4
IPI00980130	ST3GAL4	Alpha 2,3-sialyltransferase IV type A1-12	95.0%	4.0	1	1	1	8	330,119	326,728	436,059	385,279	18,978	30,394	47,536	24,435	12.9	20.8	24.4	14.2	-1.0	0.9	1.3	0.07	1.2	0.1	1.3	0.09	1.2	0.2	-1.1	0.4
IPI00984794	ST3GAL4	Uncharacterized protein	95.0%	8.5	1	1	1	8	330,119	326,728	436,059	385,279	18,978	30,394	47,536	24,435	12.9	20.8	24.4	14.2	-1.0	0.9	1.3	0.07	1.2	0.1	1.3	0.09	1.2	0.2	-1.1	0.4
				ILNPFFMEIAADK	2	95.0%	1																									
IPI00009634	SQRDL	Sulfide:quinone oxidoreductase, mitochondrial	98.5%	3.1	1	1	1	1	5,322,380	5,819,810	5,205,200	6,172,810	611,908	491,362	282,587	383,810	25.7	18.9	12.1	13.9	1.1	0.5	-1.0	0.9	1.2	0.3	-1.1	0.3	1.1	0.6	1.2	0.08
				TAAAVAAQSGILDR	2	98.5%	1																									
IPI00009659	RPRD1B	Regulation of nuclear pre-mRNA domain-containing protein 1B	100.0%	19.6	5	5	6	1	19,714,750	19,619,060	20,776,475	22,008,400	1,130,619	759,948	433,497	393,526	12.8	8.7	4.7	4.0	-1.0	0.9	1.1	0.4	1.1	0.1	1.1	0.2	1.1	0.02	1.1	0.07
				ALQDLENAASGDATVR	2	100.0%	2																									
				EFESVLVDAFSHVAR	2	99.9%	1																									
				LLNIWQER	2	94.6%	1																									
				LTFLYLANDVIQNSK	2	99.6%	1																									
				MLVEYTQNQK	2	99.6%	1																									
IPI00009700	RABL5	isoform 1 of Rab-like protein 5	94.2%	9.7	1	1	1	4	595,230	650,560	736,240	789,298	72,259	48,593	75,804	45,382	27.2	16.7	23.0	12.9	1.1	0.5	1.2	0.2	1.3	0.05	1.1	0.4	1.2	0.07	1.1	0.6
IPI00011360	RABL5	isoform 2 of Rab-like protein 5	94.2%	11.6	1	1	1	4	595,230	650,560	736,240	789,298	72,259	48,593	75,804	45,382	27.2	16.7	23.0	12.9	1.1	0.5	1.2	0.2	1.3	0.05	1.1	0.4	1.2	0.07	1.1	0.6
IPI00909609	RABL5	rab-like protein 5 isoform c	94.2%	16.7	1	1	1	4	595,230	650,560	736,240	789,298	72,259	48,593	75,804	45,382	27.2	16.7	23.0	12.9	1.1	0.5	1.2	0.2	1.3	0.05	1.1	0.4	1.2	0.07	1.1	0.6
IPI00922845	RABL5	cDNA FLJ57972, highly similar to Homo sapiens RAB, member RAS oncogene fami	94.2%	12.2	1	1	1	4	595,230	650,560	736,240	789,298	72,259	48,593	75,804	45,382	27.2	16.7	23.0	12.9	1.1	0.5	1.2	0.2	1.3	0.05	1.1	0.4	1.2	0.07	1.1	0.6
				DAHGVVIVFNADIPSHRK	2	94.2%	1																									
IPI00009747	LSS	Lanosterol synthase	100.0%	3.6	2	2	2	3	3,001,770	3,002,953	2,998,508	3,193,152	175,982	129,460	186,809	95,024	13.1	9.6	13.9	6.7	1.0	1	-1.0	1	1.1	0.4	-1.0	1	1.1	0.3	1.1	0.4
IPI00923487	LSS	lanosterol synthase isoform 3	100.0%	4.0	2	2	2	3	3,001,770	3,002,953	2,998,508	3,193,152	175,982	129,460	186,809	95,024	13.1	9.6	13.9	6.7	1.0	1	-1.0	1	1.1	0.4	-1.0	1	1.1	0.3	1.1	0.4
IPI00923506	LSS	lanosterol synthase isoform 2	100.0%	3.6	2	2	2	3	3,001,770	3,002,953	2,998,508	3,193,152	175,982	129,460	186,809	95,024	13.1	9.6	13.9	6.7	1.0	1	-1.0	1	1.1	0.4	-1.0	1	1.1	0.3	1.1	0.4
				ILGVGPDDPDLVR	2	99.9%	1																									
				LSAAEDPLVQSLR	2	99.9%	1																									
IPI00009750	LGALS4	Galectin-4	100.0%	41.2	13	17	24	1	126,822,068	131,212,819	127,623,098	147,091,960	9,108,261	3,592,173	9,853,072	4,239,311	16.1	6.1	17.3	6.4	1.0	0.7	1.0	1	1.2	0.08	-1.0	0.7	1.1	0.02	1.2	0.1
				FDGWDK	2	91.6%	1																									
				FDGWDKVVFNTLQGGK	3	100.0%	1																									
				FFVNFVVGQDPGSDVAFHFNPR	3	100.0%	1																									
				GYVPPTGK	2	80.7%	1																									
				ITHNPFGPGQFFDLSIR	2	100.0%	2																									
				ITHNPFGPGQFFDLSIR	3	100.0%	2																									
				LQGGLTAR	1	94.8%	1																									
				LSAFQR	2	80.4%	1																									
				NSLLNGSWGSEEK	2	100.0%	3																									
				NSLLNGSWGSEEKK	2	100.0%	1																									
				VGSSGDIALHINPR	2	100.0%	2																									
				VGSSGDIALHINPR	3	100.0%	1																									
				VVFNTLQGGK	2	100.0%	2																									
				VVVNGNPFYEYGHR	2	100.0%	2																									
				VVVNGNPFYEYGHR	3	98.9%	1																									
				VYANGQHLFDFAHR	2	100.0%	1																									
				VYANGQHLFDFAHR	3	100.0%	1																									
IPI00009771	LMNB2	Lamin-B2	100.0%	28.4	14	14	14	2	43,393,329	44,409,317	40,866,055	50,418,290	4,710,277	2,453,877	2,734,933	2,309,419	24.3	12.4	15.0	10.2	1.0	0.9	-1.1	0.7	1.2	0.2	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00879819	LMNB2	Lamin-B2	100.0%	29.3	14	14	14	2	43,393,329	44,409,317	40,866,055	50,418,290	4,710,277	2,453,877	2,734,933	2,309,419	24.3	12.4	15.0	10.2	1.0	0.9	-1.1	0.7	1.2	0.2	-1.1	0.4	1.1	0.1	1.2	0.03
				AGGPATPLSPTR	2	99.4%	1																									
				ALYESELADAR	2	96.5%	1																									
				DVMQQQLAEYQELLDVK	3	100.0%	1																									
				ENENGEEEEEEAEFGEEDLFHQQGDPR	3	94.6%	1																									
				EQEMTEMRDVMQQQLAEYQELLDVK	3	99.9%	1																									
				GLESDVAELR	2	100.0%	1																									
				GQSSWGTGESFR	2	90.3%	1																									
				IRELEEAMAGER	2	99.9%	1																									
				LALDMEINAYR	2	98.8%	1																									
				LESLSYQLSGLQK	2	100.0%	1																									
				MAQALEELR	2	98.3%	1																									
				QVLEGEEIAYK	2	99.9%	1																									
				RLVEVDSSR	2	100.0%	1																									
				TVLVNADGEEVAMR	2	100.0%	1																									
IPI00009790	PFKP	6-phosphofructokinase type C	100.0%	36.6	22	26	31	1	148,925,149	159,282,475	145,245,500	175,365,050	########	6,339,851	8,972,844	5,125,568	19.0	8.9	13.8	6.5	1.1	0.5	-1.0	0.8	1.2	0.09	-1.1	0.2	1.1	0.08	1.2	0.02
				AACNLLQR	2	97.3%	1																									
				AIGVLTSGGDAQGMNAAVR	2	100.0%	2																									

				AMEWITAK	2	99.2%	1																									
				ASYDVSDSGQLEHVQPWSV	2	100.0%	2																									
				EIGWTDVGGWTGQGGSILGTK	2	100.0%	2																									
				EIGWTDVGGWTGQGGSILGTK	3	100.0%	1																									
				ELVVTQLGYDTR	2	100.0%	1																									
				FLEHLSGAGK	3	93.4%	1																									
				FTTDDSICVLGISK	2	100.0%	1																									
				GITNLCVIGGDGSLTGANLFR	3	100.0%	1																									
				IIEVVDAIMTTAQSHQR	3	100.0%	1																									
				IKELVVTQLGYDTR	2	99.8%	1																									
				LAIKLPDDQIPK	2	98.3%	1																									
				LAIKLPDDQIPK	3	96.8%	1																									
				LPLMECVQMTQDVQK	2	100.0%	2																									
				LPLMECVQMTQDVQK	3	93.5%	1																									
				MGIYVGAK	2	98.4%	1																									
				MLAIYDGFDGFAK	2	100.0%	2																									
				NVIFQPVAELK	2	100.0%	1																									
				NVLGHMQQGGAPSPFDR	2	98.3%	1																									
				NVLGHMQQGGAPSPFDR	3	98.9%	1																									
				SFAGNLNTYK	2	99.9%	1																									
				TFVLEVMGR	2	99.8%	1																									
				TNCNVAVINVGAPAAGMNAAVR	3	100.0%	1																									
				VTILGHVQR	2	99.2%	1																									
				YLEEIATQMR	2	98.8%	1																									
IPI00009822	SRP54	Signal recognition particle 54 kDa protein	99.9%	4.4	2	2	2	2	17,194,785	17,126,645	16,269,835	19,452,725	1,862,784	764,373	1,012,471	848,085	24.2	10.0	13.9	9.8	-1.0	1	-1.1	0.7	1.1	0.3	-1.1	0.5	1.1	0.08	1.2	0.04
IPI00929464	SRP54	signal recognition particle 54 kDa protein isoform 2	99.9%	4.8	2	2	2	2	17,194,785	17,126,645	16,269,835	19,452,725	1,862,784	764,373	1,012,471	848,085	24.2	10.0	13.9	9.8	-1.0	1	-1.1	0.7	1.1	0.3	-1.1	0.5	1.1	0.08	1.2	0.04
				DMYEQFQNIMK	2	99.9%	1																									
				DVQELLTQYTK	2	98.8%	1																									
IPI00009841	EWSR1	RNA-binding protein EWS isoform 1	100.0%	8.0	4	4	5	5	2,609,631	2,913,103	2,742,210	3,012,194	191,732	183,423	170,404	54,747	16.4	14.1	13.9	4.1	1.1	0.3	1.1	0.6	1.2	0.1	-1.1	0.5	1.0	0.6	1.1	0.2
IPI00065554	EWSR1	RNA-binding protein EWS isoform 4	100.0%	8.8	4	4	5	5	2,609,631	2,913,103	2,742,210	3,012,194	191,732	183,423	170,404	54,747	16.4	14.1	13.9	4.1	1.1	0.3	1.1	0.6	1.2	0.1	-1.1	0.5	1.0	0.6	1.1	0.2
IPI00872855	EWSR1	isoform EWS of RNA-binding protein EWS	100.0%	8.1	4	4	5	5	2,609,631	2,913,103	2,742,210	3,012,194	191,732	183,423	170,404	54,747	16.4	14.1	13.9	4.1	1.1	0.3	1.1	0.6	1.2	0.1	-1.1	0.5	1.0	0.6	1.1	0.2
IPI00879242	EWSR1	Ewing sarcoma breakpoint region 1	100.0%	8.6	4	4	5	5	2,609,631	2,913,103	2,742,210	3,012,194	191,732	183,423	170,404	54,747	16.4	14.1	13.9	4.1	1.1	0.3	1.1	0.6	1.2	0.1	-1.1	0.5	1.0	0.6	1.1	0.2
IPI00879259	EWSR1	RNA-binding protein EWS isoform 3	100.0%	8.1	4	4	5	5	2,609,631	2,913,103	2,742,210	3,012,194	191,732	183,423	170,404	54,747	16.4	14.1	13.9	4.1	1.1	0.3	1.1	0.6	1.2	0.1	-1.1	0.5	1.0	0.6	1.1	0.2
				AAVEWFDGK	2	98.3%	1																									
				AAVEWFDGKDFQGSK	2	100.0%	1																									
				GDATVSYEDPPTAK	2	100.0%	2																									
				QDHPSSMGVYGQESGGFSGPGENR	3	100.0%	1																									
IPI00009865	KRT10	Keratin, type I cytoskeletal 10	100.0%	23.3	8	8	9	1	37,239,695	38,972,590	34,766,897	45,441,797	2,366,886	2,640,861	1,314,355	887,890	14.2	15.2	8.5	4.4	1.0	0.6	-1.1	0.4	1.2	0.02	-1.1	0.2	1.2	0.07	1.3	0.0001
				ADLEMQIESLTEELAYLKK	3	99.7%	1																									
				ALEESNYELEGK	2	100.0%	1																									
				GSLGGGFSSGGFSGGSFSR	2	99.9%	1																									
				QSLEASLAETEGR	2	100.0%	2																									
				SLLEGEGSSGGGGR	2	100.0%	1																									
				TIDDLKNQILNLTTDNANILLQIDNAR	3	100.0%	1																									
				VTMQNLNDR	2	97.6%	1																									
				YCVQLSQIQAQISALEEQLQQIR	3	100.0%	1																									
IPI00009867	KRT5	Keratin, type II cytoskeletal 5	96.9%	1.5	1	1	1	2	2,772,055	3,045,845	2,692,960	3,161,910	232,529	124,161	214,476	165,102	18.8	9.1	17.8	11.7	1.1	0.3	-1.0	0.8	1.1	0.2	-1.1	0.2	1.0	0.6	1.2	0.1
IPI00796776	KRT5	cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5	96.9%	1.6	1	1	1	2	2,772,055	3,045,845	2,692,960	3,161,910	232,529	124,161	214,476	165,102	18.8	9.1	17.8	11.7	1.1	0.3	-1.0	0.8	1.1	0.2	-1.1	0.2	1.0	0.6	1.2	0.1
				EYQELMNTK	2	96.9%	1																									
IPI00009901	NUTF2	Nuclear transport factor 2	100.0%	74.8	6	6	8	1	25,902,200	26,862,830	25,352,030	30,572,595	3,121,640	1,458,369	2,352,231	1,167,422	27.0	12.1	20.8	8.5	1.0	0.8	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.08	1.2	0.08
				ADEDPIMGFHQMFLLK	3	91.8%	1																									
				IQHSITAQDHQPTPDSCIISMVVGQLK	3	99.9%	1																									
				LALHNFG	2	99.1%	1																									
				LSSLPFQK	2	99.7%	2																									
				NINDAWVCTNDMFR	2	100.0%	2																									
				TQLGAIYIDASCLTWEGQQFQGK	3	93.9%	1																									
IPI00009904	PDIA4	Protein disulfide-isomerase A4	100.0%	47.6	28	28	39	1	184,990,303	192,101,012	187,854,511	211,164,466	########	8,497,767	########	5,831,867	21.0	9.9	12.5	6.2	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.09
				DFPEYTFAIADEEDYAGEVK	2	100.0%	2																									
				DLGLSESGEDVNAAILDESGK	2	96.1%	1																									
				DLGLSESGEDVNAAILDESGKK	3	100.0%	1																									
				EVSQPDWTPPPEVTLVLTK	2	100.0%	2																									
				FAMEPEEFDSDTLR	2	100.0%	2																									
				FDVSGYPTIK	2	93.5%	1																									
				FDVSGYPTLK	2	91.0%	1																									
				FHHTFSTEIAK	2	96.3%	1																									
				FIEEHATK	2	98.8%	1																									
				GESDPAYQQYQDAANNLR	3	99.8%	1																									
				GLVIAK	1	84.8%	1																									
				GQAVDYEGSR	2	100.0%	2																									
				GRPYDYNGPR	2	98.1%	1																									
				IDATSASVLASR	2	100.0%	1																									
				MDATANDVPSDR	2	100.0%	2																									
				QLEPVYNSLAK	2	100.0%	2																									
				RFDVSGYPTLK	2	100.0%	2																									
				RSPPIPLAK	2	99.0%	1																									
				SHMMDVQGSTQDSAIKDFVLK	3	100.0%	2																									
				TFDSIVMDPK	2	100.0%	2																									
				VDATAETDLAK	2	98.2%	1																									
				VDATAETDLAKR	2	100.0%	2																									
				VEGFPTIYFAPSGDK	2	100.0%	1																									
				VSQGQLVVMQPEK	2	100.0%	2																									
				YALPLVGHR	2	99.8%	1																									
				YGIVDYMIEQSGPPSK	3	99.8%	1																									
				YGIVDYMIEQSGPPSKEILTLK	3	100.0%	1																									
				YKVEGFPTIYFAPSGDKK	3	98.7%	1																									
IPI00009922	C14orf156	SRA stem-loop-interacting RNA-binding protein, mitochondrial	95.4%	9.2	1	1	1	1	8,377,780	9,051,950	7,312,490	9,711,350	970,959	249,915	580,423	478,584	25.9	6.2	17.8	11.0	1.1	0.5	-1.1	0.4	1.2	0.3	-1.2	0.02	1.1	0.3	1.3	0.01
				SINQPVAFVR	2	95.4%	1																									
IPI00009923	P4HA1	isoform 1 of Prolyl 4-hydroxylase subunit alpha-1	100.0%	38.4	17	21	26	1	57,127,780	62,204,310	56,366,581	63,180,390	6,157,159	2,911,081	3,339,572	2,418,562	24.1	10.5	13.3	8.6	1.1	0.5	-1.0	0.9	1.1	0.4	-1.1	0.2	1.0	0.8	1.1	0.1
				AEEDKLEQIKK	3	88.5%	1																									
				ATISNPITGDLETVHYR	2	99.9%	1																									
				ATISNPITGDLETVHYR	3	100.0%	1																									
				DPEGFVGHPVNAFK	2	100.0%	1																									
				DPEGFVGHPVNAFK	3	99.9%	1																									
				FHDIISDAEIEIVK	2	100.0%	1																									
				FILAPAKQEDEWDKPR	3	100.0%	1																									
				HAACPVLVGNK	2	100.0%	2																									
				KDEPDAFKELGTGNR	2	95.2%	1																									
				KDEPDAFKELGTGNR	3	100.0%	1																									
				LLELDPEHQR	2	99.2%	1																									
				LLELDPEHQR	3	92.9%	1																									
				LNTEWSELENLVLK	2	100.0%	2																									
				LQDTYNLDTDTISK	2	100.0%	2																									
				LTSTATKDPEGFVGHPVNAFK	3	100.0%	1																									
				QLDEGEISTIDK	2	88.8%	1																									
				QYFPNDEDQVGAAK	2	100.0%	2																									
				RLNTEWSELENLVLK	2	99.9%	1																									
				SAWLSGYENPVVSR	2	100.0%	2																									
				SFLTAEDCFELGK	2	99.9%	1																									
				YFEYIMAK	2	99.8%	1																									
IPI00009943	TPT1	Tumor protein, translationally-controlled 1	100.0%	25.0	4	5	7	2	6,477,089	6,718,470	6,114,776	7,431,453	606,913	338,815	410,441	359,968	21.0	11.3	15.0	10.8	1.0	0.7	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.04
IPI00550900	TPT1	Translationally-controlled tumor protein	100.0%	27.3	4	5	7	2	6,477,089	6,718,470	6,114,776	7,431,453	606,913	338,815	410,441	359,968	21.0	11.3	15.0	10.8	1.0	0.7	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.04
				DLISHDEMFSDIYK	3	100.0%	1																									
				EIADGLCLEVEGK	2	100.0%	2																									
				HILANFK	2	94.9%	1																									
				VKPFMTGAAEQIK	2	99.9%	2																									
				VKPFMTGAAEQIK	3	99.7%	1																									
IPI00009946	TOMM34	Mitochondrial import receptor subunit TOM34	96.0%	10.7	2	2	2	1	5,643,725	5,234,225	5,691,240	5,267,335	276,214	248,669	374,291	144,589	10.9	10.6	14.7	6.1	-1.1	0.3	1.0	0.9	-1.1	0.3	1.1	0.3	1.0	0.9	-1.1	0.3
				SSFADISNLLQIEPR	2	96.0%	1																									
				TVLQIDDNVTSAVEGINR	2	96.0%	1																									
IPI00009950	LMAN2	Vesicular integral-membrane protein VIP36	99.9%	8.7	2	2	2	4	4,395,838	4,421,830	3,701,033	4,092,123	177,461	196,627	184,529	66,107	9.0	9.9	11.2	3.6	1.0	0.9	-1.2	0.03	-1.1	0.2	-1.2	0.03	-1.1	0.2	1.1	0.1
IPI00966202	LMAN2	cDNA FLJ52285, highly similar to Vesicular integral-membrane protein VIP36	99.9%	10.9	2	2	2	4	4,395,838	4,421,830	3,701,033	4,092,123	177,461	196,627	184,529	66,107	9.0	9.9	11.2	3.6	1.0	0.9	-1.2	0.03	-1.1	0.2	-1.2	0.03	-1.1	0.2	1.1	0.1
IPI00966452	LMAN2	Uncharacterized protein	99.9%	10.8	2	2	2	4	4,395,838	4,421,830	3,701,033	4,092,123	177,461	196,627	184,529	66,107	9.0	9.9	11.2	3.6	1.0	0.9	-1.2	0.03	-1.1	0.2	-1.2	0.03	-1.1	0.2	1.1	0.1
IPI00967014	LMAN2	Uncharacterized protein	99.9%	9.5	2	2	2	4	4,395,838	4,421,830	3,701,033	4,092,123	177,461	196,627	184,529	66,107	9.0	9.9	11.2	3.6	1.0	0.9	-1.2	0.03	-1.1	0.2	-1.2	0.03	-1.1	0.2	1.1	0.1
				LFQLMVEHTPDEESIDWTK	3	99.9%	1																									
				WTELAGCTADFR	2	99.3%	1																									
IPI00009958	COPS5	COP9 signalosome complex subunit 5	98.7%	5.7	1	1	1	3	672,357	678,283	696,200	622,527	72,557	50,508	18,785	37,902	24.1	16.7	6.0	13.6	1.0	0.9	1.0	0.8	-1.1	0.6	1.0	0.8	-1.1	0.4	-1.1	0.1
IPI00980479	COPS5	Uncharacterized protein	98.7%	9.6	1	1	1	3	672,357	678,283	696,200	622,527	72,557	50,508	18,785	37,902	24.1	16.7	6.0	13.6	1.0	0.9	1.0	0.8	-1.1	0.6	1.0	0.8	-1.1	0.4	-1.1	0.1
IPI00985306	COPS5	Uncharacterized protein	98.7%	12.6	1	1	1	3	672,357	678,283	696,200	622,527	72,557	50,508	18,785	37,902	24.1	16.7	6.0	13.6	1.0	0.9	1.0	0.8	-1.1	0.6	1.0	0.8	-1.1	0.4	-1.1	0.1
				VNAQAAAYEYMAAYIENAK	3	98.7%	1																									
IPI00009960	IMMT	isoform 1 of Mitochondrial inner membrane protein	100.0%	7.7	3	3	3	7	2,573,103	2,739,719	2,527,234	3,030,776	280,440	92,223	212,106	109,157	24.4	7.5	18.8	8.1	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.08	1.2	0.07
IPI00470829	IMMT	80 kDa protein	100.0%	8.0	3	3	3	7	2,573,103	2,739,719	2,527,234	3,030,776	280,440	92,223	212,106	109,157	24.4	7.5	18.8	8.1	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.08	1.2	0.07
IPI00554469	IMMT	isoform 2 of Mitochondrial inner membrane protein	100.0%	7.8	3	3	3	7	2,573,103	2,739,719	2,527,234	3,030,776	280,440	92,223	212,106	109,157	24.4	7.5	18.8	8.1	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.08	1.2	0.07
IPI00910079	IMMT	cDNA FLJ59418, highly similar to Mitochondrial inner membrane protein	100.0%	8.8	3	3	3	7	2,573,103	2,739,719	2,527,234	3,030,776	280,440	92,223	212,106	109,157	24.4	7.5	18.8	8.1	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.08	1.2	0.07
IPI00926611	IMMT	cDNA FLJ59388, highly similar to Mitochondrial inner membrane protein	100.0%	8.2	3	3	3	7	2,573,103	2,739,719	2,527,234	3,030,776	280,440	92,223	212,106	109,157	24.4	7.5	18.8	8.1	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.08	1.2	0.07
IPI01012925	IMMT	83 kDa protein	100.0%	7.8	3	3	3	7	2,573,103	2,739,719	2,527,234	3,030,776	280,440	92,223	212,106	109,157	24.4	7.5	18.8	8.1	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.08	1.2	0.07
IPI01015181	IMMT	mitochondrial inner membrane protein isoform 2	100.0%	7.7	3	3	3	7	2,573,103	2,739,719	2,527,234	3,030,776	280,440	92,223	212,106	109,157	24.4	7.5	18.8	8.1	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.08	1.2	0.07
				IAGAGLLFVGGGIGGTILYAK	3	84.0%	1																									
				LSEQELQFR	2	97.0%	1																									
				QTASVTLQAIAAQNAAVQAVNAHSNILK	3	94.0%	1																									
IPI00010080	OXSR1	Serine/threonine-protein kinase OSR1	95.3%	2.9	1	1	1	1	2,342,400	2,507,230	2,052,760	2,671,750	167,744	143,957	123,094	183,226	16.0	12.8	13.4	15.3	1.1	0.5	-1.1	0.2	1.1	0.2	-1.2	0.04	1.1	0.5	1.3	0.02
				LASGVEGSDIPDDGK	2	95.3%	1																									
IPI00010105	EIF6	Eukaryotic translation initiation factor 6	100.0%	38.8	5	6	8	1	18,008,694	19,170,355	18,444,825	21,504,980	1,998,707	1,169,150	1,403,618	630,633	24.8	13.6	17.0	6.6	1.1	0.6	1.0	0.9	1.2	0.2	-1.0	0.7	1.1	0.1	1.2	0.08
				ASFENNCEIGCFAK	2	100.0%	1																									
				HGLLVPNNTTDQELQHIR	3	100.0%	2																									
				LNEAQPSTIATSMR	2	100.0%	1																									
				QTVADQVLVGSYCVFSNQGGLVHPK	3	99.6%	1																									
				TSIEDQDELSSLLQVPLVAGTVNR	2	100.0%	2																									

				TSIEDQDELSSLLQVPLVAGTVNR	3	99.9%	1																									
IPI00010120	CTBP2	isoform 1 of C-terminal-binding protein 2	100.0%	4.5	2	2	2	2	1,835,828	2,004,162	1,787,046	2,184,570	182,948	94,457	138,737	126,350	22.3	10.5	17.4	12.9	1.1	0.4	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.3	1.2	0.07
IPI00647506	CTBP2	C-terminal binding protein 2	100.0%	3.9	2	2	2	2	1,835,828	2,004,162	1,787,046	2,184,570	182,948	94,457	138,737	126,350	22.3	10.5	17.4	12.9	1.1	0.4	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.3	1.2	0.07
				IGSGYDNVDIK	2	99.5%	1																									
				PLVALLDGR	2	99.9%	1																									
IPI00010136	CTBP2	isoform 2 of C-terminal-binding protein 2	100.0%	3.2	3	3	3	1	10,449,898	10,507,512	10,006,156	11,232,990	692,484	1,036,937	516,422	729,485	14.8	22.1	11.5	14.5	1.0	1	-1.0	0.6	1.1	0.5	-1.1	0.7	1.1	0.6	1.1	0.2
				IGSGYDNVDIK	2	99.5%	1																									
				PLVALLDGR	2	99.9%	1																									
				TVLPEFLAFLR	2	92.4%	1																									
IPI00010141	POLE3	DNA polymerase epsilon subunit 3	99.5%	12.2	1	2	2	1	2,966,793	3,001,595	3,119,144	3,262,127	252,136	141,176	175,817	153,710	19.0	10.5	12.6	10.5	1.0	0.9	1.1	0.6	1.1	0.3	1.0	0.6	1.1	0.2	1.0	0.6
				TLNASDVLSAMEEMEFQR	2	99.5%	1																									
				TLNASDVLSAMEEMEFQR	3	94.5%	1																									
IPI00010153	RPL23	60S ribosomal protein L23	100.0%	34.3	4	4	6	2	9,919,883	9,983,967	9,909,024	11,548,918	673,658	348,527	725,601	560,131	15.2	7.8	16.4	10.9	1.0	0.9	-1.0	1	1.2	0.1	-1.0	0.9	1.2	0.05	1.2	0.1
IPI00795408	RPL23	15 kDa protein	100.0%	34.3	4	4	6	2	9,919,883	9,983,967	9,909,024	11,548,918	673,658	348,527	725,601	560,131	15.2	7.8	16.4	10.9	1.0	0.9	-1.0	1	1.2	0.1	-1.0	0.9	1.2	0.05	1.2	0.1
				GSAITGPVAK	2	99.9%	2																									
				ISLGLPVGAVINCADNTGAK	2	100.0%	1																									
				LNRLPAAGVGDMVMATVK	3	99.9%	1																									
				LPAAGVGDMVMATVK	2	100.0%	2																									
IPI00010154	GDI1	Rab GDP dissociation inhibitor alpha	100.0%	30.2	11	14	19	1	32,326,308	34,758,926	32,925,237	37,642,094	3,044,359	1,311,541	2,693,220	1,069,782	21.1	8.4	18.3	6.4	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.1	1.1	0.1
				FDLGQDVIDFTGHALALYR	2	100.0%	1																									
				FDLGQDVIDFTGHALALYR	3	100.0%	1																									
				FLMANGQLVK	2	99.5%	2																									
				FLVFVANFDENDPK	2	99.4%	1																									
				FQLLEGPPESMGR	2	99.9%	1																									
				KFDLGQDVIDFTGHALALYR	3	100.0%	2																									
				KQNDVFGEAEQ	2	99.5%	1																									
				LYSESLAR	2	99.0%	1																									
				MLLYTEVTR	2	100.0%	2																									
				QLICDPSYIPDR	2	97.9%	1																									
				SPYLYPLYGLGELPQGFAR	2	100.0%	2																									
				SPYLYPLYGLGELPQGFAR	3	100.0%	2																									
				VPSTETEALASNLMGMFEK	2	100.0%	1																									
				VPSTETEALASNLMGMFEK	3	99.9%	1																									
IPI00010157	MAT2A	S-adenosylmethionine synthase isoform type-2	100.0%	13.9	4	4	4	1	16,798,595	19,124,965	16,230,010	21,637,075	2,227,819	1,500,931	2,238,794	1,264,021	29.7	17.6	30.8	13.1	1.1	0.4	-1.0	0.9	1.3	0.1	-1.2	0.3	1.1	0.2	1.3	0.07
				FVIGGPQGDAGLTGR	2	100.0%	1																									
				IIVDTYGGWGAHGGGAFSGK	3	89.6%	1																									
				TAAYGHFGR	2	82.1%	1																									
				TQVTVQYMQDR	2	100.0%	1																									
IPI00010158	CHRAC1	Chromatin accessibility complex protein 1	97.8%	13.7	1	1	1	2	1,404,380	1,896,855	1,460,775	1,755,510	139,205	137,524	102,813	79,540	22.2	16.2	15.7	10.1	1.4	0.04	1.0	0.8	1.3	0.06	-1.3	0.03	-1.1	0.4	1.2	0.05
IPI00791751	CHRAC1	Uncharacterized protein	97.8%	32.1	1	1	1	2	1,404,380	1,896,855	1,460,775	1,755,510	139,205	137,524	102,813	79,540	22.2	16.2	15.7	10.1	1.4	0.04	1.0	0.8	1.3	0.06	-1.3	0.03	-1.1	0.4	1.2	0.05
				SSPEVSSINQEALVLTAK	2	97.8%	1																									
IPI01009593	-	62 kDa protein	100.0%	20.8	9	9	12	5	12,388,554	12,548,083	12,730,569	13,663,726	854,052	680,212	1,264,096	948,829	15.4	12.1	22.2	15.5	1.0	0.9	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.4	1.1	0.6
IPI00010180	CES1	isoform 1 of Liver carboxylesterase 1	100.0%	20.8	9	9	12	5	12,388,554	12,548,083	12,730,569	13,663,726	854,052	680,212	1,264,096	948,829	15.4	12.1	22.2	15.5	1.0	0.9	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.4	1.1	0.6
IPI00607693	CES1	liver carboxylesterase 1 isoform c precursor	100.0%	20.9	9	9	12	5	12,388,554	12,548,083	12,730,569	13,663,726	854,052	680,212	1,264,096	948,829	15.4	12.1	22.2	15.5	1.0	0.9	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.4	1.1	0.6
IPI00607801	CES1	isoform 2 of Liver carboxylesterase 1	100.0%	20.8	9	9	12	5	12,388,554	12,548,083	12,730,569	13,663,726	854,052	680,212	1,264,096	948,829	15.4	12.1	22.2	15.5	1.0	0.9	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.4	1.1	0.6
IPI00942507	CES1	cDNA FLJ57637, highly similar to Liver carboxylesterase 1	100.0%	27.3	9	9	12	5	12,388,554	12,548,083	12,730,569	13,663,726	854,052	680,212	1,264,096	948,829	15.4	12.1	22.2	15.5	1.0	0.9	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.4	1.1	0.6
				AISESGVALTSVLVK	2	100.0%	2																									
				EGYLQIGANTQAAQK	2	100.0%	1																									
				ESQPLLGTVIDGMLLLK	2	100.0%	2																									
				EVAFWTNLFAK	2	90.8%	1																									
				FLSLDLQGDPR	2	99.3%	2																									
				FWANFAR	2	87.2%	1																									
				QKTEEELLETTLK	3	99.9%	1																									
				TPEELQAER	2	99.1%	1																									
				TVIGDHGDELFSVFGAPFLK	3	92.2%	1																									
IPI00921830	-	Diazepam binding inhibitor, splice form 1D	100.0%	38.9	5	7	9	7	10,571,977	10,749,367	10,521,303	12,133,137	974,081	509,945	796,717	279,974	20.6	10.6	16.9	5.2	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.04	1.2	0.1
IPI00010182	DBI	isoform 1 of Acyl-CoA-binding protein	100.0%	64.4	5	7	9	7	10,571,977	10,749,367	10,521,303	12,133,137	974,081	509,945	796,717	279,974	20.6	10.6	16.9	5.2	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.04	1.2	0.1
IPI00218836	DBI	isoform 2 of Acyl-CoA-binding protein	100.0%	53.9	5	7	9	7	10,571,977	10,749,367	10,521,303	12,133,137	974,081	509,945	796,717	279,974	20.6	10.6	16.9	5.2	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.04	1.2	0.1
IPI00922055	DBI	acyl-CoA-binding protein isoform 4	100.0%	37.8	5	7	9	7	10,571,977	10,749,367	10,521,303	12,133,137	974,081	509,945	796,717	279,974	20.6	10.6	16.9	5.2	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.04	1.2	0.1
IPI00965476	DBI	acyl-CoA-binding protein isoform 5	100.0%	43.4	5	7	9	7	10,571,977	10,749,367	10,521,303	12,133,137	974,081	509,945	796,717	279,974	20.6	10.6	16.9	5.2	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.04	1.2	0.1
IPI00966070	DBI	acyl-CoA-binding protein isoform 6	100.0%	57.7	5	7	9	7	10,571,977	10,749,367	10,521,303	12,133,137	974,081	509,945	796,717	279,974	20.6	10.6	16.9	5.2	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.04	1.2	0.1
IPI01008823	DBI	isoform 3 of Acyl-CoA-binding protein	100.0%	63.6	5	7	9	7	10,571,977	10,749,367	10,521,303	12,133,137	974,081	509,945	796,717	279,974	20.6	10.6	16.9	5.2	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.04	1.2	0.1
				AKWDAWNELK	2	99.7%	1																									
				AKWDAWNELK	3	98.3%	1																									
				AYINKVEELK	2	99.3%	1																									
				QATVGDINTERPGMLDFTGK	2	100.0%	2																									
				QATVGDINTERPGMLDFTGK	3	100.0%	1																									
				TKPSDEEMLFIYGHYK	3	100.0%	1																									
				WDAWNELK	2	99.9%	2																									
IPI00010187	ELOVL1	Elongation of very long chain fatty acids protein 1	99.1%	4.3	1	1	2	2	2,012,452	2,386,165	2,193,775	2,423,285	305,272	144,148	223,368	90,889	33.9	13.5	22.8	8.4	1.2	0.3	1.1	0.6	1.2	0.3	-1.1	0.5	1.0	0.8	1.1	0.4
IPI00910626	ELOVL1	cDNA FLJ51720, highly similar to Elongation of very long chain fatty acids protein 1	99.1%	4.8	1	1	2	2	2,012,452	2,386,165	2,193,775	2,423,285	305,272	144,148	223,368	90,889	33.9	13.5	22.8	8.4	1.2	0.3	1.1	0.6	1.2	0.3	-1.1	0.5	1.0	0.8	1.1	0.4
				ALQQNGAPGIAK	2	99.1%	2																									
IPI00010204	SRSF3	Serine/arginine-rich splicing factor 3	100.0%	45.7	8	9	11	2	32,969,972	33,497,161	32,279,396	36,766,669	1,744,212	2,010,462	1,825,344	1,144,492	11.8	13.4	12.6	7.0	1.0	0.8	-1.0	0.8	1.1	0.1	-1.0	0.7	1.1	0.2	1.1	0.07
IPI00843996	SRSF3	cDNA FLJ52832, highly similar to Splicing factor, arginine/serine-rich 3	100.0%	60.5	8	9	11	2	32,969,972	33,497,161	32,279,396	36,766,669	1,744,212	2,010,462	1,825,344	1,144,492	11.8	13.4	12.6	7.0	1.0	0.8	-1.0	0.8	1.1	0.1	-1.0	0.7	1.1	0.2	1.1	0.07
				AFGYYGPLR	2	99.4%	1																									
				DSCPLDCK	2	98.9%	1																									
				NPPGFAFVEFEDPR	2	99.9%	1																									
				NPPGFAFVEFEDPRDAADAVR	2	99.8%	1																									
				NPPGFAFVEFEDPRDAADAVR	3	100.0%	2																									
				NRGPPPSWGR	2	92.9%	1																									
				VRVELSNGEK	3	100.0%	1																									
				VYVGNLGNNGNK	2	100.0%	2																									
				VYVGNLGNNGNKTELER	2	97.2%	1																									
IPI00010214	S100A14	Protein S100-A14	100.0%	25.0	2	2	3	1	7,340,370	7,392,530	7,545,090	7,809,050	465,205	515,379	529,792	414,389	14.2	15.6	15.7	11.9	1.0	0.9	1.0	0.8	1.1	0.5	1.0	0.8	1.1	0.5	1.0	0.7
				SANAEDAQEFSDVER	2	100.0%	1																									
				SFWELIGEAAK	2	100.0%	2																									
IPI00010248	SPG21	Maspardin	94.9%	3.6	1	1	1	2	2,210,735	1,977,025	2,097,130	2,224,215	304,714	127,139	72,730	125,848	30.8	14.4	7.8	12.7	-1.1	0.5	-1.1	0.7	1.0	1	1.1	0.4	1.1	0.2	1.1	0.4
IPI00895915	SPG21	maspardin isoform b	94.9%	3.9	1	1	1	2	2,210,735	1,977,025	2,097,130	2,224,215	304,714	127,139	72,730	125,848	30.8	14.4	7.8	12.7	-1.1	0.5	-1.1	0.7	1.0	1	1.1	0.4	1.1	0.2	1.1	0.4
				QILALTGWGYR	3	94.9%	1																									
IPI00010252	TRIM33	isoform Alpha of E3 ubiquitin-protein ligase TRIM33	90.1%	1.0	1	1	1	2	2,310,045	2,377,620	1,824,580	2,513,395	333,164	74,850	154,836	151,937	32.3	7.0	19.0	13.5	1.0	0.9	-1.3	0.2	1.1	0.6	-1.3	0.01	1.1	0.4	1.4	0.01
IPI00221114	TRIM33	isoform Beta of E3 ubiquitin-protein ligase TRIM33	90.1%	1.0	1	1	1	2	2,310,045	2,377,620	1,824,580	2,513,395	333,164	74,850	154,836	151,937	32.3	7.0	19.0	13.5	1.0	0.9	-1.3	0.2	1.1	0.6	-1.3	0.01	1.1	0.4	1.4	0.01
				SLLQQLENVTK	2	90.1%	1																									
IPI00010270	RAC2	Ras-related C3 botulinum toxin substrate 2	100.0%	5.2	1	1	2	5	634,571	621,054	616,551	672,504	91,158	77,855	29,791	58,250	32.1	28.0	10.8	19.4	-1.0	0.9	-1.0	0.9	1.1	0.7	-1.0	1	1.1	0.6	1.1	0.4
IPI00877663	RAC2	Ras-related C3 botulinum toxin substrate 2 (Rho family, small GTP binding protein R	100.0%	5.4	1	1	2	5	634,571	621,054	616,551	672,504	91,158	77,855	29,791	58,250	32.1	28.0	10.8	19.4	-1.0	0.9	-1.0	0.9	1.1	0.7	-1.0	1	1.1	0.6	1.1	0.4
IPI00878066	RAC2	Ras-related C3 botulinum toxin substrate 2	100.0%	6.8	1	1	2	5	634,571	621,054	616,551	672,504	91,158	77,855	29,791	58,250	32.1	28.0	10.8	19.4	-1.0	0.9	-1.0	0.9	1.1	0.7	-1.0	1	1.1	0.6	1.1	0.4
IPI00879948	RAC2	Ras-related C3 botulinum toxin substrate 2	100.0%	6.0	1	1	2	5	634,571	621,054	616,551	672,504	91,158	77,855	29,791	58,250	32.1	28.0	10.8	19.4	-1.0	0.9	-1.0	0.9	1.1	0.7	-1.0	1	1.1	0.6	1.1	0.4
IPI00023138	RAC3	Ras-related C3 botulinum toxin substrate 3	100.0%	5.2	1	1	2	5	634,571	621,054	616,551	672,504	91,158	77,855	29,791	58,250	32.1	28.0	10.8	19.4	-1.0	0.9	-1.0	0.9	1.1	0.7	-1.0	1	1.1	0.6	1.1	0.4
				YLECSALTQR	2	99.9%	2																									
IPI00010271	RAC1	isoform A of Ras-related C3 botulinum toxin substrate 1	100.0%	12.5	2	2	3	2	4,162,131	4,323,399	4,241,391	4,718,854	385,339	291,492	151,731	232,107	20.7	15.1	8.0	11.0	1.0	0.7	1.0	0.9	1.1	0.3	-1.0	0.8	1.1	0.3	1.1	0.1
IPI00219675	RAC1	isoform B of Ras-related C3 botulinum toxin substrate 1	100.0%	11.4	2	2	3	2	4,162,131	4,323,399	4,241,391	4,718,854	385,339	291,492	151,731	232,107	20.7	15.1	8.0	11.0	1.0	0.7	1.0	0.9	1.1	0.3	-1.0	0.8	1.1	0.3	1.1	0.1
				LTPITYPQGLAMAK	2	98.6%	1																									
				YLECSALTQR	2	99.9%	2																									
IPI00010276	ARL6IP4	25 kDa protein	97.5%	5.5	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI00434965	ARL6IP4	isoform 2 of ADP-ribosylation factor-like protein 6-interacting protein 4	97.5%	3.4	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI00434966	ARL6IP4	isoform 4 of ADP-ribosylation factor-like protein 6-interacting protein 4	97.5%	3.6	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI00792543	ARL6IP4	26 kDa protein	97.5%	5.2	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI00796038	ARL6IP4	ADP-ribosylation factor-like protein 6-interacting protein 4	97.5%	2.9	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI00877018	ARL6IP4	isoform 3 of ADP-ribosylation factor-like protein 6-interacting protein 4	97.5%	3.5	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI00877082	ARL6IP4	isoform 5 of ADP-ribosylation factor-like protein 6-interacting protein 4	97.5%	4.0	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI00883925	ARL6IP4	Similar to 2-oxoglutarate and iron-dependent oxygenase domain-containing protein	97.5%	2.8	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI00939585	ARL6IP4	24 kDa protein	97.5%	5.6	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI00942578	ARL6IP4	19 kDa protein	97.5%	7.1	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI01011960	ARL6IP4	20 kDa protein	97.5%	6.6	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI01013603	ARL6IP4	Splicing regulator SRrp37-2	97.5%	5.3	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
IPI01013635	ARL6IP4	24 kDa protein	97.5%	5.7	1	1	1	13	1,561,954	1,503,462	1,514,192	1,690,515	215,343	210,979	180,024	55,957	30.8	31.4	26.6	7.4	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	1	1.1	0.4	1.1	0.4
				GDGEVLEEIVTK	2	97.5%	1																									
IPI00010290	FABP1	FABP1 protein (Fragment)	100.0%	76.1	7	9	15	1	42,639,135	41,792,730	40,293,260	46,939,585	3,411,111	1,354,702	3,084,410	1,154,077	17.9	7.3	17.1	5.5	-1.0	0.8	-1.1	0.6	1.1	0.3	-1.0	0.7	1.1	0.02	1.2	0.1
				AIGLPEELIQK	2	100.0%	2																									
				FTITAGSK	2	95.9%	1																									
				GVSEIVQNGK	2	100.0%	2																									
				SVTELNGDIITNTMTLGDIVFK	2	100.0%	2																									
				SVTELNGDIITNTMTLGDIVFK	3	100.0%	2																									
				TVVQLEGDNKLVTTFK	3	81.2%	1																									
				VIQNEFTVGEECELETMTGEK	2	100.0%	2																									
				YQLQSQENFEAFMK	2	100.0%	2																									
				YQLQSQENFEAFMK	3	98.9%	1																									
IPI00010346	NLN	Neurolysin, mitochondrial	99.4%	3.3	2	2	2	3	2,568,479	2,805,991	2,712,983	3,271,357	174,314	210,419	365,737	320,822	15.2	16.8	30.1	21.9	1.1	0.4	1.1	0.7	1.3	0.09	-1.0	0.8	1.2	0.3	1.2	0.3
IPI00872224	NLN	cDNA FLJ14696 fis, clone NT2RP2005775, highly similar to NEUROLYSIN	99.4%	6.0	2	2	2	3	2,568,479	2,805,991	2,712,983	3,271,357	174,314	210,419	365,737	320,822	15.2	16.8	30.1	21.9	1.1	0.4	1.1	0.7	1.3	0.09	-1.0	0.8	1.2	0.3	1.2	0.3
IPI00965753	NLN	Uncharacterized protein	99.4%	3.8	2	2	2	3	2,568,479	2,805,991	2,712,983	3,271,357	174,314	210,419	365,737	320,822	15.2	16.8	30.1	21.9	1.1	0.4	1.1	0.7	1.3	0.09	-1.0	0.8	1.2	0.3	1.2	0.3
				KEGIMNPEVGMK	2	86.0%	1																									
				VTAFLDDLSQK	2	99.4%	1																									
IPI00010349	AGPS	Alkyldihydroxyacetonephosphate synthase, peroxisomal	99.8%	6.2	3	3	3	1	10,730,240	10,794,410	10,499,935	11,410,445	1,122,112	199,261	658,762	400,696	23.4	4.1	14.0	7.9	1.0	1	-1.0	0.9	1.1	0.6	-1.0	0.7	1.1	0.2	1.1	0.3
				FGGLAAGEDNGQR	2	86.2%	1																									
				IPDIVLWPTCHDDVVK	3	98.2%	1																									
				TIISLDTSQMNR	2	90.7%	1																									
IPI00010368	KIF2A	Uncharacterized protein	92.9%	2.5	1	1	1	4	690,425	650,648	621,008	778,633	102,010	76,446	33,048	35,701	33.0	26.3	11.9	10.3	-1.1	0.8	-1.1	0.5	1.1	0.5	-1.0	0.7	1.2	0.2	1.3	0.01
IPI00848334	KIF2A	isoform 4 of Kinesin-like protein KIF2A	92.9%	2.3	1	1	1	4	690,425	650,648	621,008	778,633	102,010	76,446	33,048	35,701	33.0	26.3	11.9	10.3	-1.1	0.8	-1.1	0.5	1.1	0.5	-1.0	0.7	1.2	0.2	1.3	0.01
IPI00867529	KIF2A	isoform 2 of Kinesin-like protein KIF2A	92.9%	2.6	1	1	1	4	690,425	650,648	621,008	778,633	102,010	76,446	33,048	35,701	33.0	26.3	11.9	10.3	-1.1	0.8	-1.1	0.5	1.1	0.5	-1.0	0.7	1.2	0.2	1.3	0.01
IPI00867746	KIF2A	isoform 3 of Kinesin-like protein KIF2A	92.9%	2.4	1	1	1	4	690,425	650,648	621,008	778,633	102,010	76,446	33,048	35,701	33.0	26.3	11.9	10.3	-1.1	0.8	-1.1	0.5	1.1	0.5	-1.0	0.7	1.2	0.2	1.3	0.01
				GKLHGKFSLIDLAGNER	2	92.9%	1																									
IPI00010400	PLCB3	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3	100.0%	4.1	3	4	4	1	5,860,162	5,746,856	6,047,158	6,646,902	803,235	576,859	452,759	565,326	30.7	22.5	16.7	19.0	-1.0	0.9	1.0	0.8	1.1	0.4	1.1	0.7	1.2	0.3	1.1	0.4
				DDLIASILSEVAPTPLDELR	2	97.6%	1																									
				EVLGFGGPDAR	2	98.3%	1																									
				SFDPFTEVIVDGIVANALR	2	100.0%	1																									
				SFDPFTEVIVDGIVANALR	3	99.9%	1																									
IPI00955848	-	SH3 domain binding glutamic acid-rich protein like 3, isoform CRA_a (Fragment)	100.0%	11.3	2	3	5	4	10,652,343	10,687,985	10,946,060	12,403,293	990,829	433,290	795,862	488,552	20.8	9.1	16.3	8.8	1.0	1	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.03	1.1	0.2
IPI00010402	SH3BGRL3	Putative uncharacterized protein	100.0%	12.8	2	3	5	4	10,652,343	10,687,985	10,946,060	12,403,293	990,829	433,290	795,862	488,552	20.8	9.1	16.3	8.8	1.0	1	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.03	1.1	0.2

IPI00514669	SH3BGRL3	SH3 domain binding glutamic acid-rich protein like 3	100.0%	33.0	2	3	5	4	10,652,343	10,687,985	10,946,060	12,403,293	990,829	433,290	795,862	488,552	20.8	9.1	16.3	8.8	1.0	1	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.03	1.1	0.2
IPI00746352	SH3BGRL3	SH3 domain-binding glutamic acid-rich-like protein 3	100.0%	31.2	2	3	5	4	10,652,343	10,687,985	10,946,060	12,403,293	990,829	433,290	795,862	488,552	20.8	9.1	16.3	8.8	1.0	1	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.03	1.1	0.2
				IQYQLVDISQDNALRDEMR	2	100.0%	2																									
				IQYQLVDISQDNALRDEMR	3	100.0%	1																									
				VYSTSVTGSR	2	100.0%	2																									
IPI00010404	SF3B5	Splicing factor 3B subunit 5	99.5%	15.1	1	1	1	1	6,633,920	6,653,920	6,281,680	7,119,060	361,082	183,194	212,507	469,967	12.2	6.2	7.6	14.8	1.0	1	-1.1	0.4	1.1	0.4	-1.1	0.2	1.1	0.4	1.1	0.1
				YTIHSQLEHLQSK	3	99.3%	1																									
IPI00010414	PDLIM1	PDZ and LIM domain protein 1	100.0%	46.5	9	9	9	1	64,391,210	62,614,800	64,841,525	72,074,900	5,276,540	2,658,509	4,787,955	2,489,124	18.3	9.5	16.5	7.7	-1.0	0.8	1.0	1	1.1	0.2	1.0	0.7	1.2	0.03	1.1	0.2
				AALANLCIGDVITAIDGENTSNMTHLEAQNR	3	100.0%	1																									
				DFEQPLAISR	2	100.0%	1																									
				GCTDNLTLTVAR	2	100.0%	1																									
				MNLASEPQEVLHIGSAHNR	3	86.8%	1																									
				SAMPFTASPASSTTAR	2	99.9%	1																									
				VAASIGNAQK	2	99.9%	1																									
				VITNQYNNPAGLYSSENISNFNNALESK	3	100.0%	1																									
				VTPPEGYEVVTVFPK	2	100.0%	1																									
				VWSPLVTEEGKR	3	92.2%	1																									
IPI00010415	ACOT7	isoform 1 of Cytosolic acyl coenzyme A thioester hydrolase	99.5%	3.2	1	1	1	7	1,567,914	1,573,780	1,613,409	1,682,564	172,499	121,587	126,735	115,222	24.6	17.3	17.6	15.3	1.0	1	1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.7
IPI00219451	ACOT7	isoform 5 of Cytosolic acyl coenzyme A thioester hydrolase	99.5%	3.4	1	1	1	7	1,567,914	1,573,780	1,613,409	1,682,564	172,499	121,587	126,735	115,222	24.6	17.3	17.6	15.3	1.0	1	1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.7
IPI00219452	ACOT7	isoform 6 of Cytosolic acyl coenzyme A thioester hydrolase	99.5%	3.7	1	1	1	7	1,567,914	1,573,780	1,613,409	1,682,564	172,499	121,587	126,735	115,222	24.6	17.3	17.6	15.3	1.0	1	1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.7
IPI00395748	ACOT7	cytosolic acyl coenzyme A thioester hydrolase isoform hBACHa	99.5%	3.2	1	1	1	7	1,567,914	1,573,780	1,613,409	1,682,564	172,499	121,587	126,735	115,222	24.6	17.3	17.6	15.3	1.0	1	1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.7
IPI00746126	ACOT7	isoform 3 of Cytosolic acyl coenzyme A thioester hydrolase	99.5%	4.2	1	1	1	7	1,567,914	1,573,780	1,613,409	1,682,564	172,499	121,587	126,735	115,222	24.6	17.3	17.6	15.3	1.0	1	1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.7
IPI00883762	ACOT7	isoform 2 of Cytosolic acyl coenzyme A thioester hydrolase	99.5%	4.9	1	1	1	7	1,567,914	1,573,780	1,613,409	1,682,564	172,499	121,587	126,735	115,222	24.6	17.3	17.6	15.3	1.0	1	1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.7
IPI01011431	ACOT7	cDNA FLJ60167, highly similar to Cytosolic acyl coenzyme A thioester hydrolase	99.5%	4.5	1	1	1	7	1,567,914	1,573,780	1,613,409	1,682,564	172,499	121,587	126,735	115,222	24.6	17.3	17.6	15.3	1.0	1	1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.7
				LMDEVAGIVAAR	2	99.5%	1																									
IPI00010418	MYO1C	isoform 2 of Myosin-Ic	100.0%	23.6	19	19	22	5	15,090,364	14,801,134	14,055,998	16,322,365	1,044,076	552,493	764,387	553,922	15.5	8.4	12.2	7.6	-1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.5	1.1	0.09	1.2	0.04
IPI00743335	MYO1C	isoform 1 of Myosin-Ic	100.0%	22.9	19	19	22	5	15,090,364	14,801,134	14,055,998	16,322,365	1,044,076	552,493	764,387	553,922	15.5	8.4	12.2	7.6	-1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.5	1.1	0.09	1.2	0.04
IPI00829992	MYO1C	isoform 3 of Myosin-Ic	100.0%	23.3	19	19	22	5	15,090,364	14,801,134	14,055,998	16,322,365	1,044,076	552,493	764,387	553,922	15.5	8.4	12.2	7.6	-1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.5	1.1	0.09	1.2	0.04
IPI01009308	MYO1C	120 kDa protein	100.0%	23.3	19	19	22	5	15,090,364	14,801,134	14,055,998	16,322,365	1,044,076	552,493	764,387	553,922	15.5	8.4	12.2	7.6	-1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.5	1.1	0.09	1.2	0.04
IPI01009754	MYO1C	119 kDa protein	100.0%	23.4	19	19	22	5	15,090,364	14,801,134	14,055,998	16,322,365	1,044,076	552,493	764,387	553,922	15.5	8.4	12.2	7.6	-1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.5	1.1	0.09	1.2	0.04
				DGTIDFTPGSELLITK	2	100.0%	1																									
				DNYPQSVPR	2	98.7%	1																									
				DQAVMISGESGAGK	2	100.0%	1																									
				DRVGVQDFVLLENFTSEAAFIENLR	3	99.7%	1																									
				FDEVLIR	2	99.4%	1																									
				GVSFYEVPPHLFAVADTVYR	3	100.0%	1																									
				KRPETVATQFK	2	99.5%	1																									
				KYEAFLQR	2	86.0%	1																									
				LLQSNPVLEAFGNAK	2	100.0%	2																									
				MSLLQLVEILQSK	2	100.0%	2																									
				NGHLAVVAPR	2	96.5%	1																									
				NPIMSQCFDR	2	100.0%	1																									
				PQDGVAVLVR	2	99.7%	1																									
				QLPQNVLDTSWPTPPPALR	2	99.8%	1																									
				TFTWLVGK	2	99.4%	1																									
				TLFATEDALEVR	2	95.4%	1																									
				VLQALGSEPIQYAVPVVK	2	100.0%	1																									
				YLGLLENLR	2	99.4%	1																									
				YMDVQFDFK	2	99.3%	2																									
IPI00010420	SLC25A31	ADP/ATP translocase 4	100.0%	3.8	1	1	2	2	787,998	724,095	810,633	873,198	94,669	70,450	59,390	58,092	26.9	21.8	16.4	14.9	-1.1	0.6	1.0	0.8	1.1	0.5	1.1	0.4	1.2	0.1	1.1	0.5
IPI00556601	SLC25A4	Solute carrier family 25 member 4 variant (Fragment)	100.0%	4.6	1	1	2	2	787,998	724,095	810,633	873,198	94,669	70,450	59,390	58,092	26.9	21.8	16.4	14.9	-1.1	0.6	1.0	0.8	1.1	0.5	1.1	0.4	1.2	0.1	1.1	0.5
				YFPTQALNFAFK	2	100.0%	2																									
IPI00385449	PRKCA	Protein kinase C alpha type	94.3%	1.8	1	1	1	4	239,602	199,963	299,885	290,382	21,078	18,127	43,263	22,447	19.7	20.3	32.3	17.3	-1.2	0.2	1.3	0.2	1.2	0.1	1.5	0.07	1.5	0.01	-1.0	0.9
IPI01012363	PRKCA	Protein kinase C, alpha variant (Fragment)	94.3%	2.6	1	1	1	4	239,602	199,963	299,885	290,382	21,078	18,127	43,263	22,447	19.7	20.3	32.3	17.3	-1.2	0.2	1.3	0.2	1.2	0.1	1.5	0.07	1.5	0.01	-1.0	0.9
IPI00010466	PRKCB	isoform Beta-I of Protein kinase C beta type	94.3%	1.8	1	1	1	4	239,602	199,963	299,885	290,382	21,078	18,127	43,263	22,447	19.7	20.3	32.3	17.3	-1.2	0.2	1.3	0.2	1.2	0.1	1.5	0.07	1.5	0.01	-1.0	0.9
IPI00219628	PRKCB	isoform Beta-II of Protein kinase C beta type	94.3%	1.8	1	1	1	4	239,602	199,963	299,885	290,382	21,078	18,127	43,263	22,447	19.7	20.3	32.3	17.3	-1.2	0.2	1.3	0.2	1.2	0.1	1.5	0.07	1.5	0.01	-1.0	0.9
				LTDFNFLMVLGK	2	94.3%	1																									
IPI00010471	LCP1	Plastin-2	99.4%	3.0	1	1	1	3	523,668	554,337	609,493	521,633	46,912	46,760	46,646	19,995	20.0	18.9	17.1	8.6	1.1	0.7	1.2	0.2	-1.0	1	1.1	0.4	-1.1	0.5	-1.2	0.1
IPI00643270	LCP1	Lymphocyte cytosolic protein 1	99.4%	28.8	1	1	1	3	523,668	554,337	609,493	521,633	46,912	46,760	46,646	19,995	20.0	18.9	17.1	8.6	1.1	0.7	1.2	0.2	-1.0	1	1.1	0.4	-1.1	0.5	-1.2	0.1
IPI00646259	LCP1	Lymphocyte cytosolic protein 1	99.4%	7.7	1	1	1	3	523,668	554,337	609,493	521,633	46,912	46,760	46,646	19,995	20.0	18.9	17.1	8.6	1.1	0.7	1.2	0.2	-1.0	1	1.1	0.4	-1.1	0.5	-1.2	0.1
				VDTDGNGYISFNELNDLFK	2	99.4%	1																									
IPI00010490	ARVCF	isoform Long of Armadillo repeat protein deleted in velo-cardio-facial syndrome	94.1%	3.9	2	2	2	4	1,145,405	1,036,769	1,119,294	1,121,264	202,470	75,969	140,993	86,298	39.5	16.4	28.2	17.2	-1.1	0.6	-1.0	0.9	-1.0	0.9	1.1	0.6	1.1	0.5	1.0	1
IPI00220492	ARVCF	isoform Short of Armadillo repeat protein deleted in velo-cardio-facial syndrome	94.1%	4.1	2	2	2	4	1,145,405	1,036,769	1,119,294	1,121,264	202,470	75,969	140,993	86,298	39.5	16.4	28.2	17.2	-1.1	0.6	-1.0	0.9	-1.0	0.9	1.1	0.6	1.1	0.5	1.0	1
IPI00879055	ARVCF	Uncharacterized protein	94.1%	3.9	2	2	2	4	1,145,405	1,036,769	1,119,294	1,121,264	202,470	75,969	140,993	86,298	39.5	16.4	28.2	17.2	-1.1	0.6	-1.0	0.9	-1.0	0.9	1.1	0.6	1.1	0.5	1.0	1
IPI00879180	ARVCF	Uncharacterized protein	94.1%	4.1	2	2	2	4	1,145,405	1,036,769	1,119,294	1,121,264	202,470	75,969	140,993	86,298	39.5	16.4	28.2	17.2	-1.1	0.6	-1.0	0.9	-1.0	0.9	1.1	0.6	1.1	0.5	1.0	1
				DPELPEVLAMLRHPVDPVK	3	85.0%	1																									
				PRDAEWTTVFKNTSGCLR	3	90.8%	1																									
IPI00010676	PLAUR	isoform 1 of Urokinase plasminogen activator surface receptor	99.4%	3.9	1	1	1	3	2,170,333	2,411,020	2,390,300	2,453,150	220,907	91,364	166,368	112,038	22.8	8.5	15.6	10.2	1.1	0.3	1.1	0.4	1.1	0.3	-1.0	0.9	1.0	0.8	1.0	0.8
IPI00215706	PLAUR	isoform 2 of Urokinase plasminogen activator surface receptor	99.4%	4.6	1	1	1	3	2,170,333	2,411,020	2,390,300	2,453,150	220,907	91,364	166,368	112,038	22.8	8.5	15.6	10.2	1.1	0.3	1.1	0.4	1.1	0.3	-1.0	0.9	1.0	0.8	1.0	0.8
IPI00215707	PLAUR	isoform 3 of Urokinase plasminogen activator surface receptor	99.4%	4.5	1	1	1	3	2,170,333	2,411,020	2,390,300	2,453,150	220,907	91,364	166,368	112,038	22.8	8.5	15.6	10.2	1.1	0.3	1.1	0.4	1.1	0.3	-1.0	0.9	1.0	0.8	1.0	0.8
				LWEEGEELELVEK	2	99.4%	1																									
IPI00010697	ITGA6	isoform Alpha-6X1X2B of Integrin alpha-6	100.0%	6.9	5	5	5	8	3,827,840	4,878,496	4,322,183	5,271,880	643,263	395,510	630,277	340,635	37.6	18.1	32.6	14.5	1.3	0.2	1.1	0.6	1.4	0.08	-1.1	0.5	1.1	0.5	1.2	0.2
IPI00216221	ITGA6	isoform Alpha-6X1A of Integrin alpha-6	100.0%	7.3	5	5	5	8	3,827,840	4,878,496	4,322,183	5,271,880	643,263	395,510	630,277	340,635	37.6	18.1	32.6	14.5	1.3	0.2	1.1	0.6	1.4	0.08	-1.1	0.5	1.1	0.5	1.2	0.2
IPI00216222	ITGA6	isoform Alpha-6X1B of Integrin alpha-6	100.0%	7.2	5	5	5	8	3,827,840	4,878,496	4,322,183	5,271,880	643,263	395,510	630,277	340,635	37.6	18.1	32.6	14.5	1.3	0.2	1.1	0.6	1.4	0.08	-1.1	0.5	1.1	0.5	1.2	0.2
IPI00216223	ITGA6	Uncharacterized protein	100.0%	7.2	5	5	5	8	3,827,840	4,878,496	4,322,183	5,271,880	643,263	395,510	630,277	340,635	37.6	18.1	32.6	14.5	1.3	0.2	1.1	0.6	1.4	0.08	-1.1	0.5	1.1	0.5	1.2	0.2
IPI00216224	ITGA6	isoform Alpha-6X2B of Integrin alpha-6	100.0%	7.2	5	5	5	8	3,827,840	4,878,496	4,322,183	5,271,880	643,263	395,510	630,277	340,635	37.6	18.1	32.6	14.5	1.3	0.2	1.1	0.6	1.4	0.08	-1.1	0.5	1.1	0.5	1.2	0.2
IPI00216225	ITGA6	isoform Alpha-6X1X2A of Integrin alpha-6	100.0%	7.0	5	5	5	8	3,827,840	4,878,496	4,322,183	5,271,880	643,263	395,510	630,277	340,635	37.6	18.1	32.6	14.5	1.3	0.2	1.1	0.6	1.4	0.08	-1.1	0.5	1.1	0.5	1.2	0.2
IPI00921401	ITGA6	isoform 9 of Integrin alpha-6	100.0%	7.1	5	5	5	8	3,827,840	4,878,496	4,322,183	5,271,880	643,263	395,510	630,277	340,635	37.6	18.1	32.6	14.5	1.3	0.2	1.1	0.6	1.4	0.08	-1.1	0.5	1.1	0.5	1.2	0.2
IPI00921080	ITGA6	isoform 7 of Integrin alpha-6	100.0%	8.2	5	5	5	8	3,827,840	4,878,496	4,322,183	5,271,880	643,263	395,510	630,277	340,635	37.6	18.1	32.6	14.5	1.3	0.2	1.1	0.6	1.4	0.08	-1.1	0.5	1.1	0.5	1.2	0.2
				AFIDVTAAAENIR	2	92.1%	1																									
				FGSCQQGVAATFTK	2	100.0%	1																									
				LRPIPITASVEIQEPSSR	3	99.9%	1																									
				NSYPDVAVGSLSDSVTIFR	2	100.0%	1																									
				SEDEVGSLIEYEFR	2	100.0%	1																									
IPI00893641	-	229 kDa protein	97.8%	0.7	1	1	1	8	632,545	612,985	626,796	646,876	85,236	56,019	44,909	44,411	30.1	20.4	16.0	15.4	-1.0	0.9	-1.0	1	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.8
IPI00894143	-	229 kDa protein	97.8%	0.7	1	1	1	8	632,545	612,985	626,796	646,876	85,236	56,019	44,909	44,411	30.1	20.4	16.0	15.4	-1.0	0.9	-1.0	1	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.8
IPI00010700	PRRC2A	isoform 1 of Protein PRRC2A	97.8%	0.7	1	1	1	8	632,545	612,985	626,796	646,876	85,236	56,019	44,909	44,411	30.1	20.4	16.0	15.4	-1.0	0.9	-1.0	1	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.8
IPI00642817	PRRC2A	isoform 3 of Protein PRRC2A	97.8%	0.7	1	1	1	8	632,545	612,985	626,796	646,876	85,236	56,019	44,909	44,411	30.1	20.4	16.0	15.4	-1.0	0.9	-1.0	1	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.8
IPI00885161	PRRC2A	isoform 4 of Protein PRRC2A	97.8%	1.0	1	1	1	8	632,545	612,985	626,796	646,876	85,236	56,019	44,909	44,411	30.1	20.4	16.0	15.4	-1.0	0.9	-1.0	1	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.8
IPI00893120	PRRC2A	Uncharacterized protein	97.8%	0.7	1	1	1	8	632,545	612,985	626,796	646,876	85,236	56,019	44,909	44,411	30.1	20.4	16.0	15.4	-1.0	0.9	-1.0	1	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.8
IPI00941298	PRRC2A	Uncharacterized protein	97.8%	2.7	1	1	1	8	632,545	612,985	626,796	646,876	85,236	56,019	44,909	44,411	30.1	20.4	16.0	15.4	-1.0	0.9	-1.0	1	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.8
IPI00964044	PRRC2A	Uncharacterized protein	97.8%	0.7	1	1	1	8	632,545	612,985	626,796	646,876	85,236	56,019	44,909	44,411	30.1	20.4	16.0	15.4	-1.0	0.9	-1.0	1	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.8
				GPAGNWGPPGDYPDR	2	97.8%	1																									
IPI00010706	GSS	Glutathione synthetase	100.0%	23.4	9	9	10	1	46,588,838	47,138,230	44,130,768	53,038,722	4,178,394	1,902,558	2,854,600	1,792,895	20.1	9.0	14.5	7.6	1.0	0.9	-1.1	0.6	1.1	0.2	-1.1	0.4	1.1	0.05	1.2	0.03
				AIEHADGGVAAGVAVLDNPYPV	2	100.0%	1																									
				AIENELLAR	2	99.9%	1																									
				ALAEGVLLR	2	99.3%	1																									
				ASYILMEK	2	99.3%	1																									
				CPDIATQLAGTK	2	90.1%	1																									
				EGGGNNLYGEEMVQALK	2	99.9%	1																									
				QIEINTISASFGGLASR	2	99.6%	1																									
				QYSLQNWEAR	2	98.1%	2																									
				SDYMFQR	2	99.5%	1																									
IPI00010720	CCT5	T-complex protein 1 subunit epsilon	100.0%	50.8	18	18	20	1	17,679,423	19,159,512	18,167,034	21,051,237	1,858,779	833,169	1,384,819	877,493	23.5	9.7	17.0	9.3	1.1	0.5	1.0	0.8	1.2	0.1	-1.1	0.6	1.1	0.2	1.2	0.1
				AFADALEVIPMALSENSGMNPIQTMTEVR	2	97.8%	1																									
				DVDFELIKVEGK	2	90.8%	1																									
				EKFEEMIQQIK	2	98.5%	1																									
				ETGANLAICQWGFDDEANHLLLQNNLPAVR	3	100.0%	1																									
				FEEMIQQIK	2	99.5%	1																									
				FSELTAEK	2	98.2%	1																									
				GVIVDKDFSHPQMPK	3	88.5%	1																									
				HKLDVTSVEDYK	3	94.2%	1																									
				IADGYEQAAR	2	100.0%	1																									
				IAILTCPFEPPKPK	3	99.9%	1																									
				ISDSVLVDIKDTEPLIQTAK	3	100.0%	1																									
				LDVTSVEDYK	2	100.0%	1																									
				LGFAGLVQEISFGTTK	2	100.0%	2																									
				MMVDKDGDVTVTNDGATILSMMDVDHQIAK	3	99.8%	1																									
				QMAEIAVNAVLTVADMER	3	99.8%	1																									
				QQISLATQMVR	2	98.4%	1																									
				VVYGGGAAEISCALAVSQEADK	3	92.9%	1																									
				WVGGPEIELIAIATGGR	2	100.0%	2																									
IPI00010740	SFPQ	isoform Long of Splicing factor, proline- and glutamine-rich	100.0%	23.5	12	15	17	1	61,886,534	65,514,084	60,418,319	73,245,430	5,872,801	3,063,914	5,010,514	1,618,499	21.2	10.5	18.5	4.9	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.06	1.2	0.06
				AELDDTPMR	2	99.8%	1																									
				FAQHGTFEYEYSQR	3	95.5%	1																									
				FATHAAALSVR	2	99.5%	1																									
				FATHAAALSVR	3	100.0%	1																									
				FGQGGAGPVGGQGPR	2	100.0%	1																									
				ISDSEGFK	2	91.0%	1																									
				LFVGNLPADITEDEFKR	2	100.0%	1																									
				LFVGNLPADITEDEFKR	3	99.0%	1																									
				MGGGGAMNMGDPYGSGGQK	2	100.0%	1																									
				NLSPYVSNELLEEAFSQFGPIER	2	100.0%	1																									
				PVIVEPLEQLDDEDGLPEK	2	100.0%	1																									
				PVIVEPLEQLDDEDGLPEK	3	100.0%	1																									
				REEEMMIR	2	90.0%	1																									
				RMEELHNQEMQK	3	100.0%	2																									
				YGEPGEVFINK	2	100.0%	2																									
IPI00010779	TPM4	isoform 1 of Tropomyosin alpha-4 chain	100.0%	31.1	10	10	13	1	17,909,100	19,448,546	17,196,877	20,955,989	1,452,867	792,196	1,068,368	749,076	18.1	9.1	13.9	8.0	1.1	0.4	-1.0	0.7	1.2	0.1	-1.1	0.1	1.1	0.2	1.2	0.02
				CGDLEEELKNVTNNLK	3	99.9%	1																									
				IQALQQQADEAEDR	2	100.0%	1																									
				IQLVEEELDR	2	100.0%	2																									
				KIQALQQQADEAEDR	3	99.3%	1																									
				KLVILEGELER	2	99.9%	1																									
				LATALQK	1	96.5%	2																									
				LVILEGELER	2	100.0%	1																									
				RIQLVEEELDR	2	100.0%	2																									

				RIQLVEEELDRAQER	3	99.2%	1																									
				YSEKEDKYEEEIK	3	99.2%	1																									
IPI00010796	P4HB	Protein disulfide-isomerase	100.0%	64.0	31	45	64	1	224,179,366	225,798,875	226,306,849	258,596,532	########	7,326,798	########	6,131,307	17.2	7.3	14.9	5.3	1.0	0.9	1.0	0.9	1.2	0.1	1.0	1	1.1	0.009	1.1	0.08
				ALAPEYAK	1	97.3%	1																									
				ALAPEYAK	2	99.3%	1																									
				DHENIVIAK	2	100.0%	2																									
				EADDIVNWLK	2	100.0%	2																									
				HNQLPLVIEFTEQTAPK	2	100.0%	2																									
				HNQLPLVIEFTEQTAPK	3	100.0%	2																									
				IKPHLMSQELPEDWDKQPVK	3	100.0%	2																									
				ILEFFGLK	2	99.1%	1																									
				ILFIFIDSDHTDNQR	2	100.0%	2																									
				ILFIFIDSDHTDNQR	3	99.9%	2																									
				ITEFCHR	2	81.4%	1																									
				KSNFAEALAAHK	2	100.0%	2																									
				KSNFAEALAAHK	3	100.0%	1																									
				LGETYKDHENIVIAK	2	100.0%	1																									
				LGETYKDHENIVIAK	3	100.0%	2																									
				LITLEEEMTK	2	100.0%	2																									
				LKAEGSEIR	2	87.3%	1																									
				MDSTANEVEAVK	2	100.0%	1																									
				NFEDVAFDEK	2	99.8%	2																									
				NFEDVAFDEKK	2	99.9%	1																									
				NFEDVAFDEKK	3	100.0%	1																									
				NNFEGEVTK	2	99.8%	1																									
				NNFEGEVTKENLLDFIK	3	100.0%	2																									
				NVFVEFYAPWCGHCK	2	99.9%	1																									
				NVFVEFYAPWCGHCK	3	99.7%	1																									
				QFLQAAEAIDDIPFGITSNSDVFSK	2	100.0%	2																									
				QFLQAAEAIDDIPFGITSNSDVFSK	3	100.0%	1																									
				QLAPIWDK	2	99.7%	2																									
				SNFAEALAAHK	2	100.0%	1																									
				SNFAEALAAHK	3	84.0%	1																									
				TAAESFK	1	98.5%	2																									
				TAAESFKGKILFIFIDSDHTDNQR	3	99.1%	1																									
				TGPAATTLPDGAAAESLVESSEVAVIGFFK	2	100.0%	2																									
				TGPAATTLPDGAAAESLVESSEVAVIGFFK	3	100.0%	1																									
				THILLFLPK	2	99.9%	1																									
				THILLFLPK	3	99.9%	1																									
				TVIDYNGER	2	100.0%	2																									
				VDATEESDLAQQYGVR	2	100.0%	1																									
				VDATEESDLAQQYGVR	3	100.0%	1																									
				VHSFPTLK	2	88.9%	1																									
				YKPESEELTAER	2	100.0%	2																									
				YKPESEELTAER	3	100.0%	1																									
				YQLDKDGVVLFK	2	100.0%	1																									
				YQLDKDGVVLFK	3	100.0%	2																									
				YQLDKDGVVLFKK	3	95.2%	1																									
IPI00010810	ETFA	Electron transfer flavoprotein subunit alpha, mitochondrial	100.0%	35.4	8	8	10	1	15,563,932	16,515,967	15,652,233	18,869,508	1,359,979	653,479	1,166,863	554,006	19.5	8.9	16.7	6.6	1.1	0.5	1.0	1	1.2	0.05	-1.1	0.5	1.1	0.03	1.2	0.04
				AAVDAGFVPNDMQVGQTGK	2	100.0%	2																									
				DPEAPIFQVADYGIVADLFK	2	100.0%	1																									
				GLLPEELTPLILATQK	2	100.0%	1																									
				GTSFDAAATSGGSASSEK	2	100.0%	1																									
				LEVAPISDIIAIK	2	99.9%	1																									
				LGGEVSCLVAGTK	2	100.0%	2																									
				TIVAINKDPEAPIFQVADYGIVADLFK	3	100.0%	1																									
				TIYAGNALCTVK	2	100.0%	1																									
IPI00010845	NDUFS8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	99.6%	9.5	2	2	2	5	642,859	642,709	709,397	687,574	33,352	34,166	54,509	27,139	11.6	11.9	17.2	8.8	-1.0	1	1.1	0.3	1.1	0.3	1.1	0.3	1.1	0.3	-1.0	0.7
IPI00908766	NDUFS8	cDNA FLJ57061, highly similar to NADH-ubiquinone oxidoreductase 23 kDa subunit	99.6%	11.7	2	2	2	5	642,859	642,709	709,397	687,574	33,352	34,166	54,509	27,139	11.6	11.9	17.2	8.8	-1.0	1	1.1	0.3	1.1	0.3	1.1	0.3	1.1	0.3	-1.0	0.7
IPI00982019	NDUFS8	Uncharacterized protein	99.6%	10.9	2	2	2	5	642,859	642,709	709,397	687,574	33,352	34,166	54,509	27,139	11.6	11.9	17.2	8.8	-1.0	1	1.1	0.3	1.1	0.3	1.1	0.3	1.1	0.3	-1.0	0.7
IPI00984633	NDUFS8	Uncharacterized protein	99.6%	14.5	2	2	2	5	642,859	642,709	709,397	687,574	33,352	34,166	54,509	27,139	11.6	11.9	17.2	8.8	-1.0	1	1.1	0.3	1.1	0.3	1.1	0.3	1.1	0.3	-1.0	0.7
IPI01008912	NDUFS8	14 kDa protein	99.6%	16.1	2	2	2	5	642,859	642,709	709,397	687,574	33,352	34,166	54,509	27,139	11.6	11.9	17.2	8.8	-1.0	1	1.1	0.3	1.1	0.3	1.1	0.3	1.1	0.3	-1.0	0.7
				EPATINYPFEK	2	86.8%	1																									
				TLLWTELFR	2	98.2%	1																									
IPI00010860	PSMD9	isoform p27-L of 26S proteasome non-ATPase regulatory subunit 9	95.5%	4.9	1	1	1	6	1,392,825	1,204,412	1,388,118	1,369,425	131,679	70,894	163,241	116,178	21.1	13.2	26.3	19.0	-1.2	0.2	-1.0	1	-1.0	0.9	1.2	0.3	1.1	0.3	-1.0	0.9
IPI00216220	PSMD9	isoform p27-S of 26S proteasome non-ATPase regulatory subunit 9	95.5%	5.3	1	1	1	6	1,392,825	1,204,412	1,388,118	1,369,425	131,679	70,894	163,241	116,178	21.1	13.2	26.3	19.0	-1.2	0.2	-1.0	1	-1.0	0.9	1.2	0.3	1.1	0.3	-1.0	0.9
IPI01013452	PSMD9	14 kDa protein	95.5%	8.6	1	1	1	6	1,392,825	1,204,412	1,388,118	1,369,425	131,679	70,894	163,241	116,178	21.1	13.2	26.3	19.0	-1.2	0.2	-1.0	1	-1.0	0.9	1.2	0.3	1.1	0.3	-1.0	0.9
IPI01013622	PSMD9	20 kDa protein	95.5%	6.2	1	1	1	6	1,392,825	1,204,412	1,388,118	1,369,425	131,679	70,894	163,241	116,178	21.1	13.2	26.3	19.0	-1.2	0.2	-1.0	1	-1.0	0.9	1.2	0.3	1.1	0.3	-1.0	0.9
IPI01014017	PSMD9	17 kDa protein	95.5%	7.2	1	1	1	6	1,392,825	1,204,412	1,388,118	1,369,425	131,679	70,894	163,241	116,178	21.1	13.2	26.3	19.0	-1.2	0.2	-1.0	1	-1.0	0.9	1.2	0.3	1.1	0.3	-1.0	0.9
IPI01014410	PSMD9	25 kDa protein	95.5%	5.0	1	1	1	6	1,392,825	1,204,412	1,388,118	1,369,425	131,679	70,894	163,241	116,178	21.1	13.2	26.3	19.0	-1.2	0.2	-1.0	1	-1.0	0.9	1.2	0.3	1.1	0.3	-1.0	0.9
				HNIICLQNDHK	3	95.5%	1																									
IPI00010865	CSNK2B	Casein kinase II subunit beta	95.1%	5.1	1	1	1	4	2,941,873	3,047,343	2,725,033	3,104,558	264,060	212,882	232,236	241,972	20.1	15.6	19.1	17.4	1.0	0.8	-1.1	0.6	1.1	0.7	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00514910	CSNK2B	Casein kinase 2, beta polypeptide	95.1%	4.8	1	1	1	4	2,941,873	3,047,343	2,725,033	3,104,558	264,060	212,882	232,236	241,972	20.1	15.6	19.1	17.4	1.0	0.8	-1.1	0.6	1.1	0.7	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00640088	CSNK2B	Casein kinase 2, beta polypeptide, isoform CRA_d	95.1%	4.7	1	1	1	4	2,941,873	3,047,343	2,725,033	3,104,558	264,060	212,882	232,236	241,972	20.1	15.6	19.1	17.4	1.0	0.8	-1.1	0.6	1.1	0.7	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00647922	LY6G5B	Uncharacterized protein	95.1%	5.0	1	1	1	4	2,941,873	3,047,343	2,725,033	3,104,558	264,060	212,882	232,236	241,972	20.1	15.6	19.1	17.4	1.0	0.8	-1.1	0.6	1.1	0.7	-1.1	0.3	1.0	0.9	1.1	0.3
				YQQGDFGYCPR	2	95.1%	1																									
IPI00010882	DFFA	isoform DFF45 of DNA fragmentation factor subunit alpha (Fragment)	99.4%	7.0	2	2	2	1	10,347,691	7,760,440	8,710,210	8,479,375	1,560,617	1,285,014	899,649	755,997	33.7	37.0	23.1	19.9	-1.3	0.2	-1.2	0.4	-1.2	0.3	1.1	0.6	1.1	0.6	-1.0	0.8
				ALAVALNWDIK	2	98.0%	1																									
				QLLQLYLQALEK	2	99.3%	1																									
IPI00010896	CLIC1	Chloride intracellular channel protein 1	100.0%	63.9	14	16	24	1	148,479,865	145,341,711	141,538,246	167,642,899	########	5,781,780	9,417,128	6,282,570	20.7	8.9	14.9	8.4	-1.0	0.8	-1.0	0.7	1.1	0.2	-1.0	0.7	1.2	0.03	1.2	0.05
				EEFASTCPDDEEIELAYEQVAK	2	100.0%	2																									
				FLDGNELTLADCNLLPK	2	98.6%	2																									
				GFTIPEAFR	2	95.5%	1																									
				GVTFNVTTVDTK	2	100.0%	2																									
				GVTFNVTTVDTKR	2	97.1%	1																									
				IGNCPFSQR	2	100.0%	2																									
				LAALNPESNTAGLDIFAK	2	100.0%	2																									
				LFMVLWLK	2	99.7%	2																									
				LHIVQVVCK	2	99.9%	1																									
				LHIVQVVCKK	2	98.9%	1																									
				LHIVQVVCKK	3	100.0%	1																									
				NSNPALNDNLEK	2	100.0%	2																									
				VLDNYLTSPLPEEVDETSAEDEGVSQR	2	100.0%	2																									
				VLDNYLTSPLPEEVDETSAEDEGVSQR	3	96.7%	1																									
				VLDNYLTSPLPEEVDETSAEDEGVSQRK	3	100.0%	1																									
				YLSNAYAR	2	99.9%	1																									
IPI00010949	SIAE	isoform 1 of Sialate O-acetylesterase	99.9%	2.9	1	1	2	2	563,559	545,868	662,021	720,340	51,580	48,564	55,333	49,762	20.5	19.9	18.7	15.5	-1.0	0.8	1.2	0.2	1.3	0.06	1.2	0.2	1.3	0.04	1.1	0.5
IPI00759728	SIAE	isoform 2 of Sialate O-acetylesterase	99.9%	3.1	1	1	2	2	563,559	545,868	662,021	720,340	51,580	48,564	55,333	49,762	20.5	19.9	18.7	15.5	-1.0	0.8	1.2	0.2	1.3	0.06	1.2	0.2	1.3	0.04	1.1	0.5
				FFPFGLVQLSSDLSK	2	99.9%	2																									
IPI00010951	EPPK1	Epiplakin	100.0%	9.6	31	31	34	1	159,046,237	167,636,533	168,623,450	197,988,509	########	5,543,632	########	5,339,758	22.8	7.4	20.2	6.0	1.1	0.6	1.1	0.7	1.2	0.07	1.0	1	1.2	0.004	1.2	0.1
				AEIIDQDLYER	2	100.0%	2																									
				AGTLTVEELGATLTSLLAQAQAQAR	2	100.0%	1																									
				AMLAQQYQEGTLSVEK	2	100.0%	1																									
				ASLSLWQAMEK	2	99.9%	2																									
				AVPVWDVLASGYVSGAAR	3	99.9%	1																									
				EGQGEGETQEAAAAAAAAR	3	97.4%	1																									
				ELIQEYGAQSGGLEK	2	100.0%	1																									
				ELSEQLGQAER	2	99.9%	1																									
				GCSVSLWDLLLSEYVGADK	2	100.0%	1																									
				GFFDPNTHENLTYLQLLER	3	99.9%	1																									
				GFFDPNTHENLTYVQLLR	3	100.0%	1																									
				GSAVHQLSEELR	2	100.0%	1																									
				GYFDEEMNR	2	100.0%	2																									
				LLEAETQR	2	92.5%	1																									
				LLEAQIATGGIIDPVHSHR	3	100.0%	1																									
				LLEAQIATGGVIDPVHSHR	3	99.7%	1																									
				LLEIITTTIEETETQNQGIK	3	99.9%	1																									
				LPLEAALR	2	95.4%	1																									
				LSVEEAVAAGVVGGEIQEK	2	100.0%	1																									
				LTAIIEEAEEAPGARPQLQDAWR	3	100.0%	1																									
				MSIYQAMWK	2	99.7%	1																									
				QVSASELHTSGILGPETLR	3	99.8%	1																									
				QVVSAVTALVEAAER	2	100.0%	1																									
				RDELLAQHAAGALGLPDLVAVLTR	3	100.0%	1																									
				SLEGGNFIAGVLIQGTQER	3	99.8%	1																									
				VLADPSDDTK	2	82.7%	1																									
				VPVDVAYR	2	99.8%	1																									
				VSAWELINSEYFSEGR	2	99.8%	1																									
				YLCGLGAVGGVR	2	99.1%	1																									
				YLEGTSCIAGVLVPAK	2	100.0%	1																									
				YLQGTGCIAGLLLPGSQER	2	93.0%	1																									
IPI00011107	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	100.0%	17.3	7	8	9	2	22,151,121	22,887,562	23,000,855	27,128,860	2,184,263	1,215,436	2,237,466	702,920	22.1	11.9	21.8	5.8	1.0	0.8	1.0	0.8	1.2	0.08	1.0	1	1.2	0.02	1.2	0.1
IPI01015385	IDH2	Isocitrate dehydrogenase	100.0%	19.5	7	8	9	2	22,151,121	22,887,562	23,000,855	27,128,860	2,184,263	1,215,436	2,237,466	702,920	22.1	11.9	21.8	5.8	1.0	0.8	1.0	0.8	1.2	0.08	1.0	1	1.2	0.02	1.2	0.1
				GKLDGNQDLIR	2	99.5%	1																									
				LIDDMVAQVLK	2	100.0%	2																									
				LNEHFLNTTDFLDTIK	2	99.5%	1																									
				LNEHFLNTTDFLDTIK	3	100.0%	1																									
				LNEHFLNTTDFLDTIKSNLDRALGR	3	84.9%	1																									
				NILGGTVFR	2	99.3%	1																									
				TIEAEAAHGTVTR	2	100.0%	1																									
				YFDLGLPNR	2	91.7%	1																									
IPI00011126	PSMC1	26S protease regulatory subunit 4	100.0%	18.4	5	6	7	1	10,080,637	10,186,358	10,082,525	11,795,757	670,966	593,822	608,153	577,068	14.9	13.0	13.5	10.9	1.0	0.9	1.0	1	1.2	0.09	-1.0	0.9	1.2	0.09	1.2	0.08
				AVANQTSATFLR	2	100.0%	1																									
				IKDYLLMEEEFIR	3	99.9%	1																									
				TMLELLNQLDGFDSR	2	100.0%	2																									
				VAEEHAPSIVFIDEIDAIGTK	3	100.0%	1																									
				VHAVIGVLMDDTDPLVTVMK	2	96.8%	1																									

				VHAVIGVLMDDTDPLVTVMK	3	100.0%	1																									
IPI00011134	HSPA7	Putative heat shock 70 kDa protein 7	100.0%	3.0	1	1	1	1	703,447	721,692	682,965	850,490	47,476	40,076	66,087	28,161	15.1	12.4	21.6	7.4	1.0	0.8	-1.0	0.8	1.2	0.03	-1.1	0.6	1.2	0.03	1.2	0.05
				VEILANDQGNR	1	98.1%	1																									
IPI00011177	EIF3FP2	IFP38	100.0%	3.5	1	1	1	1	729,728	824,112	763,558	880,752	51,375	75,853	59,899	47,087	15.7	20.6	17.5	12.0	1.1	0.3	1.0	0.7	1.2	0.06	-1.1	0.5	1.1	0.5	1.2	0.2
				AYVSTLMGVPGR	2	100.0%	1																									
IPI00011200	PHGDH	D-3-phosphoglycerate dehydrogenase	100.0%	26.5	11	12	16	1	38,663,481	41,653,022	39,772,436	45,318,414	2,523,492	1,599,953	2,220,753	2,752,325	14.6	8.6	12.5	13.6	1.1	0.3	1.0	0.7	1.2	0.1	-1.0	0.5	1.1	0.3	1.1	0.2
				AGTGVDNVDLEAATR	2	100.0%	2																									
				ALVDHENVISCPHLGASTK	3	100.0%	1																									
				CGEEIAVQFVDMVK	2	100.0%	1																									
				DLPLLLFR	2	99.9%	1																									
				GGIVDEGALLR	2	99.9%	1																									
				ILQDGGLQVVEK	2	100.0%	2																									
				KILQDGGLQVVEK	2	99.6%	1																									
				NAGNCLSPAVIVGLLK	2	100.0%	2																									
				TQTSDPAMLPTMIGLLAEAGVR	2	100.0%	2																									
				TQTSDPAMLPTMIGLLAEAGVR	3	100.0%	1																									
				VLISDSLDPCCR	2	97.2%	1																									
				VTADVINAAEK	2	91.2%	1																									
IPI00011201	ME2	NAD-dependent malic enzyme, mitochondrial	99.4%	3.1	1	1	1	2	2,148,380	2,497,655	2,180,355	2,823,080	251,149	171,211	169,367	217,603	26.1	15.3	17.4	17.2	1.2	0.3	1.0	0.9	1.3	0.08	-1.1	0.2	1.1	0.3	1.3	0.05
IPI00643577	ME2	NAD-dependent malic enzyme, mitochondrial isoform 2 precursor	99.4%	3.8	1	1	1	2	2,148,380	2,497,655	2,180,355	2,823,080	251,149	171,211	169,367	217,603	26.1	15.3	17.4	17.2	1.2	0.3	1.0	0.9	1.3	0.08	-1.1	0.2	1.1	0.3	1.3	0.05
				ILGLGDLGVYGMGIPVGK	2	99.4%	1																									
IPI00011229	CTSD	Cathepsin D	100.0%	32.3	9	11	16	1	55,872,505	58,471,209	51,665,085	63,843,432	4,495,419	4,020,474	3,240,390	4,162,696	18.0	15.4	14.0	14.6	1.0	0.7	-1.1	0.5	1.1	0.2	-1.1	0.2	1.1	0.4	1.2	0.05
				AIGAVPLIQGEYMIPCEK	2	100.0%	2																									
				AIGAVPLIQGEYMIPCEK	3	100.0%	1																									
				AYWQVHLDQVEVASGLTLCK	3	98.7%	1																									
				DPDAQPGGELMLGGTDSK	2	100.0%	2																									
				EGCEAIVDTGTSLMVGPVDEVR	2	100.0%	1																									
				FDGILGMAYPR	2	100.0%	2																									
				ISVNNVLPVFDNLMQQK	2	100.0%	2																									
				ISVNNVLPVFDNLMQQK	3	100.0%	2																									
				LLDIACWIHHK	3	99.4%	1																									
				QVFGEATK	2	95.4%	1																									
				VGFAEAAR	2	99.9%	1																									
IPI00011250	UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	100.0%	30.0	5	6	8	1	21,928,485	20,797,585	22,027,332	25,842,475	2,152,408	846,544	1,652,055	958,601	22.0	9.1	16.8	8.3	-1.1	0.6	1.0	1	1.2	0.1	1.1	0.5	1.2	0.004	1.2	0.08
				FLEESVSMSPEER	2	100.0%	2																									
				MHFESGSTLKK	3	98.8%	1																									
				VTHETSAHEGQTEAPSIDEK	3	84.9%	1																									
				WLPLEANPEVTNQFLK	2	100.0%	2																									
				WLPLEANPEVTNQFLK	3	98.8%	1																									
				YLENYDAIR	2	100.0%	1																									
IPI00011253	RPS3	40S ribosomal protein S3	100.0%	42.8	8	8	11	1	10,898,805	11,985,820	10,995,798	12,352,110	1,257,406	682,592	1,052,468	592,456	25.8	12.7	21.4	10.7	1.1	0.5	1.0	1	1.1	0.3	-1.1	0.5	1.0	0.7	1.1	0.3
				AELNEFLTR	2	97.8%	1																									
				ELAEDGYSGVEVR	2	100.0%	2																									
				FGFPEGSVELYAEK	2	100.0%	2																									
				FVDGLMIHSGDPVNYYVDTAVR	3	100.0%	1																									
				GCEVVVSGK	2	99.8%	1																									
				GGKPEPPAMPQPVPTA	2	100.0%	2																									
				GLCAIAQAESLR	2	100.0%	1																									
				KFVADGIFK	2	96.7%	1																									
IPI00011268	RALY	cDNA FLJ77422, highly similar to Homo sapiens RNA binding protein, autoantigenic	100.0%	9.8	3	3	4	2	2,470,140	2,472,514	2,355,848	3,069,082	219,766	136,990	221,504	106,054	19.9	12.4	21.0	7.7	1.0	1	-1.0	0.7	1.2	0.04	-1.0	0.7	1.2	0.009	1.3	0.02
IPI00216044	RALY	isoform 1 of RNA-binding protein Raly	100.0%	10.3	3	3	4	2	2,470,140	2,472,514	2,355,848	3,069,082	219,766	136,990	221,504	106,054	19.9	12.4	21.0	7.7	1.0	1	-1.0	0.7	1.2	0.04	-1.0	0.7	1.2	0.009	1.3	0.02
				GYAFVQYSNER	2	99.9%	1																									
				KSDVETIFSK	2	99.0%	1																									
				LEQIAAEQK	2	98.9%	2																									
IPI00011274	HNRPDL	isoform 1 of Heterogeneous nuclear ribonucleoprotein D-like	100.0%	10.7	5	5	6	3	5,143,181	5,354,966	5,054,502	6,107,587	546,890	339,516	361,784	341,566	23.8	14.2	16.0	12.5	1.0	0.8	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.2	1.2	0.07
IPI00045498	HNRPDL	isoform 3 of Heterogeneous nuclear ribonucleoprotein D-like	100.0%	18.4	5	5	6	3	5,143,181	5,354,966	5,054,502	6,107,587	546,890	339,516	361,784	341,566	23.8	14.2	16.0	12.5	1.0	0.8	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.2	1.2	0.07
IPI00845282	HNRPDL	isoform 2 of Heterogeneous nuclear ribonucleoprotein D-like	100.0%	15.0	5	5	6	3	5,143,181	5,354,966	5,054,502	6,107,587	546,890	339,516	361,784	341,566	23.8	14.2	16.0	12.5	1.0	0.8	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.2	1.2	0.07
				DLTEYLSR	2	99.8%	1																									
				GFGFVLFK	2	100.0%	2																									
				MFIGGLSWDTSK	2	99.9%	1																									
				MFIGGLSWDTSKK	2	99.9%	1																									
				VFVGGLSPDTSEEQIK	2	97.5%	1																									
IPI00011276	BCKDHB	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	99.5%	4.3	1	1	1	3	377,347	334,397	379,419	328,134	37,052	18,504	38,060	19,440	22.0	12.4	22.4	13.3	-1.1	0.3	1.0	1	-1.1	0.3	1.1	0.3	-1.0	0.8	-1.2	0.3
IPI00642832	BCKDHB	Branched chain keto acid dehydrogenase E1, beta polypeptide (Maple syrup urine d	99.5%	7.8	1	1	1	3	377,347	334,397	379,419	328,134	37,052	18,504	38,060	19,440	22.0	12.4	22.4	13.3	-1.1	0.3	1.0	1	-1.1	0.3	1.1	0.3	-1.0	0.8	-1.2	0.3
IPI01011008	BCKDHB	cDNA, FLJ79444, highly similar to 2-oxoisovalerate dehydrogenase subunit beta, mi	99.5%	5.3	1	1	1	3	377,347	334,397	379,419	328,134	37,052	18,504	38,060	19,440	22.0	12.4	22.4	13.3	-1.1	0.3	1.0	1	-1.1	0.3	1.1	0.3	-1.0	0.8	-1.2	0.3
				MNLFQSVTSALDNSLAK	2	99.5%	1																									
IPI00011284	COMT	isoform Membrane-bound of Catechol O-methyltransferase	100.0%	41.7	7	8	10	2	19,256,526	22,176,213	20,055,340	24,562,382	1,697,561	1,176,425	1,817,138	758,619	19.7	11.9	20.3	6.9	1.2	0.2	1.0	0.8	1.3	0.02	-1.1	0.4	1.1	0.1	1.2	0.05
IPI00375513	COMT	isoform Soluble of Catechol O-methyltransferase	100.0%	51.1	7	8	10	2	19,256,526	22,176,213	20,055,340	24,562,382	1,697,561	1,176,425	1,817,138	758,619	19.7	11.9	20.3	6.9	1.2	0.2	1.0	0.8	1.3	0.02	-1.1	0.4	1.1	0.1	1.2	0.05
				AIYKGPGSEAGP	2	99.2%	1																									
				GSSCFECTHYQSFLEYR	3	92.6%	1																									
				GTVLLADNVICPGAPDFLAHVR	3	100.0%	2																									
				LITIEINPDCAAITQR	3	100.0%	1																									
				VTLVVGASQDIIPQLK	2	99.8%	1																									
				YDVDTLDMVFLDHWK	2	100.0%	1																									
				YDVDTLDMVFLDHWK	3	100.0%	1																									
				YLPDTLLLEECGLLR	2	100.0%	2																									
IPI00011285	CAPN1	Calpain-1 catalytic subunit	100.0%	26.8	12	12	14	1	37,974,823	37,440,554	37,582,792	44,134,218	3,940,975	1,553,557	3,190,810	1,013,247	23.2	9.3	19.0	5.1	-1.0	0.9	-1.0	0.9	1.2	0.2	1.0	1	1.2	0.007	1.2	0.1
				DMETIGFAVYEVPPELVGQPAVHLK	3	86.2%	1																									
				FRLPPGEYVVVPSTFEPNKEGDFVLR	3	99.6%	1																									
				LEICNLTPDALK	2	99.9%	2																									
				LVFVHSAEGNEFWSALLEK	3	100.0%	1																									
				LYELIITR	2	98.8%	1																									
				QLAGEDMEISVK	2	100.0%	2																									
				SAGTVELDDQIQANLPDEQVLSEEEIDENFK	3	100.0%	1																									
				SGSMSAYEMR	2	99.9%	1																									
				SMVNLMDR	2	99.4%	1																									
				WNTTLYEGTWR	2	98.1%	1																									
				YLGQDYEQLR	2	99.9%	1																									
				YSEPDLAVDFDNFVCCLVR	2	99.9%	1																									
IPI00011302	CD59	CD59 glycoprotein	99.5%	9.4	1	2	2	4	2,016,968	2,349,016	2,005,641	2,300,843	136,543	169,043	149,450	188,490	15.1	16.1	16.7	18.3	1.2	0.2	-1.0	1	1.1	0.3	-1.2	0.2	-1.0	0.9	1.1	0.3
IPI00980045	CD59	Uncharacterized protein	99.5%	9.2	1	2	2	4	2,016,968	2,349,016	2,005,641	2,300,843	136,543	169,043	149,450	188,490	15.1	16.1	16.7	18.3	1.2	0.2	-1.0	1	1.1	0.3	-1.2	0.2	-1.0	0.9	1.1	0.3
IPI00983417	CD59	Uncharacterized protein	99.5%	11.1	1	2	2	4	2,016,968	2,349,016	2,005,641	2,300,843	136,543	169,043	149,450	188,490	15.1	16.1	16.7	18.3	1.2	0.2	-1.0	1	1.1	0.3	-1.2	0.2	-1.0	0.9	1.1	0.3
IPI00983742	CD59	Conserved hypothetical protein	99.5%	16.9	1	2	2	4	2,016,968	2,349,016	2,005,641	2,300,843	136,543	169,043	149,450	188,490	15.1	16.1	16.7	18.3	1.2	0.2	-1.0	1	1.1	0.3	-1.2	0.2	-1.0	0.9	1.1	0.3
				FEHCNFNDVTTR	2	91.7%	1																									
				FEHCNFNDVTTR	3	99.5%	1																									
IPI00011416	ECH1	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	100.0%	36.0	8	9	14	1	42,586,992	37,779,337	39,645,849	46,753,810	3,988,139	979,233	2,255,534	1,075,571	20.9	5.8	12.7	5.1	-1.1	0.3	-1.1	0.5	1.1	0.4	1.0	0.5	1.2	0.0003	1.2	0.02
				DHSVAESLNYVASWNMSMLQTQDLVK	3	100.0%	1																									
				EVDVGLAADVGTLQR	2	100.0%	1																									
				MFTAGIDLMDMASDILQPK	2	100.0%	2																									
				MFTAGIDLMDMASDILQPK	3	100.0%	1																									
				MMADEALGSGLVSR	2	100.0%	2																									
				VIGNQSLVNELAFTAR	2	100.0%	2																									
				VNLLYSR	2	96.8%	1																									
				YCAQDAFFQVK	2	100.0%	2																									
				YQETFNVIER	2	100.0%	2																									
IPI00011448	MUC13	mucin-13	100.0%	11.1	4	4	5	1	23,383,360	25,338,710	23,851,885	28,061,975	1,886,084	930,357	1,758,820	983,774	18.0	8.2	16.5	7.8	1.1	0.4	1.0	0.9	1.2	0.06	-1.1	0.5	1.1	0.08	1.2	0.07
				DSQMQNPYSR	2	98.3%	1																									
				HSMAYQDLHSEITSLFK	3	99.9%	1																									
				ISVTVSETFDPEEK	2	100.0%	1																									
				STGFTNLGAEGSVFPK	2	100.0%	2																									
IPI00011454	GANAB	isoform 2 of Neutral alpha-glucosidase AB	100.0%	28.6	19	20	23	2	43,190,422	43,699,469	45,370,209	49,781,625	3,289,027	1,513,651	2,735,685	1,410,466	17.0	7.8	13.5	6.3	1.0	0.9	1.1	0.6	1.2	0.1	1.0	0.6	1.1	0.02	1.1	0.2
IPI00383581	GANAB	cDNA FLJ61290, highly similar to Neutral alpha-glucosidase AB	100.0%	27.7	19	20	23	2	43,190,422	43,699,469	45,370,209	49,781,625	3,289,027	1,513,651	2,735,685	1,410,466	17.0	7.8	13.5	6.3	1.0	0.9	1.1	0.6	1.2	0.1	1.0	0.6	1.1	0.02	1.1	0.2
				DENSVELTMAEGPYK	2	100.0%	1																									
				FGAVWTGDNTAEWDHLK	3	100.0%	1																									
				FRIDELEPR	3	93.3%	1																									
				FSFSGNTLVSSSADPEGHFETPIWIER	3	100.0%	2																									
				GLLEFEHQR	2	99.3%	1																									
				HHGPQTLYLPVTLSSIPVFQR	2	97.1%	1																									
				LSFQHDPETSVLVLR	3	100.0%	1																									
				LVAIVDPHIK	2	99.9%	1																									
				LVAIVDPHIK	3	99.7%	1																									
				MMDYLQGSGETPQTDVR	2	100.0%	2																									
				NPEPELLVR	2	98.3%	1																									
				QYASLTGTQALPPLFSLGYHQSR	3	100.0%	1																									
				SLLLSVNAR	2	99.8%	1																									
				TCEESSFCKR	2	100.0%	1																									
				TRDGSDYEGWCWPGSAGYPDFTNPTMR	3	99.4%	1																									
				VLLVLELQGLQK	2	100.0%	1																									
				VTEGGEPYR	2	98.6%	1																									
				VVIIGAGKPAAVVLQTK	2	100.0%	1																									
				WYQMGAYQPFFR	2	100.0%	2																									
				YFTWDPSR	2	98.7%	1																									
IPI00011522	ACAA1	cDNA, FLJ79450, highly similar to 3-ketoacyl-CoA thiolase, peroxisomal	100.0%	26.1	2	2	2	1	788,976	839,007	825,982	828,827	65,015	60,060	68,917	25,345	18.4	16.0	18.7	6.8	1.1	0.6	1.0	0.7	1.1	0.6	-1.0	0.9	-1.0	0.9	1.0	1
				GGFKDTTPDELLSAVMTAVLK	3	100.0%	1																									
				IAQFLSDIPETVPLSTVNR	2	98.2%	1																									
IPI00011569	ACACA	isoform 1 of Acetyl-CoA carboxylase 1	98.4%	2.3	4	4	4	6	3,567,767	3,881,298	3,787,660	4,215,905	316,069	108,962	242,792	112,048	19.8	6.3	14.3	5.9	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.06	1.1	0.1
IPI00396015	ACACA	isoform 4 of Acetyl-CoA carboxylase 1	98.4%	2.3	4	4	4	6	3,567,767	3,881,298	3,787,660	4,215,905	316,069	108,962	242,792	112,048	19.8	6.3	14.3	5.9	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.06	1.1	0.1
IPI00396018	ACACA	isoform 3 of Acetyl-CoA carboxylase 1	98.4%	2.4	4	4	4	6	3,567,767	3,881,298	3,787,660	4,215,905	316,069	108,962	242,792	112,048	19.8	6.3	14.3	5.9	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.06	1.1	0.1
IPI00793409	ACACA	265 kDa protein	98.4%	2.3	4	4	4	6	3,567,767	3,881,298	3,787,660	4,215,905	316,069	108,962	242,792	112,048	19.8	6.3	14.3	5.9	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.06	1.1	0.1
IPI00847501	ACACA	isoform 2 of Acetyl-CoA carboxylase 1	98.4%	2.4	4	4	4	6	3,567,767	3,881,298	3,787,660	4,215,905	316,069	108,962	242,792	112,048	19.8	6.3	14.3	5.9	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.06	1.1	0.1
IPI00942045	ACACA	268 kDa protein	98.4%	2.3	4	4	4	6	3,567,767	3,881,298	3,787,660	4,215,905	316,069	108,962	242,792	112,048	19.8	6.3	14.3	5.9	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.06	1.1	0.1
				DVDDGLQAAEEVGYPVMIK	3	84.6%	1																									
				GSVLEPEGTVEIK	2	81.0%	1																									
				IGSFGPQEDLLFLR	2	90.2%	1																									
				MGGMVSFR	2	87.1%	1																									
IPI00011592	DYNC1LI2	Cytoplasmic dynein 1 light intermediate chain 2	98.7%	2.4	1	1	1	2	4,389,450	4,921,530	4,530,520	4,368,840	953,381	747,249	431,166	487,055	48.6	34.0	21.3	24.9	1.1	0.7	1.0	0.9	-1.0	1	-1.1	0.7	-1.1	0.6	-1.0	0.8
IPI00909090	DYNC1LI2	cDNA FLJ52924, highly similar to Cytoplasmic dynein 1 light intermediate chain 2	98.7%	2.9	1	1	1	2	4,389,450	4,921,530	4,530,520	4,368,840	953,381	747,249	431,166	487,055	48.6	34.0	21.3	24.9	1.1	0.7	1.0	0.9	-1.0	1	-1.1	0.7	-1.1	0.6	-1.0	0.8

				TVLSNVQEELDR	2	98.7%	1																									
IPI00011603	PSMD3	26S proteasome non-ATPase regulatory subunit 3	99.9%	3.9	2	2	2	2	3,431,663	3,388,470	3,352,345	4,050,053	439,373	150,539	233,698	214,383	28.6	9.9	15.6	11.8	-1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.04	1.2	0.06
IPI01015295	PSMD3	cDNA FLJ30049 fis, clone ADRGL1000033, highly similar to 26S proteasome non-A	99.9%	4.0	2	2	2	2	3,431,663	3,388,470	3,352,345	4,050,053	439,373	150,539	233,698	214,383	28.6	9.9	15.6	11.8	-1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.04	1.2	0.06
				AIQLEYSEAR	2	99.9%	1																									
				FNQVLDQFGEK	2	95.3%	1																									
IPI00011604	GCSH	Glycine cleavage system H protein, mitochondrial	99.6%	11.6	1	1	1	2	799,815	804,050	850,995	904,310	118,721	44,471	101,439	36,198	33.2	12.4	26.7	9.0	1.0	1	1.1	0.8	1.1	0.4	1.1	0.7	1.1	0.1	1.1	0.6
IPI00738964	LOC654085	glycine cleavage system H protein, mitochondrial-like isoform 2	99.6%	11.6	1	1	1	2	799,815	804,050	850,995	904,310	118,721	44,471	101,439	36,198	33.2	12.4	26.7	9.0	1.0	1	1.1	0.8	1.1	0.4	1.1	0.7	1.1	0.1	1.1	0.6
				MTLSNPSELDELMSEEAYEK	2	99.6%	1																									
IPI00011662	SPINT2	Kunitz-type protease inhibitor 2	99.5%	8.7	2	2	2	1	6,960,178	7,434,490	7,282,328	7,740,597	723,062	350,928	447,995	233,233	23.2	10.6	13.8	6.7	1.1	0.6	1.0	0.7	1.1	0.4	-1.0	0.8	1.0	0.5	1.1	0.4
				NAADSSVPSAPR	2	99.5%	1																									
				SIHDFCLVSK	3	83.1%	1																									
IPI00011698	SAP18	histone deacetylase complex subunit SAP18	99.6%	11.1	1	1	1	2	869,252	949,720	995,880	1,203,200	157,625	102,286	85,729	43,656	40.6	24.1	19.3	8.1	1.1	0.7	1.1	0.5	1.4	0.1	1.0	0.7	1.3	0.05	1.2	0.06
IPI00927280	SAP18	Protein	99.6%	11.9	1	1	1	2	869,252	949,720	995,880	1,203,200	157,625	102,286	85,729	43,656	40.6	24.1	19.3	8.1	1.1	0.7	1.1	0.5	1.4	0.1	1.0	0.7	1.3	0.05	1.2	0.06
				GNVPSSELQIYTWMDATLK	2	99.6%	1																									
IPI00011876	MTAP	cDNA FLJ59758, highly similar to S-methyl-5-thioadenosine phosphorylase	100.0%	29.0	5	5	5	1	24,324,348	24,188,535	22,910,644	26,970,764	1,652,724	752,387	2,297,212	1,242,777	15.2	7.0	22.4	10.3	-1.0	0.9	-1.1	0.6	1.1	0.2	-1.1	0.6	1.1	0.09	1.2	0.2
				GTMVTIEGPR	2	100.0%	1																									
				IGIIGGTGLDDPEILEGR	2	100.0%	1																									
				SLLLTTIPQIGSTEWSETLHNLK	3	99.9%	1																									
				TWGADVINMTTVPEVVLAK	2	100.0%	1																									
				YVDTPFGKPSDALILGK	3	99.4%	1																									
IPI00011898	EIF2B5	Translation initiation factor eIF-2B subunit epsilon	93.2%	1.8	1	1	1	2	2,397,165	2,618,955	2,603,135	2,975,435	193,205	176,728	139,496	143,077	18.0	15.1	12.0	10.8	1.1	0.4	1.1	0.4	1.2	0.04	-1.0	0.9	1.1	0.2	1.1	0.1
IPI00925085	EIF2B5	Uncharacterized protein	93.2%	1.8	1	1	1	2	2,397,165	2,618,955	2,603,135	2,975,435	193,205	176,728	139,496	143,077	18.0	15.1	12.0	10.8	1.1	0.4	1.1	0.4	1.2	0.04	-1.0	0.9	1.1	0.2	1.1	0.1
				SKWCRPTSLNVVR	3	91.2%	1																									
IPI00011913	HNRNPA0	Heterogeneous nuclear ribonucleoprotein A0	100.0%	17.4	3	3	4	1	22,176,220	24,190,670	23,082,150	25,955,920	2,497,467	1,165,094	2,451,184	793,746	25.2	10.8	23.8	6.8	1.1	0.5	1.0	0.8	1.2	0.2	-1.0	0.7	1.1	0.2	1.1	0.3
				AVPKEDIYSGGGGGGSR	2	99.6%	1																									
				GDVAEGDLIEHFSQFGTVEK	3	100.0%	1																									
				LFIGGLNVQTSESGLR	2	100.0%	2																									
IPI00011916	AIMP2	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	98.8%	7.8	1	1	1	1	3,475,580	3,550,980	3,242,810	3,898,100	369,880	104,112	266,144	131,942	23.8	6.6	18.4	7.6	1.0	0.9	-1.1	0.6	1.1	0.3	-1.1	0.3	1.1	0.07	1.2	0.06
				SYGPAPGAGHVQEESNLSLQALESR	3	98.8%	1																									
IPI00011919	FADD	Protein FADD	100.0%	21.2	2	2	2	1	7,587,510	9,081,810	8,897,940	9,422,110	387,782	796,585	1,049,120	757,399	11.4	19.6	26.4	18.0	1.2	0.1	1.2	0.3	1.2	0.06	-1.0	0.9	1.0	0.8	1.1	0.7
				SCQMNLVADLVQEVQQAR	2	99.9%	1																									
				VQSGLDLFSMLLEQNDLEPGHTELLR	3	100.0%	1																									
IPI00011937	PRDX4	Peroxiredoxin-4	100.0%	17.0	5	6	8	1	10,716,482	11,070,234	10,860,636	12,279,314	823,673	573,194	821,631	776,514	17.2	11.6	16.9	14.1	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.2	1.1	0.2
				GLFIIDDK	2	100.0%	2																									
				GLFIIDDKGILR	2	98.7%	1																									
				IPLLSDLTHQISK	2	94.0%	1																									
				IPLLSDLTHQISK	3	93.5%	1																									
				LVQAFQYTDK	2	98.3%	1																									
				QITLNDLPVGR	2	100.0%	2																									
IPI00011954	AQP9	Aquaporin-9	96.4%	5.8	1	1	1	1	343,683	349,805	384,495	360,953	23,606	31,397	54,853	19,733	15.4	20.1	31.9	12.2	1.0	0.9	1.1	0.5	1.1	0.6	1.1	0.6	1.0	0.8	-1.1	0.7
				TEQSEDKPEKYELSVIM	2	96.4%	1																									
IPI00011996	UBE2Z	isoform 1 of Ubiquitin-conjugating enzyme E2 Z	100.0%	5.9	2	2	2	2	5,527,240	6,633,825	6,005,250	6,213,070	609,425	326,833	548,852	385,904	24.7	11.0	20.4	13.9	1.2	0.1	1.1	0.6	1.1	0.4	-1.1	0.4	-1.1	0.4	1.0	0.8
IPI00829749	UBE2Z	Ubiquitin-conjugating enzyme E2Z (Putative), isoform CRA_a	100.0%	7.0	2	2	2	2	5,527,240	6,633,825	6,005,250	6,213,070	609,425	326,833	548,852	385,904	24.7	11.0	20.4	13.9	1.2	0.1	1.1	0.6	1.1	0.4	-1.1	0.4	-1.1	0.4	1.0	0.8
				GHFDYQSLLMR	2	98.9%	1																									
				VAVCDMMEGK	2	98.9%	1																									
IPI00012007	AHCY	Adenosylhomocysteinase	100.0%	34.3	11	12	16	1	73,812,487	75,657,176	70,506,728	83,630,565	5,891,739	2,518,734	5,185,332	3,067,728	17.9	7.4	16.4	8.2	1.0	0.8	-1.0	0.7	1.1	0.2	-1.1	0.4	1.1	0.08	1.2	0.06
				DGPLNMILDDGGDLTNLIHTK	3	100.0%	2																									
				GETDEEYLWCIEQTLYFK	2	100.0%	1																									
				GISEETTTGVHNLYK	2	100.0%	2																									
				KLDEAVAEAHLGK	3	100.0%	1																									
				QAQYLGMSCDGPFKPDHYR	3	86.7%	1																									
				RIILLAEGR	2	99.9%	1																									
				VADIGLAAWGR	2	100.0%	1																									
				VAVVAGYGDVGK	2	100.0%	2																									
				VNIKPQVDR	2	99.6%	1																									
				VNIKPQVDR	3	97.9%	1																									
				VPAINVNDSVTK	2	100.0%	2																									
				YPQLLPGIR	2	98.7%	1																									
IPI00012011	CFL1	Cofilin-1	100.0%	70.5	13	15	21	2	69,413,562	72,714,894	72,245,695	81,407,452	5,731,134	3,196,496	5,973,202	1,811,603	18.5	9.8	18.5	5.0	1.0	0.6	1.0	0.7	1.2	0.1	-1.0	0.9	1.1	0.05	1.1	0.2
IPI00984795	CFL1	Uncharacterized protein	100.0%	57.4	13	15	21	2	69,413,562	72,714,894	72,245,695	81,407,452	5,731,134	3,196,496	5,973,202	1,811,603	18.5	9.8	18.5	5.0	1.0	0.6	1.0	0.7	1.2	0.1	-1.0	0.9	1.1	0.05	1.1	0.2
				EDLVFIFWAPESAPLK	2	99.9%	1																									
				EILVGDVGQTVDDPYATFVK	2	100.0%	2																									
				ESKKEDLVFIFWAPESAPLK	3	99.0%	1																									
				HELQANCYEEVKDR	2	100.0%	1																									
				HELQANCYEEVKDR	3	100.0%	2																									
				KEDLVFIFWAPESAPLK	3	100.0%	2																									
				LGGSAVISLEGKPL	2	100.0%	2																									
				LTGIKHELQANCYEEVKDR	3	100.0%	1																									
				MIYASSK	1	100.0%	1																									
				MIYASSKDAIK	2	98.2%	1																									
				MLPDKDCR	2	97.7%	1																									
				NIILEEGKEILVGDVGQTVDDPYATFVK	2	100.0%	2																									
				NIILEEGKEILVGDVGQTVDDPYATFVK	3	100.0%	1																									
				VFNDMK	2	99.2%	1																									
				YALYDATYETK	2	100.0%	2																									
IPI00012048	NME1	isoform 1 of Nucleoside diphosphate kinase A	100.0%	81.6	9	13	19	2	34,680,083	35,304,368	34,061,697	39,923,394	3,147,345	1,196,203	2,480,831	1,146,945	20.3	7.6	16.3	6.4	1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.7	1.1	0.02	1.2	0.06
IPI00375531	NME2	isoform 2 of Nucleoside diphosphate kinase A	100.0%	70.1	9	13	19	2	34,680,083	35,304,368	34,061,697	39,923,394	3,147,345	1,196,203	2,480,831	1,146,945	20.3	7.6	16.3	6.4	1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.7	1.1	0.02	1.2	0.06
				DRPFFAGLVK	2	99.9%	1																									
				DRPFFAGLVK	3	99.9%	1																									
				EIGLWFHPEELVDYTSCAQNWIYE	2	99.8%	1																									
				FMQASEDLLK	2	99.6%	2																									
				GDFCIQVGR	2	100.0%	2																									
				GLVGEIIKR	2	99.9%	2																									
				NIIHGSDSVESAEK	2	100.0%	1																									
				NIIHGSDSVESAEK	3	100.0%	1																									
				TFIAIKPDGVQR	2	100.0%	2																									
				TFIAIKPDGVQR	3	99.7%	1																									
				VMLGETNPADSKPGTIR	2	100.0%	2																									
				VMLGETNPADSKPGTIR	3	100.0%	1																									
				YMHSGPVVAMVWEGLNVVK	3	100.0%	2																									
IPI00012066	PCBP2	poly(rC)-binding protein 2 isoform b	100.0%	31.2	9	10	14	3	7,635,913	8,025,441	7,421,822	8,977,200	786,326	316,947	449,123	415,240	23.0	8.8	13.5	10.3	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.03
IPI00470509	PCBP2	poly(rC)-binding protein 2 isoform c	100.0%	34.1	9	10	14	3	7,635,913	8,025,441	7,421,822	8,977,200	786,326	316,947	449,123	415,240	23.0	8.8	13.5	10.3	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.03
IPI00790627	PCBP2	poly(rC)-binding protein 2 isoform e	100.0%	31.3	9	10	14	3	7,635,913	8,025,441	7,421,822	8,977,200	786,326	316,947	449,123	415,240	23.0	8.8	13.5	10.3	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.03
				AFAMIIDK	2	94.2%	1																									
				AITIAGIPQSIIECVK	2	100.0%	2																									
				ESTGAQVQVAGDMLPNSTER	2	100.0%	2																									
				ESTGAQVQVAGDMLPNSTER	3	99.9%	1																									
				EVGSIIGK	2	94.3%	1																									
				IANPVEGSTDR	2	100.0%	1																									
				IITLAGPTNAIFK	2	99.8%	1																									
				INISEGNCPER	2	100.0%	2																									
				LVVPASQCGSLIGK	2	100.0%	1																									
				QICVVMLESPPK	2	99.0%	2																									
IPI00012069	NQO1	NAD(P)H dehydrogenase [quinone] 1	100.0%	8.4	2	2	2	4	2,629,920	2,288,970	2,408,278	2,274,803	129,366	169,322	77,542	130,858	11.0	16.5	7.2	12.9	-1.1	0.1	-1.1	0.2	-1.2	0.09	1.1	0.5	-1.0	0.9	-1.1	0.4
IPI00619898	NQO1	NQO1 protein (Fragment)	100.0%	9.6	2	2	2	4	2,629,920	2,288,970	2,408,278	2,274,803	129,366	169,322	77,542	130,858	11.0	16.5	7.2	12.9	-1.1	0.1	-1.1	0.2	-1.2	0.09	1.1	0.5	-1.0	0.9	-1.1	0.4
IPI00619966	NQO1	NAD(P)H dehydrogenase [quinone] 1 isoform b	100.0%	9.6	2	2	2	4	2,629,920	2,288,970	2,408,278	2,274,803	129,366	169,322	77,542	130,858	11.0	16.5	7.2	12.9	-1.1	0.1	-1.1	0.2	-1.2	0.09	1.1	0.5	-1.0	0.9	-1.1	0.4
IPI00910902	NQO1	cDNA FLJ50573, highly similar to Homo sapiens NAD(P)H dehydrogenase, quinone	100.0%	11.4	2	2	2	4	2,629,920	2,288,970	2,408,278	2,274,803	129,366	169,322	77,542	130,858	11.0	16.5	7.2	12.9	-1.1	0.1	-1.1	0.2	-1.2	0.09	1.1	0.5	-1.0	0.9	-1.1	0.4
				ALIVLAHSER	2	99.9%	1																									
				EGHLSPDIVAEQK	2	99.9%	1																									
IPI00012074	HNRNPR	isoform 1 of Heterogeneous nuclear ribonucleoprotein R	100.0%	13.3	6	6	8	2	4,242,389	4,227,716	4,337,747	4,832,677	286,070	185,923	205,231	184,082	15.1	9.8	10.6	8.5	-1.0	1	1.0	0.8	1.1	0.1	1.0	0.7	1.1	0.05	1.1	0.1
IPI00941649	HNRNPR	Uncharacterized protein	100.0%	13.2	6	6	8	2	4,242,389	4,227,716	4,337,747	4,832,677	286,070	185,923	205,231	184,082	15.1	9.8	10.6	8.5	-1.0	1	1.0	0.8	1.1	0.1	1.0	0.7	1.1	0.05	1.1	0.1
				DLYEDELVPLFEK	2	100.0%	1																									
				LCDSYEIRPGK	2	99.3%	1																									
				LMMDPLSGQNR	2	100.0%	2																									
				NLATTVTEEILEK	2	100.0%	1																									
				TGYTLDVTTGQR	2	100.0%	2																									
				VWGNVVTVEWADPVEEPDPEVMAK	2	100.0%	1																									
IPI00012079	EIF4B	cDNA FLJ54492, highly similar to Eukaryotic translation initiation factor 4B	100.0%	13.8	5	5	5	2	10,988,741	10,664,357	9,644,868	11,875,808	505,793	665,535	534,354	566,642	10.3	14.0	12.4	10.7	-1.0	0.7	-1.1	0.1	1.1	0.3	-1.1	0.3	1.1	0.2	1.2	0.02
IPI00908588	EIF4B	cDNA FLJ59206, highly similar to Eukaryotic translation initiation factor 4B	100.0%	14.5	5	5	5	2	10,988,741	10,664,357	9,644,868	11,875,808	505,793	665,535	534,354	566,642	10.3	14.0	12.4	10.7	-1.0	0.7	-1.1	0.1	1.1	0.3	-1.1	0.3	1.1	0.2	1.2	0.02
				GFGYAEFEDLDSLLSALSLNEESLGNRR	3	100.0%	1																									
				GLNISAVR	2	88.6%	1																									
				RGDDSFGDKYR	3	99.1%	1																									
				SPPYTAFLGNLPYDVTEESIKEFFR	3	100.0%	1																									
				VAPAQPSEEGPGR	2	97.0%	1																									
IPI00012102	GNS	N-acetylglucosamine-6-sulfatase	99.4%	4.7	2	2	2	5	919,938	837,802	1,019,284	987,552	40,869	86,525	28,926	49,366	9.9	23.1	6.4	11.2	-1.1	0.4	1.1	0.08	1.1	0.3	1.2	0.1	1.2	0.2	-1.0	0.6
IPI00908404	GNS	cDNA FLJ51188, highly similar to N-acetylglucosamine-6-sulfatase	99.4%	4.5	2	2	2	5	919,938	837,802	1,019,284	987,552	40,869	86,525	28,926	49,366	9.9	23.1	6.4	11.2	-1.1	0.4	1.1	0.08	1.1	0.3	1.2	0.1	1.2	0.2	-1.0	0.6
IPI00979679	GNS	Putative uncharacterized protein DKFZp686E12166	99.4%	5.2	2	2	2	5	919,938	837,802	1,019,284	987,552	40,869	86,525	28,926	49,366	9.9	23.1	6.4	11.2	-1.1	0.4	1.1	0.08	1.1	0.3	1.2	0.1	1.2	0.2	-1.0	0.6
IPI01011079	GNS	cDNA FLJ54262, highly similar to N-acetylglucosamine-6-sulfatase	99.4%	4.9	2	2	2	5	919,938	837,802	1,019,284	987,552	40,869	86,525	28,926	49,366	9.9	23.1	6.4	11.2	-1.1	0.4	1.1	0.08	1.1	0.3	1.2	0.1	1.2	0.2	-1.0	0.6
IPI01010051	GNS	39 kDa protein	99.4%	7.6	2	2	2	5	919,938	837,802	1,019,284	987,552	40,869	86,525	28,926	49,366	9.9	23.1	6.4	11.2	-1.1	0.4	1.1	0.08	1.1	0.3	1.2	0.1	1.2	0.2	-1.0	0.6
				TQMDGMSLLPILR	2	98.5%	1																									
				WQTLLSVDDLVEK	2	98.0%	1																									
IPI00012149	MPHOSPH10	U3 small nucleolar ribonucleoprotein protein MPP10	96.1%	1.9	1	1	1	2	1,557,985	1,553,930	1,605,650	1,681,750	141,453	133,628	29,202	154,047	20.3	19.2	4.1	20.5	-1.0	1	1.0	0.8	1.1	0.6	1.0	0.7	1.1	0.5	1.0	0.7
IPI00927397	MPHOSPH10	Uncharacterized protein	96.1%	2.4	1	1	1	2	1,557,985	1,553,930	1,605,650	1,681,750	141,453	133,628	29,202	154,047	20.3	19.2	4.1	20.5	-1.0	1	1.0	0.8	1.1	0.6	1.0	0.7	1.1	0.5	1.0	0.7
				LSLAEIYEQEYIK	2	88.3%	1																									
IPI00012197	DCTPP1	dCTP pyrophosphatase 1	93.2%	7.7	1	1	1	1	3,355,340	3,338,410	3,129,560	3,798,610	248,289	271,332	145,753	144,653	16.6	18.2	10.4	8.5	-1.0	1	-1.1	0.5	1.1	0.2	-1.1	0.5	1.1	0.2	1.2	0.01
				TDGEPGPQGWSPR	2	93.2%	1																									
IPI00012268	PSMD2	26S proteasome non-ATPase regulatory subunit 2	100.0%	18.2	11	12	12	2	14,292,600	15,613,408	15,189,080	17,276,145	1,050,474	258,119	907,317	376,531	16.4	3.7	13.4	4.9	1.1	0.3	1.1	0.5	1.2	0.04	-1.0	0.7	1.1	0.007	1.1	0.07
IPI01014808	PSMD2	cDNA FLJ53357, highly similar to 26S proteasome non-ATPase regulatory subunit 2	100.0%	18.3	11	12	12	2	14,292,600	15,613,408	15,189,080	17,276,145	1,050,474	258,119	907,317	376,531	16.4	3.7	13.4	4.9	1.1	0.3	1.1	0.5	1.2	0.04	-1.0	0.7	1.1	0.007	1.1	0.07
				APVQPQQSPAAAPGGTDEKPSGK	3	87.4%	1																									
				AVPLALALISVSNPR	2	98.6%	1																									
				LAQGLTHLGK	2	81.0%	1																									
				MLVTFDEELRPLPVSVR	3	97.3%	1																									
				MNLASSFVNGFVNAAFGQDK	2	100.0%	1																									
				MNLASSFVNGFVNAAFGQDK	3	98.4%	1																									
				NECDPALALLSDYVLHNSNTMR	3	99.7%	1																									
				SETELKDTYAR	2	91.6%	1																									
				SGALLACGIVNSGVR	2	100.0%	1																									

				VGQAVDVVGQAGKPK	3	99.9%	1																									
				YGEPTLR	2	88.6%	1																									
				YLYSSEDYIK	2	99.5%	1																									
IPI00012280	TOR1AIP1	isoform 2 of Torsin-1A-interacting protein 1	90.7%	3.7	1	1	1	5	808,780	714,278	895,272	761,522	116,104	44,129	117,142	41,320	32.1	13.8	29.3	12.1	-1.1	0.5	1.1	0.6	-1.1	0.7	1.3	0.2	1.1	0.5	-1.2	0.3
IPI00936738	TOR1AIP1	isoform 1 of Torsin-1A-interacting protein 1	90.7%	2.4	1	1	1	5	808,780	714,278	895,272	761,522	116,104	44,129	117,142	41,320	32.1	13.8	29.3	12.1	-1.1	0.5	1.1	0.6	-1.1	0.7	1.3	0.2	1.1	0.5	-1.2	0.3
IPI00952955	TOR1AIP1	Uncharacterized protein	90.7%	3.7	1	1	1	5	808,780	714,278	895,272	761,522	116,104	44,129	117,142	41,320	32.1	13.8	29.3	12.1	-1.1	0.5	1.1	0.6	-1.1	0.7	1.3	0.2	1.1	0.5	-1.2	0.3
IPI00977372	TOR1AIP1	14 kDa protein	90.7%	12.1	1	1	1	5	808,780	714,278	895,272	761,522	116,104	44,129	117,142	41,320	32.1	13.8	29.3	12.1	-1.1	0.5	1.1	0.6	-1.1	0.7	1.3	0.2	1.1	0.5	-1.2	0.3
IPI00979278	TOR1AIP1	Protein	90.7%	7.1	1	1	1	5	808,780	714,278	895,272	761,522	116,104	44,129	117,142	41,320	32.1	13.8	29.3	12.1	-1.1	0.5	1.1	0.6	-1.1	0.7	1.3	0.2	1.1	0.5	-1.2	0.3
				SIQEAPVSEDLVIR	2	90.7%	1																									
IPI00012303	SELENBP1	Uncharacterized protein	100.0%	16.5	6	6	7	1	13,259,320	13,557,291	13,078,910	14,927,345	1,123,664	293,973	1,004,308	732,896	19.0	4.9	17.2	11.0	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.1	1.1	0.2
				GGFVLLDGETFEVK	2	99.9%	1																									
				GGPVQVLEDEELK	2	88.5%	1																									
				HNVMISTEWAAPNVLR	2	99.8%	1																									
				IYVVDVGSEPR	2	99.7%	1																									
				LTGQLFLGGSIVK	2	99.5%	2																									
				NTGTEAPDYLATVDVDPK	2	100.0%	1																									
IPI00012340	SRSF9	Serine/arginine-rich splicing factor 9	100.0%	14.9	3	3	4	1	8,706,365	10,230,561	9,716,525	10,854,470	703,237	382,083	867,597	454,668	18.1	8.4	20.0	9.4	1.2	0.09	1.1	0.4	1.2	0.03	-1.1	0.6	1.1	0.3	1.1	0.3
				EAGDVCYADVQK	2	99.5%	1																									
				IYVGNLPTDVR	2	99.7%	1																									
				SHEGETSYIR	2	99.8%	2																									
IPI00012341	SRSF5	isoform SRP40-1 of Serine/arginine-rich splicing factor 5	100.0%	8.8	2	2	2	3	3,734,408	4,210,003	3,693,690	4,586,997	545,019	362,390	376,387	293,206	32.6	19.3	22.8	14.3	1.1	0.5	-1.0	1	1.2	0.2	-1.1	0.4	1.1	0.4	1.2	0.1
IPI00413654	SRSF5	isoform SRP40-4 of Serine/arginine-rich splicing factor 5	100.0%	8.9	2	2	2	3	3,734,408	4,210,003	3,693,690	4,586,997	545,019	362,390	376,387	293,206	32.6	19.3	22.8	14.3	1.1	0.5	-1.0	1	1.2	0.2	-1.1	0.4	1.1	0.4	1.2	0.1
IPI00915825	SRSF5	CS0DF038YO05 variant (Fragment)	100.0%	7.4	2	2	2	3	3,734,408	4,210,003	3,693,690	4,586,997	545,019	362,390	376,387	293,206	32.6	19.3	22.8	14.3	1.1	0.5	-1.0	1	1.2	0.2	-1.1	0.4	1.1	0.4	1.2	0.1
				LIVENLSSR	2	99.9%	1																									
				LNEGVVEFASYGDLK	2	100.0%	1																									
IPI00012345	SRSF6	isoform SRP55-1 of Serine/arginine-rich splicing factor 6	100.0%	14.8	6	6	7	3	9,180,034	9,794,005	9,091,812	11,953,443	1,091,830	656,474	718,818	590,577	26.6	15.0	17.7	11.1	1.1	0.6	-1.0	0.9	1.3	0.06	-1.1	0.5	1.2	0.04	1.3	0.02
IPI00215879	SRSF6	isoform SRP55-3 of Serine/arginine-rich splicing factor 6	100.0%	15.2	6	6	7	3	9,180,034	9,794,005	9,091,812	11,953,443	1,091,830	656,474	718,818	590,577	26.6	15.0	17.7	11.1	1.1	0.6	-1.0	0.9	1.3	0.06	-1.1	0.5	1.2	0.04	1.3	0.02
IPI00556297	SRSF6	Arginine/serine-rich splicing factor 6 variant (Fragment)	100.0%	18.3	6	6	7	3	9,180,034	9,794,005	9,091,812	11,953,443	1,091,830	656,474	718,818	590,577	26.6	15.0	17.7	11.1	1.1	0.6	-1.0	0.9	1.3	0.06	-1.1	0.5	1.2	0.04	1.3	0.02
				CSWQDLK	2	98.8%	1																									
				LIVENLSSR	2	99.9%	1																									
				NGYGFVEFEDSR	2	99.7%	1																									
				QAGEVTYADAHK	2	100.0%	1																									
				QAGEVTYADAHKER	3	99.9%	1																									
				TNEGVIEFR	2	100.0%	2																									
IPI00012433	F8A2	Factor VIII intron 22 protein	95.9%	4.3	1	1	1	1	6,000,660	5,547,260	5,431,970	6,525,090	669,318	600,569	391,815	527,326	24.9	24.2	16.1	18.1	-1.1	0.6	-1.1	0.5	1.1	0.6	-1.0	0.9	1.2	0.3	1.2	0.1
				KPNVAEAGEQFGQLGR	3	95.9%	1																									
IPI00012440	FUCA2	Plasma alpha-L-fucosidase	93.2%	3.6	1	1	1	2	1,314,705	1,337,155	1,226,045	1,336,365	184,741	97,392	65,555	46,653	31.4	16.3	12.0	7.8	1.0	0.9	-1.1	0.7	1.0	0.9	-1.1	0.4	-1.0	1	1.1	0.2
IPI00385460	FUCA2	cDNA FLJ50101, highly similar to Plasma alpha-L-fucosidase	93.2%	10.3	1	1	1	2	1,314,705	1,337,155	1,226,045	1,336,365	184,741	97,392	65,555	46,653	31.4	16.3	12.0	7.8	1.0	0.9	-1.1	0.7	1.0	0.9	-1.1	0.4	-1.0	1	1.1	0.2
				FFNANQWADIFQASGAK	2	93.2%	1																									
IPI00012442	G3BP1	Ras GTPase-activating protein-binding protein 1	100.0%	15.0	5	7	9	1	29,161,148	32,127,055	28,608,488	33,098,715	3,650,742	1,852,309	1,869,032	1,420,196	28.0	12.9	14.6	9.6	1.1	0.5	-1.0	0.9	1.1	0.4	-1.1	0.2	1.0	0.7	1.2	0.09
				FMQTFVLAPEGSVANK	2	100.0%	1																									
				FYVHNDIFR	2	99.9%	1																									
				FYVHNDIFR	3	100.0%	2																									
				LPNFGFVVFDDSEPVQK	2	100.0%	2																									
				LPNFGFVVFDDSEPVQK	3	100.0%	1																									
				SSSPAPADIAQTVQEDLR	2	100.0%	1																									
				TFSWASVTSK	2	99.5%	1																									
IPI00012462	EIF2A	Eukaryotic translation initiation factor 2A	99.4%	4.9	2	2	2	4	1,535,400	1,496,654	1,467,562	1,693,689	106,955	59,320	90,964	91,105	15.6	8.9	13.9	12.0	-1.0	0.8	-1.0	0.6	1.1	0.3	-1.0	0.8	1.1	0.1	1.2	0.1
IPI00845305	EIF2A	cDNA FLJ57962, highly similar to Homo sapiens eukaryotic translation initiation facto	99.4%	5.7	2	2	2	4	1,535,400	1,496,654	1,467,562	1,693,689	106,955	59,320	90,964	91,105	15.6	8.9	13.9	12.0	-1.0	0.8	-1.0	0.6	1.1	0.3	-1.0	0.8	1.1	0.1	1.2	0.1
IPI00945725	EIF2A	cDNA FLJ58035, highly similar to Homo sapiens eukaryotic translation initiation facto	99.4%	5.4	2	2	2	4	1,535,400	1,496,654	1,467,562	1,693,689	106,955	59,320	90,964	91,105	15.6	8.9	13.9	12.0	-1.0	0.8	-1.0	0.6	1.1	0.3	-1.0	0.8	1.1	0.1	1.2	0.1
IPI00982376	EIF2A	Uncharacterized protein	99.4%	5.2	2	2	2	4	1,535,400	1,496,654	1,467,562	1,693,689	106,955	59,320	90,964	91,105	15.6	8.9	13.9	12.0	-1.0	0.8	-1.0	0.6	1.1	0.3	-1.0	0.8	1.1	0.1	1.2	0.1
				ETALLQELEDLELGI	2	98.4%	1																									
				KATAVLVIASTDVDK	2	87.9%	1																									
IPI00012463	TATDN1	isoform 1 of Putative deoxyribonuclease TATDN1	100.0%	12.1	3	3	4	5	2,138,013	2,171,011	2,070,602	2,534,806	226,819	98,545	160,564	65,625	23.7	10.2	17.3	5.8	1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.6	1.2	0.02	1.2	0.03
IPI00795107	TATDN1	38 kDa protein	100.0%	10.8	3	3	4	5	2,138,013	2,171,011	2,070,602	2,534,806	226,819	98,545	160,564	65,625	23.7	10.2	17.3	5.8	1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.6	1.2	0.02	1.2	0.03
IPI01015120	TATDN1	Uncharacterized protein	100.0%	11.2	3	3	4	5	2,138,013	2,171,011	2,070,602	2,534,806	226,819	98,545	160,564	65,625	23.7	10.2	17.3	5.8	1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.6	1.2	0.02	1.2	0.03
IPI01015660	TATDN1	24 kDa protein	100.0%	17.4	3	3	4	5	2,138,013	2,171,011	2,070,602	2,534,806	226,819	98,545	160,564	65,625	23.7	10.2	17.3	5.8	1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.6	1.2	0.02	1.2	0.03
IPI00981859	TATDN1	Protein	100.0%	17.8	3	3	4	5	2,138,013	2,171,011	2,070,602	2,534,806	226,819	98,545	160,564	65,625	23.7	10.2	17.3	5.8	1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.6	1.2	0.02	1.2	0.03
				FMITGGNLQDSK	2	98.5%	1																									
				HQDDLQDVIGR	2	100.0%	2																									
				VVAIGECGLDFDR	2	94.7%	1																									
IPI00012479	NACAP1	Putative nascent polypeptide-associated complex subunit alpha-like protein	99.6%	7.0	1	1	1	1	4,041,810	4,470,240	3,919,180	4,452,930	255,875	155,023	296,020	258,254	14.2	7.8	16.9	13.0	1.1	0.2	-1.0	0.8	1.1	0.3	-1.1	0.1	-1.0	1	1.1	0.2
				IEDLSQEAQLAAAEK	2	99.6%	1																									
IPI00012493	RPS20	40S ribosomal protein S20	100.0%	19.3	2	3	4	2	6,052,798	6,901,648	6,264,358	7,405,067	501,139	444,389	418,111	657,990	18.5	14.4	14.9	19.9	1.1	0.2	1.0	0.8	1.2	0.1	-1.1	0.3	1.1	0.5	1.2	0.2
IPI00794659	RPS20	40S ribosomal protein S20 isoform 1	100.0%	16.2	2	3	4	2	6,052,798	6,901,648	6,264,358	7,405,067	501,139	444,389	418,111	657,990	18.5	14.4	14.9	19.9	1.1	0.2	1.0	0.8	1.2	0.1	-1.1	0.3	1.1	0.5	1.2	0.2
				LIDLHSPSEIVK	2	100.0%	2																									
				LIDLHSPSEIVK	3	95.5%	1																									
				TPVEPEVAIHR	3	100.0%	1																									
IPI00012501	REG4	isoform 1 of Regenerating islet-derived protein 4	99.9%	8.9	1	1	2	2	8,386,465	9,834,500	8,628,730	11,199,500	1,245,520	408,336	1,280,778	593,410	33.2	9.3	33.2	11.9	1.2	0.3	1.0	0.9	1.3	0.08	-1.1	0.4	1.1	0.09	1.3	0.1
IPI00168727	REG4	Regenerating islet-derived family, member 4	99.9%	11.3	1	1	2	2	8,386,465	9,834,500	8,628,730	11,199,500	1,245,520	408,336	1,280,778	593,410	33.2	9.3	33.2	11.9	1.2	0.3	1.0	0.9	1.3	0.08	-1.1	0.4	1.1	0.09	1.3	0.1
				EASTIAEYISGYQR	2	99.9%	2																									
IPI00012503	PSAP	isoform Sap-mu-0 of Proactivator polypeptide	100.0%	22.7	9	11	15	2	18,895,301	20,025,494	18,975,648	22,675,586	1,761,251	576,756	1,362,429	744,616	20.8	6.4	16.1	7.3	1.1	0.6	1.0	1	1.2	0.08	-1.1	0.5	1.1	0.02	1.2	0.04
IPI00219825	PSAP	Prosaposin	100.0%	21.3	9	11	15	2	18,895,301	20,025,494	18,975,648	22,675,586	1,761,251	576,756	1,362,429	744,616	20.8	6.4	16.1	7.3	1.1	0.6	1.0	1	1.2	0.08	-1.1	0.5	1.1	0.02	1.2	0.04
				EICALVGFCDEVK	2	99.4%	1																									
				EIVDSYLPVILDIIK	2	100.0%	2																									
				EIVDSYLPVILDIIK	3	100.0%	1																									
				GCSFLPDPYQK	2	99.9%	2																									
				GEMSRPGEVCSALNLCESLQK	3	99.4%	1																									
				LGPGMADICK	2	100.0%	2																									
				LVGYLDR	2	99.5%	1																									
				NYISQYSEIAIQMMMHMQPK	2	100.0%	1																									
				NYISQYSEIAIQMMMHMQPK	3	100.0%	1																									
				QEILAALEK	2	99.4%	1																									
				SDVYCEVCEFLVK	2	100.0%	2																									
IPI00012535	DNAJA1	DnaJ homolog subfamily A member 1	99.9%	6.6	2	2	2	1	3,522,470	3,443,580	3,826,483	4,025,320	457,837	191,010	140,666	286,073	29.1	12.4	8.2	15.9	-1.0	0.9	1.1	0.6	1.1	0.4	1.1	0.1	1.2	0.1	1.1	0.6
				QISQAYEVLSDAK	2	99.9%	1																									
				TIVITSHPGQIVK	2	91.4%	1																									
IPI00012545	TGOLN2	isoform TGN51 of Trans-Golgi network integral membrane protein 2	90.1%	2.9	1	1	1	8	562,763	567,946	645,065	599,683	38,518	33,388	72,712	58,291	15.3	13.2	25.2	21.7	1.0	0.9	1.1	0.3	1.1	0.6	1.1	0.4	1.1	0.6	-1.1	0.6
IPI00219049	TGOLN2	isoform TGN48 of Trans-Golgi network integral membrane protein 2	90.1%	3.1	1	1	1	8	562,763	567,946	645,065	599,683	38,518	33,388	72,712	58,291	15.3	13.2	25.2	21.7	1.0	0.9	1.1	0.3	1.1	0.6	1.1	0.4	1.1	0.6	-1.1	0.6
IPI00297543	TGOLN2	isoform TGN46 of Trans-Golgi network integral membrane protein 2	90.1%	3.2	1	1	1	8	562,763	567,946	645,065	599,683	38,518	33,388	72,712	58,291	15.3	13.2	25.2	21.7	1.0	0.9	1.1	0.3	1.1	0.6	1.1	0.4	1.1	0.6	-1.1	0.6
IPI00445166	TGOLN2	isoform 6 of Trans-Golgi network integral membrane protein 2	90.1%	5.0	1	1	1	8	562,763	567,946	645,065	599,683	38,518	33,388	72,712	58,291	15.3	13.2	25.2	21.7	1.0	0.9	1.1	0.3	1.1	0.6	1.1	0.4	1.1	0.6	-1.1	0.6
IPI00855725	TGOLN2	isoform 4 of Trans-Golgi network integral membrane protein 2	90.1%	3.7	1	1	1	8	562,763	567,946	645,065	599,683	38,518	33,388	72,712	58,291	15.3	13.2	25.2	21.7	1.0	0.9	1.1	0.3	1.1	0.6	1.1	0.4	1.1	0.6	-1.1	0.6
IPI00855872	TGOLN2	isoform 5 of Trans-Golgi network integral membrane protein 2	90.1%	3.1	1	1	1	8	562,763	567,946	645,065	599,683	38,518	33,388	72,712	58,291	15.3	13.2	25.2	21.7	1.0	0.9	1.1	0.3	1.1	0.6	1.1	0.4	1.1	0.6	-1.1	0.6
IPI00953223	TGOLN2	Uncharacterized protein	90.1%	5.0	1	1	1	8	562,763	567,946	645,065	599,683	38,518	33,388	72,712	58,291	15.3	13.2	25.2	21.7	1.0	0.9	1.1	0.3	1.1	0.6	1.1	0.4	1.1	0.6	-1.1	0.6
IPI00969380	TGOLN2	Trans-golgi network protein 2, isoform CRA_b	90.1%	2.9	1	1	1	8	562,763	567,946	645,065	599,683	38,518	33,388	72,712	58,291	15.3	13.2	25.2	21.7	1.0	0.9	1.1	0.3	1.1	0.6	1.1	0.4	1.1	0.6	-1.1	0.6
				SGAEEQGPIDGPSK	2	90.1%	1																									
IPI00012575	PIR	Pirin	99.9%	4.1	1	1	1	1	404,180	374,437	446,579	546,316	64,141	31,271	18,369	47,355	35.5	18.7	9.2	19.4	-1.1	0.7	1.1	0.6	1.4	0.1	1.2	0.08	1.5	0.02	1.2	0.1
				NLDPFLLFDEFK	2	99.9%	1																									
IPI00012578	KPNA4	Importin subunit alpha-4	100.0%	6.7	2	2	2	1	3,281,450	3,470,695	3,441,015	3,399,285	335,541	285,209	140,428	204,648	22.9	18.4	9.1	13.5	1.1	0.7	1.0	0.7	1.0	0.8	-1.0	0.9	-1.0	0.8	-1.0	0.9
				EAAWAISNLTISGR	2	99.5%	1																									
				MAEDEAETIGNLIEECGGLEK	2	99.7%	1																									
IPI00012585	HEXB	Beta-hexosaminidase subunit beta	99.3%	2.2	1	1	1	4	3,036,360	3,016,485	2,956,023	3,482,700	471,517	204,439	380,562	134,808	34.7	15.2	28.8	8.7	-1.0	1	-1.0	0.9	1.1	0.4	-1.0	0.9	1.2	0.09	1.2	0.2
IPI00963880	HEXB	Protein	99.3%	5.9	1	1	1	4	3,036,360	3,016,485	2,956,023	3,482,700	471,517	204,439	380,562	134,808	34.7	15.2	28.8	8.7	-1.0	1	-1.0	0.9	1.1	0.4	-1.0	0.9	1.2	0.09	1.2	0.2
IPI00964815	HEXB	Protein	99.3%	7.1	1	1	1	4	3,036,360	3,016,485	2,956,023	3,482,700	471,517	204,439	380,562	134,808	34.7	15.2	28.8	8.7	-1.0	1	-1.0	0.9	1.1	0.4	-1.0	0.9	1.2	0.09	1.2	0.2
IPI00967527	HEXB	ENC-1AS	99.3%	3.6	1	1	1	4	3,036,360	3,016,485	2,956,023	3,482,700	471,517	204,439	380,562	134,808	34.7	15.2	28.8	8.7	-1.0	1	-1.0	0.9	1.1	0.4	-1.0	0.9	1.2	0.09	1.2	0.2
				GSIVWQEVFDDK	2	99.3%	1																									
IPI00012726	PABPC4	isoform 1 of Polyadenylate-binding protein 4	100.0%	17.6	9	10	13	4	9,939,907	11,203,275	9,825,429	13,509,029	1,916,467	944,555	893,192	615,094	43.1	18.9	20.3	10.2	1.1	0.6	-1.0	1	1.4	0.1	-1.1	0.3	1.2	0.08	1.4	0.009
IPI00555747	PABPC4	isoform 2 of Polyadenylate-binding protein 4	100.0%	17.9	9	10	13	4	9,939,907	11,203,275	9,825,429	13,509,029	1,916,467	944,555	893,192	615,094	43.1	18.9	20.3	10.2	1.1	0.6	-1.0	1	1.4	0.1	-1.1	0.3	1.2	0.08	1.4	0.009
IPI00642904	PABPC4	polyadenylate-binding protein 4 isoform 1	100.0%	17.1	9	10	13	4	9,939,907	11,203,275	9,825,429	13,509,029	1,916,467	944,555	893,192	615,094	43.1	18.9	20.3	10.2	1.1	0.6	-1.0	1	1.4	0.1	-1.1	0.3	1.2	0.08	1.4	0.009
IPI00642944	PABPC4	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	100.0%	18.4	9	10	13	4	9,939,907	11,203,275	9,825,429	13,509,029	1,916,467	944,555	893,192	615,094	43.1	18.9	20.3	10.2	1.1	0.6	-1.0	1	1.4	0.1	-1.1	0.3	1.2	0.08	1.4	0.009
				AKEFTNVYIK	2	90.8%	1																									
				AKEFTNVYIK	3	99.9%	1																									
				ALDTMNFDVIK	2	100.0%	2																									
				EFSPFGSITSAK	2	99.2%	1																									
				ITGMLLEIDNSELLHMLESPESLR	3	100.0%	1																									
				MNGMLLNDR	2	95.6%	1																									
				NFGEEVDDESLKELFSQFGK	2	99.9%	2																									
				RSLGYAYVNFQQPADAER	3	99.1%	1																									
				SGVGNVFIK	2	96.1%	1																									
				SLGYAYVNFQQPADAER	2	100.0%	2																									
IPI00012728	ACSL1	isoform 1 of Long-chain-fatty-acid--CoA ligase 1	99.1%	2.9	2	2	2	5	1,652,065	1,715,822	1,732,001	1,720,398	47,014	83,666	81,021	70,580	6.4	10.9	10.5	9.2	1.0	0.5	1.0	0.4	1.0	0.4	1.0	0.9	1.0	1	-1.0	0.9
IPI00401448	ACSL1	isoform 2 of Long-chain-fatty-acid--CoA ligase 1	99.1%	2.9	2	2	2	5	1,652,065	1,715,822	1,732,001	1,720,398	47,014	83,666	81,021	70,580	6.4	10.9	10.5	9.2	1.0	0.5	1.0	0.4	1.0	0.4	1.0	0.9	1.0	1	-1.0	0.9
IPI00942534	ACSL1	cDNA FLJ54220, highly similar to Long-chain-fatty-acid--CoA ligase 1	99.1%	3.0	2	2	2	5	1,652,065	1,715,822	1,732,001	1,720,398	47,014	83,666	81,021	70,580	6.4	10.9	10.5	9.2	1.0	0.5	1.0	0.4	1.0	0.4	1.0	0.9	1.0	1	-1.0	0.9
IPI00965893	ACSL1	cDNA FLJ59311, highly similar to Long-chain-fatty-acid--CoA ligase 1	99.1%	2.9	2	2	2	5	1,652,065	1,715,822	1,732,001	1,720,398	47,014	83,666	81,021	70,580	6.4	10.9	10.5	9.2	1.0	0.5	1.0	0.4	1.0	0.4	1.0	0.9	1.0	1	-1.0	0.9
IPI00982418	ACSL1	cDNA FLJ53511, highly similar to Long-chain-fatty-acid--CoA ligase 1	99.1%	3.8	2	2	2	5	1,652,065	1,715,822	1,732,001	1,720,398	47,014	83,666	81,021	70,580	6.4	10.9	10.5	9.2	1.0	0.5	1.0	0.4	1.0	0.4	1.0	0.9	1.0	1	-1.0	0.9
				IGFFQGDIR	2	99.1%	1																									
				LAQGEYIAPEK	2	92.3%	1																									
IPI00012738	CDK5R2	Cyclin-dependent kinase 5 activator 2	99.6%	4.6	1	1	1	2	1,444,875	1,619,795	1,488,715	1,643,415	132,437	90,021	118,076	34,321	20.5	12.4	17.7	4.7	1.1	0.3	1.0	0.8	1.1	0.2	-1.1	0.4	1.0	0.8	1.1	0.3
IPI00985276	CDK5R2	Cyclin-dependent kinase 5, regulatory subunit 2	99.6%	4.6	1	1	1	2	1,444,875	1,619,795	1,488,715	1,643,415	132,437	90,021	118,076	34,321	20.5	12.4	17.7	4.7	1.1	0.3	1.0	0.8	1.1	0.2	-1.1	0.4	1.0	0.8	1.1	0.3
				VTPKPASTGPDPLVQQR	2	98.0%	1																									
IPI00012750	RPS25	40S ribosomal protein S25	100.0%	16.0	2	2	2	1	8,598,270	8,898,500	9,133,370	9,973,120	605,797	602,305	475,958	500,882	15.8	15.1	11.7	11.2	1.0	0.7	1.1	0.5	1.2	0.1	1.0	0.8	1.1	0.2	1.1	0.3
				AALQELLSK	2	99.9%	1																									
				DKLNNLVLFDK	2	98.1%	1																									
IPI00012795	EIF3I	Eukaryotic translation initiation factor 3 subunit I	100.0%	7.1	2	2	2	1	7,550,650	7,602,820	6,554,900	8,030,490	544,966	582,152	528,937	338,416	16.1	17.1	18.0	9.4	1.0	0.9	-1.2	0.2	1.1	0.5	-1.2	0.2	1.1	0.5	1.2	0.05
				LFDSTTLEHQK	2	97.9%	1																									
				SYSSGGEDGYVR	2	99.9%	1																									
IPI00012828	ACAA1	3-ketoacyl-CoA thiolase, peroxisomal	100.0%	24.3	6	7	7	1	14,734,119	15,602,183	16,451,872	18,078,841	1,875,108	1,013,980	1,521,117	598,050	28.5	14.5	20.7	7.4	1.1	0.7	1.1	0.5	1.2	0.2	1.1	0.7	1.2	0.07	1.1	0.4
				AEELGLPILGVLR	2	99.9%	1																									
				DGSTTAGNSSQVSDGAAAILLAR	2	100.0%	1																									
				DGSTTAGNSSQVSDGAAAILLAR	3	100.0%	1																									
				GGFKDTTPDELLSAVMTAVLK	3	100.0%	1																									
				IAQFLSDIPETVPLSTVNR	2	98.2%	1																									
				QCSSGLQAVASIAGGIR	2	100.0%	1																									
				QVITLLNELK	2	96.5%	1																									
IPI00012833	PPP4C	Serine/threonine-protein phosphatase 4 catalytic subunit	100.0%	8.1	2	2	2	1	22,605,700	23,328,675	22,611,075	25,388,750	2,071,972	953,439	1,637,421	663,879	20.5	9.1	16.2	5.9	1.0	0.8	1.0	1	1.1	0.3	-1.0	0.7	1.1	0.1	1.1	0.2
				EILVEESNVQR	2	95.3%	1																									
				QITQVYGFYDECLR	2	100.0%	1																									

IPI00012835	CTBP1	C-terminal-binding protein 1	100.0%	18.4	4	4	4	2	1,931,675	2,276,683	1,987,689	2,366,171	173,094	110,338	176,193	109,127	20.0	10.8	19.8	10.3	1.2	0.1	1.0	0.8	1.2	0.07	-1.1	0.2	1.0	0.6	1.2	0.1
IPI00554626	CTBP1	C-terminal-binding protein 1 isoform 2	100.0%	18.9	4	4	4	2	1,931,675	2,276,683	1,987,689	2,366,171	173,094	110,338	176,193	109,127	20.0	10.8	19.8	10.3	1.2	0.1	1.0	0.8	1.2	0.07	-1.1	0.2	1.0	0.6	1.2	0.1
				AFGFNVLFYDPYLSDGVER	2	100.0%	1																									
				GAALDVHESEPFSFSQGPLK	3	89.9%	1																									
				PLVALLDGR	2	99.9%	1																									
				SAGDLGIAVCNVPAASVEETADSTLCHILNLYR	3	96.3%	1																									
IPI00012837	KIF5B	Kinesin-1 heavy chain	100.0%	23.0	16	16	16	1	66,288,757	69,471,391	69,512,013	76,918,531	3,873,106	2,420,127	3,724,119	1,271,705	13.1	7.8	12.0	3.7	1.0	0.5	1.0	0.6	1.2	0.05	1.0	1	1.1	0.03	1.1	0.1
				DQDNMQAELNR	2	100.0%	1																									
				EYELLSDELNQK	2	92.6%	1																									
				IVQDIFNYIYSMDENLEFHIK	3	100.0%	1																									
				LFVQDLATR	2	99.7%	1																									
				LITDLQDQNQK	2	100.0%	1																									
				LYLVDLAGSEK	2	99.8%	1																									
				NGETVPIDEQFDKEK	3	93.1%	1																									
				NTIQWLENELNR	2	99.7%	1																									
				QAVEQQIQSHR	2	97.7%	1																									
				QLDDKDEEINQQSQLVEK	3	99.5%	1																									
				QLEESVDALSEELVQLR	2	100.0%	1																									
				SATLASIDAELQK	2	100.0%	1																									
				SLSALGNVISALAEGSTYVPYR	2	100.0%	1																									
				SLTEYLQNVEQK	2	100.0%	1																									
				TGAEGAVLDEAK	2	95.5%	1																									
				TQMLDQEELLASTR	2	100.0%	1																									
IPI00012895	CA12	isoform 1 of Carbonic anhydrase 12	96.4%	5.7	1	1	1	3	1,364,100	1,265,070	1,471,610	1,499,920	144,488	171,631	127,556	103,065	23.7	30.3	19.4	15.4	-1.1	0.7	1.1	0.6	1.1	0.5	1.2	0.4	1.2	0.3	1.0	0.9
IPI00221392	CA12	isoform 2 of Carbonic anhydrase 12	96.4%	5.8	1	1	1	3	1,364,100	1,265,070	1,471,610	1,499,920	144,488	171,631	127,556	103,065	23.7	30.3	19.4	15.4	-1.1	0.7	1.1	0.6	1.1	0.5	1.2	0.4	1.2	0.3	1.0	0.9
IPI00903233	CA12	cDNA FLJ39526 fis, clone PUAEN2003018, highly similar to CARBONIC ANHYDRA	96.4%	7.1	1	1	1	3	1,364,100	1,265,070	1,471,610	1,499,920	144,488	171,631	127,556	103,065	23.7	30.3	19.4	15.4	-1.1	0.7	1.1	0.6	1.1	0.5	1.2	0.4	1.2	0.3	1.0	0.9
				YKGQEAFVPGFNIEELLPER	3	96.4%	1																									
IPI00012902	SYT7	Synaptotagmin-7	93.8%	4.5	1	1	1	6	248,247	282,812	256,728	339,468	33,304	8,488	26,407	43,761	30.0	6.7	23.0	28.8	1.1	0.4	1.0	0.8	1.4	0.1	-1.1	0.4	1.2	0.3	1.3	0.1
IPI01013332	SYT7	51 kDa protein	93.8%	4.0	1	1	1	6	248,247	282,812	256,728	339,468	33,304	8,488	26,407	43,761	30.0	6.7	23.0	28.8	1.1	0.4	1.0	0.8	1.4	0.1	-1.1	0.4	1.2	0.3	1.3	0.1
IPI01014240	SYT7	58 kDa protein	93.8%	3.5	1	1	1	6	248,247	282,812	256,728	339,468	33,304	8,488	26,407	43,761	30.0	6.7	23.0	28.8	1.1	0.4	1.0	0.8	1.4	0.1	-1.1	0.4	1.2	0.3	1.3	0.1
IPI01014982	SYT7	53 kDa protein	93.8%	3.8	1	1	1	6	248,247	282,812	256,728	339,468	33,304	8,488	26,407	43,761	30.0	6.7	23.0	28.8	1.1	0.4	1.0	0.8	1.4	0.1	-1.1	0.4	1.2	0.3	1.3	0.1
IPI01015502	SYT7	68 kDa protein	93.8%	3.0	1	1	1	6	248,247	282,812	256,728	339,468	33,304	8,488	26,407	43,761	30.0	6.7	23.0	28.8	1.1	0.4	1.0	0.8	1.4	0.1	-1.1	0.4	1.2	0.3	1.3	0.1
IPI01016059	SYT7	76 kDa protein	93.8%	2.6	1	1	1	6	248,247	282,812	256,728	339,468	33,304	8,488	26,407	43,761	30.0	6.7	23.0	28.8	1.1	0.4	1.0	0.8	1.4	0.1	-1.1	0.4	1.2	0.3	1.3	0.1
				NLNPIFNESFAFDIPTEK	2	93.8%	1																									
IPI00012970	PPP6C	isoform 1 of Serine/threonine-protein phosphatase 6 catalytic subunit	93.7%	6.2	1	1	1	3	930,517	925,290	938,273	891,423	92,961	70,661	152,520	45,809	22.3	17.1	36.4	11.5	-1.0	1	1.0	1	-1.0	0.7	1.0	0.9	-1.0	0.7	-1.1	0.8
IPI00514237	PPP6C	Serine/threonine-protein phosphatase	93.7%	15.2	1	1	1	3	930,517	925,290	938,273	891,423	92,961	70,661	152,520	45,809	22.3	17.1	36.4	11.5	-1.0	1	1.0	1	-1.0	0.7	1.0	0.9	-1.0	0.7	-1.1	0.8
IPI00890743	PPP6C	serine/threonine-protein phosphatase 6 catalytic subunit isoform a	93.7%	5.6	1	1	1	3	930,517	925,290	938,273	891,423	92,961	70,661	152,520	45,809	22.3	17.1	36.4	11.5	-1.0	1	1.0	1	-1.0	0.7	1.0	0.9	-1.0	0.7	-1.1	0.8
				TGGQVPDTNYIFMGDFVDR	2	93.7%	1																									
IPI00012989	MAN2B1	Lysosomal alpha-mannosidase	98.1%	1.5	1	1	1	3	928,700	835,473	957,707	1,157,093	115,122	44,687	103,124	117,269	27.7	12.0	24.1	22.7	-1.1	0.5	1.0	0.9	1.2	0.2	1.1	0.3	1.4	0.05	1.2	0.2
IPI00644131	MAN2B1	lysosomal alpha-mannosidase isoform 2 precursor	98.1%	1.5	1	1	1	3	928,700	835,473	957,707	1,157,093	115,122	44,687	103,124	117,269	27.7	12.0	24.1	22.7	-1.1	0.5	1.0	0.9	1.2	0.2	1.1	0.3	1.4	0.05	1.2	0.2
IPI00925850	MAN2B1	cDNA FLJ54572, highly similar to Lysosomal alpha-mannosidase	98.1%	1.6	1	1	1	3	928,700	835,473	957,707	1,157,093	115,122	44,687	103,124	117,269	27.7	12.0	24.1	22.7	-1.1	0.5	1.0	0.9	1.2	0.2	1.1	0.3	1.4	0.05	1.2	0.2
				ELVDYFLNVATAQGR	2	98.1%	1																									
IPI00012998	CPSF6	isoform 1 of Cleavage and polyadenylation specificity factor subunit 6	100.0%	4.5	2	2	2	3	1,769,513	1,836,443	1,732,183	2,091,410	188,585	117,655	145,996	95,741	23.8	14.3	18.9	10.2	1.0	0.8	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.1	1.2	0.07
IPI00030654	CPSF6	isoform 2 of Cleavage and polyadenylation specificity factor subunit 6	100.0%	4.3	2	2	2	3	1,769,513	1,836,443	1,732,183	2,091,410	188,585	117,655	145,996	95,741	23.8	14.3	18.9	10.2	1.0	0.8	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.1	1.2	0.07
IPI00647126	CPSF6	Uncharacterized protein	100.0%	5.2	2	2	2	3	1,769,513	1,836,443	1,732,183	2,091,410	188,585	117,655	145,996	95,741	23.8	14.3	18.9	10.2	1.0	0.8	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.1	1.2	0.07
				GFALVGVGSEASSK	2	100.0%	1																									
				QFLSQFEMQSR	2	100.0%	1																									
IPI00013004	PDXK	isoform 1 of Pyridoxal kinase	100.0%	27.9	6	6	6	2	8,756,526	8,768,045	8,666,485	9,813,869	677,590	236,822	396,219	209,900	17.3	6.0	10.2	4.8	1.0	1	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.01	1.1	0.03
IPI00418202	PDXK	isoform 3 of Pyridoxal kinase	100.0%	32.0	6	6	6	2	8,756,526	8,768,045	8,666,485	9,813,869	677,590	236,822	396,219	209,900	17.3	6.0	10.2	4.8	1.0	1	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.01	1.1	0.03
				AQAGEGVRPSPMQLELR	3	99.6%	1																									
				GQVLNSDELQELYEGLR	3	99.9%	1																									
				RNPAGSVVMER	2	82.5%	1																									
				TVSTLHHVLQR	2	99.7%	1																									
				VVPLADIITPNQFEAELLSGR	2	99.8%	1																									
				YDYVLTGYTR	2	100.0%	1																									
IPI00013043	TPPP	Tubulin polymerization-promoting protein	100.0%	19.6	3	3	4	1	18,130,015	18,159,600	17,754,589	20,951,410	2,447,793	942,852	2,002,024	1,023,175	30.2	11.6	25.2	10.9	1.0	1	-1.0	0.9	1.2	0.3	-1.0	0.9	1.2	0.08	1.2	0.2
				NVTVTDVDIVFSK	2	99.4%	1																									
				TITFEQFQEALEELAK	2	100.0%	2																									
				VDLVDESGYVSGYK	2	99.5%	1																									
IPI00013068	EIF3E	Eukaryotic translation initiation factor 3 subunit E	100.0%	22.5	7	7	7	1	8,344,353	8,380,748	8,704,654	9,792,776	562,239	374,525	548,700	349,812	15.1	10.0	14.1	8.0	1.0	1	1.0	0.7	1.2	0.06	1.0	0.6	1.2	0.02	1.1	0.1
				HLVFPLLEFLSVK	2	99.7%	1																									
				LASEILMQNWDAAMEDLTR	2	100.0%	1																									
				LDLLSDTNMVDFAMDVYK	2	100.0%	1																									
				LGHVVMGNNAVSPYQQVIEK	3	99.7%	1																									
				MFEDPETTR	2	93.2%	1																									
				QLQAETEPIVK	2	100.0%	1																									
				YLTTAVITNK	2	95.7%	1																									
IPI00013070	HNRNPUL1	isoform 1 of Heterogeneous nuclear ribonucleoprotein U-like protein 1	100.0%	17.8	10	10	10	4	9,641,226	9,549,426	9,657,004	11,297,507	859,447	394,484	588,507	333,940	19.9	9.2	13.6	6.6	-1.0	0.9	1.0	1	1.2	0.1	1.0	0.9	1.2	0.01	1.2	0.04
IPI00167147	HNRNPUL1	isoform 2 of Heterogeneous nuclear ribonucleoprotein U-like protein 1	100.0%	18.9	10	10	10	4	9,641,226	9,549,426	9,657,004	11,297,507	859,447	394,484	588,507	333,940	19.9	9.2	13.6	6.6	-1.0	0.9	1.0	1	1.2	0.1	1.0	0.9	1.2	0.01	1.2	0.04
IPI00736859	HNRNPUL1	isoform 4 of Heterogeneous nuclear ribonucleoprotein U-like protein 1	100.0%	20.1	10	10	10	4	9,641,226	9,549,426	9,657,004	11,297,507	859,447	394,484	588,507	333,940	19.9	9.2	13.6	6.6	-1.0	0.9	1.0	1	1.2	0.1	1.0	0.9	1.2	0.01	1.2	0.04
IPI01009355	HNRNPUL1	cDNA FLJ56481, highly similar to Heterogeneous nuclear ribonucleoprotein U-like pr	100.0%	19.8	10	10	10	4	9,641,226	9,549,426	9,657,004	11,297,507	859,447	394,484	588,507	333,940	19.9	9.2	13.6	6.6	-1.0	0.9	1.0	1	1.2	0.1	1.0	0.9	1.2	0.01	1.2	0.04
				AEPYCSVLPGFTFIQHLPLSER	3	97.4%	1																									
				EALGGQALYPHVLVK	2	99.9%	1																									
				INEEISVK	2	88.2%	1																									
				NCAVEFNFGQR	2	100.0%	1																									
				NYILDQTNVYGSAQR	2	99.9%	1																									
				QGAPTSFLPPEASQLKPDR	3	97.9%	1																									
				QNQFYDTQVIKQENESGYER	3	100.0%	1																									
				RPLEMEQQQAYRPEMK	3	82.3%	1																									
				WDVLIQQATQCLNR	2	100.0%	1																									
				YNILGTNAIMDK	2	99.7%	1																									
IPI00013122	CDC37	Hsp90 co-chaperone Cdc37	100.0%	14.0	5	5	5	1	24,124,840	25,241,720	22,679,580	27,828,300	1,284,279	834,474	1,517,952	1,484,764	11.9	7.4	15.0	11.9	1.0	0.5	-1.1	0.5	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.04
				ASEAKEGEEAGPGDPLLEAVPK	3	100.0%	1																									
				DVQMLQDAISK	2	100.0%	1																									
				EGEEAGPGDPLLEAVPK	2	99.9%	1																									
				LQAEAQQLR	2	97.8%	1																									
				SMPWNVDTLSK	2	98.3%	1																									
IPI00013174	RBM14	isoform 1 of RNA-binding protein 14	100.0%	8.2	4	4	5	1	7,416,509	7,588,220	7,427,374	8,514,916	501,507	814,442	563,815	606,354	15.1	24.0	17.0	15.9	1.0	0.9	1.0	1	1.1	0.2	-1.0	0.9	1.1	0.4	1.1	0.2
				AQPSVSLGAAYR	2	95.5%	1																									
				ASYVAPLTAQPATYR	2	100.0%	1																									
				IFVGNVSAACTSQELR	2	100.0%	1																									
				KGPGLAVQSGDK	2	100.0%	2																									
IPI00013195	MRPL49	39S ribosomal protein L49, mitochondrial	99.5%	7.2	1	1	1	3	1,264,870	1,208,233	1,385,837	1,324,397	69,658	78,660	77,199	117,719	12.3	14.6	12.5	19.9	-1.0	0.6	1.1	0.3	1.0	0.7	1.1	0.1	1.1	0.4	-1.0	0.7
IPI00555553	MRPL49	Mitochondrial ribosomal protein L49 variant (Fragment)	99.5%	8.4	1	1	1	3	1,264,870	1,208,233	1,385,837	1,324,397	69,658	78,660	77,199	117,719	12.3	14.6	12.5	19.9	-1.0	0.6	1.1	0.3	1.0	0.7	1.1	0.1	1.1	0.4	-1.0	0.7
IPI00981529	MRPL49	Protein	99.5%	9.5	1	1	1	3	1,264,870	1,208,233	1,385,837	1,324,397	69,658	78,660	77,199	117,719	12.3	14.6	12.5	19.9	-1.0	0.6	1.1	0.3	1.0	0.7	1.1	0.1	1.1	0.4	-1.0	0.7
				DVEDFLSPLLGK	2	99.5%	1																									
IPI00013214	MCM3	cDNA FLJ55599, highly similar to DNA replication licensing factor MCM3	99.8%	1.6	1	1	1	2	2,770,625	2,641,905	3,674,035	4,240,220	400,635	428,267	603,223	295,692	32.3	36.3	36.7	15.6	-1.0	0.8	1.3	0.2	1.5	0.02	1.4	0.2	1.6	0.02	1.2	0.4
IPI00940786	MCM3	cDNA FLJ50873, highly similar to DNA replication licensing factor MCM3	99.8%	1.8	1	1	1	2	2,770,625	2,641,905	3,674,035	4,240,220	400,635	428,267	603,223	295,692	32.3	36.3	36.7	15.6	-1.0	0.8	1.3	0.2	1.5	0.02	1.4	0.2	1.6	0.02	1.2	0.4
				LLNNAFEELVAFQR	2	99.7%	1																									
IPI00013256	CSTF2	isoform 1 of Cleavage stimulation factor subunit 2	100.0%	7.6	2	2	2	5	1,770,366	1,885,066	1,843,807	2,057,332	140,982	89,597	140,857	45,517	17.8	10.6	17.1	5.0	1.1	0.5	1.0	0.7	1.2	0.1	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00607841	CSTF2	isoform 2 of Cleavage stimulation factor subunit 2	100.0%	7.9	2	2	2	5	1,770,366	1,885,066	1,843,807	2,057,332	140,982	89,597	140,857	45,517	17.8	10.6	17.1	5.0	1.1	0.5	1.0	0.7	1.2	0.1	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00902991	CSTF2	BetaCstF-64 variant 2	100.0%	7.4	2	2	2	5	1,770,366	1,885,066	1,843,807	2,057,332	140,982	89,597	140,857	45,517	17.8	10.6	17.1	5.0	1.1	0.5	1.0	0.7	1.2	0.1	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00909622	CSTF2	cDNA FLJ58787, highly similar to Cleavage stimulation factor 64 kDa subunit	100.0%	8.0	2	2	2	5	1,770,366	1,885,066	1,843,807	2,057,332	140,982	89,597	140,857	45,517	17.8	10.6	17.1	5.0	1.1	0.5	1.0	0.7	1.2	0.1	-1.0	0.8	1.1	0.1	1.1	0.2
IPI01012987	CSTF2	Uncharacterized protein	100.0%	10.1	2	2	2	5	1,770,366	1,885,066	1,843,807	2,057,332	140,982	89,597	140,857	45,517	17.8	10.6	17.1	5.0	1.1	0.5	1.0	0.7	1.2	0.1	-1.0	0.8	1.1	0.1	1.1	0.2
				GGTLLSVTGEVEPR	2	96.1%	1																									
				SVFVGNIPYEATEEQLKDIFSEVGPVVSFR	3	99.9%	1																									
IPI00013272	GOLGA4	isoform 1 of Golgin subfamily A member 4	96.1%	0.5	1	1	1	5	2,325,770	2,153,210	4,552,940	2,042,826	559,409	297,680	1,073,987	292,198	53.8	30.9	52.8	32.0	-1.1	0.8	2.0	0.1	-1.1	0.7	2.1	0.09	-1.1	0.8	-2.2	0.08
IPI00220522	GOLGA4	isoform 4 of Golgin subfamily A member 4	96.1%	0.5	1	1	1	5	2,325,770	2,153,210	4,552,940	2,042,826	559,409	297,680	1,073,987	292,198	53.8	30.9	52.8	32.0	-1.1	0.8	2.0	0.1	-1.1	0.7	2.1	0.09	-1.1	0.8	-2.2	0.08
IPI00925587	GOLGA4	Uncharacterized protein	96.1%	1.9	1	1	1	5	2,325,770	2,153,210	4,552,940	2,042,826	559,409	297,680	1,073,987	292,198	53.8	30.9	52.8	32.0	-1.1	0.8	2.0	0.1	-1.1	0.7	2.1	0.09	-1.1	0.8	-2.2	0.08
IPI00927614	GOLGA4	Golgin subfamily A member 4 isoform 1	96.1%	0.5	1	1	1	5	2,325,770	2,153,210	4,552,940	2,042,826	559,409	297,680	1,073,987	292,198	53.8	30.9	52.8	32.0	-1.1	0.8	2.0	0.1	-1.1	0.7	2.1	0.09	-1.1	0.8	-2.2	0.08
IPI01009738	GOLGA4	isoform 3 of Golgin subfamily A member 4	96.1%	0.5	1	1	1	5	2,325,770	2,153,210	4,552,940	2,042,826	559,409	297,680	1,073,987	292,198	53.8	30.9	52.8	32.0	-1.1	0.8	2.0	0.1	-1.1	0.7	2.1	0.09	-1.1	0.8	-2.2	0.08
				DQINQLELLLK	2	96.1%	1																									
IPI00013290	HDGFRP2	isoform 1 of Hepatoma-derived growth factor-related protein 2	100.0%	4.1	2	2	2	1	2,530,785	2,526,532	2,649,825	2,758,562	124,132	177,142	111,646	198,032	11.0	15.7	9.4	16.1	-1.0	1	1.0	0.5	1.1	0.4	1.0	0.6	1.1	0.4	1.0	0.6
				CLNALEELGTLQVTSQILQK	3	99.5%	1																									
				GYPHWPAR	2	99.0%	1																									
IPI00013296	RPS18	40S ribosomal protein S18	100.0%	30.9	5	5	6	1	31,835,718	33,078,650	30,063,438	36,457,780	2,660,743	1,712,058	1,681,095	1,842,766	18.7	11.6	12.5	11.3	1.0	0.7	-1.1	0.6	1.1	0.2	-1.1	0.2	1.1	0.2	1.2	0.03
				IAFAITAIK	2	92.1%	1																									
				IPDWFLNR	2	99.9%	2																									
				VITIMQNPR	2	96.0%	1																									
				VLNTNIDGR	2	99.7%	1																									
				YSQVLANGLDNK	2	99.9%	1																									
IPI00013297	PDAP1	28 kDa heat- and acid-stable phosphoprotein	100.0%	22.7	5	5	6	1	37,545,660	35,651,305	35,229,530	42,201,365	2,240,616	586,082	2,134,159	1,998,926	13.3	3.7	13.6	10.6	-1.1	0.5	-1.1	0.5	1.1	0.2	-1.0	0.9	1.2	0.03	1.2	0.04
				GVEGLIDIENPNR	2	99.1%	1																									
				KGVEGLIDIENPNR	2	96.3%	1																									
				KVTQLDLDGPK	2	99.8%	1																									
				QYTSPEEIDAQLQAEK	2	100.0%	2																									
				VTQLDLDGPK	2	87.5%	1																									
IPI00013396	SNRPC	U1 small nuclear ribonucleoprotein C	100.0%	13.2	3	3	4	2	6,849,495	6,964,420	7,121,335	8,121,035	389,861	198,868	182,539	475,906	12.7	6.4	5.7	13.1	1.0	0.8	1.0	0.5	1.2	0.07	1.0	0.6	1.2	0.06	1.1	0.1
IPI00641788	SNRPC	U1 small nuclear ribonucleoprotein C	100.0%	11.7	3	3	4	2	6,849,495	6,964,420	7,121,335	8,121,035	389,861	198,868	182,539	475,906	12.7	6.4	5.7	13.1	1.0	0.8	1.0	0.5	1.2	0.07	1.0	0.6	1.2	0.06	1.1	0.1
				TTAAFQQGK	2	98.8%	1																									
				WMEEQAQSLIDK	2	99.6%	2																									
				WMEEQAQSLIDKTTAAFQQGK	3	89.3%	1																									
IPI00013415	RPS7	40S ribosomal protein S7	100.0%	33.0	4	5	6	1	7,615,400	7,114,188	8,560,957	8,825,490	980,030	649,364	735,218	388,756	28.8	20.4	19.2	9.9	-1.1	0.7	1.1	0.5	1.2	0.3	1.2	0.2	1.2	0.05	1.0	0.8
				DVNFEFPEFQL	2	100.0%	2																									
				IVKPNGEKPDEFESGISQALLELEMNSDLK	3	98.8%	1																									
				TLTAVHDAILEDLVFPSEIVGK	2	100.0%	1																									
				TLTAVHDAILEDLVFPSEIVGK	3	99.8%	1																									
				TLTAVHDAILEDLVFPSEIVGKR	3	100.0%	1																									
IPI00013452	EPRS	Bifunctional aminoacyl-tRNA synthetase	100.0%	15.7	16	16	16	1	74,342,930	77,253,090	72,504,670	83,901,935	6,862,192	2,683,071	5,660,200	1,280,902	20.6	7.8	17.5	3.4	1.0	0.7	-1.0	0.8	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.1
				FAGGDYTTTIEAFISASGR	3	99.8%	1																									
				GNAAWQEQLK	2	94.1%	1																									
				HEELMLGDPCLK	2	99.7%	1																									
				INEAVECLLSLK	2	99.9%	1																									
				KGDIIQLQR	2	86.5%	1																									
				LNLNNTVLSK	2	99.8%	1																									
				LNQWCNVVR	2	99.6%	1																									
				LTWFVNEGLVDGWDDPR	2	83.8%	1																									

				MFEIVFEDPKIPGEK	2	81.1%	1																								
				QFAYQNSWGLTTR	2	99.9%	1																								
				QFIAAQGSSR	2	97.3%	1																								
				SLYDEVAAQGEVVR	2	99.4%	1																								
				TELAEPIAIRPTSETVMYPAYAK	3	99.1%	1																								
				TGQEYKPGNPPAEIGQNISSNSSASILESK	3	100.0%	1																								
				TTARDQDLEPGAPSMGAK	3	99.8%	1																								
				WFGFLEAQQAFQSVGTK	2	100.0%	1																								
IPI00013466	ASNA1	ATPase ASNA1	100.0%	9.8	2	2	2	1	6,036,170	6,046,275	5,756,020	5,398,345	361,485	226,286	480,889	225,187	13.4	8.4	18.7	9.3	1.0	1	-1.0	0.7	-1.1	0.2	-1.1	0.6	-1.1	0.08	-1.1	0.5
				VNTFSALLLEPYKPPSAQ	3	91.1%	1																								
				YLDQMEDLYEDFHIVK	3	99.6%	1																								
IPI00013468	BUB3	isoform 1 of Mitotic checkpoint protein BUB3	100.0%	20.7	6	6	7	2	11,950,148	11,302,393	11,801,438	12,960,343	1,067,266	543,313	586,550	689,704	20.0	10.8	11.1	11.9	-1.1	0.6	-1.0	0.9	1.1	0.4	1.0	0.5	1.1	0.1	1.1	0.2
IPI00514701	BUB3	isoform 2 of Mitotic checkpoint protein BUB3	100.0%	20.9	6	6	7	2	11,950,148	11,302,393	11,801,438	12,960,343	1,067,266	543,313	586,550	689,704	20.0	10.8	11.1	11.9	-1.1	0.6	-1.0	0.9	1.1	0.4	1.0	0.5	1.1	0.1	1.1	0.2
				LNQPPEDGISSVK	2	99.3%	1																								
				LYDVPANSMR	2	98.9%	1																								
				QGYVLSSIEGR	2	99.8%	1																								
				QVTDAETKPK	2	89.2%	1																								
				VAVEYLDPSPEVQK	2	100.0%	2																								
				VYTLSVSGDR	2	99.4%	1																								
IPI00013475	TUBB2A	Tubulin beta-2A chain	100.0%	32.4	6	7	11	2	18,338,834	17,380,728	18,818,167	21,758,196	2,444,663	1,157,778	2,058,555	970,349	29.8	14.9	24.5	10.0	-1.1	0.7	1.0	0.9	1.2	0.2	1.1	0.6	1.3	0.02	1.2	0.2
IPI00930715	TUBB2A	cDNA, FLJ93005, highly similar to Homo sapiens tubulin, beta polypeptide (TUBB),	100.0%	32.4	6	7	11	2	18,338,834	17,380,728	18,818,167	21,758,196	2,444,663	1,157,778	2,058,555	970,349	29.8	14.9	24.5	10.0	-1.1	0.7	1.0	0.9	1.2	0.2	1.1	0.6	1.3	0.02	1.2	0.2
				EIVHIQAGQCGNQIGAK	2	99.5%	2																								
				ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	3	99.9%	1																								
				FWEVISDEHGIDPTGSYHGDSDLQLER	3	98.2%	1																								
				LTTPTYGDLNHLVSATMSGVTTCLR	2	100.0%	2																								
				MSATFIGNSTAIQELFK	2	99.2%	1																								
				SGPFGQIFRPDNFVFGQSGAGNNWAK	2	100.0%	2																								
				SGPFGQIFRPDNFVFGQSGAGNNWAK	3	100.0%	2																								
IPI00871956	-	Similar to Ribosomal protein S2	100.0%	15.2	2	2	3	2	3,494,675	3,382,410	3,643,035	4,041,203	290,689	157,164	241,457	99,381	18.6	10.4	14.8	5.5	-1.0	0.7	1.0	0.7	1.2	0.1	1.1	0.4	1.2	0.008	1.1	0.2
IPI00013485	RPS2	40S ribosomal protein S2	100.0%	9.6	2	2	3	2	3,494,675	3,382,410	3,643,035	4,041,203	290,689	157,164	241,457	99,381	18.6	10.4	14.8	5.5	-1.0	0.7	1.0	0.7	1.2	0.1	1.1	0.4	1.2	0.008	1.1	0.2
				AFVAIGDYNGHVGLGVK	2	99.8%	1																								
				TYSYLTPDLWK	2	100.0%	2																								
IPI00013508	ACTN1	Alpha-actinin-1	100.0%	20.2	14	15	19	5	25,688,535	25,959,029	25,219,664	29,323,175	2,143,219	888,327	1,705,462	969,926	18.7	7.7	15.1	7.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.07
IPI00759776	ACTN1	alpha-actinin-1 isoform a	100.0%	19.7	14	15	19	5	25,688,535	25,959,029	25,219,664	29,323,175	2,143,219	888,327	1,705,462	969,926	18.7	7.7	15.1	7.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.07
IPI00909239	ACTN1	alpha-actinin-1 isoform c	100.0%	20.3	14	15	19	5	25,688,535	25,959,029	25,219,664	29,323,175	2,143,219	888,327	1,705,462	969,926	18.7	7.7	15.1	7.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.07
IPI00921118	ACTN1	Actinin alpha 1 isoform 3	100.0%	19.4	14	15	19	5	25,688,535	25,959,029	25,219,664	29,323,175	2,143,219	888,327	1,705,462	969,926	18.7	7.7	15.1	7.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.07
IPI01011340	ACTN1	95 kDa protein	100.0%	21.9	14	15	19	5	25,688,535	25,959,029	25,219,664	29,323,175	2,143,219	888,327	1,705,462	969,926	18.7	7.7	15.1	7.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.07
				ASIHEAWTDGK	2	100.0%	2																								
				DDPLTNLNTAFDVAEK	2	99.8%	1																								
				DYETATLSEIK	2	99.1%	1																								
				GISQEQMNEFR	2	100.0%	1																								
				HRPELIDYGK	3	100.0%	1																								
				ICDQWDNLGALTQK	2	100.0%	1																								
				IDQLEGDHQLIQEALIFDNK	3	100.0%	1																								
				LASDLLEWIR	2	100.0%	2																								
				LLETIDQLYLEYAK	2	99.3%	1																								
				MLDAEDIVGTARPDEK	2	95.1%	1																								
				MLDAEDIVGTARPDEK	3	98.8%	1																								
				MVSDINNAWGCLEQVEK	2	100.0%	1																								
				TINEVENQILTR	2	100.0%	2																								
				VGWEQLLTTIAR	2	100.0%	2																								
				YLDIPK	2	96.1%	1																								
IPI00013654	DCTN3	isoform 2 of Dynactin subunit 3	95.7%	6.3	1	1	1	5	1,322,876	1,368,684	1,245,248	1,475,028	137,361	140,437	132,120	148,282	23.2	22.9	23.7	22.5	1.0	0.8	-1.1	0.7	1.1	0.5	-1.1	0.5	1.1	0.6	1.2	0.3
IPI00027014	DCTN3	isoform 1 of Dynactin subunit 3	95.7%	5.9	1	1	1	5	1,322,876	1,368,684	1,245,248	1,475,028	137,361	140,437	132,120	148,282	23.2	22.9	23.7	22.5	1.0	0.8	-1.1	0.7	1.1	0.5	-1.1	0.5	1.1	0.6	1.2	0.3
IPI00385809	DCTN3	cDNA FLJ34342 fis, clone FEBRA2009986, moderately similar to Dynactin 3	95.7%	6.4	1	1	1	5	1,322,876	1,368,684	1,245,248	1,475,028	137,361	140,437	132,120	148,282	23.2	22.9	23.7	22.5	1.0	0.8	-1.1	0.7	1.1	0.5	-1.1	0.5	1.1	0.6	1.2	0.3
IPI00514971	DCTN3	isoform 3 of Dynactin subunit 3	95.7%	7.0	1	1	1	5	1,322,876	1,368,684	1,245,248	1,475,028	137,361	140,437	132,120	148,282	23.2	22.9	23.7	22.5	1.0	0.8	-1.1	0.7	1.1	0.5	-1.1	0.5	1.1	0.6	1.2	0.3
IPI00747408	DCTN3	12 kDa protein	95.7%	10.6	1	1	1	5	1,322,876	1,368,684	1,245,248	1,475,028	137,361	140,437	132,120	148,282	23.2	22.9	23.7	22.5	1.0	0.8	-1.1	0.7	1.1	0.5	-1.1	0.5	1.1	0.6	1.2	0.3
				VQVALGNISSK	2	95.7%	1																								
IPI01013705	MC1R	cDNA, FLJ95457, highly similar to Homo sapiens tubulin, beta, 4 (TUBB4), mRNA	100.0%	15.3	3	3	4	3	2,904,183	3,224,526	2,566,153	3,152,107	392,818	246,862	153,080	255,641	30.2	17.1	13.3	18.1	1.1	0.5	-1.1	0.5	1.1	0.6	-1.3	0.05	-1.0	0.8	1.2	0.08
IPI01015284	MC1R	Tubulin, beta, 4 variant (Fragment)	100.0%	15.3	3	3	4	3	2,904,183	3,224,526	2,566,153	3,152,107	392,818	246,862	153,080	255,641	30.2	17.1	13.3	18.1	1.1	0.5	-1.1	0.5	1.1	0.6	-1.3	0.05	-1.0	0.8	1.2	0.08
IPI00013683	TUBB3	Tubulin beta-3 chain	100.0%	15.3	3	3	4	3	2,904,183	3,224,526	2,566,153	3,152,107	392,818	246,862	153,080	255,641	30.2	17.1	13.3	18.1	1.1	0.5	-1.1	0.5	1.1	0.6	-1.3	0.05	-1.0	0.8	1.2	0.08
				EIVHIQAGQCGNQIGAK	2	99.5%	2																								
				FWEVISDEHGIDPSGNYVGDSDLQLER	3	99.8%	1																								
				LATPTYGDLNHLVSATMSGVTTSLR	3	91.7%	1																								
IPI00013698	ASAH1	N-acylsphingosine amidohydrolase (Acid ceramidase) 1, isoform CRA_c	100.0%	7.1	3	3	3	3	5,313,455	5,070,921	5,030,258	5,655,011	399,133	314,061	486,010	238,389	16.8	13.9	21.6	9.4	-1.0	0.6	-1.1	0.7	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00418446	ASAH1	isoform 2 of Acid ceramidase	100.0%	9.5	3	3	3	3	5,313,455	5,070,921	5,030,258	5,655,011	399,133	314,061	486,010	238,389	16.8	13.9	21.6	9.4	-1.0	0.6	-1.1	0.7	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00940046	ASAH1	Uncharacterized protein	100.0%	10.5	3	3	3	3	5,313,455	5,070,921	5,030,258	5,655,011	399,133	314,061	486,010	238,389	16.8	13.9	21.6	9.4	-1.0	0.6	-1.1	0.7	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.3
				ESLDVYELDAK	2	99.8%	1																								
				LPGLLGNFPGPFEEEMK	2	100.0%	1																								
				NMINTFVPSGK	2	99.0%	1																								
IPI00013721	PRPF4B	Serine/threonine-protein kinase PRP4 homolog	96.5%	1.1	1	1	1	2	7,213,150	7,037,350	6,583,200	7,692,850	326,250	296,202	369,103	360,587	10.1	9.4	12.5	10.5	-1.0	0.7	-1.1	0.2	1.1	0.4	-1.1	0.4	1.1	0.2	1.2	0.06
IPI00976830	PRPF4B	HCG1820375, isoform CRA_a	96.5%	1.1	1	1	1	2	7,213,150	7,037,350	6,583,200	7,692,850	326,250	296,202	369,103	360,587	10.1	9.4	12.5	10.5	-1.0	0.7	-1.1	0.2	1.1	0.4	-1.1	0.4	1.1	0.2	1.2	0.06
				AELDNELMEGK	2	96.5%	1																								
IPI00013723	PIN1	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	99.4%	11.7	1	1	1	2	3,366,810	3,567,680	3,194,770	3,640,845	290,902	138,182	231,920	275,680	19.3	8.7	16.2	16.9	1.1	0.6	-1.1	0.7	1.1	0.5	-1.1	0.2	1.0	0.8	1.1	0.3
IPI00644298	PIN1	PIN1 protein	99.4%	42.2	1	1	1	2	3,366,810	3,567,680	3,194,770	3,640,845	290,902	138,182	231,920	275,680	19.3	8.7	16.2	16.9	1.1	0.6	-1.1	0.7	1.1	0.5	-1.1	0.2	1.0	0.8	1.1	0.3
				TGEMSGPVFTDSGIHIILR	3	99.4%	1																								
IPI00013774	HDAC1	Histone deacetylase 1	96.9%	3.5	1	1	1	2	1,136,555	1,305,850	1,641,030	1,457,880	215,125	197,032	305,720	115,345	42.3	33.7	41.7	17.7	1.1	0.6	1.4	0.2	1.3	0.2	1.3	0.4	1.1	0.5	-1.1	0.6
IPI01010320	HDAC1	Putative uncharacterized protein DKFZp686H12203	96.9%	5.9	1	1	1	2	1,136,555	1,305,850	1,641,030	1,457,880	215,125	197,032	305,720	115,345	42.3	33.7	41.7	17.7	1.1	0.6	1.4	0.2	1.3	0.2	1.3	0.4	1.1	0.5	-1.1	0.6
				SFNLPMLMLGGGGYTIR	2	96.9%	1																								
IPI00013808	ACTN4	Alpha-actinin-4	100.0%	65.3	48	59	76	1	331,935,541	335,182,457	342,378,523	386,149,461	########	########	########	########	17.8	8.1	12.8	6.1	1.0	0.9	1.0	0.8	1.2	0.09	1.0	0.8	1.2	0.01	1.1	0.09
				AGTQIENIDEDFRDGLK	3	100.0%	1																								
				AIMTYVSSFYHAFSGAQK	2	99.4%	1																								
				ALDFIASK	2	98.5%	1																								
				ASFNHFDKDHGGALGPEEFK	3	100.0%	1																								
				ASIHEAWTDGK	2	100.0%	2																								
				CQLEINFNTLQTK	2	100.0%	2																								
				DDPVTNLNNAFEVAEK	2	100.0%	1																								
				DGLAFNALIHR	2	99.9%	1																								
				DGLAFNALIHR	3	100.0%	1																								
				DYETATLSDIK	2	100.0%	2																								
				EAILAIHK	2	99.9%	1																								
				ETTDTDTADQVIASFK	2	100.0%	2																								
				FAIQDISVEETSAK	2	100.0%	2																								
				GISQEQMQEFR	2	100.0%	2																								
				GYEEWLLNEIR	2	100.0%	2																								
				HRDYETATLSDIK	2	99.9%	1																								
				HRDYETATLSDIK	3	100.0%	1																								
				HRPELIEYDK	2	94.4%	1																								
				HRPELIEYDK	3	99.9%	1																								
				HRPELIEYDKLR	3	99.7%	1																								
				HTNYTMEHIR	3	100.0%	1																								
				ICDQWDALGSLTHSR	2	100.0%	1																								
				ICDQWDALGSLTHSR	3	100.0%	1																								
				IMSLVDPNHSGLVTFQAFIDFMSR	3	100.0%	1																								
				ISIEMNGTLEDQLSHLK	2	99.8%	2																								
				ISIEMNGTLEDQLSHLK	3	100.0%	1																								
				KAGTQIENIDEDFRDGLK	3	100.0%	1																								
				KDDPVTNLNNAFEVAEK	2	100.0%	1																								
				KDDPVTNLNNAFEVAEK	3	100.0%	1																								
				KHEAFESDLAAHQDR	3	100.0%	1																								
				KTFTAWCNSHLR	3	98.3%	1																								
				LASDLLEWIR	2	100.0%	2																								
				LSGSNPYTTVTPQIINSK	2	100.0%	2																								
				LVSIGAEEIVDGNAK	2	100.0%	2																								
				MAPYQGPDAVPGALDYK	2	100.0%	2																								
				MLDAEDIVNTARPDEK	2	100.0%	1																								
				MLDAEDIVNTARPDEK	3	100.0%	1																								
				MVSDINNGWQHLEQAEK	3	98.3%	1																								
				NVNVQNFHISWK	2	100.0%	2																								
				QFASQANVVGPWIQTK	2	100.0%	1																								
				QFASQANVVGPWIQTK	3	99.9%	1																								
				QLEAIDQLHLEYAK	2	100.0%	1																								
				QLEAIDQLHLEYAK	3	100.0%	1																								
				RDHALLEEQSK	2	100.0%	2																								
				RQFASQANVVGPWIQTK	3	98.7%	1																								
				SFSTALYGESDL	1	100.0%	1																								
				SIVDYKPNLDLLEQQHQLIQEALIFDNK	3	100.0%	1																								
				TFTAWCNSHLR	2	100.0%	1																								
				TINEVENQILTR	2	100.0%	2																								
				TIPWLEDRVPQK	2	90.3%	1																								
				TIQEMQQK	1	98.2%	1																								
				VEQIAAIAQELNELDYYDSHNVNTR	3	100.0%	1																								
				VGWEQLLTTIAR	2	100.0%	2																								
				VLAGDKNFITAEELR	2	100.0%	1																								
				VLAVNQENEHLMEDYEK	2	100.0%	1																								
				VLAVNQENEHLMEDYEK	3	99.9%	1																								
				VQQLVPK	1	94.9%	1																								
				VQQLVPK	2	99.7%	2																								
				YLDIPK	2	96.1%	1																								
IPI00910816	-	cDNA FLJ59238, highly similar to SNW domain-containing protein 1	99.4%	4.4	1	1	1	3	929,337	1,028,230	1,003,590	1,202,487	133,905	124,217	83,103	32,131	32.2	27.0	18.5	6.0	1.1	0.6	1.1	0.7	1.3	0.1	-1.0	0.9	1.2	0.2	1.2	0.07
IPI00013830	SNW1	SNW domain-containing protein 1	99.4%	4.7	1	1	1	3	929,337	1,028,230	1,003,590	1,202,487	133,905	124,217	83,103	32,131	32.2	27.0	18.5	6.0	1.1	0.6	1.1	0.7	1.3	0.1	-1.0	0.9	1.2	0.2	1.2	0.07
IPI00943237	SNW1	SNW1 protein (Fragment)	99.4%	8.7	1	1	1	3	929,337	1,028,230	1,003,590	1,202,487	133,905	124,217	83,103	32,131	32.2	27.0	18.5	6.0	1.1	0.6	1.1	0.7	1.3	0.1	-1.0	0.9	1.2	0.2	1.2	0.07
				LLEDFGDGGAFPEIHVAQYPLDMGR	3	99.4%	1																								
IPI00013847	UQCRC1	Cytochrome b-c1 complex subunit 1, mitochondrial	100.0%	16.0	5	6	6	1	22,042,350	23,487,630	23,255,200	25,903,160	2,562,706	793,620	1,948,938	686,022	26.0	7.6	18.7	5.9	1.1	0.6	1.1	0.7	1.2	0.2	-1.0	0.9	1.1	0.05	1.1	0.3
				ADLTEYLSTHYK	2	100.0%	1																								
				ADLTEYLSTHYK	3	90.4%	1																								
				LCTSATESEVAR	2	99.9%	1																								

				MVLAAAGGVEHQQLLDLAQK	3	99.9%	1																									
				NALVSHLDGTTPVCEDIGR	3	100.0%	1																									
				NNGAGYFLEHLAFK	2	100.0%	1																									
IPI00013860	HIBADH	3-hydroxyisobutyrate dehydrogenase, mitochondrial	99.5%	9.5	2	2	2	1	6,660,215	6,541,665	6,917,890	7,478,405	396,148	375,227	318,208	355,493	13.3	12.8	10.3	10.6	-1.0	0.8	1.0	0.6	1.1	0.2	1.1	0.5	1.1	0.1	1.1	0.3
				MGAVFMDAPVSGGVGAAR	2	99.5%	1																									
				SPILLGSLAHQIYR	3	98.7%	1																									
IPI00013862	DTYMK	Thymidylate kinase	97.7%	10.4	2	2	2	3	3,866,273	3,578,848	3,636,838	4,229,384	125,266	345,172	284,819	232,469	7.2	21.6	17.5	12.3	-1.1	0.5	-1.1	0.5	1.1	0.2	1.0	0.9	1.2	0.2	1.2	0.1
IPI00787559	DTYMK	thymidylate kinase isoform 2	97.7%	11.7	2	2	2	3	3,866,273	3,578,848	3,636,838	4,229,384	125,266	345,172	284,819	232,469	7.2	21.6	17.5	12.3	-1.1	0.5	-1.1	0.5	1.1	0.2	1.0	0.9	1.2	0.2	1.2	0.1
IPI00892966	DTYMK	Protein	97.7%	11.5	2	2	2	3	3,866,273	3,578,848	3,636,838	4,229,384	125,266	345,172	284,819	232,469	7.2	21.6	17.5	12.3	-1.1	0.5	-1.1	0.5	1.1	0.2	1.0	0.9	1.2	0.2	1.2	0.1
				SIEAVHEDIR	2	97.7%	1																									
				YAFSGVAFTGAK	2	94.7%	1																									
IPI00013877	HNRNPH3	isoform 1 of Heterogeneous nuclear ribonucleoprotein H3	100.0%	38.2	7	9	13	2	9,602,460	9,914,441	9,084,475	10,929,605	936,248	401,628	614,572	605,203	21.8	9.1	15.1	12.4	1.0	0.8	-1.1	0.7	1.1	0.3	-1.1	0.3	1.1	0.2	1.2	0.06
IPI00216493	HNRNPH3	isoform 3 of Heterogeneous nuclear ribonucleoprotein H3	100.0%	44.4	7	9	13	2	9,602,460	9,914,441	9,084,475	10,929,605	936,248	401,628	614,572	605,203	21.8	9.1	15.1	12.4	1.0	0.8	-1.1	0.7	1.1	0.3	-1.1	0.3	1.1	0.2	1.2	0.06
				ATENDIANFFSPLNPIR	2	100.0%	2																									
				ATENDIANFFSPLNPIR	3	100.0%	1																									
				ATGEADVEFVTHEDAVAAMSK	3	100.0%	1																									
				DGMDNQGGYGSVGR	2	100.0%	2																									
				RGGDGYDGGYGGFDDYGGYNNYGYGNDGFDDR	3	100.0%	1																									
				STGEAFVQFASK	2	100.0%	2																									
				VHIDIGADGR	2	100.0%	2																									
				VHIDIGADGR	3	99.8%	1																									
				YIELFLNSTPGGGSGMGGSGMGGYGR	2	100.0%	1																									
IPI00013881	HNRNPH1	Heterogeneous nuclear ribonucleoprotein H	100.0%	22.3	6	6	9	2	12,942,554	13,023,366	13,088,669	14,750,058	1,453,859	194,815	1,239,481	947,077	25.1	3.3	21.2	14.4	1.0	1	1.0	0.9	1.1	0.3	1.0	1	1.1	0.1	1.1	0.3
IPI00479191	HNRNPH1	51 kDa protein	100.0%	21.2	6	6	9	2	12,942,554	13,023,366	13,088,669	14,750,058	1,453,859	194,815	1,239,481	947,077	25.1	3.3	21.2	14.4	1.0	1	1.0	0.9	1.1	0.3	1.0	1	1.1	0.1	1.1	0.3
				ATENDIYNFFSPLNPVR	3	100.0%	1																									
				EGRPSGEAFVELESEDEVK	3	99.9%	1																									
				HTGPNSPDTANDGFVR	2	100.0%	2																									
				SNNVEMDWVLK	2	100.0%	2																									
				STGEAFVQFASQEIAEK	2	100.0%	2																									
				YVELFLNSTAGASGGAYEHR	3	99.8%	1																									
IPI00013890	SFN	isoform 1 of 14-3-3 protein sigma	100.0%	25.8	5	7	8	1	27,862,423	28,624,992	25,013,516	31,742,444	3,074,116	1,616,544	2,127,213	839,204	24.7	12.6	19.0	5.9	1.0	0.8	-1.1	0.5	1.1	0.3	-1.1	0.2	1.1	0.1	1.3	0.03
				SAYQEAMDISK	2	100.0%	1																									
				SAYQEAMDISKK	2	100.0%	2																									
				SAYQEAMDISKK	3	99.9%	1																									
				TTFDEAMADLHTLSEDSYK	2	100.0%	1																									
				TTFDEAMADLHTLSEDSYK	3	100.0%	1																									
				VETELQGVCDTVLGLLDSHLIK	3	100.0%	1																									
				YLAEVATGDDK	2	100.0%	1																									
IPI00013891	TRA2A	isoform Long of Transformer-2 protein homolog alpha	99.9%	5.0	1	1	1	3	883,527	790,273	836,420	852,723	56,427	36,467	88,700	106,495	14.3	10.3	23.7	27.9	-1.1	0.2	-1.1	0.7	-1.0	0.8	1.1	0.6	1.1	0.6	1.0	0.9
IPI00220447	TRA2A	cDNA FLJ50614, highly similar to Transformer-2 protein homolog	99.9%	7.8	1	1	1	3	883,527	790,273	836,420	852,723	56,427	36,467	88,700	106,495	14.3	10.3	23.7	27.9	-1.1	0.2	-1.1	0.7	-1.0	0.8	1.1	0.6	1.1	0.6	1.0	0.9
IPI01014274	TRA2A	cDNA FLJ50689, highly similar to Transformer-2 protein homolog	99.9%	7.7	1	1	1	3	883,527	790,273	836,420	852,723	56,427	36,467	88,700	106,495	14.3	10.3	23.7	27.9	-1.1	0.2	-1.1	0.7	-1.0	0.8	1.1	0.6	1.1	0.6	1.0	0.9
				YGPLSGVNVVYDQR	2	99.9%	1																									
IPI00013894	STIP1	Stress-induced-phosphoprotein 1	100.0%	47.7	23	25	28	2	70,081,323	71,403,925	71,034,218	79,555,608	4,851,247	2,810,425	3,717,352	1,782,478	15.5	8.8	11.7	5.0	1.0	0.8	1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.04	1.1	0.07
IPI00479946	STIP1	STIP1 protein	100.0%	43.9	23	25	28	2	70,081,323	71,403,925	71,034,218	79,555,608	4,851,247	2,810,425	3,717,352	1,782,478	15.5	8.8	11.7	5.0	1.0	0.8	1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.04	1.1	0.07
				AAALEAMKDYTK	2	100.0%	1																									
				ALDLDSSCKEAADGYQR	3	99.8%	1																									
				ALSVGNIDDALQCYSEAIK	2	100.0%	2																									
				AMADPEVQQIMSDPAMR	2	100.0%	2																									
				AMADPEVQQIMSDPAMR	3	85.2%	1																									
				CMMAQYNR	2	99.5%	1																									
				DPQALSEHLK	2	100.0%	1																									
				DPQALSEHLKNPVIAQK	3	100.0%	2																									
				EGLQNMEAR	2	98.9%	1																									
				ELDPTNMTYITNQAAVYFEK	2	100.0%	1																									
				ELDPTNMTYITNQAAVYFEK	3	100.0%	1																									
				ETKPEPMEEDLPENKK	3	99.9%	1																									
				FMNPFNMPNLYQK	2	99.9%	1																									
				GDYPQAMK	2	99.8%	1																									
				HYTEAIK	2	99.6%	1																									
				IGNSYFKEEK	2	91.7%	1																									
				KAAALEAMKDYTK	2	84.5%	1																									
				KAAALEFLNR	2	100.0%	1																									
				LAYINPDLALEEK	2	100.0%	1																									
				LILEQMQK	2	98.5%	1																									
				LLEFQLALK	2	91.6%	1																									
				TLLSDPTYR	2	96.4%	1																									
				TVDLKPDWGK	2	99.2%	1																									
				TYEEGLKHEANNPQLK	3	100.0%	1																									
				YKDAIHFYNK	3	99.5%	1																									
IPI00013895	S100A11	Protein S100-A11	100.0%	52.4	6	6	9	1	59,500,110	58,839,200	59,372,020	67,563,120	4,600,946	1,968,670	4,570,744	1,801,080	17.3	7.5	17.2	6.0	-1.0	0.9	-1.0	1	1.1	0.2	1.0	0.9	1.1	0.01	1.1	0.2
				CIESLIAVFQK	2	100.0%	2																									
				DGYNYTLSK	2	100.0%	1																									
				DPGVLDR	2	99.9%	2																									
				ISSPTETER	2	99.3%	1																									
				NQKDPGVLDR	2	99.3%	1																									
				TEFLSFMNTELAAFTK	2	100.0%	2																									
IPI00013917	RPS12	40S ribosomal protein S12	100.0%	45.5	5	6	7	1	50,824,810	50,624,990	47,624,670	58,201,830	4,150,589	2,039,898	2,747,721	2,596,696	18.3	9.0	12.9	10.0	-1.0	1	-1.1	0.5	1.1	0.2	-1.1	0.4	1.1	0.05	1.2	0.02
				DVIEEYFK	2	91.2%	1																									
				LGEWVGLCK	2	100.0%	2																									
				LVEALCAEHQINLIK	2	100.0%	1																									
				QAHLCVLASNCDEPMYVK	3	100.0%	1																									
				TALIHDGLAR	2	99.8%	1																									
				TALIHDGLAR	3	94.1%	1																									
IPI00013930	STX6	Syntaxin-6	99.3%	9.8	1	1	1	2	906,141	968,680	1,130,305	1,214,940	108,632	60,065	122,292	80,121	26.8	13.9	24.2	14.8	1.1	0.6	1.2	0.2	1.3	0.05	1.2	0.3	1.3	0.04	1.1	0.6
IPI01012471	STX6	cDNA FLJ57566, highly similar to Syntaxin-6	99.3%	16.2	1	1	1	2	906,141	968,680	1,130,305	1,214,940	108,632	60,065	122,292	80,121	26.8	13.9	24.2	14.8	1.1	0.6	1.2	0.2	1.3	0.05	1.2	0.3	1.3	0.04	1.1	0.6
				IGGELEEQAVMLEDFSHELESTQSR	3	99.3%	1																									
IPI00013933	DSP	isoform DPI of Desmoplakin	100.0%	20.9	44	46	54	1	234,663,485	238,998,960	227,139,571	267,009,715	########	8,001,326	########	8,779,944	16.3	7.5	17.8	7.4	1.0	0.8	-1.0	0.8	1.1	0.1	-1.1	0.6	1.1	0.05	1.2	0.08
				AELIVQPELK	2	99.9%	1																									
				AFIGFEGVK	2	99.6%	1																									
				AITGFDDPFSGK	2	100.0%	2																									
				ALLQAILQTEDMLK	2	100.0%	1																									
				FGDSNTVMR	2	98.0%	1																									
				FLDQNLQKYQAECSQFKAK	3	87.6%	1																									
				FLEFQYLTGGLVDPEVHGR	3	100.0%	2																									
				GGGGYTCQSGSGWDEFTK	2	100.0%	1																									
				GIVDSITGQR	2	100.0%	1																									
				GLPSPYNMSSAPGSR	2	96.6%	1																									
				GYFNEELSEILSDPSDDTK	2	100.0%	2																									
				IEVLEEELR	2	96.8%	1																									
				IGLVRPGTALELLEAQAATGFIVDPVSNLR	3	100.0%	1																									
				IKDFLQGSSCIAGIYNETTK	3	99.9%	1																									
				IQSQFTDAQK	2	99.7%	1																									
				KQQLEVELR	2	83.8%	1																									
				LASLEELKR	2	81.4%	1																									
				LGIYEAMK	2	99.9%	1																									
				LISPESTVMLLEAQAATGGIIDPHR	3	95.9%	1																									
				LLEAQIASGGVVDPVNSVFLPK	2	100.0%	2																									
				LLEAQIASGGVVDPVNSVFLPK	3	100.0%	1																									
				LLEAQIATGGIIDPK	2	100.0%	2																									
				LLQLQEQMR	2	99.8%	1																									
				LNDSILQATEQR	2	100.0%	1																									
				LSLQDAVSQGVIDQDMATR	2	100.0%	1																									
				LTVDSAIAR	2	99.9%	2																									
				NNYDEEIISLK	2	99.9%	1																									
				NQFETEINITK	2	99.9%	1																									
				NSQGSEMFGDDDK	2	96.5%	1																									
				NTLTQTTENLR	2	99.3%	1																									
				QLQNIIQATSR	2	100.0%	1																									
				RGLVGIEFK	2	93.7%	1																									
				RQDSLESMK	2	99.8%	2																									
				SAIYQLEEEYENLLK	2	100.0%	1																									
				SAIYQLEEEYENLLK	3	100.0%	1																									
				SGSLSLTQFADMISLK	2	100.0%	2																									
				SMVEDITGLR	2	98.3%	1																									
				SQLQISNNR	2	99.8%	1																									
				SRELDECFAQANDQMEILDSLIR	3	100.0%	1																									
				SVEEVASEIQPFLR	2	95.4%	1																									
				SVQNDSQAIAEVLNQLK	2	99.9%	1																									
				TIADLELHYQEFIR	2	99.9%	1																									
				TMIQSPSGVILQEAADVHAR	3	100.0%	1																									
				TVSVSEAIKK	2	91.9%	1																									
				VLLQEEGTR	2	99.5%	1																									
				YGDGIQLTR	2	99.9%	1																									
IPI00013939	RPA2	isoform 1 of Replication protein A 32 kDa subunit	97.2%	5.9	1	1	1	4	697,368	691,720	713,523	666,878	84,502	65,185	57,690	33,207	27.1	21.1	18.1	11.1	-1.0	1	1.0	0.9	-1.0	0.8	1.0	0.8	-1.0	0.7	-1.1	0.5
IPI00646500	RPA2	isoform 3 of Replication protein A 32 kDa subunit	97.2%	4.5	1	1	1	4	697,368	691,720	713,523	666,878	84,502	65,185	57,690	33,207	27.1	21.1	18.1	11.1	-1.0	1	1.0	0.9	-1.0	0.8	1.0	0.8	-1.0	0.7	-1.1	0.5
IPI00646957	RPA2	Replication protein A2, 32kDa	97.2%	8.9	1	1	1	4	697,368	691,720	713,523	666,878	84,502	65,185	57,690	33,207	27.1	21.1	18.1	11.1	-1.0	1	1.0	0.9	-1.0	0.8	1.0	0.8	-1.0	0.7	-1.1	0.5
IPI00647667	RPA2	isoform 2 of Replication protein A 32 kDa subunit	97.2%	5.8	1	1	1	4	697,368	691,720	713,523	666,878	84,502	65,185	57,690	33,207	27.1	21.1	18.1	11.1	-1.0	1	1.0	0.9	-1.0	0.8	1.0	0.8	-1.0	0.7	-1.1	0.5
				IGNVEISQVTIVGIIR	2	97.2%	1																									
IPI00013949	SGTA	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	99.8%	4.5	1	1	1	2	4,378,075	4,522,635	3,532,610	4,197,115	389,824	755,700	544,765	758,902	19.9	37.4	34.5	40.4	1.0	0.9	-1.2	0.2	-1.0	0.8	-1.3	0.3	-1.1	0.8	1.2	0.5
IPI00908410	SGTA	cDNA FLJ56566, highly similar to Small glutamine-rich tetratricopeptiderepeat-conta	99.8%	4.8	1	1	1	2	4,378,075	4,522,635	3,532,610	4,197,115	389,824	755,700	544,765	758,902	19.9	37.4	34.5	40.4	1.0	0.9	-1.2	0.2	-1.0	0.8	-1.3	0.3	-1.1	0.8	1.2	0.5
				LAYAIIQFLHDQLR	2	99.7%	1																									
IPI00853358	-	MUC1 isoform T9	99.3%	10.0	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00013955	MUC1	isoform 1 of Mucin-1	99.3%	0.9	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00218163	MUC1	isoform 2 of Mucin-1	99.3%	0.9	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00218164	MUC1	isoform 3 of Mucin-1	99.3%	0.9	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00218165	MUC1	isoform 4 of Mucin-1	99.3%	0.9	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00218169	MUC1	isoform 7 of Mucin-1	99.3%	4.3	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7

IPI00385161	MUC1	Mucin short variant SV10	99.3%	7.4	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00607569	MUC1	mucin-1 isoform 2 precursor	99.3%	4.2	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00607673	MUC1	isoform 8 of Mucin-1	99.3%	4.0	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00889553	MUC1	mucin-1 isoform 9 precursor	99.3%	2.3	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00916285	MUC1	mucin-1 isoform 11 precursor	99.3%	3.9	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00975472	MUC1	mucin-1 isoform 10 precursor	99.3%	2.3	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00982300	MUC1	mucin-1 isoform 12 precursor	99.3%	5.0	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
IPI00982802	MUC1	mucin-1 isoform 17 precursor	99.3%	5.6	1	1	1	14	562,152	524,783	542,540	568,159	53,564	24,761	38,678	42,667	21.3	10.6	15.9	16.8	-1.1	0.5	-1.0	0.8	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
				DISEMFLQIYK	2	99.3%	1																									
IPI00013976	LAMB1	Laminin subunit beta-1	99.6%	1.1	1	1	1	2	170,361	197,059	278,966	233,371	19,279	28,629	41,858	9,611	25.3	32.5	33.6	9.2	1.2	0.5	1.6	0.05	1.4	0.02	1.4	0.1	1.2	0.3	-1.2	0.3
IPI00853454	LAMB1	200 kDa protein	99.6%	1.1	1	1	1	2	170,361	197,059	278,966	233,371	19,279	28,629	41,858	9,611	25.3	32.5	33.6	9.2	1.2	0.5	1.6	0.05	1.4	0.02	1.4	0.1	1.2	0.3	-1.2	0.3
				AMDLDQDVLSALAEVEQLSK	2	99.6%	1																									
IPI00909308	-	cDNA FLJ57891, highly similar to Tropomyosin beta chain	99.3%	7.0	1	1	1	3	366,525	311,653	313,742	366,575	59,163	24,099	31,126	23,145	36.1	17.3	22.2	14.1	-1.2	0.4	-1.2	0.5	1.0	1	1.0	1	1.2	0.1	1.2	0.2
IPI00013991	TPM2	isoform 1 of Tropomyosin beta chain	99.3%	3.9	1	1	1	3	366,525	311,653	313,742	366,575	59,163	24,099	31,126	23,145	36.1	17.3	22.2	14.1	-1.2	0.4	-1.2	0.5	1.0	1	1.0	1	1.2	0.1	1.2	0.2
IPI00513698	TPM2	Tropomyosin 2	99.3%	3.4	1	1	1	3	366,525	311,653	313,742	366,575	59,163	24,099	31,126	23,145	36.1	17.3	22.2	14.1	-1.2	0.4	-1.2	0.5	1.0	1	1.0	1	1.2	0.1	1.2	0.2
				QLEEEQQALQK	2	99.7%	1																									
IPI00847576	LOC729057	Similar to Mitochondrial import receptor subunit TOM40 homolog	99.1%	16.1	1	1	1	2	1,645,430	1,757,140	1,556,280	1,817,025	171,923	203,110	117,693	128,827	23.4	25.9	16.9	15.9	1.1	0.7	-1.1	0.7	1.1	0.4	-1.1	0.4	1.0	0.8	1.2	0.2
IPI00014053	TOMM40	isoform 1 of Mitochondrial import receptor subunit TOM40 homolog	99.1%	4.2	1	1	1	2	1,645,430	1,757,140	1,556,280	1,817,025	171,923	203,110	117,693	128,827	23.4	25.9	16.9	15.9	1.1	0.7	-1.1	0.7	1.1	0.4	-1.1	0.4	1.0	0.8	1.2	0.2
				GSVDSNWIVGATLEK	2	99.1%	1																									
IPI00014068	PAK4	isoform 1 of Serine/threonine-protein kinase PAK 4	99.5%	3.1	1	1	1	3	101,684	94,411	116,176	107,123	16,528	10,267	16,698	8,072	36.4	24.3	32.1	16.9	-1.1	0.7	1.1	0.6	1.1	0.8	1.2	0.3	1.1	0.4	-1.1	0.6
IPI00178714	PAK4	isoform 2 of Serine/threonine-protein kinase PAK 4	99.5%	4.2	1	1	1	3	101,684	94,411	116,176	107,123	16,528	10,267	16,698	8,072	36.4	24.3	32.1	16.9	-1.1	0.7	1.1	0.6	1.1	0.8	1.2	0.3	1.1	0.4	-1.1	0.6
IPI00384231	PAK4	isoform 4 of Serine/threonine-protein kinase PAK 4	99.5%	3.6	1	1	1	3	101,684	94,411	116,176	107,123	16,528	10,267	16,698	8,072	36.4	24.3	32.1	16.9	-1.1	0.7	1.1	0.6	1.1	0.8	1.2	0.3	1.1	0.4	-1.1	0.6
				DGALTLLLDEFENMSVTR	2	99.5%	1																									
IPI00014151	PSMD6	26S proteasome non-ATPase regulatory subunit 6	100.0%	9.0	3	3	3	2	2,542,930	2,834,053	2,568,927	2,946,648	232,096	91,316	234,434	61,964	20.4	7.2	20.4	4.7	1.1	0.3	1.0	0.9	1.2	0.2	-1.1	0.3	1.0	0.3	1.1	0.2
IPI00793381	PSMD6	Uncharacterized protein	100.0%	7.9	3	3	3	2	2,542,930	2,834,053	2,568,927	2,946,648	232,096	91,316	234,434	61,964	20.4	7.2	20.4	4.7	1.1	0.3	1.0	0.9	1.2	0.2	-1.1	0.3	1.0	0.3	1.1	0.2
				FLLSLPEHR	3	96.6%	1																									
				IGLFYMDNDLITR	2	99.7%	1																									
				SLDWQIDVDLLNK	2	99.9%	1																									
IPI00014177	SEP2	isoform 1 of Septin-2	100.0%	27.7	7	7	8	3	5,512,602	5,585,513	5,278,139	6,140,298	648,364	370,919	435,328	173,068	26.3	14.9	18.4	6.3	1.0	0.9	-1.0	0.8	1.1	0.4	-1.1	0.6	1.1	0.2	1.2	0.1
IPI00871851	SEP2	isoform 2 of Septin-2	100.0%	25.3	7	7	8	3	5,512,602	5,585,513	5,278,139	6,140,298	648,364	370,919	435,328	173,068	26.3	14.9	18.4	6.3	1.0	0.9	-1.0	0.8	1.1	0.4	-1.1	0.6	1.1	0.2	1.2	0.1
IPI00894340	SEP2	Uncharacterized protein	100.0%	31.2	7	7	8	3	5,512,602	5,585,513	5,278,139	6,140,298	648,364	370,919	435,328	173,068	26.3	14.9	18.4	6.3	1.0	0.9	-1.0	0.8	1.1	0.4	-1.1	0.6	1.1	0.2	1.2	0.1
				ILDEIEEHNIK	2	100.0%	1																									
				KVENEDMNKDQILLEK	3	97.9%	1																									
				LTVVDTPGYGDAINCR	2	100.0%	1																									
				MQAQMQMQMQGGDGDGGALGHHV	3	100.0%	1																									
				RMQEMIAR	2	97.5%	1																									
				TIISYIDEQFER	2	100.0%	2																									
				TVQIEASTVEIEER	2	100.0%	1																									
IPI00014197	CDV3	isoform 1 of Protein CDV3 homolog	100.0%	26.7	3	3	3	2	2,443,319	2,732,359	2,472,230	2,813,361	274,474	140,706	279,070	166,051	25.1	11.5	25.2	13.2	1.1	0.4	1.0	0.9	1.2	0.3	-1.1	0.4	1.0	0.7	1.1	0.3
IPI00793920	CDV3	CDV3 homolog (Mouse), isoform CRA_a	100.0%	26.7	3	3	3	2	2,443,319	2,732,359	2,472,230	2,813,361	274,474	140,706	279,070	166,051	25.1	11.5	25.2	13.2	1.1	0.4	1.0	0.9	1.2	0.3	-1.1	0.4	1.0	0.7	1.1	0.3
				KTPQGPPEIYSDTQFPSLQSTAK	3	100.0%	1																									
				LQLDNQYAVLENQK	2	99.9%	1																									
				TAPVQAPPAPVIVTETPEPAMTSGVYRPPGAR	3	98.7%	1																									
IPI00014198	EXOSC7	Exosome complex component RRP42	91.0%	5.2	1	1	1	1	4,211,920	4,018,180	3,920,370	4,103,520	356,204	340,315	250,492	126,524	18.9	18.9	14.3	6.9	-1.0	0.7	-1.1	0.5	-1.0	0.8	-1.0	0.8	1.0	0.8	1.0	0.5
				GGDDLGTEIANTLYR	2	91.0%	1																									
IPI00014230	C1QBP	Complement component 1 Q subcomponent-binding protein, mitochondrial	100.0%	22.0	4	4	5	1	23,803,613	25,259,752	21,070,933	26,581,482	2,876,562	833,775	2,052,258	621,770	27.0	7.4	21.8	5.2	1.1	0.6	-1.1	0.5	1.1	0.4	-1.2	0.1	1.1	0.2	1.3	0.05
				AFVDFLSDEIKEER	2	99.6%	1																									
				EVSFQSTGESEWK	2	99.5%	1																									
				MSGGWELELNGTEAK	2	100.0%	2																									
				VEEQEPELTSTPNFVVEVIK	3	85.5%	1																									
IPI00014236	SLC39A14	isoform 1 of Zinc transporter ZIP14	99.4%	4.1	1	1	1	3	2,441,950	2,831,190	2,837,353	3,291,850	359,807	114,150	295,625	168,591	33.0	9.0	23.3	11.5	1.2	0.4	1.2	0.4	1.3	0.06	1.0	1	1.2	0.05	1.2	0.2
IPI00303452	SLC39A14	isoform 2 of Zinc transporter ZIP14	99.4%	4.2	1	1	1	3	2,441,950	2,831,190	2,837,353	3,291,850	359,807	114,150	295,625	168,591	33.0	9.0	23.3	11.5	1.2	0.4	1.2	0.4	1.3	0.06	1.0	1	1.2	0.05	1.2	0.2
IPI00973181	SLC39A14	isoform 3 of Zinc transporter ZIP14	99.4%	4.1	1	1	1	3	2,441,950	2,831,190	2,837,353	3,291,850	359,807	114,150	295,625	168,591	33.0	9.0	23.3	11.5	1.2	0.4	1.2	0.4	1.3	0.06	1.0	1	1.2	0.05	1.2	0.2
				IGSSELQEFCPTILQQLDSR	3	99.4%	1																									
IPI00014238	KARS	isoform Cytoplasmic of Lysyl-tRNA synthetase	100.0%	9.4	5	5	6	2	14,835,388	14,578,432	14,355,441	15,958,675	1,162,179	566,071	833,124	429,651	17.5	8.7	13.0	6.0	-1.0	0.8	-1.0	0.7	1.1	0.4	-1.0	0.8	1.1	0.09	1.1	0.1
IPI00307092	KARS	isoform Mitochondrial of Lysyl-tRNA synthetase	100.0%	9.0	5	5	6	2	14,835,388	14,578,432	14,355,441	15,958,675	1,162,179	566,071	833,124	429,651	17.5	8.7	13.0	6.0	-1.0	0.8	-1.0	0.7	1.1	0.4	-1.0	0.8	1.1	0.09	1.1	0.1
				INMVEELEK	2	98.6%	1																									
				LPETNLFETEETRK	3	100.0%	1																									
				MLVVGGIDR	2	98.5%	1																									
				RGDIIGVQGNPGK	2	99.9%	1																									
				YLDLILNDFVR	2	100.0%	2																									
IPI00014263	EIF4H	isoform Long of Eukaryotic translation initiation factor 4H	100.0%	20.2	2	2	2	1	6,783,450	7,261,015	4,662,025	7,128,075	884,979	639,421	685,629	709,271	29.2	19.7	32.9	22.3	1.1	0.7	-1.5	0.09	1.1	0.8	-1.6	0.02	-1.0	0.9	1.5	0.04
				ELPTEPPYTAYVGNLPFNTVQGDIDAIFK	3	100.0%	1																									
				TVATPLNQVANPNSAIFGGAR	2	100.0%	1																									
IPI00014361	TSTA3	GDP-L-fucose synthase	100.0%	7.8	2	2	2	1	2,651,980	2,757,783	3,489,300	3,093,093	167,466	191,601	419,532	341,929	14.1	15.5	26.9	24.7	1.0	0.7	1.3	0.1	1.2	0.3	1.3	0.2	1.1	0.4	-1.1	0.5
				TASNSK	1	83.2%	1																									
				VVADGAGLPGEDWVFVSSK	2	100.0%	1																									
IPI00410496	FLJ44635	TPT1-like protein	100.0%	9.3	1	1	2	3	322,877	313,570	296,810	339,843	35,916	23,669	26,751	23,453	24.9	16.9	20.2	15.4	-1.0	0.8	-1.1	0.6	1.1	0.7	-1.1	0.7	1.1	0.5	1.1	0.3
IPI00014402	HUWE1	CDNA FLJ20030 fis, clone ADSU02156	100.0%	3.2	1	1	2	3	322,877	313,570	296,810	339,843	35,916	23,669	26,751	23,453	24.9	16.9	20.2	15.4	-1.0	0.8	-1.1	0.6	1.1	0.7	-1.1	0.7	1.1	0.5	1.1	0.3
IPI00643765	TPT1	Tumor protein, translationally-controlled 1, isoform CRA_a	100.0%	9.4	1	1	2	3	322,877	313,570	296,810	339,843	35,916	23,669	26,751	23,453	24.9	16.9	20.2	15.4	-1.0	0.8	-1.1	0.6	1.1	0.7	-1.1	0.7	1.1	0.5	1.1	0.3
				VKPFMTGAAEQIK	2	99.9%	2																									
IPI00014424	EEF1A2	Elongation factor 1-alpha 2	100.0%	18.6	5	6	10	1	18,200,651	18,899,944	18,263,993	21,246,507	1,629,500	904,927	1,739,980	836,568	20.0	10.7	21.3	8.8	1.0	0.7	1.0	1	1.2	0.1	-1.0	0.8	1.1	0.09	1.2	0.2
				IGGIGTVPVGR	2	100.0%	3																									
				NMITGTSQADCAVLIVAAGVGEFEAGISK	2	100.0%	2																									
				NMITGTSQADCAVLIVAAGVGEFEAGISK	3	100.0%	1																									
				STTTGHLIYK	2	100.0%	2																									
				VETGILRPGMVVTFAPVNITTEVK	3	99.6%	1																									
				YYITIIDAPGHR	2	98.9%	1																									
IPI00014439	QDPR	Dihydropteridine reductase	99.5%	5.3	1	1	1	2	4,763,040	4,859,760	4,360,350	5,621,165	644,417	372,105	180,716	432,954	30.3	17.1	9.3	17.2	1.0	0.9	-1.1	0.6	1.2	0.3	-1.1	0.3	1.2	0.2	1.3	0.03
IPI00902534	QDPR	cDNA FLJ42391 fis, clone 3NB692002806, highly similar to Dihydropteridine reducta	99.5%	6.1	1	1	1	2	4,763,040	4,859,760	4,360,350	5,621,165	644,417	372,105	180,716	432,954	30.3	17.1	9.3	17.2	1.0	0.9	-1.1	0.6	1.2	0.3	-1.1	0.3	1.2	0.2	1.3	0.03
				GAVHQLCQSLAGK	2	99.5%	1																									
IPI00014481	AAMP	Angio-associated migratory cell protein	92.9%	2.5	1	1	1	4	1,329,268	1,291,835	1,421,400	1,643,000	109,569	68,385	130,077	161,486	18.4	11.8	20.5	22.0	-1.0	0.8	1.1	0.6	1.2	0.1	1.1	0.4	1.3	0.08	1.2	0.3
IPI00924477	AAMP	Uncharacterized protein	92.9%	2.7	1	1	1	4	1,329,268	1,291,835	1,421,400	1,643,000	109,569	68,385	130,077	161,486	18.4	11.8	20.5	22.0	-1.0	0.8	1.1	0.6	1.2	0.1	1.1	0.4	1.3	0.08	1.2	0.3
IPI00924705	AAMP	Uncharacterized protein	92.9%	5.5	1	1	1	4	1,329,268	1,291,835	1,421,400	1,643,000	109,569	68,385	130,077	161,486	18.4	11.8	20.5	22.0	-1.0	0.8	1.1	0.6	1.2	0.1	1.1	0.4	1.3	0.08	1.2	0.3
IPI00927731	AAMP	Uncharacterized protein	92.9%	2.5	1	1	1	4	1,329,268	1,291,835	1,421,400	1,643,000	109,569	68,385	130,077	161,486	18.4	11.8	20.5	22.0	-1.0	0.8	1.1	0.6	1.2	0.1	1.1	0.4	1.3	0.08	1.2	0.3
				AVVGYEDGTIR	2	92.9%	1																									
IPI00922175	-	cDNA FLJ51678, highly similar to Ras-related protein Rab-18	99.5%	15.2	2	2	2	4	2,354,457	2,568,733	2,428,400	2,189,095	170,089	188,727	284,828	217,430	16.2	16.4	26.2	22.2	1.1	0.4	1.0	0.8	-1.1	0.6	-1.1	0.7	-1.2	0.2	-1.1	0.5
IPI00014577	RAB18	Ras-related protein Rab-18	99.5%	14.6	2	2	2	4	2,354,457	2,568,733	2,428,400	2,189,095	170,089	188,727	284,828	217,430	16.2	16.4	26.2	22.2	1.1	0.4	1.0	0.8	-1.1	0.6	-1.1	0.7	-1.2	0.2	-1.1	0.5
IPI00478787	RAB18	RAB18, member RAS oncogene family	99.5%	10.3	2	2	2	4	2,354,457	2,568,733	2,428,400	2,189,095	170,089	188,727	284,828	217,430	16.2	16.4	26.2	22.2	1.1	0.4	1.0	0.8	-1.1	0.6	-1.1	0.7	-1.2	0.2	-1.1	0.5
IPI00844361	RAB18	RAB18 long isoform 1	99.5%	12.8	2	2	2	4	2,354,457	2,568,733	2,428,400	2,189,095	170,089	188,727	284,828	217,430	16.2	16.4	26.2	22.2	1.1	0.4	1.0	0.8	-1.1	0.6	-1.1	0.7	-1.2	0.2	-1.1	0.5
				FTDDTFDPELAATIGVDFK	2	99.3%	1																									
				NDIVNMLVGNK	2	97.9%	1																									
IPI00014587	CLTA	isoform Brain of Clathrin light chain A	99.6%	8.5	1	1	1	4	563,353	564,768	529,723	649,860	44,708	29,445	36,139	59,120	17.8	11.7	15.3	20.3	1.0	1	-1.1	0.6	1.2	0.3	-1.1	0.5	1.2	0.2	1.2	0.1
IPI00790571	CLTA	isoform 3 of Clathrin light chain A	99.6%	8.9	1	1	1	4	563,353	564,768	529,723	649,860	44,708	29,445	36,139	59,120	17.8	11.7	15.3	20.3	1.0	1	-1.1	0.6	1.2	0.3	-1.1	0.5	1.2	0.2	1.2	0.1
IPI00945731	CLTA	clathrin light chain A isoform d	99.6%	9.1	1	1	1	4	563,353	564,768	529,723	649,860	44,708	29,445	36,139	59,120	17.8	11.7	15.3	20.3	1.0	1	-1.1	0.6	1.2	0.3	-1.1	0.5	1.2	0.2	1.2	0.1
IPI00946844	CLTA	Uncharacterized protein	99.6%	10.7	1	1	1	4	563,353	564,768	529,723	649,860	44,708	29,445	36,139	59,120	17.8	11.7	15.3	20.3	1.0	1	-1.1	0.6	1.2	0.3	-1.1	0.5	1.2	0.2	1.2	0.1
				AAEEAFVNDIDESSPGTEWER	2	100.0%	1																									
IPI00014589	CLTB	isoform Brain of Clathrin light chain B	100.0%	7.9	2	2	3	2	6,408,792	6,067,757	5,928,568	6,701,490	327,176	308,793	407,200	194,242	11.4	11.4	15.4	6.5	-1.1	0.5	-1.1	0.4	1.0	0.5	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00216472	CLTB	isoform Non-brain of Clathrin light chain B	100.0%	8.5	2	2	3	2	6,408,792	6,067,757	5,928,568	6,701,490	327,176	308,793	407,200	194,242	11.4	11.4	15.4	6.5	-1.1	0.5	-1.1	0.4	1.0	0.5	-1.0	0.8	1.1	0.1	1.1	0.1
				DLEEWNQR	2	97.9%	1																									
				VAQLCDFNPK	2	99.9%	2																									
IPI00014718	DNAJC9	RcDNAJ9 (Fragment)	99.2%	7.9	1	1	1	1	818,520	899,470	870,180	895,675	65,245	98,144	40,153	48,116	17.8	24.4	10.3	12.0	1.1	0.5	1.1	0.5	1.1	0.4	-1.0	0.8	-1.0	1	1.0	0.7
				NIIQQAIDAGEVPSYNAFVK	2	99.2%	1																									
IPI00014808	PAFAH1B3	Platelet-activating factor acetylhydrolase IB subunit gamma	100.0%	26.8	4	4	4	1	23,401,220	22,684,570	21,383,150	27,403,050	2,587,066	1,148,811	1,694,324	699,629	24.7	11.3	17.7	5.7	-1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.5	1.2	0.008	1.3	0.01
				AIVQLVNER	2	98.8%	1																									
				ELFSPLHALNFGIGGDGTQHVLWR	3	100.0%	1																									
				LENGELEHIRPK	2	98.6%	1																									
				LLAQDQGQGAPLLEPAP	2	99.6%	1																									
IPI00014845	DNAH8	isoform 1 of Dynein heavy chain 8, axonemal	94.7%	0.6	1	1	1	4	301,486	360,395	402,227	400,870	16,070	21,968	41,572	37,977	11.9	13.6	23.1	21.2	1.2	0.06	1.3	0.07	1.3	0.04	1.1	0.4	1.1	0.4	-1.0	1
IPI00478021	DNAH8	isoform 2 of Dynein heavy chain 8, axonemal	94.7%	0.6	1	1	1	4	301,486	360,395	402,227	400,870	16,070	21,968	41,572	37,977	11.9	13.6	23.1	21.2	1.2	0.06	1.3	0.07	1.3	0.04	1.1	0.4	1.1	0.4	-1.0	1
IPI00552749	DNAH8	478 kDa protein	94.7%	0.6	1	1	1	4	301,486	360,395	402,227	400,870	16,070	21,968	41,572	37,977	11.9	13.6	23.1	21.2	1.2	0.06	1.3	0.07	1.3	0.04	1.1	0.4	1.1	0.4	-1.0	1
IPI00873991	DNAH8	537 kDa protein	94.7%	0.6	1	1	1	4	301,486	360,395	402,227	400,870	16,070	21,968	41,572	37,977	11.9	13.6	23.1	21.2	1.2	0.06	1.3	0.07	1.3	0.04	1.1	0.4	1.1	0.4	-1.0	1
				QVVETMGLFHDMVSESCESYFQRYRR	3	94.7%	1																									
IPI00014898	PLEC	isoform 1 of Plectin	100.0%	23.2	83	85	96	8	75,001,389	76,098,049	74,396,922	84,779,963	6,310,324	2,761,586	4,839,722	3,041,543	18.8	8.1	14.6	8.0	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.07	1.1	0.1
IPI00186711	PLEC	isoform 2 of Plectin	100.0%	23.7	83	85	96	8	75,001,389	76,098,049	74,396,922	84,779,963	6,310,324	2,761,586	4,839,722	3,041,543	18.8	8.1	14.6	8.0	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.07	1.1	0.1
IPI00398775	PLEC	isoform 9 of Plectin	100.0%	24.0	83	85	96	8	75,001,389	76,098,049	74,396,922	84,779,963	6,310,324	2,761,586	4,839,722	3,041,543	18.8	8.1	14.6	8.0	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.07	1.1	0.1
IPI00398776	PLEC	isoform 7 of Plectin	100.0%	24.1	83	85	96	8	75,001,389	76,098,049	74,396,922	84,779,963	6,310,324	2,761,586	4,839,722	3,041,543	18.8	8.1	14.6	8.0	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.07	1.1	0.1
IPI00398777	PLEC	isoform 5 of Plectin	100.0%	23.9	83	85	96	8	75,001,389	76,098,049	74,396,922	84,779,963	6,310,324	2,761,586	4,839,722	3,041,543	18.8	8.1	14.6	8.0	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.07	1.1	0.1
IPI00398778	PLEC	isoform 6 of Plectin	100.0%	23.9	83	85	96	8	75,001,389	76,098,049	74,396,922	84,779,963	6,310,324	2,761,586	4,839,722	3,041,543	18.8	8.1	14.6	8.0	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.07	1.1	0.1
IPI00398779	PLEC	isoform 4 of Plectin	100.0%	23.9	83	85	96	8	75,001,389	76,098,049	74,396,922	84,779,963	6,310,324	2,761,586	4,839,722	3,041,543	18.8	8.1	14.6	8.0	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.07	1.1	0.1
IPI00420096	PLEC	isoform 8 of Plectin	100.0%	24.0	83	85	96	8	75,001,389	76,098,049	74,396,922	84,779,963	6,310,324	2,761,586	4,839,722	3,041,543	18.8	8.1	14.6	8.0	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.07	1.1	0.1
				AELELELGR	2	99.1%	1																									
				AFCGFEDPR	2	91.4%	1																									
				AGTLSITEFADMLSGNAGGFR	2	100.0%	2																									
				AGVAAPATQVAQVTLQSVQR	2	100.0%	1																									
				AGVAAPATQVAQVTLQSVQR	3	99.4%	1																									
				AGVVGPELHEQLLSAEK	3	92.1%	1																									
				AKLEQLFQDEVAK	2	99.0%	1																									
				APVPASELLASGVLSR	2	100.0%	2																									
				AQLEPVASPAK	2	99.9%	1																									
				AQVEQELTTLR	2	100.0%	1																									
				ARQEELYSELQAR	2	99.2%	1																									
				ATTAALLLEAQAATGFLVDPVR	3	100.0%	1																									
				CDNFTSSWR	2	99.9%	1																									
				DDGTGQLLLPLSDAR	2	99.4%	1																									
				DLSELGSVR	2	97.7%	1																									
				DPYSGSTISLFQAMQK	2	100.0%	1																									
				DSQDAGGFGPEDR	2	95.4%	1																									
				EGLTSIEEVTK	2	100.0%	1																									
				EQELQQTLQQEQSVLDQLR	2	100.0%	1																									
				ESADPLGAWLQDAR	2	100.0%	2																									
				FAEQTLR	2	97.2%	1																									
				FLEGTSCIAGVFVDATK	2	100.0%	1																									
				FLEVQYLTGGLIEPDTPGR	2	100.0%	1																									
				FLEVQYLTGGLIEPDTPGR	3	99.4%	1																									
				FLEVQYLTGGLIEPDTPGRVPLDEALQR	3	100.0%	1																									
				FRELAEEAAR	2	88.2%	1																									

				GANVIAGVWLEEAGQK	2	100.0%	1																									
				GFFDPNTEENLTYLQLMER	2	100.0%	1																									
				GFFDPNTHENLTYLQLLER	3	99.9%	1																									
				GGELVYTDSEAR	2	100.0%	2																									
				GLFDEEMNEILTDPSDDTK	2	100.0%	1																									
				GLHQSIEEFR	2	98.6%	1																									
				GYFDEEMNR	2	100.0%	2																									
				IIITVVEEQEQK	2	100.0%	1																									
				ISYKDALDR	2	98.5%	1																									
				KGLVGPELHDR	3	99.5%	1																									
				LAAEQELIR	2	98.9%	1																									
				LEQLFQDEVAK	2	100.0%	1																									
				LKAEAELLQQQK	2	99.2%	1																									
				LLDAQLATGGIVDPR	2	100.0%	2																									
				LLDAQLSTGGIVDPSK	2	100.0%	2																									
				LLDPEDVDVPQPDEK	2	90.6%	1																									
				LLEAAAQSTK	2	99.9%	2																									
				LLEAQACTGGIIDPSTGERFPVTDAVNK	3	87.1%	1																									
				LLEAQIATGGIIDPVHSHR	3	100.0%	1																									
				LLEAQIATGGVIDPVHSHR	3	99.7%	1																									
				LLLEAQAATGFLLDPVKGER	3	99.9%	1																									
				LQNVQIALDYLR	2	100.0%	1																									
				LREQLQLLEEQHR	3	95.2%	1																									
				LRIEEEIR	3	91.3%	1																									
				LTAEDLFEAR	2	98.5%	1																									
				LTVDEAVR	2	93.3%	1																									
				MGIVGPEFK	2	100.0%	1																									
				MQAVQEATR	2	99.0%	2																									
				MVEGYQGLR	2	80.9%	1																									
				NLVDNITGQR	2	99.8%	1																									
				QITMEELVR	2	91.5%	1																									
				QLLEEELAR	2	98.0%	1																									
				QVEEEILALK	2	97.3%	1																									
				QVQVALETAQR	2	99.9%	1																									
				QYDIDDAIAK	2	99.9%	1																									
				QYINAIKDYELQLVTYK	3	98.2%	1																									
				RASFAEK	2	83.5%	1																									
				RPELEDSTLR	2	99.9%	1																									
				SEEMQTVQQEQLLQETQALQQSFLSEK	3	95.6%	1																									
				SELELTLGK	2	80.0%	1																									
				SIQEELQQLR	2	99.9%	1																									
				SKEQAELEAAR	2	94.1%	1																									
				SLQEEHVAVAQLR	2	99.7%	1																									
				SLVPAAELLESR	2	99.9%	1																									
				SQVEEELFSVR	2	99.9%	1																									
				SQVMDEATALQLR	2	100.0%	2																									
				SYVDPSTDER	2	99.6%	1																									
				TPVEVPVGGFK	2	100.0%	1																									
				TVTIWEIINSEYFTAEQR	2	99.8%	1																									
				VDGAEWGVDLPSVEAQLGSHR	3	100.0%	1																									
				VIDRELYQQLQR	3	95.2%	1																									
				VLADPSDDTK	2	82.7%	1																									
				VPDVQDGVR	2	99.9%	1																									
				VPLDVACAR	2	99.8%	1																									
				VPVDVAYQR	2	99.9%	2																									
				VPVDVAYR	2	99.8%	1																									
				VQSGSESVIQEYVDLR	2	100.0%	1																									
				VSAQRLQEAGILSAEELQRLAQGHTTVDELAR	3	99.0%	1																									
				YLQDLLAWVEENQHR	3	100.0%	1																									
IPI00014938	SARNP	SAP domain-containing ribonucleoprotein	100.0%	20.5	4	4	4	2	7,024,042	7,401,900	7,697,892	8,538,715	735,386	233,418	620,652	194,807	23.4	7.1	18.0	5.1	1.1	0.6	1.1	0.5	1.2	0.1	1.0	0.7	1.2	0.006	1.1	0.3
IPI01015600	SARNP	CIP29 protein	100.0%	28.7	4	4	4	2	7,024,042	7,401,900	7,697,892	8,538,715	735,386	233,418	620,652	194,807	23.4	7.1	18.0	5.1	1.1	0.6	1.1	0.5	1.2	0.1	1.0	0.7	1.2	0.006	1.1	0.3
				FGISSVPTK	2	99.0%	1																									
				FGLNVSSISR	2	99.8%	1																									
				GLSSDNKPMVNLDK	2	99.3%	1																									
				ITSEIPQTER	2	90.4%	1																									
IPI00014958	PON2	isoform 1 of Serum paraoxonase/arylesterase 2	98.7%	4.5	1	1	1	5	922,972	754,042	886,480	699,460	62,410	48,218	22,405	49,240	15.1	14.3	5.7	15.7	-1.2	0.06	-1.0	0.6	-1.3	0.02	1.2	0.04	-1.1	0.5	-1.3	0.009
IPI00290945	PON2	serum paraoxonase/arylesterase 2 isoform 1	98.7%	4.5	1	1	1	5	922,972	754,042	886,480	699,460	62,410	48,218	22,405	49,240	15.1	14.3	5.7	15.7	-1.2	0.06	-1.0	0.6	-1.3	0.02	1.2	0.04	-1.1	0.5	-1.3	0.009
IPI00742670	PON2	cDNA FLJ55597, highly similar to Serum paraoxonase/arylesterase 2	98.7%	4.3	1	1	1	5	922,972	754,042	886,480	699,460	62,410	48,218	22,405	49,240	15.1	14.3	5.7	15.7	-1.2	0.06	-1.0	0.6	-1.3	0.02	1.2	0.04	-1.1	0.5	-1.3	0.009
IPI00844348	PON2	39 kDa protein	98.7%	4.6	1	1	1	5	922,972	754,042	886,480	699,460	62,410	48,218	22,405	49,240	15.1	14.3	5.7	15.7	-1.2	0.06	-1.0	0.6	-1.3	0.02	1.2	0.04	-1.1	0.5	-1.3	0.009
IPI00976213	PON2	serum paraoxonase/arylesterase 2 isoform 2	98.7%	4.7	1	1	1	5	922,972	754,042	886,480	699,460	62,410	48,218	22,405	49,240	15.1	14.3	5.7	15.7	-1.2	0.06	-1.0	0.6	-1.3	0.02	1.2	0.04	-1.1	0.5	-1.3	0.009
				LFVYDPNNPPSSEVLR	2	98.7%	1																									
IPI00015018	PPA1	Inorganic pyrophosphatase	100.0%	44.3	10	13	14	1	63,321,427	62,257,227	61,848,075	73,793,610	6,302,720	2,325,080	4,336,203	2,746,671	22.3	8.4	15.7	8.3	-1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.01	1.2	0.05
				AAPFSLEYR	2	99.9%	1																									
				DKDFAIDIIK	2	97.4%	1																									
				DKDFAIDIIK	3	99.6%	1																									
				DPLNPIK	2	92.5%	1																									
				GEIIGVK	2	87.3%	1																									
				GISCMNTTLSESPFK	2	100.0%	1																									
				GYIWNYGAIPQTWEDPGHNDK	3	100.0%	1																									
				HTGCCGDNDPIDVCEIGSK	3	91.6%	1																									
				LKPGYLEATVDWFR	2	99.8%	1																									
				LKPGYLEATVDWFR	3	100.0%	1																									
				MEIATKDPLNPIKQDVK	3	100.0%	1																									
				VLGILAMIDEGETDWK	2	100.0%	2																									
				VLGILAMIDEGETDWK	3	100.0%	1																									
IPI00015029	PTGES3	Prostaglandin E synthase 3	100.0%	32.5	4	4	5	3	4,155,596	4,341,263	4,289,669	4,934,236	371,966	110,661	289,784	98,594	20.0	5.7	15.1	4.5	1.0	0.7	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.004	1.2	0.09
IPI00789101	PTGES3	cDNA FLJ40895 fis, clone UTERU2002294, highly similar to Prostaglandin E syntha	100.0%	31.5	4	4	5	3	4,155,596	4,341,263	4,289,669	4,934,236	371,966	110,661	289,784	98,594	20.0	5.7	15.1	4.5	1.0	0.7	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.004	1.2	0.09
IPI00908647	PTGES3	cDNA FLJ59942, highly similar to Prostaglandin E synthase 3	100.0%	37.4	4	4	5	3	4,155,596	4,341,263	4,289,669	4,934,236	371,966	110,661	289,784	98,594	20.0	5.7	15.1	4.5	1.0	0.7	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.004	1.2	0.09
				HLNEIDLFHCIDPNDSK	3	100.0%	1																									
				KGESGQSWPR	2	100.0%	2																									
				LNWLSVDFNNWK	2	100.0%	1																									
				LTFSCLGGSDNFK	2	100.0%	1																									
IPI00015077	EIF1	Eukaryotic translation initiation factor 1	99.6%	15.9	2	2	2	1	2,269,502	1,545,396	2,215,002	2,106,153	225,499	144,473	368,103	238,337	22.2	20.9	37.2	25.3	-1.5	0.03	-1.0	0.9	-1.1	0.6	1.4	0.1	1.4	0.08	-1.1	0.8
				NICQFLVEIGLAK	2	99.6%	1																									
				NICQFLVEIGLAKDDQLK	3	97.7%	1																									
IPI00794756	-	10 kDa protein	97.0%	12.7	1	1	1	4	873,480	867,418	712,538	874,568	98,085	75,245	45,774	78,091	25.1	19.4	14.4	20.0	-1.0	1	-1.2	0.2	1.0	1	-1.2	0.1	1.0	0.9	1.2	0.1
IPI00015104	CKS1B	Cyclin-dependent kinases regulatory subunit 1	97.0%	12.7	1	1	1	4	873,480	867,418	712,538	874,568	98,085	75,245	45,774	78,091	25.1	19.4	14.4	20.0	-1.0	1	-1.2	0.2	1.0	1	-1.2	0.1	1.0	0.9	1.2	0.1
IPI00514250	CKS1B	CDC28 protein kinase regulatory subunit 1B	97.0%	14.9	1	1	1	4	873,480	867,418	712,538	874,568	98,085	75,245	45,774	78,091	25.1	19.4	14.4	20.0	-1.0	1	-1.2	0.2	1.0	1	-1.2	0.1	1.0	0.9	1.2	0.1
IPI00643512	CKS1B	PNAS-18	97.0%	15.9	1	1	1	4	873,480	867,418	712,538	874,568	98,085	75,245	45,774	78,091	25.1	19.4	14.4	20.0	-1.0	1	-1.2	0.2	1.0	1	-1.2	0.1	1.0	0.9	1.2	0.1
				THLMSESEWR	2	97.0%	1																									
IPI00019345	RAP1A	Ras-related protein Rap-1A	100.0%	12.5	2	2	2	6	1,140,139	1,222,963	1,053,824	1,147,210	84,771	75,474	59,678	53,396	16.6	13.8	12.7	10.4	1.1	0.5	-1.1	0.4	1.0	0.9	-1.2	0.1	-1.1	0.4	1.1	0.3
IPI00877120	RAP1A	RAP1A, member of RAS oncogene family	100.0%	12.5	2	2	2	6	1,140,139	1,222,963	1,053,824	1,147,210	84,771	75,474	59,678	53,396	16.6	13.8	12.7	10.4	1.1	0.5	-1.1	0.4	1.0	0.9	-1.2	0.1	-1.1	0.4	1.1	0.3
IPI00015148	RAP1B	Ras-related protein Rap-1b	100.0%	12.5	2	2	2	6	1,140,139	1,222,963	1,053,824	1,147,210	84,771	75,474	59,678	53,396	16.6	13.8	12.7	10.4	1.1	0.5	-1.1	0.4	1.0	0.9	-1.2	0.1	-1.1	0.4	1.1	0.3
IPI00908754	RAP1B	cDNA FLJ50714, moderately similar to Ras-related protein Rap-1b	100.0%	16.8	2	2	2	6	1,140,139	1,222,963	1,053,824	1,147,210	84,771	75,474	59,678	53,396	16.6	13.8	12.7	10.4	1.1	0.5	-1.1	0.4	1.0	0.9	-1.2	0.1	-1.1	0.4	1.1	0.3
IPI01014435	RAP1B	cDNA FLJ51696, highly similar to Ras-related protein Rap-1b	100.0%	13.9	2	2	2	6	1,140,139	1,222,963	1,053,824	1,147,210	84,771	75,474	59,678	53,396	16.6	13.8	12.7	10.4	1.1	0.5	-1.1	0.4	1.0	0.9	-1.2	0.1	-1.1	0.4	1.1	0.3
IPI01015962	RAP1B	cDNA FLJ50711, moderately similar to Ras-related protein Rap-1b	100.0%	16.2	2	2	2	6	1,140,139	1,222,963	1,053,824	1,147,210	84,771	75,474	59,678	53,396	16.6	13.8	12.7	10.4	1.1	0.5	-1.1	0.4	1.0	0.9	-1.2	0.1	-1.1	0.4	1.1	0.3
				INVNEIFYDLVR	2	100.0%	1																									
				LVVLGSGGVGK	2	96.0%	1																									
IPI00015262	CNN2	Calponin-2	100.0%	18.5	4	4	4	2	5,751,370	5,286,933	6,048,933	5,830,773	184,159	175,458	188,426	298,552	7.2	7.4	7.0	11.5	-1.1	0.1	1.1	0.3	1.0	0.8	1.1	0.02	1.1	0.2	-1.0	0.6
IPI00910593	CNN2	cDNA FLJ52765, highly similar to Calponin-2	100.0%	17.3	4	4	4	2	5,751,370	5,286,933	6,048,933	5,830,773	184,159	175,458	188,426	298,552	7.2	7.4	7.0	11.5	-1.1	0.1	1.1	0.3	1.0	0.8	1.1	0.02	1.1	0.2	-1.0	0.6
				CASQVGMTAPGTR	2	99.1%	1																									
				GPSYGLSAEVK	2	98.6%	1																									
				SMQNWHQLENLSNFIK	3	98.8%	1																									
				TWIEGLTGLSIGPDFQK	2	100.0%	1																									
IPI00015286	DOCK1	Dedicator of cytokinesis protein 1	98.6%	1.2	1	1	1	2	238,990	280,592	380,471	277,848	76,798	73,566	90,097	42,892	71.9	58.6	53.0	34.5	1.2	0.7	1.6	0.3	1.2	0.7	1.4	0.4	-1.0	1	-1.4	0.3
IPI00872808	DOCK1	Uncharacterized protein	98.6%	1.1	1	1	1	2	238,990	280,592	380,471	277,848	76,798	73,566	90,097	42,892	71.9	58.6	53.0	34.5	1.2	0.7	1.6	0.3	1.2	0.7	1.4	0.4	-1.0	1	-1.4	0.3
				GQHETVIPGDLPLIQEVTTTLR	2	98.6%	1																									
IPI00015351	PITHD1	isoform 1 of PITH domain-containing protein 1	96.7%	5.2	1	1	1	4	1,376,995	1,348,195	1,432,693	1,602,100	170,652	100,159	225,456	110,842	27.7	16.6	35.2	15.5	-1.0	0.9	1.0	0.8	1.2	0.3	1.1	0.7	1.2	0.1	1.1	0.5
IPI00643061	PITHD1	8 kDa protein	96.7%	15.7	1	1	1	4	1,376,995	1,348,195	1,432,693	1,602,100	170,652	100,159	225,456	110,842	27.7	16.6	35.2	15.5	-1.0	0.9	1.0	0.8	1.2	0.3	1.1	0.7	1.2	0.1	1.1	0.5
IPI00643524	PITHD1	isoform 2 of PITH domain-containing protein 1	96.7%	5.2	1	1	1	4	1,376,995	1,348,195	1,432,693	1,602,100	170,652	100,159	225,456	110,842	27.7	16.6	35.2	15.5	-1.0	0.9	1.0	0.8	1.2	0.3	1.1	0.7	1.2	0.1	1.1	0.5
IPI00910270	PITHD1	cDNA FLJ60641	96.7%	9.3	1	1	1	4	1,376,995	1,348,195	1,432,693	1,602,100	170,652	100,159	225,456	110,842	27.7	16.6	35.2	15.5	-1.0	0.9	1.0	0.8	1.2	0.3	1.1	0.7	1.2	0.1	1.1	0.5
				DLTGELEYATK	2	96.7%	1																									
IPI00015361	PFDN5	Prefoldin subunit 5	100.0%	21.4	2	3	3	1	3,471,226	3,132,161	3,808,968	3,113,733	313,530	112,363	277,760	159,260	20.2	8.0	16.3	11.4	-1.1	0.4	1.1	0.4	-1.1	0.3	1.2	0.05	-1.0	0.9	-1.2	0.06
				IQQLTALGAAQATAK	2	100.0%	1																									
				NQLDQEVEFLSTSIAQLK	2	100.0%	1																									
				NQLDQEVEFLSTSIAQLK	3	100.0%	1																									
IPI00015568	KBTBD11	Kelch repeat and BTB domain-containing protein 11	98.0%	2.1	1	1	1	1	4,966,100	4,245,000	4,832,380	5,189,400	552,199	198,527	501,110	515,056	24.9	10.5	23.2	22.2	-1.2	0.3	-1.0	0.9	1.0	0.8	1.1	0.3	1.2	0.1	1.1	0.6
				SADMVALDGFIYR	2	98.0%	1																									
IPI00015602	TOMM70A	Mitochondrial import receptor subunit TOM70	98.7%	3.0	1	1	1	2	410,217	500,665	462,264	519,069	65,626	89,015	81,624	34,319	35.8	39.8	39.5	14.8	1.2	0.4	1.1	0.6	1.3	0.2	-1.1	0.8	1.0	0.9	1.1	0.5
IPI01015765	TOMM70A	cDNA FLJ57240, highly similar to Mitochondrial proteins import receptor	98.7%	3.6	1	1	1	2	410,217	500,665	462,264	519,069	65,626	89,015	81,624	34,319	35.8	39.8	39.5	14.8	1.2	0.4	1.1	0.6	1.3	0.2	-1.1	0.8	1.0	0.9	1.1	0.5
				ILLDQVEEAVADFDECIR	2	98.7%	1																									
IPI00015671	TUBAL3	isoform 1 of Tubulin alpha chain-like 3	91.4%	3.1	1	1	1	2	2,711,700	3,296,540	2,610,215	3,326,755	255,171	630,660	338,212	254,330	21.0	42.8	29.0	17.1	1.2	0.4	-1.0	0.8	1.2	0.1	-1.3	0.4	1.0	1	1.3	0.1
IPI00879904	TUBAL3	isoform 2 of Tubulin alpha chain-like 3	91.4%	3.5	1	1	1	2	2,711,700	3,296,540	2,610,215	3,326,755	255,171	630,660	338,212	254,330	21.0	42.8	29.0	17.1	1.2	0.4	-1.0	0.8	1.2	0.1	-1.3	0.4	1.0	1	1.3	0.1
				LVVQVVSSITASLR	3	91.4%	1																									
IPI00015736	UBA5	isoform 1 of Ubiquitin-like modifier-activating enzyme 5	99.4%	10.2	2	2	2	5	1,732,776	1,549,990	1,921,365	1,708,410	65,418	175,076	236,433	93,945	8.4	25.3	27.5	12.3	-1.1	0.4	1.1	0.5	-1.0	0.8	1.2	0.2	1.1	0.4	-1.1	0.4
IPI00383579	UBA5	isoform 2 of Ubiquitin-like modifier-activating enzyme 5	99.4%	11.8	2	2	2	5	1,732,776	1,549,990	1,921,365	1,708,410	65,418	175,076	236,433	93,945	8.4	25.3	27.5	12.3	-1.1	0.4	1.1	0.5	-1.0	0.8	1.2	0.2	1.1	0.4	-1.1	0.4
IPI00791004	UBA5	Uncharacterized protein	99.4%	10.9	2	2	2	5	1,732,776	1,549,990	1,921,365	1,708,410	65,418	175,076	236,433	93,945	8.4	25.3	27.5	12.3	-1.1	0.4	1.1	0.5	-1.0	0.8	1.2	0.2	1.1	0.4	-1.1	0.4
IPI00946703	UBA5	Uncharacterized protein	99.4%	36.9	2	2	2	5	1,732,776	1,549,990	1,921,365	1,708,410	65,418	175,076	236,433	93,945	8.4	25.3	27.5	12.3	-1.1	0.4	1.1	0.5	-1.0	0.8	1.2	0.2	1.1	0.4	-1.1	0.4
IPI00968261	UBA5	Uncharacterized protein	99.4%	11.8	2	2	2	5	1,732,776	1,549,990	1,921,365	1,708,410	65,418	175,076	236,433	93,945	8.4	25.3	27.5	12.3	-1.1	0.4	1.1	0.5	-1.0	0.8	1.2	0.2	1.1	0.4	-1.1	0.4
				ISNGGLEEGKPVDLVLSCVDNFEAR	3	99.4%	1																									
				LLLFDYDKVELANMNR	3	94.0%	1																									
IPI00015833	CHCHD3	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	100.0%	14.5	2	2	2	3	1,127,182	1,398,740	1,212,693	1,319,691	69,452	145,796	151,654	97,684	13.8	23.3	28.0	16.6	1.2	0.1	1.1	0.6	1.2	0.1	-1.2	0.4	-1.1	0.7	1.1	0.6
IPI00926903	CHCHD3	Uncharacterized protein	100.0%	14.2	2	2	2	3	1,127,182	1,398,740	1,212,693	1,319,691	69,452	145,796	151,654	97,684	13.8	23.3	28.0	16.6	1.2	0.1	1.1	0.6	1.2	0.1	-1.2	0.4	-1.1	0.7	1.1	0.6
IPI00927150	CHCHD3	28 kDa protein	100.0%	13.7	2	2	2	3	1,127,182	1,398,740	1,212,693	1,319,691	69,452	145,796	151,654	97,684	13.8	23.3	28.0	16.6	1.2	0.1	1.1	0.6	1.2	0.1	-1.2	0.4	-1.1	0.7	1.1	0.6
				LEERSSEFYRVTTEQYQK	3	92.9%	1																									
				YSGAYGASVSDEELK	2	100.0%	1																									
IPI00015842	RCN1	Reticulocalbin-1	100.0%	25.7	5	6	8	1	9,285,061	10,301,947	9,745,829	10,916,602	854,078	416,519	712,219	243,252	20.6	9.0	16.3	5.0	1.1	0.3	1.0	0.7	1.2	0.1	-1.1	0.5	1.1	0.2	1.1	0.2

				AADLNGDLTATR	2	100.0%	1																									
				HWILPQDYDHAQAEAR	3	100.0%	1																									
				IDNDGDGFVTTEELK	2	100.0%	2																									
				TFDQLTPDESKER	2	100.0%	2																									
				TFDQLTPDESKER	3	95.9%	1																									
				VVRPDSELGERPPEDNQSFQYDHEAFLGK	3	95.8%	1																									
IPI00015856	DNPEP	aspartyl aminopeptidase	100.0%	11.6	3	3	3	4	1,368,028	1,394,127	1,373,654	1,558,116	75,841	61,523	131,892	85,736	12.4	9.9	21.5	12.3	1.0	0.8	1.0	1	1.1	0.1	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00029820	DNPEP	DNPEP protein (Fragment)	100.0%	14.8	3	3	3	4	1,368,028	1,394,127	1,373,654	1,558,116	75,841	61,523	131,892	85,736	12.4	9.9	21.5	12.3	1.0	0.8	1.0	1	1.1	0.1	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00982108	DNPEP	cDNA FLJ56420, highly similar to Aspartyl aminopeptidase	100.0%	11.4	3	3	3	4	1,368,028	1,394,127	1,373,654	1,558,116	75,841	61,523	131,892	85,736	12.4	9.9	21.5	12.3	1.0	0.8	1.0	1	1.1	0.1	-1.0	0.9	1.1	0.2	1.1	0.3
IPI01015812	DNPEP	Uncharacterized protein	100.0%	13.7	3	3	3	4	1,368,028	1,394,127	1,373,654	1,558,116	75,841	61,523	131,892	85,736	12.4	9.9	21.5	12.3	1.0	0.8	1.0	1	1.1	0.1	-1.0	0.9	1.1	0.2	1.1	0.3
				GFFELFPSLSHNLLVD	2	95.4%	1																									
				NINENFGPNTEMHLVPILATAIQEELEK	3	99.3%	1																									
				YASNAVSEALIR	2	99.9%	1																									
IPI00015865	ADPRHL2	Poly(ADP-ribose) glycohydrolase ARH3	99.1%	8.8	2	2	2	3	2,459,977	2,493,447	2,381,487	2,787,230	247,763	200,522	130,679	179,823	22.5	18.0	12.3	14.4	1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.3	1.2	0.1
IPI01012710	ADPRHL2	cDNA, FLJ79248, highly similar to Homo sapiens ADP-ribosylhydrolase like 2 (ADPR	99.1%	15.3	2	2	2	3	2,459,977	2,493,447	2,381,487	2,787,230	247,763	200,522	130,679	179,823	22.5	18.0	12.3	14.4	1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.3	1.2	0.1
IPI01013974	ADPRHL2	cDNA FLJ51852, highly similar to Homo sapiens ADP-ribosylhydrolase like 2 (ADPR	99.1%	11.3	2	2	2	3	2,459,977	2,493,447	2,381,487	2,787,230	247,763	200,522	130,679	179,823	22.5	18.0	12.3	14.4	1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.3	1.2	0.1
				IGELLDQASVTR	2	94.0%	1																									
				QLLGHMEDLEGDAQSVLDAR	3	99.1%	1																									
IPI00015872	TSPAN8	Tetraspanin-8	99.5%	10.1	2	2	2	1	10,318,270	11,890,790	10,281,980	11,458,580	2,224,328	932,206	830,338	385,463	48.2	17.5	18.1	7.5	1.2	0.5	-1.0	1	1.1	0.6	-1.2	0.2	-1.0	0.7	1.1	0.2
				LLSATGESEK	2	98.3%	1																									
				QFQEAIIVFQEEFK	2	99.5%	1																									
IPI00015891	PFDN4	Prefoldin subunit 4	100.0%	20.2	2	2	3	2	7,032,630	6,572,175	6,520,975	7,471,755	828,423	349,254	362,429	376,027	26.3	11.9	12.4	11.3	-1.1	0.6	-1.1	0.6	1.1	0.6	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00980273	PFDN4	Uncharacterized protein	100.0%	19.9	2	2	3	2	7,032,630	6,572,175	6,520,975	7,471,755	828,423	349,254	362,429	376,027	26.3	11.9	12.4	11.3	-1.1	0.6	-1.1	0.6	1.1	0.6	-1.0	0.9	1.1	0.1	1.1	0.1
				AAAEDVNVTFEDQQK	2	100.0%	1																									
				NLQEEIDALESR	2	99.9%	2																									
IPI00015894	CDC42EP4	Cdc42 effector protein 4	99.0%	3.9	1	1	1	2	4,666,865	4,848,400	4,666,135	5,496,775	331,482	256,234	321,461	233,996	15.9	11.8	15.4	9.5	1.0	0.7	-1.0	1	1.2	0.08	-1.0	0.7	1.1	0.1	1.2	0.07
IPI00902538	CDC42EP4	cDNA FLJ40516 fis, clone TESTI2046569, highly similar to Cdc42 effector protein 4	99.0%	4.9	1	1	1	2	4,666,865	4,848,400	4,666,135	5,496,775	331,482	256,234	321,461	233,996	15.9	11.8	15.4	9.5	1.0	0.7	-1.0	1	1.2	0.08	-1.0	0.7	1.1	0.1	1.2	0.07
				AGDAFGDTSFLNSK	2	99.0%	1																									
IPI00015897	CHORDC1	isoform 1 of Cysteine and histidine-rich domain-containing protein 1	100.0%	13.6	3	3	3	2	2,377,581	2,338,125	2,510,131	2,615,305	239,036	30,024	249,072	137,465	22.5	2.9	22.2	11.8	-1.0	0.9	1.1	0.7	1.1	0.4	1.1	0.5	1.1	0.1	1.0	0.7
IPI00977749	CHORDC1	Uncharacterized protein	100.0%	24.5	3	3	3	2	2,377,581	2,338,125	2,510,131	2,615,305	239,036	30,024	249,072	137,465	22.5	2.9	22.2	11.8	-1.0	0.9	1.1	0.7	1.1	0.4	1.1	0.5	1.1	0.1	1.0	0.7
				FQEHIIQAPKPVEAIK	3	95.0%	1																									
				RPSPDEPMTNLELK	2	99.9%	1																									
				TTDFSDFLSIVGCTK	2	100.0%	1																									
IPI00015911	DLD	Dihydrolipoyl dehydrogenase, mitochondrial	100.0%	17.7	5	5	5	2	5,732,543	6,097,110	5,871,278	6,814,718	409,318	259,678	503,200	266,756	16.0	9.5	19.2	8.8	1.1	0.5	1.0	0.8	1.2	0.06	-1.0	0.7	1.1	0.09	1.2	0.1
IPI01011421	DLD	Dihydrolipoyl dehydrogenase	100.0%	19.6	5	5	5	2	5,732,543	6,097,110	5,871,278	6,814,718	409,318	259,678	503,200	266,756	16.0	9.5	19.2	8.8	1.1	0.5	1.0	0.8	1.2	0.06	-1.0	0.7	1.1	0.09	1.2	0.1
				ALTGGIAHLFK	2	99.6%	1																									
				EANLAASFGK	2	99.3%	1																									
				IPNIYAIGDVVAGPMLAHK	3	100.0%	1																									
				NETLGGTCLNVGCIPSK	2	90.4%	1																									
				VLGAHILGPGAGEMVNEAALALEYGASCEDIAR	3	100.0%	1																									
IPI00015916	QSOX1	Bone-derived growth factor (Fragment)	100.0%	3.7	2	2	2	1	4,285,905	4,494,419	4,259,601	4,410,347	171,468	188,536	347,241	200,813	9.0	9.4	18.2	10.2	1.0	0.4	-1.0	0.9	1.0	0.7	-1.1	0.6	-1.0	0.8	1.0	0.7
				EVALDLSQHK	2	96.4%	1																									
				SALYSPSDPLTLLQADTVR	2	100.0%	1																									
IPI00015924	TFIP11	isoform 1 of Tuftelin-interacting protein 11	93.5%	1.8	1	1	1	4	706,825	697,263	771,613	742,025	52,169	58,168	17,848	35,608	16.5	18.7	5.2	10.7	-1.0	0.9	1.1	0.3	1.0	0.6	1.1	0.3	1.1	0.5	-1.0	0.5
IPI00220893	TFIP11	isoform 2 of Tuftelin-interacting protein 11	93.5%	7.7	1	1	1	4	706,825	697,263	771,613	742,025	52,169	58,168	17,848	35,608	16.5	18.7	5.2	10.7	-1.0	0.9	1.1	0.3	1.0	0.6	1.1	0.3	1.1	0.5	-1.0	0.5
IPI00910595	TFIP11	cDNA FLJ58206, highly similar to Tuftelin-interacting protein 11	93.5%	2.9	1	1	1	4	706,825	697,263	771,613	742,025	52,169	58,168	17,848	35,608	16.5	18.7	5.2	10.7	-1.0	0.9	1.1	0.3	1.0	0.6	1.1	0.3	1.1	0.5	-1.0	0.5
IPI00941082	TFIP11	Uncharacterized protein	93.5%	3.3	1	1	1	4	706,825	697,263	771,613	742,025	52,169	58,168	17,848	35,608	16.5	18.7	5.2	10.7	-1.0	0.9	1.1	0.3	1.0	0.6	1.1	0.3	1.1	0.5	-1.0	0.5
				AEEHNIVFMPVIGKR	2	93.5%	1																									
IPI00909800	-	cDNA FLJ56703, highly similar to Tyrosine-protein kinase 6	97.3%	11.2	1	1	1	2	1,036,750	972,730	1,051,295	1,091,100	165,406	76,399	98,224	55,836	35.7	17.6	20.9	11.4	-1.1	0.7	1.0	0.9	1.1	0.8	1.1	0.5	1.1	0.2	1.0	0.7
IPI00015927	PTK6	Protein-tyrosine kinase 6	97.3%	3.3	1	1	1	2	1,036,750	972,730	1,051,295	1,091,100	165,406	76,399	98,224	55,836	35.7	17.6	20.9	11.4	-1.1	0.7	1.0	0.9	1.1	0.8	1.1	0.5	1.1	0.2	1.0	0.7
				RLQAEGNATGAFLIR	2	97.3%	1																									
IPI00015947	DNAJB1	DnaJ homolog subfamily B member 1	99.2%	5.9	2	2	2	2	7,634,020	7,515,310	7,590,210	8,891,075	432,343	439,092	594,664	315,909	12.7	13.1	17.5	7.9	-1.0	0.9	-1.0	1	1.2	0.05	1.0	0.9	1.2	0.03	1.2	0.09
IPI01010489	DNAJB1	cDNA FLJ59093, highly similar to DnaJ homolog subfamily B member 1	99.2%	8.3	2	2	2	2	7,634,020	7,515,310	7,590,210	8,891,075	432,343	439,092	594,664	315,909	12.7	13.1	17.5	7.9	-1.0	0.9	-1.0	1	1.2	0.05	1.0	0.9	1.2	0.03	1.2	0.09
				DGSDVIYPAR	2	97.1%	1																									
				NPFDTFFGQR	2	99.2%	1																									
IPI00015952	EIF4G2	cDNA FLJ59571, highly similar to Eukaryotic translation initiation factor 4gamma 2	99.5%	4.7	3	3	3	2	1,910,625	2,101,935	2,149,497	2,355,393	104,509	113,191	128,500	139,220	12.2	12.0	13.4	13.2	1.1	0.2	1.1	0.2	1.2	0.03	1.0	0.8	1.1	0.2	1.1	0.3
IPI00782985	EIF4G2	isoform 2 of Eukaryotic translation initiation factor 4 gamma 2	99.5%	5.3	3	3	3	2	1,910,625	2,101,935	2,149,497	2,355,393	104,509	113,191	128,500	139,220	12.2	12.0	13.4	13.2	1.1	0.2	1.1	0.2	1.2	0.03	1.0	0.8	1.1	0.2	1.1	0.3
				DMGEDLECLCQIMR	2	91.1%	1																									
				HFLPEMLSK	2	92.6%	1																									
				QEGIATSDNFMQAFLNVLDQCPK	3	99.5%	1																									
IPI00015953	DDX21	isoform 1 of Nucleolar RNA helicase 2	97.6%	1.9	1	1	1	4	1,302,608	1,215,563	1,120,418	1,281,360	88,810	58,003	42,715	68,817	15.3	10.7	8.5	12.0	-1.1	0.4	-1.2	0.1	-1.0	0.9	-1.1	0.2	1.1	0.5	1.1	0.08
IPI00477179	DDX21	isoform 2 of Nucleolar RNA helicase 2	97.6%	2.1	1	1	1	4	1,302,608	1,215,563	1,120,418	1,281,360	88,810	58,003	42,715	68,817	15.3	10.7	8.5	12.0	-1.1	0.4	-1.2	0.1	-1.0	0.9	-1.1	0.2	1.1	0.5	1.1	0.08
IPI00031554	DDX50	ATP-dependent RNA helicase DDX50	97.6%	2.0	1	1	1	4	1,302,608	1,215,563	1,120,418	1,281,360	88,810	58,003	42,715	68,817	15.3	10.7	8.5	12.0	-1.1	0.4	-1.2	0.1	-1.0	0.9	-1.1	0.2	1.1	0.5	1.1	0.08
IPI01011782	DDX50	cDNA FLJ61430, highly similar to ATP-dependent RNA helicase DDX50	97.6%	2.1	1	1	1	4	1,302,608	1,215,563	1,120,418	1,281,360	88,810	58,003	42,715	68,817	15.3	10.7	8.5	12.0	-1.1	0.4	-1.2	0.1	-1.0	0.9	-1.1	0.2	1.1	0.5	1.1	0.08
				EGAFSNFPISEETIK	2	97.6%	1																									
IPI00015954	SAR1A	GTP-binding protein SAR1a	100.0%	17.2	2	2	2	1	3,346,238	3,212,772	2,951,444	3,049,204	411,468	148,704	238,760	78,319	27.5	10.4	18.1	5.7	-1.0	0.8	-1.1	0.4	-1.1	0.5	-1.1	0.4	-1.1	0.4	1.0	0.7
				LVFLGLDNAGK	2	99.4%	1																									
				VELNALMTDETISNVPILILGNK	3	90.6%	1																									
IPI00016006	GPHN	isoform 1 of Gephyrin	92.7%	2.7	1	1	1	5	268,549	262,449	309,509	312,400	45,345	24,596	30,725	44,740	37.8	21.0	22.2	32.0	-1.0	0.9	1.2	0.5	1.2	0.5	1.2	0.3	1.2	0.4	1.0	1
IPI00184477	GPHN	isoform 2 of Gephyrin	92.7%	2.6	1	1	1	5	268,549	262,449	309,509	312,400	45,345	24,596	30,725	44,740	37.8	21.0	22.2	32.0	-1.0	0.9	1.2	0.5	1.2	0.5	1.2	0.3	1.2	0.4	1.0	1
IPI00922682	GPHN	cDNA FLJ54713, highly similar to Gephyrin	92.7%	2.6	1	1	1	5	268,549	262,449	309,509	312,400	45,345	24,596	30,725	44,740	37.8	21.0	22.2	32.0	-1.0	0.9	1.2	0.5	1.2	0.5	1.2	0.3	1.2	0.4	1.0	1
IPI01010764	GPHN	76 kDa protein	92.7%	2.8	1	1	1	5	268,549	262,449	309,509	312,400	45,345	24,596	30,725	44,740	37.8	21.0	22.2	32.0	-1.0	0.9	1.2	0.5	1.2	0.5	1.2	0.3	1.2	0.4	1.0	1
IPI01012429	GPHN	71 kDa protein	92.7%	3.0	1	1	1	5	268,549	262,449	309,509	312,400	45,345	24,596	30,725	44,740	37.8	21.0	22.2	32.0	-1.0	0.9	1.2	0.5	1.2	0.5	1.2	0.3	1.2	0.4	1.0	1
				AFITVLEMTPVLGTEIINYR	2	92.7%	1																									
IPI00016179	S100A13	Protein S100-A13	100.0%	39.8	7	7	7	1	35,432,846	38,434,778	33,223,190	40,508,375	4,177,586	2,483,034	2,656,262	1,603,028	26.4	14.5	17.9	8.9	1.1	0.6	-1.1	0.7	1.1	0.3	-1.2	0.2	1.1	0.5	1.2	0.05
				DSLSVNEFK	2	97.3%	1																									
				DSLSVNEFKELVTQQLPHLLK	3	90.4%	1																									
				ELVTQQLPHLLK	2	99.6%	1																									
				FNEYWR	2	93.6%	1																									
				KDSLSVNEFK	3	99.4%	1																									
				SLDVNQDSELK	2	100.0%	1																									
				SLDVNQDSELKFNEYWR	3	96.9%	1																									
IPI00016249	FXR1	isoform 1 of Fragile X mental retardation syndrome-related protein 1	100.0%	5.2	2	2	2	7	1,252,866	1,275,951	1,100,323	1,336,605	173,090	96,597	130,221	85,056	30.9	16.9	26.5	14.2	1.0	0.9	-1.1	0.5	1.1	0.7	-1.2	0.3	1.0	0.7	1.2	0.2
IPI00479630	FXR1	isoform 3 of Fragile X mental retardation syndrome-related protein 1	100.0%	6.0	2	2	2	7	1,252,866	1,275,951	1,100,323	1,336,605	173,090	96,597	130,221	85,056	30.9	16.9	26.5	14.2	1.0	0.9	-1.1	0.5	1.1	0.7	-1.2	0.3	1.0	0.7	1.2	0.2
IPI00554715	FXR1	isoform 2 of Fragile X mental retardation syndrome-related protein 1	100.0%	5.9	2	2	2	7	1,252,866	1,275,951	1,100,323	1,336,605	173,090	96,597	130,221	85,056	30.9	16.9	26.5	14.2	1.0	0.9	-1.1	0.5	1.1	0.7	-1.2	0.3	1.0	0.7	1.2	0.2
IPI00797887	FXR1	cDNA FLJ58199, highly similar to Fragile X mental retardation syndrome-related pro	100.0%	5.7	2	2	2	7	1,252,866	1,275,951	1,100,323	1,336,605	173,090	96,597	130,221	85,056	30.9	16.9	26.5	14.2	1.0	0.9	-1.1	0.5	1.1	0.7	-1.2	0.3	1.0	0.7	1.2	0.2
IPI00945864	FXR1	cDNA FLJ58644, highly similar to Fragile X mental retardation syndrome-related pro	100.0%	5.3	2	2	2	7	1,252,866	1,275,951	1,100,323	1,336,605	173,090	96,597	130,221	85,056	30.9	16.9	26.5	14.2	1.0	0.9	-1.1	0.5	1.1	0.7	-1.2	0.3	1.0	0.7	1.2	0.2
IPI00947266	FXR1	Uncharacterized protein	100.0%	7.1	2	2	2	7	1,252,866	1,275,951	1,100,323	1,336,605	173,090	96,597	130,221	85,056	30.9	16.9	26.5	14.2	1.0	0.9	-1.1	0.5	1.1	0.7	-1.2	0.3	1.0	0.7	1.2	0.2
IPI00947512	FXR1	Uncharacterized protein	100.0%	6.5	2	2	2	7	1,252,866	1,275,951	1,100,323	1,336,605	173,090	96,597	130,221	85,056	30.9	16.9	26.5	14.2	1.0	0.9	-1.1	0.5	1.1	0.7	-1.2	0.3	1.0	0.7	1.2	0.2
				GFLEFVEDFIQVPR	3	99.9%	1																									
				KVPGVTAIELDEDTGTFR	3	99.5%	1																									
IPI00016339	RAB5C	Ras-related protein Rab-5C	100.0%	6.5	1	1	2	2	1,979,170	2,274,565	1,825,955	2,052,780	186,324	237,468	118,246	116,264	21.1	23.3	14.5	12.7	1.1	0.4	-1.1	0.5	1.0	0.7	-1.2	0.1	-1.1	0.4	1.1	0.2
IPI00789439	RAB5C	19 kDa protein	100.0%	7.9	1	1	2	2	1,979,170	2,274,565	1,825,955	2,052,780	186,324	237,468	118,246	116,264	21.1	23.3	14.5	12.7	1.1	0.4	-1.1	0.5	1.0	0.7	-1.2	0.1	-1.1	0.4	1.1	0.2
				QASPNIVIALAGNK	2	99.9%	2																									
IPI00016342	RAB7A	Ras-related protein Rab-7a	100.0%	28.5	5	5	7	1	18,310,583	17,597,464	18,571,767	19,589,502	927,130	434,311	942,553	533,412	11.3	5.5	11.4	6.1	-1.0	0.5	1.0	0.8	1.1	0.3	1.1	0.4	1.1	0.02	1.1	0.4
				ATIGADFLTK	2	98.3%	1																									
				EAINVEQAFQTIAR	2	100.0%	1																									
				FQSLGVAFYR	2	98.5%	2																									
				LVTMQIWDTAGQER	2	100.0%	2																									
				NNIPYFETSAK	2	93.6%	1																									
IPI00016346	PROSC	Proline synthetase co-transcribed homolog (Bacterial), isoform CRA_b	100.0%	14.2	3	3	3	4	2,758,065	3,169,277	3,047,264	3,100,947	240,988	323,004	243,917	97,716	19.5	22.8	17.9	7.1	1.1	0.3	1.1	0.4	1.1	0.2	-1.0	0.8	-1.0	0.8	1.0	0.8
IPI00902466	PROSC	cDNA FLJ11861 fis, clone HEMBA1006885, highly similar to Proline synthetase co-t	100.0%	18.7	3	3	3	4	2,758,065	3,169,277	3,047,264	3,100,947	240,988	323,004	243,917	97,716	19.5	22.8	17.9	7.1	1.1	0.3	1.1	0.4	1.1	0.2	-1.0	0.8	-1.0	0.8	1.0	0.8
IPI00983028	PROSC	Uncharacterized protein	100.0%	32.1	3	3	3	4	2,758,065	3,169,277	3,047,264	3,100,947	240,988	323,004	243,917	97,716	19.5	22.8	17.9	7.1	1.1	0.3	1.1	0.4	1.1	0.2	-1.0	0.8	-1.0	0.8	1.0	0.8
IPI00984829	PROSC	Protein	100.0%	18.0	3	3	3	4	2,758,065	3,169,277	3,047,264	3,100,947	240,988	323,004	243,917	97,716	19.5	22.8	17.9	7.1	1.1	0.3	1.1	0.4	1.1	0.2	-1.0	0.8	-1.0	0.8	1.0	0.8
				HGLPPSETIAIVEHINAK	3	99.9%	1																									
				ILSLCPEIK	2	84.4%	1																									
				LMAVPNLFMLETVDSVK	2	100.0%	1																									
IPI00016513	RAB10	Ras-related protein Rab-10	100.0%	19.0	3	3	4	1	5,395,554	5,848,294	6,217,462	6,148,528	421,884	177,787	362,829	84,186	17.5	6.8	13.1	3.1	1.1	0.4	1.2	0.2	1.1	0.1	1.1	0.4	1.1	0.2	-1.0	0.9
				AFLTLAEDILR	2	100.0%	2																									
				GAMGIMLVYDITNGK	2	85.8%	1																									
				NIDEHANEDVER	2	99.8%	1																									
IPI00973950	AK3	HCG2031840, isoform CRA_c	98.3%	5.3	1	1	1	2	5,776,230	7,228,550	5,597,865	8,298,700	514,431	483,031	578,489	464,240	19.9	14.9	23.1	12.5	1.3	0.07	-1.0	0.8	1.4	0.007	-1.3	0.06	1.1	0.1	1.5	0.007
IPI00016568	AK4	Adenylate kinase isoenzyme 4, mitochondrial	98.3%	4.0	1	1	1	2	5,776,230	7,228,550	5,597,865	8,298,700	514,431	483,031	578,489	464,240	19.9	14.9	23.1	12.5	1.3	0.07	-1.0	0.8	1.4	0.007	-1.3	0.06	1.1	0.1	1.5	0.007
				LMMSELENR	2	98.3%	1																									
IPI00745343	LOC100130932	Small nuclear ribonucleoprotein G-like protein	99.8%	17.1	2	2	2	5	1,733,422	1,616,946	1,856,124	1,894,730	121,404	91,112	57,907	128,477	15.7	12.6	7.0	15.2	-1.1	0.5	1.1	0.4	1.1	0.4	1.1	0.06	1.2	0.1	1.0	0.8
IPI00016572	SNRPG	Small nuclear ribonucleoprotein G	99.8%	17.1	2	2	2	5	1,733,422	1,616,946	1,856,124	1,894,730	121,404	91,112	57,907	128,477	15.7	12.6	7.0	15.2	-1.1	0.5	1.1	0.4	1.1	0.4	1.1	0.06	1.2	0.1	1.0	0.8
IPI00924895	SNRPG	SNRPG protein	99.8%	20.3	2	2	2	5	1,733,422	1,616,946	1,856,124	1,894,730	121,404	91,112	57,907	128,477	15.7	12.6	7.0	15.2	-1.1	0.5	1.1	0.4	1.1	0.4	1.1	0.06	1.2	0.1	1.0	0.8
IPI00925251	SNRPG	Uncharacterized protein	99.8%	15.1	2	2	2	5	1,733,422	1,616,946	1,856,124	1,894,730	121,404	91,112	57,907	128,477	15.7	12.6	7.0	15.2	-1.1	0.5	1.1	0.4	1.1	0.4	1.1	0.06	1.2	0.1	1.0	0.8
IPI01015663	SNRPG	8 kDa protein	99.8%	19.1	2	2	2	5	1,733,422	1,616,946	1,856,124	1,894,730	121,404	91,112	57,907	128,477	15.7	12.6	7.0	15.2	-1.1	0.5	1.1	0.4	1.1	0.4	1.1	0.06	1.2	0.1	1.0	0.8
				GNSIIMLEALER	2	99.9%	1																									
				GNSIIMLEALERV	2	98.8%	1																									
IPI00016605	C1orf123	UPF0587 protein C1orf123	98.2%	14.4	1	1	1	2	3,171,870	3,073,785	3,243,710	3,651,960	261,208	134,596	323,484	132,788	18.4	9.8	22.3	8.1	-1.0	0.7	1.0	0.9	1.2	0.1	1.1	0.6	1.2	0.02	1.1	0.3
IPI00514522	C1orf123	Chromosome 1 open reading frame 123	98.2%	16.8	1	1	1	2	3,171,870	3,073,785	3,243,710	3,651,960	261,208	134,596	323,484	132,788	18.4	9.8	22.3	8.1	-1.0	0.7	1.0	0.9	1.2	0.1	1.1	0.6	1.2	0.02	1.1	0.3
				ENSIEILSSTIKPYNAEDNENFK	3	97.0%	1																									
IPI00016610	PCBP1	Poly(rC)-binding protein 1	100.0%	45.5	11	13	19	1	46,173,061	47,715,815	46,568,222	54,681,566	3,795,441	1,720,617	2,698,171	1,809,468	18.4	8.1	13.0	7.4	1.0	0.7	1.0	0.9	1.2	0.08	-1.0	0.7	1.1	0.02	1.2	0.04
				AFAMIIDK	2	94.2%	1																									
				AITIAGVPQSVTECVK	2	100.0%	2																									
				ESTGAQVQVAGDMLPNSTER	2	100.0%	2																									
				ESTGAQVQVAGDMLPNSTER	3	99.9%	1																									
				EVGSIIGK	2	94.3%	1																									
				IANPVEGSSGR	2	100.0%	3																									
				IITLTGPTNAIFK	2	100.0%	2																									
				INISEGNCPER	2	100.0%	2																									
				LVVPATQCGSLIGK	2	100.0%	1																									
				QICLVMLETLSQSPQGR	2	99.4%	1																									
				QVTITGSAASISLAQYLINAR	2	100.0%	1																									
				QVTITGSAASISLAQYLINAR	3	100.0%	1																									
				VMTIPYQPMPASSPVICAGGQDR	2	100.0%	1																									
IPI00016613	CSNK2A1	CSNK2A1 protein	100.0%	8.6	3	3	3	3	14,094,353	13,934,973	14,061,067	16,354,173	1,296,677	785,630	936,917	497,348	20.6	12.6	14.9	6.8	-1.0	0.9	-1.0	1	1.2	0.2	1.0	0.9	1.2	0.03	1.2	0.06
IPI00741317	CSNK2A1	Uncharacterized protein	100.0%	8.8	3	3	3	3	14,094,353	13,934,973	14,061,067	16,354,173	1,296,677	785,630	936,917	497,348	20.6	12.6	14.9	6.8	-1.0	0.9	-1.0	1	1.2	0.2	1.0	0.9	1.2	0.03	1.2	0.06
IPI00744507	CSNK2A1	Casein kinase II subunit alpha	100.0%	8.7	3	3	3	3	14,094,353	13,934,973	14,061,067	16,354,173	1,296,677	785,630	936,917	497,348	20.6	12.6	14.9	6.8	-1.0	0.9	-1.0	1	1.2	0.2	1.0	0.9	1.2	0.03	1.2	0.06
				FNDILGR	2	98.7%	1																									
				QLYQTLTDYDIR	2	98.6%	1																									
				TPALVFEHVNNTDFK	3	99.9%	1																									
IPI00016621	AP2A2	isoform 2 of AP-2 complex subunit alpha-2	100.0%	8.6	5	5	5	2	4,447,707	4,108,621	4,349,740	4,856,567	318,227	166,316	265,930	117,222	16.0	9.1	13.7	5.4	-1.1	0.4	-1.0	0.8	1.1	0.3	1.1	0.5	1.2	0.006	1.1	0.1
IPI00914938	AP2A2	isoform 1 of AP-2 complex subunit alpha-2	100.0%	8.6	5	5	5	2	4,447,707	4,108,621	4,349,740	4,856,567	318,227	166,316	265,930	117,222	16.0	9.1	13.7	5.4	-1.1	0.4	-1.0	0.8	1.1	0.3	1.1	0.5	1.2	0.006	1.1	0.1
				EMAEAFAGEIPK	2	96.0%	1																									

				EMAEAFAGEIPKVLVAGDTMDSVK	3	97.3%	1																										
				IIGFGSALLEEVDPNPANFVGAGIIHTK	3	100.0%	1																										
				THIETVINALK	2	86.0%	1																										
				VGGYILGEFGNLIAGDPR	2	100.0%	1																										
IPI00016626	MTAP	Uncharacterized protein	100.0%	15.2	1	1	1	1	1,216,855	1,248,940	1,125,650	1,223,210	74,014	103,675	115,490	61,757	13.6	18.6	22.9	11.3	1.0	0.8	-1.1	0.5	1.0	0.9	-1.1	0.4	-1.0	0.8	1.1	0.5
				TWGADVINMTTVPEVVLAK	2	100.0%	1																										
IPI00016634	C20orf11	Protein C20orf11	99.3%	9.7	1	1	1	1	789,420	854,293	939,166	910,414	79,211	125,982	166,133	55,384	22.4	33.0	39.6	13.6	1.1	0.7	1.2	0.4	1.2	0.2	1.1	0.7	1.1	0.7	-1.0	0.9
				GQIQEAIALINSLHPELLDTNR	3	99.3%	1																										
IPI00016637	OXSM	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	99.9%	2.6	1	1	1	2	1,203,055	1,037,935	1,165,005	1,592,810	44,945	85,067	109,599	166,344	8.4	18.3	21.0	23.4	-1.2	0.1	-1.0	0.8	1.3	0.08	1.1	0.4	1.5	0.02	1.4	0.06
IPI00922369	OXSM	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial isoform 2 precursor	99.9%	3.2	1	1	1	2	1,203,055	1,037,935	1,165,005	1,592,810	44,945	85,067	109,599	166,344	8.4	18.3	21.0	23.4	-1.2	0.1	-1.0	0.8	1.3	0.08	1.1	0.4	1.5	0.02	1.4	0.06
				DHAYALAVSSTK	2	99.7%	1																										
IPI00016670	LAMTOR1	Ragulator complex protein LAMTOR1	96.3%	8.1	1	1	1	5	1,024,706	1,081,478	1,000,402	1,083,054	146,295	85,080	110,690	91,822	31.9	17.6	24.7	19.0	1.1	0.7	-1.0	0.9	1.1	0.7	-1.1	0.6	1.0	1	1.1	0.6
IPI00980723	LAMTOR1	Conserved hypothetical protein	96.3%	8.1	1	1	1	5	1,024,706	1,081,478	1,000,402	1,083,054	146,295	85,080	110,690	91,822	31.9	17.6	24.7	19.0	1.1	0.7	-1.0	0.9	1.1	0.7	-1.1	0.6	1.0	1	1.1	0.6
IPI01010893	LAMTOR1	Protein	96.3%	16.5	1	1	1	5	1,024,706	1,081,478	1,000,402	1,083,054	146,295	85,080	110,690	91,822	31.9	17.6	24.7	19.0	1.1	0.7	-1.0	0.9	1.1	0.7	-1.1	0.6	1.0	1	1.1	0.6
IPI01013627	LAMTOR1	11 kDa protein	96.3%	13.1	1	1	1	5	1,024,706	1,081,478	1,000,402	1,083,054	146,295	85,080	110,690	91,822	31.9	17.6	24.7	19.0	1.1	0.7	-1.0	0.9	1.1	0.7	-1.1	0.6	1.0	1	1.1	0.6
IPI01014026	LAMTOR1	16 kDa protein	96.3%	9.2	1	1	1	5	1,024,706	1,081,478	1,000,402	1,083,054	146,295	85,080	110,690	91,822	31.9	17.6	24.7	19.0	1.1	0.7	-1.0	0.9	1.1	0.7	-1.1	0.6	1.0	1	1.1	0.6
				TDEQALLSSILAK	2	96.3%	1																										
IPI00016703	DHCR24	Delta(24)-sterol reductase	95.4%	2.5	1	1	1	4	1,738,460	1,874,603	1,738,610	2,072,568	183,179	90,910	166,506	88,176	23.6	10.8	21.4	9.5	1.1	0.5	1.0	1	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.1
IPI01008932	DHCR24	cDNA FLJ53870, highly similar to 24-dehydrocholesterol reductase	95.4%	2.7	1	1	1	4	1,738,460	1,874,603	1,738,610	2,072,568	183,179	90,910	166,506	88,176	23.6	10.8	21.4	9.5	1.1	0.5	1.0	1	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00922718	DHCR24	cDNA FLJ53131, highly similar to 24-dehydrocholesterol reductase	95.4%	5.4	1	1	1	4	1,738,460	1,874,603	1,738,610	2,072,568	183,179	90,910	166,506	88,176	23.6	10.8	21.4	9.5	1.1	0.5	1.0	1	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00922928	DHCR24	cDNA FLJ52052, highly similar to 24-dehydrocholesterol reductase	95.4%	4.3	1	1	1	4	1,738,460	1,874,603	1,738,610	2,072,568	183,179	90,910	166,506	88,176	23.6	10.8	21.4	9.5	1.1	0.5	1.0	1	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.1
				LGCQDAFPEVYDK	2	95.4%	1																										
IPI00016709	CACNA1C	isoform 1 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00216095	CACNA1C	isoform 2 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00384621	CACNA1C	Voltage-gated L-type calcium channel Cav1.2 alpha 1 subunit, splice variant 9*	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00607583	CACNA1C	isoform 24 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00744784	CACNA1C	isoform 34 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00793099	CACNA1C	isoform 21 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00793792	CACNA1C	isoform 27 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00794300	CACNA1C	isoform 12 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00794357	CACNA1C	isoform 25 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00797606	CACNA1C	isoform 33 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00798235	CACNA1C	isoform 32 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827513	CACNA1C	isoform 3 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827543	CACNA1C	isoform 30 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827553	CACNA1C	isoform 20 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827578	CACNA1C	isoform 31 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827633	CACNA1C	isoform 15 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827681	CACNA1C	isoform 26 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827766	CACNA1C	isoform 18 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827775	CACNA1C	isoform 11 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827851	CACNA1C	isoform 7 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827855	CACNA1C	isoform 29 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827887	CACNA1C	isoform 8 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827942	CACNA1C	isoform 9 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827956	CACNA1C	isoform 13 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00827998	CACNA1C	isoform 14 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00828000	CACNA1C	isoform 22 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00828035	CACNA1C	isoform 23 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00828116	CACNA1C	isoform 10 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00828128	CACNA1C	isoform 4 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00828174	CACNA1C	Uncharacterized protein	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00828206	CACNA1C	isoform 6 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00828210	CACNA1C	isoform 19 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00853140	CACNA1C	voltage-dependent L-type calcium channel subunit alpha-1C isoform 22	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00900275	CACNA1C	isoform 35 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00954938	CACNA1C	voltage-dependent L-type calcium channel subunit alpha-1C isoform 21	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI01009352	CACNA1C	isoform 5 of Voltage-dependent L-type calcium channel subunit alpha-1C	98.1%	0.8	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
IPI00977469	LOC100510450	voltage-dependent L-type calcium channel subunit alpha-1C-like, partial	98.1%	2.1	1	1	1	37	141,208	136,540	144,365	140,031	12,006	4,074	9,786	5,415	19.0	6.7	15.2	8.7	-1.0	0.7	1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.6	-1.0	0.7
				DAGQDRAGGEEDAGCVR	3	98.1%	1																										
IPI00016746	CBFB	isoform 1 of Core-binding factor subunit beta	98.9%	7.1	1	1	1	2	2,103,965	2,083,235	2,102,670	2,144,880	102,837	183,493	226,078	98,656	10.9	19.7	24.0	10.3	-1.0	0.9	-1.0	1	1.0	0.8	1.0	0.9	1.0	0.8	1.0	0.9
IPI00024871	CBFB	isoform 2 of Core-binding factor subunit beta	98.9%	7.0	1	1	1	2	2,103,965	2,083,235	2,102,670	2,144,880	102,837	183,493	226,078	98,656	10.9	19.7	24.0	10.3	-1.0	0.9	-1.0	1	1.0	0.8	1.0	0.9	1.0	0.8	1.0	0.9
				APMILNGVCVIWK	2	98.9%	1																										
IPI00148061	LDHAL6A	L-lactate dehydrogenase A-like 6A	100.0%	2.7	1	1	2	2	11,377,133	11,514,900	9,385,167	12,970,467	1,762,296	793,869	1,042,472	474,692	34.6	15.4	24.8	8.2	1.0	0.9	-1.2	0.4	1.1	0.4	-1.2	0.1	1.1	0.2	1.4	0.01
IPI00016768	LDHAL6B	L-lactate dehydrogenase A-like 6B	100.0%	2.4	1	1	2	2	11,377,133	11,514,900	9,385,167	12,970,467	1,762,296	793,869	1,042,472	474,692	34.6	15.4	24.8	8.2	1.0	0.9	-1.2	0.4	1.1	0.4	-1.2	0.1	1.1	0.2	1.4	0.01
				LVIITAGAR	2	99.7%	2																										
IPI00909484	-	cDNA FLJ54776, highly similar to Cell division control protein 42 homolog	100.0%	29.7	6	7	9	2	22,801,083	24,754,621	24,248,445	27,058,853	1,393,304	674,938	2,130,247	729,238	13.7	6.1	19.6	6.0	1.1	0.2	1.1	0.6	1.2	0.03	-1.0	0.8	1.1	0.05	1.1	0.3
IPI00016786	CDC42	isoform 2 of Cell division control protein 42 homolog	100.0%	36.7	6	7	9	2	22,801,083	24,754,621	24,248,445	27,058,853	1,393,304	674,938	2,130,247	729,238	13.7	6.1	19.6	6.0	1.1	0.2	1.1	0.6	1.2	0.03	-1.0	0.8	1.1	0.05	1.1	0.3
				NVFDEAILAALEPPEPK	2	97.4%	1																										
				NVFDEAILAALEPPEPK	3	100.0%	1																										
				QKPITPETAEK	3	84.6%	1																										
				TCLLISYTTNK	2	99.0%	1																										
				TPFLLVGTQIDLR	2	100.0%	2																										
				TPFLLVGTQIDLRDDPSTIEK	3	92.4%	1																										
				YVECSALTQK	2	100.0%	2																										
IPI00016801	GLUD1	Glutamate dehydrogenase 1, mitochondrial	100.0%	24.9	11	12	12	2	14,539,927	15,927,383	15,052,060	17,451,955	1,326,501	434,369	1,198,422	519,985	20.4	6.1	17.8	6.7	1.1	0.4	1.0	0.8	1.2	0.09	-1.1	0.5	1.1	0.05	1.2	0.1
IPI01014382	GLUD1	cDNA FLJ55493, highly similar to Glutamate dehydrogenase 1, mitochondrial	100.0%	27.3	11	12	12	2	14,539,927	15,927,383	15,052,060	17,451,955	1,326,501	434,369	1,198,422	519,985	20.4	6.1	17.8	6.7	1.1	0.4	1.0	0.8	1.2	0.09	-1.1	0.5	1.1	0.05	1.2	0.1
				ALASLMTYK	2	99.8%	1																										
				DDGSWEVIEGYR	2	100.0%	1																										
				DSNYHLLMSVQESLER	2	95.3%	1																										
				DSNYHLLMSVQESLER	3	99.9%	1																										
				GFIGPGIDVPAPDMSTGER	2	100.0%	1																										
				HGGTIPIVPTAEFQDR	2	100.0%	1																										
				IIAEGANGPTTPEADKIFLER	3	100.0%	1																										
				MVEGFFDR	2	99.2%	1																										
				NLNHVSYGR	2	99.9%	1																										
				TAAYVNAIEK	2	99.7%	1																										
				YNLGLDLR	2	100.0%	1																										
				YSTDVSVDEVK	2	100.0%	1																										
IPI00016832	PSMA1	isoform Short of Proteasome subunit alpha type-1	100.0%	22.8	5	5	6	2	7,133,558	7,724,298	6,960,645	7,973,699	375,721	205,406	242,547	407,748	11.8	6.0	7.8	11.4	1.1	0.2	-1.0	0.7	1.1	0.2	-1.1	0.04	1.0	0.6	1.1	0.07
IPI00472442	PSMA1	isoform Long of Proteasome subunit alpha type-1	100.0%	22.3	5	5	6	2	7,133,558	7,724,298	6,960,645	7,973,699	375,721	205,406	242,547	407,748	11.8	6.0	7.8	11.4	1.1	0.2	-1.0	0.7	1.1	0.2	-1.1	0.04	1.0	0.6	1.1	0.07
				DLEFTIYDDDDVSPFLEGLEERPQR	3	100.0%	1																										
				DLEFTIYDDDDVSPFLEGLEERPQRK	3	98.2%	1																										
				ETLPAEQDLTTK	2	100.0%	2																										
				IHQIEYAMEAVK	2	99.9%	1																										
				THAVLVALKR	2	85.2%	1																										
IPI00016862	GSR	isoform Mitochondrial of Glutathione reductase, mitochondrial	100.0%	23.0	7	7	8	3	10,107,090	10,059,042	9,950,718	11,528,005	546,882	406,209	458,159	384,636	12.1	9.0	10.3	7.5	-1.0	0.9	-1.0	0.8	1.1	0.07	-1.0	0.9	1.1	0.03	1.2	0.03
IPI00759575	GSR	isoform Cytoplasmic of Glutathione reductase, mitochondrial	100.0%	25.1	7	7	8	3	10,107,090	10,059,042	9,950,718	11,528,005	546,882	406,209	458,159	384,636	12.1	9.0	10.3	7.5	-1.0	0.9	-1.0	0.8	1.1	0.07	-1.0	0.9	1.1	0.03	1.2	0.03
IPI00953236	GSR	glutathione reductase, mitochondrial isoform 2 precursor	100.0%	24.3	7	7	8	3	10,107,090	10,059,042	9,950,718	11,528,005	546,882	406,209	458,159	384,636	12.1	9.0	10.3	7.5	-1.0	0.9	-1.0	0.8	1.1	0.07	-1.0	0.9	1.1	0.03	1.2	0.03
				ADFDNTVAIHPTSSEELVTLR	3	100.0%	1																										
				ALLTPVAIAAGR	2	85.6%	1																										
				LGGTCVNVGCVPK	2	100.0%	1																										
				LGIQTDDKGHIIVDEFQNTNVK	3	100.0%	1																										
				LNAIYQNNLTK	2	100.0%	2																										
				QEPQPQGPPPAAGAVASYDYLVIGGGSGGLASAR	3	98.8%	1																										
				YGIENVK	2	88.7%	1																										
IPI00023526	RAB6A	isoform 1 of Ras-related protein Rab-6A	93.7%	5.8	1	1	1	9	849,137	976,157	650,217	669,107	184,536	252,202	83,339	79,721	48.6	57.8	28.7	26.6	1.1	0.7	-1.3	0.4	-1.3	0.4	-1.5	0.3	-1.5	0.3	1.0	0.9
IPI00217943	RAB6A	isoform 2 of Ras-related protein Rab-6A	93.7%	5.8	1	1	1	9	849,137	976,157	650,217	669,107	184,536	252,202	83,339	79,721	48.6	57.8	28.7	26.6	1.1	0.7	-1.3	0.4	-1.3	0.4	-1.5	0.3	-1.5	0.3	1.0	0.9
IPI00872108	RAB6A	Protein	93.7%	6.9	1	1	1	9	849,137	976,157	650,217	669,107	184,536	252,202	83,339	79,721	48.6	57.8	28.7	26.6	1.1	0.7	-1.3	0.4	-1.3	0.4	-1.5	0.3	-1.5	0.3	1.0	0.9
IPI01009243	RAB6A	RAB6A protein	93.7%	5.8	1	1	1	9	849,137	976,157	650,217	669,107	184,536	252,202	83,339	79,721	48.6	57.8	28.7	26.6	1.1	0.7	-1.3	0.4	-1.3	0.4	-1.5	0.3	-1.5	0.3	1.0	0.9
IPI01013015	RAB6A	cDNA FLJ52284, highly similar to Ras-related protein Rab-6A	93.7%	6.9	1	1	1	9	849,137	976,157	650,217	669,107	184,536	252,202	83,339	79,721	48.6	57.8	28.7	26.6	1.1	0.7	-1.3	0.4	-1.3	0.4	-1.5	0.3	-1.5	0.3	1.0	0.9
IPI00016891	RAB6B	Ras-related protein Rab-6B	93.7%	5.8	1	1	1	9	849,137	976,157	650,217	669,107	184,536	252,202	83,339	79,721	48.6	57.8	28.7	26.6	1.1	0.7	-1.3	0.4	-1.3	0.4	-1.5	0.3	-1.5	0.3	1.0	0.9
IPI00945534	RAB6B	14 kDa protein	93.7%	9.7	1	1	1	9	849,137	976,157	650,217	669,107	184,536	252,202	83,339	79,721	48.6	57.8	28.7	26.6	1.1	0.7	-1.3	0.4	-1.3	0.4	-1.5	0.3	-1.5	0.3	1.0	0.9
IPI00946019	RAB6B	cDNA FLJ57728, highly similar to Ras-related protein Rab-6B	93.7%	6.2	1	1	1	9	849,137	976,157	650,217	669,107	184,536	252,202	83,339	79,721	48.6	57.8	28.7	26.6	1.1	0.7	-1.3	0.4	-1.3	0.4	-1.5	0.3	-1.5	0.3	1.0	0.9
IPI00946537	RAB6B	Uncharacterized protein	93.7%	14.5	1	1	1	9	849,137	976,157	650,217	669,107	184,536	252,202	83,339	79,721	48.6	57.8	28.7	26.6	1.1	0.7	-1.3	0.4	-1.3	0.4	-1.5	0.3	-1.5	0.3	1.0	0.9
				GSDVIIMLVGNK	2	93.7%	1																										
IPI00016910	EIF3CL;EIF3C	Eukaryotic translation initiation factor 3 subunit C	100.0%	8.1	6	6	6	8	4,410,362	4,472,763	4,194,635	4,927,477	232,335	143,168	260,618	117,559	11.8	7.2	13.9	5.3	1.0	0.8	-1.1	0.6	1.1	0.08	-1.1	0.4	1.1	0.04	1.2	0.03
IPI00646839	EIF3CL;EIF3C	Uncharacterized protein	100.0%	8.1	6	6	6	8	4,410,362	4,472,763	4,194,635	4,927,477	232,335	143,168	260,618	117,559	11.8	7.2	13.9	5.3	1.0	0.8	-1.1	0.6	1.1	0.08	-1.1	0.4	1.1	0.04	1.2	0.03
IPI00910003	EIF3CL;EIF3C	88 kDa protein	100.0%	9.7	6	6	6	8	4,410,362	4,472,763	4,194,635	4,927,477	232,335	143,168	260,618	117,559	11.8	7.2	13.9	5.3	1.0	0.8	-1.1	0.6	1.1	0.08	-1.1	0.4	1.1	0.04	1.2	0.03
IPI00922360	EIF3CL;EIF3C	cDNA FLJ54488, highly similar to Eukaryotic translation initiation factor 3 subunit 8	100.0%	9.3	6	6	6	8	4,410,362	4,472,763	4,194,635	4,927,477	232,335	143,168	260,618	117,559	11.8	7.2	13.9	5.3	1.0	0.8	-1.1	0.6	1.1	0.08	-1.1	0.4	1.1	0.04	1.2	0.03
IPI01009614	EIF3CL;EIF3C	cDNA FLJ55450, highly similar to Eukaryotic translation initiation factor 3 subunit 8	100.0%	8.2	6	6	6	8	4,410,362	4,472,763	4,194,635	4,927,477	232,335	143,168	260,618	117,559	11.8	7.2	13.9	5.3	1.0	0.8	-1.1	0.6	1.1	0.08	-1.1	0.4	1.1	0.04	1.2	0.03
IPI01011218	EIF3CL;EIF3C	Uncharacterized protein	100.0%	9.3	6	6	6	8	4,410,362	4,472,763	4,194,635	4,927,477	232,335	143,168	260,618	117,559	11.8	7.2	13.9	5.3	1.0	0.8	-1.1	0.6	1.1	0.08	-1.1	0.4	1.1	0.04	1.2	0.03
IPI01013710	EIF3CL;EIF3C	cDNA FLJ53378, highly similar to Eukaryotic translation initiation factor 3 subunit 8	100.0%	9.7	6	6	6	8	4,410,362	4,472,763	4,194,635	4,927,477	232,335	143,168	260,618	117,559	11.8	7.2	13.9	5.3	1.0	0.8	-1.1	0.6	1.1	0.08	-1.1	0.4	1.1	0.04	1.2	0.03
IPI01013816	EIF3CL;EIF3C	104 kDa protein	100.0%	8.2	6	6	6	8	4,410,362	4,472,763	4,194,635	4,927,477	232,335	143,168	260,618	117,559	11.8	7.2	13.9	5.3	1.0	0.8	-1.1	0.6	1.1	0.08	-1.1	0.4	1.1	0.04	1.2	0.03
				ILADLEDYLNELWEDKEGK	3	99.6%	1																										
				KLNEILQAR	2	95.1%	1																										
				LGSLVENNER	2	99.9%	1																										
				QGTYGGYFR	2	89.1%	1																										
				TEPTAQQNLALQLAEK	2	100.0%	1																										
				TMVQLGICAFR	2	99.9%	1																										
IPI00016968	SDHC	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	97.1%	4.7	1	1	1	3	1,511,917	1,383,913	1,378,997	1,621,210	300,593	169,913	98,438	200,589	44.5	27.5	16.0	27.7	-1.1	0.7	-1.1	0.7	1.1	0.8	-1.0	1	1.2	0.4	1.2	0.3
IPI00655681	SDHC	succinate dehydrogenase cytochrome b560 subunit, mitochondrial isoform 4 precurs	97.1%	6.9	1	1	1	3	1,511,917	1,383,913	1,378,997	1,621,210	300,593	169,913	98,438	200,589	44.5	27.5	16.0	27.7	-1.1	0.7	-1.1	0.7	1.1	0.8	-1.0	1	1.2	0.4	1.2	0.3
IPI00943958	SDHC	succinate dehydrogenase cytochrome b560 subunit, mitochondrial isoform 3 precurs	97.1%	5.9	1	1	1	3	1,511,917	1,383,913	1,378,997	1,621,210	300,593	169,913	98,438	200,589	44.5	27.5	16.0	27.7	-1.1	0.7	-1.1	0.7	1.1	0.8	-1.0	1	1.2	0.4	1.2	0.3
				HLMWDLGK	2	97.1%	1																										
IPI00017163	HECW2	isoform 1 of E3 ubiquitin-protein ligase HECW2	98.6%	1.0	1	1	1	1	1,786,490	1,690,159	1,845,590	1,862,224	144,429	271,409	157,547	157,174	18.1	35.9	19.1	18.9	-1.1	0.8	1.0	0.8	1.0	0.7	1.1	0.6	1.1	0.6	1.0	0.9
				YSFFALLTDVLEIEIK	2	98.6%	1																										
IPI00017184	EHD1	EH domain-containing protein 1	100.0%	12.9	5	5	5	2	13,208,001	13,172,499	12,976,084	14,801,986	839,971	640,421	684,185	594,178	14.2	10.9	11.8	9.0	-1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.08
IPI00853165	EHD1	cDNA FLJ55347, highly similar to EH-domain-containing protein 1	100.0%	13.5	5	5	5	2	13,208,001	13,172,499	12,976,084	14,801,986	839,971	640,421	684,185	594,178	14.2	10.9	11.8	9.0	-1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.08
				HLIEQDFPGMR	2	100.0%	1																										
				LADVDKDGLLDDEEFALANHLIK	3	100.0%	1																										
				LNAFGNAFLNR	2	99.9%	1																										
				MQELLQTQDFSK	2	100.0%	1																										
				QEESLMPSQVVK	2	99.9%	1																										
IPI00017256	RSU1	Ras suppressor protein 1	95.7%	9.4	1	1	1	3	117,269	114,908	141,861	120,751	13,265	12,143	17,654	7,452	25.3	23.6	27.8	13.8	-1.0	0.9	1.2	0.3	1.0	0.8	1.2	0.2	1.1	0.7	-1.2	0.3
IPI00377066	RSU1	ras suppressor protein 1 isoform 2	95.7%	11.6	1	1	1	3	117,269	114,908	141,861	120,751	13,265	12,143	17,654	7,452	25.3	23.6	27.8	13.8	-1.0	0.9	1.2	0.3	1.0	0.8	1.2	0.2	1.1	0.7	-1.2	0.3
IPI00847168	RSU1	RSU1 protein (Fragment)	95.7%	9.3	1	1	1	3	117,269	114,908	141,861	120,751	13,265	12,143	17,654	7,452	25.3	23.6	27.8	13.8	-1.0	0.9	1.2	0.3	1.0	0.8	1.2	0.2	1.1	0.7	-1.2	0.3
				AENNPWVTPIADQFQLGVSHVFEYIR	3	95.7%	1																										

IPI00017283	IARS2	Isoleucyl-tRNA synthetase, mitochondrial	100.0%	7.6	6	6	6	1	18,018,277	20,495,245	19,941,781	22,513,036	2,064,598	586,300	1,918,189	1,491,756	25.6	6.4	21.5	14.8	1.1	0.3	1.1	0.5	1.2	0.1	-1.0	0.8	1.1	0.3	1.1	0.3
				AVLEEGTDVVIK	2	99.9%	1																									
				FLINLEGGDIR	2	96.6%	1																									
				QQPDTELEIQQK	2	99.7%	1																									
				QWFINITDIK	2	99.3%	1																									
				SCQTALVEILDVIVR	2	99.9%	1																									
				TALAEAELEYNPEHVSR	2	88.9%	1																									
IPI00017290	SMEK1	isoform 5 of Serine/threonine-protein phosphatase 4 regulatory subunit 3A	100.0%	2.2	1	1	1	4	2,057,000	2,037,400	1,849,771	2,134,514	124,005	89,582	69,867	117,665	13.5	9.8	8.5	12.3	-1.0	0.9	-1.1	0.2	1.0	0.7	-1.1	0.1	1.0	0.5	1.2	0.07
IPI00414323	SMEK2	isoform 1 of Serine/threonine-protein phosphatase 4 regulatory subunit 3B	100.0%	1.4	1	1	1	4	2,057,000	2,037,400	1,849,771	2,134,514	124,005	89,582	69,867	117,665	13.5	9.8	8.5	12.3	-1.0	0.9	-1.1	0.2	1.0	0.7	-1.1	0.1	1.0	0.5	1.2	0.07
IPI00551045	SMEK2	isoform 2 of Serine/threonine-protein phosphatase 4 regulatory subunit 3B	100.0%	1.5	1	1	1	4	2,057,000	2,037,400	1,849,771	2,134,514	124,005	89,582	69,867	117,665	13.5	9.8	8.5	12.3	-1.0	0.9	-1.1	0.2	1.0	0.7	-1.1	0.1	1.0	0.5	1.2	0.07
IPI00746325	SMEK2	isoform 3 of Serine/threonine-protein phosphatase 4 regulatory subunit 3B	100.0%	1.6	1	1	1	4	2,057,000	2,037,400	1,849,771	2,134,514	124,005	89,582	69,867	117,665	13.5	9.8	8.5	12.3	-1.0	0.9	-1.1	0.2	1.0	0.7	-1.1	0.1	1.0	0.5	1.2	0.07
				AESDGSLLLESK	2	99.9%	1																									
IPI00017292	CTNNB1	isoform 1 of Catenin beta-1	100.0%	14.1	8	9	10	2	23,068,879	24,348,896	22,326,458	26,368,432	2,799,184	1,318,297	2,006,458	1,198,497	27.1	12.1	20.1	10.2	1.1	0.7	-1.0	0.8	1.1	0.3	-1.1	0.4	1.1	0.3	1.2	0.1
IPI00927799	CTNNB1	cDNA FLJ57878, highly similar to Beta-catenin	100.0%	14.2	8	9	10	2	23,068,879	24,348,896	22,326,458	26,368,432	2,799,184	1,318,297	2,006,458	1,198,497	27.1	12.1	20.1	10.2	1.1	0.7	-1.0	0.8	1.1	0.3	-1.1	0.4	1.1	0.3	1.2	0.1
				AAMFPETLDEGMQIPSTQFDAAHPTNVQR	3	100.0%	1																									
				HQEAEMAQNAVR	2	100.0%	1																									
				LHYGLPVVVK	2	97.4%	1																									
				LHYGLPVVVK	3	99.6%	1																									
				LIILASGGPQALVNIMR	2	99.9%	2																									
				LLNDEDQVVVNK	2	100.0%	1																									
				LSVELTSSLFR	2	99.8%	1																									
				LVQLLVR	2	96.3%	1																									
				TMQNTNDVETAR	2	95.9%	1																									
IPI00017297	SNHG4;MATR3	Matrin-3	100.0%	24.0	14	15	20	2	18,875,643	18,910,004	18,474,401	20,215,936	922,363	484,069	1,155,015	716,718	10.9	5.7	14.0	7.9	1.0	1	-1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.2	1.1	0.2
IPI00789551	SNHG4;MATR3	Uncharacterized protein	100.0%	22.7	14	15	20	2	18,875,643	18,910,004	18,474,401	20,215,936	922,363	484,069	1,155,015	716,718	10.9	5.7	14.0	7.9	1.0	1	-1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.2	1.1	0.2
				DLDELSRYPEDKITPENLPQILLQLK	3	98.0%	1																									
				DLSAAGIGLLAAATQSLSMPASLGR	2	100.0%	2																									
				DSFDDRGPSLNPVLDYDHGSR	3	95.6%	1																									
				GDADQASNILASFGLSAR	2	100.0%	2																									
				GDADQASNILASFGLSAR	3	100.0%	1																									
				GNLGAGNGNLQGPR	2	99.9%	1																									
				ITPENLPQILLQLK	2	100.0%	2																									
				KDGSASAAAKK	2	91.3%	1																									
				SFQQSSLSR	2	100.0%	1																									
				SQAFIEMETR	2	100.0%	2																									
				SQESGYYDR	2	99.9%	1																									
				TEEGPTLSYGR	2	99.9%	2																									
				VIHLSNLPHSGYSDSAVLK	3	100.0%	1																									
				VVHIMDFQR	3	99.9%	1																									
				YQLLQLVEPFGVISNHLILNK	3	100.0%	1																									
IPI00017303	MSH2	DNA mismatch repair protein Msh2	99.6%	3.3	2	2	2	3	137,752	131,042	122,137	143,856	13,795	6,710	10,465	7,227	22.4	11.5	19.2	11.2	-1.1	0.7	-1.1	0.4	1.0	0.7	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00893933	MSH2	Uncharacterized protein	99.6%	3.4	2	2	2	3	137,752	131,042	122,137	143,856	13,795	6,710	10,465	7,227	22.4	11.5	19.2	11.2	-1.1	0.7	-1.1	0.4	1.0	0.7	-1.1	0.5	1.1	0.2	1.2	0.1
IPI01014700	MSH2	cDNA FLJ51193, highly similar to DNA mismatch repair protein Msh2	99.6%	3.6	2	2	2	3	137,752	131,042	122,137	143,856	13,795	6,710	10,465	7,227	22.4	11.5	19.2	11.2	-1.1	0.7	-1.1	0.4	1.0	0.7	-1.1	0.5	1.1	0.2	1.2	0.1
				GVSTFMAEMLETASILR	2	98.4%	1																									
				LNLVEAFVEDAELR	2	99.6%	1																									
IPI00017305	RPS6KA1	Ribosomal protein S6 kinase alpha-1	93.2%	2.2	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI00477982	RPS6KA1	ribosomal protein S6 kinase alpha-1 isoform b	93.2%	2.2	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI00513863	RPS6KA1	Uncharacterized protein	93.2%	2.2	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI00640510	RPS6KA1	Uncharacterized protein	93.2%	2.2	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI00981144	RPS6KA1	Uncharacterized protein	93.2%	14.3	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI01011967	RPS6KA1	cDNA FLJ54535, highly similar to Ribosomal protein S6 kinase alpha-1	93.2%	2.5	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI00300321	RPS6KA2	isoform 1 of Ribosomal protein S6 kinase alpha-2	93.2%	2.2	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI00478653	RPS6KA2	isoform 2 of Ribosomal protein S6 kinase alpha-2	93.2%	2.1	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI00513934	RPS6KA2	Ribosomal protein S6 kinase, 90kDa, polypeptide 2	93.2%	9.6	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI00966051	RPS6KA2	ribosomal protein S6 kinase alpha-2 isoform b	93.2%	2.2	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI00967123	RPS6KA2	cDNA FLJ55331, highly similar to Ribosomal protein S6 kinase alpha-2	93.2%	2.5	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
IPI00967630	RPS6KA2	Uncharacterized protein	93.2%	12.8	1	1	1	12	260,619	248,014	259,623	279,008	33,012	18,667	25,559	9,089	28.3	16.8	22.0	7.3	-1.1	0.7	-1.0	1	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.5
				DLKPENILLDEEGHIK	3	93.2%	1																									
IPI00017334	PHB	Prohibitin	100.0%	56.6	11	14	18	1	29,805,176	30,660,215	31,247,060	34,088,155	2,127,658	855,318	1,847,201	970,045	16.0	6.2	13.2	6.4	1.0	0.7	1.0	0.6	1.1	0.1	1.0	0.8	1.1	0.03	1.1	0.2
				AAELIANSLATAGDGLIELR	2	99.9%	1																									
				AAELIANSLATAGDGLIELR	3	100.0%	1																									
				AAIISAEGDSK	2	100.0%	2																									
				AATFGLILDDVSLTHLTFGK	2	99.7%	1																									
				AATFGLILDDVSLTHLTFGK	3	99.9%	1																									
				DLQNVNITLR	2	100.0%	2																									
				FDAGELITQR	2	100.0%	2																									
				FGLALAVAGGVVNSALYNVDAGHR	3	99.9%	1																									
				IFTSIGEDYDER	2	100.0%	2																									
				ILFRPVASQLPR	2	98.5%	1																									
				ILFRPVASQLPR	3	100.0%	1																									
				NITYLPAGQSVLLQLPQ	3	100.0%	1																									
				VFESIGK	2	96.6%	1																									
				VLPSITTEILK	2	99.5%	1																									
IPI00017337	ANXA13	isoform A of Annexin A13	100.0%	51.9	13	14	17	2	112,892,563	116,771,834	106,942,859	135,184,428	########	5,553,878	########	5,329,200	27.0	10.6	23.1	8.8	1.0	0.8	-1.1	0.7	1.2	0.2	-1.1	0.4	1.2	0.04	1.3	0.05
IPI00465213	ANXA13	isoform B of Annexin A13	100.0%	45.9	13	14	17	2	112,892,563	116,771,834	106,942,859	135,184,428	########	5,553,878	########	5,329,200	27.0	10.6	23.1	8.8	1.0	0.8	-1.1	0.7	1.2	0.2	-1.1	0.4	1.2	0.04	1.3	0.05
				ASSPQGFDVDRDAK	2	94.6%	1																									
				ATFQAYQILIGKDIEEAIEEETSGDLQK	3	99.9%	1																									
				DIEEAIEEETSGDLQK	2	100.0%	1																									
				DIEEAIEEETSGDLQK	3	99.6%	1																									
				DLYDAGEGR	2	90.7%	1																									
				GAGTDEETLIR	2	100.0%	1																									
				GLGTDESVLIEVLCTR	2	100.0%	1																									
				GMGTNEAAIIEILSGR	2	100.0%	2																									
				LLVALLH	2	83.6%	1																									
				SDTSGDFRK	2	100.0%	2																									
				SELSGNFEK	2	99.4%	1																									
				SLESDVKGDTSGNLKK	3	85.1%	1																									
				TALALLDRPSEYAAR	2	97.6%	1																									
				WGTDELAFNEVLAK	2	100.0%	2																									
IPI00017339	SF3B4	Splicing factor 3B subunit 4	99.6%	3.3	1	1	1	1	1,166,056	1,385,801	1,079,144	1,476,807	156,462	96,918	45,784	212,409	30.0	15.6	9.5	32.2	1.2	0.3	-1.1	0.6	1.3	0.3	-1.3	0.02	1.1	0.7	1.4	0.1
				NQDATVYVGGLDEK	2	99.6%	1																									
IPI00017341	SF3A2	SF3A2 protein (Fragment)	99.4%	3.7	1	1	1	1	7,241,310	7,938,850	7,566,850	8,968,250	769,101	287,145	662,295	400,570	23.8	8.1	19.6	10.0	1.1	0.4	1.0	0.8	1.2	0.08	-1.0	0.6	1.1	0.07	1.2	0.1
				MEKPPAPPSLPAGPPGVK	3	99.4%	1																									
IPI00017344	RAB5B	Ras-related protein Rab-5B	100.0%	13.0	2	2	2	1	4,602,770	4,858,510	4,941,505	5,324,765	338,801	230,233	338,630	98,294	16.5	10.6	15.3	4.1	1.1	0.5	1.1	0.5	1.2	0.1	1.0	0.8	1.1	0.1	1.1	0.3
				QASPSIVIALAGNK	2	99.9%	1																									
				TAMNVNDLFLAIAK	2	99.9%	1																									
IPI00017367	RDX	Radixin, isoform CRA_a	100.0%	11.8	5	5	5	2	8,049,925	7,950,809	7,618,599	9,057,531	713,904	354,360	613,431	202,181	19.8	10.0	18.0	5.0	-1.0	0.9	-1.1	0.7	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.08
IPI00903145	RDX	Radixin	100.0%	12.2	5	5	5	2	8,049,925	7,950,809	7,618,599	9,057,531	713,904	354,360	613,431	202,181	19.8	10.0	18.0	5.0	-1.0	0.9	-1.1	0.7	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.08
				AFAAQEDLEK	2	99.2%	1																									
				FFPEDVSEELIQEITQR	3	96.5%	1																									
				IAQDLEMYGVNYFEIK	2	85.9%	1																									
				NQEQLAAELAEFTAK	2	100.0%	1																									
				QLQALSSELAQAR	2	99.9%	1																									
IPI00017373	RPA3	Replication protein A 14 kDa subunit	100.0%	41.3	3	4	5	2	4,575,568	4,642,095	4,764,428	5,443,765	397,010	119,949	425,006	210,751	19.4	5.8	20.0	8.7	1.0	0.9	1.0	0.8	1.2	0.09	1.0	0.8	1.2	0.01	1.1	0.2
IPI00894460	RPA3	Uncharacterized protein	100.0%	61.0	3	4	5	2	4,575,568	4,642,095	4,764,428	5,443,765	397,010	119,949	425,006	210,751	19.4	5.8	20.0	8.7	1.0	0.9	1.0	0.8	1.2	0.09	1.0	0.8	1.2	0.01	1.1	0.2
				IIHDFPQFYPLGIVQHD	3	100.0%	1																									
				MFILSDGEGK	2	100.0%	1																									
				NGTIELMEPLDEEISGIVEVVGR	2	100.0%	2																									
				NGTIELMEPLDEEISGIVEVVGR	3	100.0%	1																									
IPI00017375	SEC23A	Protein transport protein Sec23A	100.0%	9.8	5	5	5	2	14,202,583	14,369,352	14,073,589	16,289,831	1,020,300	541,152	761,362	501,778	16.1	8.4	12.1	6.9	1.0	0.9	-1.0	0.9	1.1	0.1	-1.0	0.8	1.1	0.03	1.2	0.04
IPI01011937	SEC23A	83 kDa protein	100.0%	10.2	5	5	5	2	14,202,583	14,369,352	14,073,589	16,289,831	1,020,300	541,152	761,362	501,778	16.1	8.4	12.1	6.9	1.0	0.9	-1.0	0.9	1.1	0.1	-1.0	0.8	1.1	0.03	1.2	0.04
				AVLNPLCQVDYR	2	91.1%	1																									
				HLLQAPVDDAQEILHSR	3	100.0%	1																									
				IMMFIGGPATQGPGMVVGDELK	2	99.5%	1																									
				ISGAIGPCVSLNSK	2	99.2%	1																									
				MGFGGTLEIK	2	99.6%	1																									
IPI00017376	SEC23B	Protein transport protein Sec23B	100.0%	10.8	6	6	6	2	17,101,344	16,950,249	16,891,160	19,911,857	1,227,688	766,335	1,348,378	779,647	16.1	10.1	17.9	8.8	-1.0	0.9	-1.0	0.9	1.2	0.09	-1.0	1	1.2	0.03	1.2	0.09
IPI00956024	SEC23B	protein transport protein Sec23B isoform 2	100.0%	11.1	6	6	6	2	17,101,344	16,950,249	16,891,160	19,911,857	1,227,688	766,335	1,348,378	779,647	16.1	10.1	17.9	8.8	-1.0	0.9	-1.0	0.9	1.2	0.09	-1.0	1	1.2	0.03	1.2	0.09
				AVLNPLCQVDYR	2	91.1%	1																									
				HYEMLANR	2	84.9%	1																									
				IAGAIGPCVSLNVK	2	97.2%	1																									
				IDMNLTDLLGELQRDPWPVTQGK	3	98.9%	1																									
				MVVPLACLLTPLK	2	92.4%	1																									
				PAQPQEHPFASSR	3	97.5%	1																									
IPI00017381	RFC4	Replication factor C subunit 4	99.2%	5.5	1	1	1	7	255,713	279,723	254,586	296,143	31,160	11,428	37,328	35,305	27.3	9.1	32.8	26.7	1.1	0.5	-1.0	1	1.2	0.4	-1.1	0.5	1.1	0.7	1.2	0.4
IPI00792595	RFC4	cDNA FLJ60688, highly similar to Replication factor C subunit 4	99.2%	6.6	1	1	1	7	255,713	279,723	254,586	296,143	31,160	11,428	37,328	35,305	27.3	9.1	32.8	26.7	1.1	0.5	-1.0	1	1.2	0.4	-1.1	0.5	1.1	0.7	1.2	0.4
IPI00795756	RFC4	Uncharacterized protein	99.2%	16.3	1	1	1	7	255,713	279,723	254,586	296,143	31,160	11,428	37,328	35,305	27.3	9.1	32.8	26.7	1.1	0.5	-1.0	1	1.2	0.4	-1.1	0.5	1.1	0.7	1.2	0.4
IPI00924737	RFC4	Uncharacterized protein	99.2%	21.1	1	1	1	7	255,713	279,723	254,586	296,143	31,160	11,428	37,328	35,305	27.3	9.1	32.8	26.7	1.1	0.5	-1.0	1	1.2	0.4	-1.1	0.5	1.1	0.7	1.2	0.4
IPI00925227	RFC4	10 kDa protein	99.2%	20.6	1	1	1	7	255,713	279,723	254,586	296,143	31,160	11,428	37,328	35,305	27.3	9.1	32.8	26.7	1.1	0.5	-1.0	1	1.2	0.4	-1.1	0.5	1.1	0.7	1.2	0.4
IPI00925397	RFC4	Uncharacterized protein	99.2%	12.0	1	1	1	7	255,713	279,723	254,586	296,143	31,160	11,428	37,328	35,305	27.3	9.1	32.8	26.7	1.1	0.5	-1.0	1	1.2	0.4	-1.1	0.5	1.1	0.7	1.2	0.4
IPI00925945	RFC4	Uncharacterized protein	99.2%	6.0	1	1	1	7	255,713	279,723	254,586	296,143	31,160	11,428	37,328	35,305	27.3	9.1	32.8	26.7	1.1	0.5	-1.0	1	1.2	0.4	-1.1	0.5	1.1	0.7	1.2	0.4
				SLEGADLPNLLFYGPPGTGK	2	99.2%	1																									
IPI00937239	RPS21	40S ribosomal protein S21	100.0%	49.4	5	5	8	2	18,590,114	21,783,189	18,268,299	23,212,839	1,582,208	980,257	1,373,783	536,604	19.0	10.1	16.8	5.2	1.2	0.1	-1.0	0.9	1.2	0.04	-1.2	0.07	1.1	0.2	1.3	0.02
IPI00017448	RPS21	40S ribosomal protein S21	100.0%	48.2	5	5	8	2	18,590,114	21,783,189	18,268,299	23,212,839	1,582,208	980,257	1,373,783	536,604	19.0	10.1	16.8	5.2	1.2	0.1	-1.0	0.9	1.2	0.04	-1.2	0.07	1.1	0.2	1.3	0.02
				DHASIQMNVAEVDK	2	100.0%	1																									
				FNGQFK	1	96.2%	1																									
				MGESDDSILR	2	100.0%	2																									
				RMGESDDSILR	2	100.0%	2																									
				TYAICGAIR	2	100.0%	2																									
IPI00017451	SF3A1	Splicing factor 3A subunit 1	100.0%	21.1	11	11	11	1	20,199,112	20,659,937	20,733,129	22,919,815	1,411,233	507,511	1,320,990	577,029	15.6	5.5	14.3	5.6	1.0	0.8	1.0	0.8	1.1	0.1	1.0	1	1.1	0.02	1.1	0.2
				ASKPLPPAPAPDEYLVSPITGEK	3	100.0%	1																									
				EKQSDDEVYAPGLDIESSLK	3	89.8%	1																									
				EPPPEFEFIADPPSISAFDLDVVK	3	100.0%	1																									
				FNFLNPNDPYHAYYR	3	99.7%	1																									
				IHEATGMPAGK	2	81.0%	1																									
				QSDDEVYAPGLDIESSLK	2	95.9%	1																									
				TDIFGVEETAIGK	2	98.6%	1																									

				TQQAAQANITLQEQIEAIHK	3	99.9%	1																									
				VMQQQQQTTQQQLPQK	3	99.6%	1																									
				VQAQVIQETIVPK	2	100.0%	1																									
				VTWDGHSGSMAR	2	97.3%	1																									
IPI00017454	TUBA4B	Putative tubulin-like protein alpha-4B	100.0%	16.6	3	4	7	1	23,944,948	24,132,213	23,651,665	27,973,905	2,283,987	920,488	1,825,419	607,720	21.3	8.5	17.3	4.9	1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.8	1.2	0.008	1.2	0.08
				LISQIVSSITASLR	2	100.0%	2																									
				LISQIVSSITASLR	3	100.0%	2																									
				NLDIERPTYTNLNR	3	100.0%	1																									
				QIFHPEQLITGK	2	91.9%	2																									
IPI00017469	SPR	Sepiapterin reductase	100.0%	31.8	5	6	7	1	16,530,683	15,862,273	16,607,177	18,012,266	1,061,972	317,004	617,175	310,280	14.4	4.5	8.3	3.9	-1.0	0.6	1.0	1	1.1	0.2	1.0	0.3	1.1	0.001	1.1	0.08
				LLLINNAGSLGDVSK	2	100.0%	1																									
				QLEAELGAER	2	98.1%	1																									
				TLAPLLASLLSPGSVLVLSAR	3	98.8%	1																									
				VLNYAPGPLDTDMQQLAR	2	99.9%	1																									
				VPADLGAEAGLQQLLGALR	2	100.0%	2																									
				VPADLGAEAGLQQLLGALR	3	99.4%	1																									
IPI00017510	MT-CO2	Cytochrome c oxidase subunit 2	100.0%	8.8	1	1	1	1	5,380,420	4,722,330	5,134,330	4,947,700	151,794	229,495	241,435	299,958	6.3	10.9	10.5	13.6	-1.1	0.04	-1.0	0.4	-1.1	0.2	1.1	0.3	1.0	0.6	-1.0	0.6
				MMITSQDVLHSWAVPTLGLK	3	100.0%	1																									
IPI00017526	S100P	Protein S100-P	100.0%	28.4	2	3	3	1	30,443,820	29,504,910	28,298,100	33,176,550	1,723,687	1,092,604	1,691,384	787,876	12.7	8.3	13.4	5.3	-1.0	0.7	-1.1	0.4	1.1	0.2	-1.0	0.6	1.1	0.03	1.2	0.03
				ELPGFLQSGK	2	99.8%	1																									
				YSGSEGSTQTLTKGELK	2	99.9%	1																									
				YSGSEGSTQTLTKGELK	3	97.3%	1																									
IPI00017596	MAPRE1	Microtubule-associated protein RP/EB family member 1	100.0%	42.5	7	9	10	1	20,522,524	21,757,652	20,306,176	24,525,583	1,926,822	842,725	1,314,839	1,101,574	21.0	8.7	14.5	10.0	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.08	1.2	0.04
				FQDNFEFVQWFK	2	100.0%	2																									
				HDMLAWINESLQLNLTK	2	97.7%	1																									
				HDMLAWINESLQLNLTK	3	100.0%	1																									
				IEQLCSGAAYCQFMDMLFPGSIALKK	3	99.7%	1																									
				LEHEYIQNFK	2	99.9%	1																									
				LEHEYIQNFK	3	98.0%	1																									
				LTVEDLEKER	3	80.4%	1																									
				NIELICQENEGENDPVLQR	3	99.9%	1																									
				QGQETAVAPSLVAPALNKPK	3	100.0%	1																									
IPI00017597	MAPRE3	isoform 1 of Microtubule-associated protein RP/EB family member 3	100.0%	10.3	2	2	2	3	1,723,579	2,016,998	1,957,058	1,994,377	194,578	312,436	209,227	103,240	25.2	34.6	23.9	11.6	1.2	0.4	1.1	0.4	1.2	0.3	-1.0	0.9	-1.0	0.9	1.0	0.9
IPI00553216	MAPRE3	isoform 2 of Microtubule-associated protein RP/EB family member 3	100.0%	10.9	2	2	2	3	1,723,579	2,016,998	1,957,058	1,994,377	194,578	312,436	209,227	103,240	25.2	34.6	23.9	11.6	1.2	0.4	1.1	0.4	1.2	0.3	-1.0	0.9	-1.0	0.9	1.0	0.9
IPI00892961	MAPRE3	Uncharacterized protein	100.0%	13.3	2	2	2	3	1,723,579	2,016,998	1,957,058	1,994,377	194,578	312,436	209,227	103,240	25.2	34.6	23.9	11.6	1.2	0.4	1.1	0.4	1.2	0.3	-1.0	0.9	-1.0	0.9	1.0	0.9
				FFDANYDGKDYNPLLAR	3	89.2%	1																									
				FQDNFEFIQWFK	2	99.5%	1																									
IPI00017603	F8	Coagulation factor VIII	94.5%	1.1	1	1	1	1	403,191	439,319	520,857	498,132	42,487	39,581	64,972	53,969	23.6	20.2	27.9	24.2	1.1	0.6	1.3	0.2	1.2	0.2	1.2	0.3	1.1	0.4	-1.0	0.8
				GEEENLEGLGNQTKQIVEKYACTTR	3	91.8%	1																									
IPI00017617	DDX5	Probable ATP-dependent RNA helicase DDX5	100.0%	11.7	6	6	7	3	15,292,422	16,338,093	15,440,918	18,572,896	1,265,739	912,970	1,314,203	642,417	18.5	12.5	19.0	7.7	1.1	0.5	1.0	0.9	1.2	0.05	-1.1	0.6	1.1	0.08	1.2	0.06
IPI00798375	DDX5	cDNA FLJ59357, highly similar to Probable ATP-dependent RNA helicase DDX5	100.0%	13.2	6	6	7	3	15,292,422	16,338,093	15,440,918	18,572,896	1,265,739	912,970	1,314,203	642,417	18.5	12.5	19.0	7.7	1.1	0.5	1.0	0.9	1.2	0.05	-1.1	0.6	1.1	0.08	1.2	0.06
IPI00947363	DDX5	cDNA FLJ53366, highly similar to Probable ATP-dependent RNA helicase DDX5	100.0%	11.9	6	6	7	3	15,292,422	16,338,093	15,440,918	18,572,896	1,265,739	912,970	1,314,203	642,417	18.5	12.5	19.0	7.7	1.1	0.5	1.0	0.9	1.2	0.05	-1.1	0.6	1.1	0.08	1.2	0.06
				APILIATDVASR	2	100.0%	2																									
				ELAQQVQQVAAEYCR	2	99.8%	1																									
				FVINYDYPNSSEDYIHR	3	99.9%	1																									
				LLQLVEDR	2	85.6%	1																									
				LMEEIMSEK	2	87.6%	1																									
				NFYQEHPDLAR	2	99.8%	1																									
IPI00017672	PNP	cDNA FLJ25678 fis, clone TST04067, highly similar to PURINE NUCLEOSIDE PHO	100.0%	59.0	13	14	17	1	89,992,728	91,274,339	92,853,218	108,009,879	9,157,125	5,406,647	7,000,558	3,856,483	22.8	13.3	16.9	8.0	1.0	0.9	1.0	0.8	1.2	0.1	1.0	0.9	1.2	0.04	1.2	0.09
				ANHEEVLAAGK	2	100.0%	2																									
				DHINLPGFSGQNPLR	2	99.9%	1																									
				FEVGDIMLIR	2	100.0%	2																									
				FGDRFPAMSDAYDR	3	100.0%	1																									
				FHMYEGYPLWK	2	98.8%	1																									
				FPAMSDAYDR	2	99.7%	1																									
				HRPQVAIICGSGLGGLTDK	2	96.3%	1																									
				HRPQVAIICGSGLGGLTDK	3	99.9%	1																									
				LEQFVSILMASIPLPDK	3	99.3%	1																									
				LGADAVGMSTVPEVIVAR	2	100.0%	2																									
				LTQAQIFDYGEIPNFPR	2	100.0%	1																									
				LVFGFLNGR	2	99.6%	1																									
				VFGFSLITNK	2	99.6%	1																									
				VFHLLGVDTLVVTNAAGGLNPK	3	100.0%	1																									
IPI00017704	COTL1	Coactosin-like protein	100.0%	15.5	2	3	4	1	5,529,243	5,862,487	5,555,752	6,579,436	511,671	194,923	570,450	212,904	20.7	7.4	23.0	7.2	1.1	0.6	1.0	1	1.2	0.09	-1.1	0.6	1.1	0.04	1.2	0.2
				FALITWIGENVSGLQR	2	100.0%	2																									
				FALITWIGENVSGLQR	3	100.0%	1																									
				LFAFVR	2	91.4%	1																									
IPI00017726	HSD17B10	isoform 1 of 3-hydroxyacyl-CoA dehydrogenase type-2	100.0%	54.4	7	7	9	1	22,643,858	25,331,205	24,477,323	27,096,913	2,491,323	1,209,247	1,183,163	309,909	24.6	10.7	10.8	2.6	1.1	0.4	1.1	0.5	1.2	0.1	-1.0	0.6	1.1	0.2	1.1	0.09
				GGIVGMTLPIAR	2	100.0%	2																									
				GLVAVITGGASGLGLATAER	2	82.4%	1																									
				LGDPAEYAHLVQAIIENPFLNGEVIR	3	100.0%	1																									
				LGNNCVFAPADVTSEKDVQTALALAK	3	86.4%	1																									
				LVGQGASAVLLDLPNSGGEAQAK	2	100.0%	1																									
				VDVAVNCAGIAVASK	2	100.0%	1																									
				VMTIAPGLFGTPLLTSLPEK	2	100.0%	2																									
IPI00017763	NAP1L4	44 kDa protein	100.0%	14.5	4	5	6	1	2,093,190	2,144,083	2,023,539	2,564,008	189,643	136,196	139,591	71,999	20.3	14.2	15.4	6.3	1.0	0.8	-1.0	0.8	1.2	0.07	-1.1	0.6	1.2	0.03	1.3	0.009
				FYEEVHDLER	2	100.0%	1																									
				LDNVPHTPSSYIETLPK	3	100.0%	1																									
				NVDMLSELVQEYDEPILK	2	100.0%	2																									
				NVDMLSELVQEYDEPILK	3	99.6%	1																									
				YAALYQPLFDK	2	99.7%	1																									
IPI00017855	ACO2	Aconitate hydratase, mitochondrial	100.0%	8.3	4	5	6	2	5,170,636	5,385,217	4,684,570	5,539,178	350,194	198,603	469,678	277,412	15.1	8.3	22.4	11.2	1.0	0.6	-1.1	0.4	1.1	0.4	-1.1	0.2	1.0	0.7	1.2	0.2
IPI00790739	ACO2	Aconitase 2, mitochondrial	100.0%	8.1	4	5	6	2	5,170,636	5,385,217	4,684,570	5,539,178	350,194	198,603	469,678	277,412	15.1	8.3	22.4	11.2	1.0	0.6	-1.1	0.4	1.1	0.4	-1.1	0.2	1.0	0.7	1.2	0.2
				LTGSLSGWSSPK	2	99.2%	1																									
				NAVTQEFGPVPDTAR	2	99.9%	1																									
				QGLLPLTFADPADYNK	2	99.9%	1																									
				VAMQDATAQMAMLQFISSGLSK	2	99.9%	2																									
				VAMQDATAQMAMLQFISSGLSK	3	99.9%	1																									
IPI00017891	APC2	isoform 2 of Adenomatous polyposis coli protein 2	99.6%	1.5	2	2	2	4	3,410,198	3,970,085	3,428,438	4,174,243	291,834	149,762	132,247	133,268	19.1	8.4	8.6	7.1	1.2	0.1	1.0	1	1.2	0.04	-1.2	0.03	1.1	0.3	1.2	0.004
IPI00025190	APC2	isoform 1 of Adenomatous polyposis coli protein 2	99.6%	1.4	2	2	2	4	3,410,198	3,970,085	3,428,438	4,174,243	291,834	149,762	132,247	133,268	19.1	8.4	8.6	7.1	1.2	0.1	1.0	1	1.2	0.04	-1.2	0.03	1.1	0.3	1.2	0.004
IPI00793844	APC2	132 kDa protein	99.6%	2.5	2	2	2	4	3,410,198	3,970,085	3,428,438	4,174,243	291,834	149,762	132,247	133,268	19.1	8.4	8.6	7.1	1.2	0.1	1.0	1	1.2	0.04	-1.2	0.03	1.1	0.3	1.2	0.004
IPI00880059	APC2	isoform 3 of Adenomatous polyposis coli protein 2	99.6%	1.4	2	2	2	4	3,410,198	3,970,085	3,428,438	4,174,243	291,834	149,762	132,247	133,268	19.1	8.4	8.6	7.1	1.2	0.1	1.0	1	1.2	0.04	-1.2	0.03	1.1	0.3	1.2	0.004
				HQAAATAVSPGSCVPSLYVR	2	96.3%	1																									
				QRPTGRPTSAR	3	89.6%	1																									
IPI00017895	GPD2	isoform 1 of Glycerol-3-phosphate dehydrogenase, mitochondrial	99.9%	8.0	4	4	4	2	21,549,390	23,026,252	22,814,572	25,174,447	3,659,787	4,351,621	2,266,623	2,723,345	38.0	42.3	22.2	24.2	1.1	0.8	1.1	0.8	1.2	0.4	-1.0	1	1.1	0.7	1.1	0.5
IPI00719611	GPD2	isoform 2 of Glycerol-3-phosphate dehydrogenase, mitochondrial	99.9%	9.7	4	4	4	2	21,549,390	23,026,252	22,814,572	25,174,447	3,659,787	4,351,621	2,266,623	2,723,345	38.0	42.3	22.2	24.2	1.1	0.8	1.1	0.8	1.2	0.4	-1.0	1	1.1	0.7	1.1	0.5
				LAFLNVQAAEEALPR	2	95.8%	1																									
				NGQVELNEFLQLMSAIQK	2	94.1%	1																									
				VIFFLPWQK	2	92.9%	1																									
				YGAATANYMEVVSLLK	2	99.8%	1																									
IPI00017963	SNRPD2	Small nuclear ribonucleoprotein Sm D2	100.0%	15.3	2	2	2	2	9,144,275	9,219,145	9,607,820	9,840,440	270,536	466,482	299,880	524,890	6.6	11.3	7.0	11.9	1.0	0.9	1.1	0.3	1.1	0.3	1.0	0.5	1.1	0.4	1.0	0.7
IPI00930678	SNRPD2	small nuclear ribonucleoprotein Sm D2 isoform 2	100.0%	16.7	2	2	2	2	9,144,275	9,219,145	9,607,820	9,840,440	270,536	466,482	299,880	524,890	6.6	11.3	7.0	11.9	1.0	0.9	1.1	0.3	1.1	0.3	1.0	0.5	1.1	0.4	1.0	0.7
				EMWTEVPK	2	94.5%	1																									
				HCNMVLENVK	2	100.0%	1																									
IPI00017964	SNRPD3	Small nuclear ribonucleoprotein Sm D3	100.0%	15.1	2	2	3	3	2,057,720	2,178,180	2,131,027	2,295,923	193,382	44,279	145,878	108,537	21.0	4.6	15.3	10.6	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.8	1.1	0.3	1.1	0.4
IPI00878876	SNRPD3	cDNA FLJ51872, highly similar to Small nuclear ribonucleoprotein Sm D3	100.0%	15.8	2	2	3	3	2,057,720	2,178,180	2,131,027	2,295,923	193,382	44,279	145,878	108,537	21.0	4.6	15.3	10.6	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.8	1.1	0.3	1.1	0.4
IPI00879750	SNRPD3	19 kDa protein	100.0%	10.9	2	2	3	3	2,057,720	2,178,180	2,131,027	2,295,923	193,382	44,279	145,878	108,537	21.0	4.6	15.3	10.6	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.8	1.1	0.3	1.1	0.4
				FLILPDMLK	2	91.9%	1																									
				VAQLEQVYIR	2	100.0%	2																									
IPI00018079	SSTR5	Somatostatin receptor type 5	95.4%	6.3	2	2	2	1	743,771,490	739,604,900	728,763,860	745,892,630	########	9,505,616	########	########	4.0	2.9	7.0	3.9	-1.0	0.8	-1.0	0.6	1.0	0.9	-1.0	0.7	1.0	0.7	1.0	0.5
				AAANGLMQTSKL	2	95.4%	1																									
				QQQEATPPAHR	3	81.4%	1																									
IPI00018111	TAF7	Transcription initiation factor TFIID subunit 7	90.2%	3.4	1	1	1	1	3,449,970	3,567,120	3,662,740	3,936,220	469,395	206,277	492,720	410,904	30.4	12.9	30.1	23.3	1.0	0.8	1.1	0.8	1.1	0.5	1.0	0.9	1.1	0.4	1.1	0.7
				LLSTDAEAVSTR	2	90.2%	1																									
IPI00018140	SYNCRIP	isoform 1 of Heterogeneous nuclear ribonucleoprotein Q	100.0%	24.7	11	12	18	6	8,447,686	8,521,633	8,388,279	9,406,920	622,659	264,697	491,995	387,212	16.5	7.0	13.1	9.2	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00402182	SYNCRIP	isoform 2 of Heterogeneous nuclear ribonucleoprotein Q	100.0%	26.2	11	12	18	6	8,447,686	8,521,633	8,388,279	9,406,920	622,659	264,697	491,995	387,212	16.5	7.0	13.1	9.2	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00402183	SYNCRIP	isoform 3 of Heterogeneous nuclear ribonucleoprotein Q	100.0%	27.4	11	12	18	6	8,447,686	8,521,633	8,388,279	9,406,920	622,659	264,697	491,995	387,212	16.5	7.0	13.1	9.2	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00402184	SYNCRIP	isoform 4 of Heterogeneous nuclear ribonucleoprotein Q	100.0%	29.2	11	12	18	6	8,447,686	8,521,633	8,388,279	9,406,920	622,659	264,697	491,995	387,212	16.5	7.0	13.1	9.2	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00930205	SYNCRIP	heterogeneous nuclear ribonucleoprotein Q isoform 5	100.0%	27.5	11	12	18	6	8,447,686	8,521,633	8,388,279	9,406,920	622,659	264,697	491,995	387,212	16.5	7.0	13.1	9.2	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00983581	SYNCRIP	SYNCRIP protein (Fragment)	100.0%	34.0	11	12	18	6	8,447,686	8,521,633	8,388,279	9,406,920	622,659	264,697	491,995	387,212	16.5	7.0	13.1	9.2	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
				AIEALKEFNEDGALAVLQQFK	2	100.0%	1																									
				AIEALKEFNEDGALAVLQQFK	3	100.0%	2																									
				DLFEDELVPLFEK	2	100.0%	2																									
				EFNEDGALAVLQQFK	2	99.3%	1																									
				KYGGPPPDSVYSGQQPSVGTEIFVGK	3	100.0%	1																									
				LMMDPLTGLNR	2	99.9%	2																									
				LYNNHEIR	2	99.9%	1																									
				NLANTVTEEILEK	2	100.0%	2																									
				TGYTLDVTTGQR	2	100.0%	2																									
				TKEQILEEFSK	2	83.1%	1																									
				VAEKLDEIYVAGLVAHSDLDER	3	100.0%	1																									
				VTEGLTDVILYHQPDDK	3	100.0%	2																									
IPI00018146	YWHAQ	14-3-3 protein theta	100.0%	34.7	10	11	14	1	50,717,390	57,853,750	51,906,895	64,434,020	6,601,509	4,841,174	3,572,458	3,040,936	29.1	18.7	15.4	10.6	1.1	0.4	1.0	0.9	1.3	0.1	-1.1	0.4	1.1	0.3	1.2	0.03
				AVTEQGAELSNEER	2	100.0%	2																									
				KQTIDNSQGAYQEAFDISK	3	100.0%	1																									
				KQTIDNSQGAYQEAFDISKK	3	100.0%	1																									
				QTIDNSQGAYQEAFDISK	2	100.0%	1																									
				QTIDNSQGAYQEAFDISK	3	98.9%	1																									
				QTIDNSQGAYQEAFDISKK	3	100.0%	2																									
				SICTTVLELLDK	2	100.0%	2																									
				TAFDEAIAELDTLNEDSYK	2	100.0%	1																									
				YDDMATCMK	2	100.0%	1																									
				YLAEVACGDDR	2	100.0%	1																									
				YLAEVACGDDRK	3	99.8%	1																									
IPI00018188	NECAP2	isoform 1 of Adaptin ear-binding coat-associated protein 2	97.7%	5.3	1	1	1	5	2,021,732	1,908,612	2,065,106	2,097,024	97,234	85,526	67,875	64,685	10.8	10.0	7.4	6.9	-1.1	0.4	1.0	0.7	1.0	0.5	1.1	0.2	1.1	0.1	1.0	0.7
IPI00073436	NECAP2	isoform 2 of Adaptin ear-binding coat-associated protein 2	97.7%	5.1	1	1	1	5	2,021,732	1,908,612	2,065,106	2,097,024	97,234	85,526	67,875	64,685	10.8	10.0	7.4	6.9	-1.1	0.4	1.0	0.7	1.0	0.5	1.1	0.2	1.1	0.1	1.0	0.7
IPI00965130	NECAP2	Uncharacterized protein	97.7%	13.9	1	1	1	5	2,021,732	1,908,612	2,065,106	2,097,024	97,234	85,526	67,875	64,685	10.8	10.0	7.4	6.9	-1.1	0.4	1.0	0.7	1.0	0.5	1.1	0.2	1.1	0.1	1.0	0.7

IPI00965384	NECAP2	Protein	97.7%	22.2	1	1	1	5	2,021,732	1,908,612	2,065,106	2,097,024	97,234	85,526	67,875	64,685	10.8	10.0	7.4	6.9	-1.1	0.4	1.0	0.7	1.0	0.5	1.1	0.2	1.1	0.1	1.0	0.7
IPI00967036	NECAP2	cDNA FLJ52763, highly similar to Adaptin ear-binding coat-associated protein 2	97.7%	7.2	1	1	1	5	2,021,732	1,908,612	2,065,106	2,097,024	97,234	85,526	67,875	64,685	10.8	10.0	7.4	6.9	-1.1	0.4	1.0	0.7	1.0	0.5	1.1	0.2	1.1	0.1	1.0	0.7
				AAEWQLDQPSWSGR	2	98.5%	1																									
IPI00018195	MAPK3	Mitogen-activated protein kinase 3	99.5%	8.4	2	2	2	5	2,766,120	2,883,651	2,748,115	3,192,813	308,572	172,014	177,270	150,760	24.9	13.3	14.4	10.6	1.0	0.7	-1.0	1	1.2	0.2	-1.0	0.6	1.1	0.2	1.2	0.09
IPI00304111	MAPK3	mitogen-activated protein kinase 3 isoform 3	99.5%	9.6	2	2	2	5	2,766,120	2,883,651	2,748,115	3,192,813	308,572	172,014	177,270	150,760	24.9	13.3	14.4	10.6	1.0	0.7	-1.0	1	1.2	0.2	-1.0	0.6	1.1	0.2	1.2	0.09
IPI00742900	MAPK3	mitogen-activated protein kinase 3 isoform 2	99.5%	9.0	2	2	2	5	2,766,120	2,883,651	2,748,115	3,192,813	308,572	172,014	177,270	150,760	24.9	13.3	14.4	10.6	1.0	0.7	-1.0	1	1.2	0.2	-1.0	0.6	1.1	0.2	1.2	0.09
IPI00975595	MAPK3	Uncharacterized protein	99.5%	10.1	2	2	2	5	2,766,120	2,883,651	2,748,115	3,192,813	308,572	172,014	177,270	150,760	24.9	13.3	14.4	10.6	1.0	0.7	-1.0	1	1.2	0.2	-1.0	0.6	1.1	0.2	1.2	0.09
IPI00983657	MAPK3	Uncharacterized protein	99.5%	9.4	2	2	2	5	2,766,120	2,883,651	2,748,115	3,192,813	308,572	172,014	177,270	150,760	24.9	13.3	14.4	10.6	1.0	0.7	-1.0	1	1.2	0.2	-1.0	0.6	1.1	0.2	1.2	0.09
				APEIMLNSK	2	98.4%	1																									
				YTQLQYIGEGAYGMVSSAYDHVR	3	99.3%	1																									
IPI00018206	GOT2	Aspartate aminotransferase, mitochondrial	100.0%	21.9	7	7	8	1	27,985,015	27,916,025	26,552,524	30,206,870	1,584,698	1,453,232	1,270,049	1,034,579	12.7	11.6	10.7	7.7	-1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.5	1.1	0.2	1.1	0.06
				ASAELALGENSEVLK	2	100.0%	1																									
				DAGMQLQGYR	2	100.0%	1																									
				FVTVQTISGTGALR	2	100.0%	1																									
				IAAAILNTPDLR	2	100.0%	2																									
				IGASFLQR	2	99.9%	1																									
				TCGFDFTGAVEDISK	2	100.0%	1																									
				VLPGIAAAFHPGLAAAASAR	2	93.1%	1																									
IPI00018235	PEF1	Peflin	100.0%	10.2	2	2	3	1	4,385,403	4,627,820	4,915,000	5,238,990	396,414	536,415	370,332	269,100	20.2	25.9	16.9	11.5	1.1	0.7	1.1	0.4	1.2	0.1	1.1	0.7	1.1	0.3	1.1	0.5
				FIQVCTQLQVLTEAFR	2	91.5%	1																									
				LSFEDFVTMTASR	2	100.0%	2																									
IPI00018236	GM2A	Ganglioside GM2 activator	99.2%	10.4	1	1	1	1	1,296,618	1,473,656	1,233,071	1,221,080	270,915	183,607	96,551	144,419	46.7	27.9	17.5	26.5	1.1	0.6	-1.1	0.8	-1.1	0.8	-1.2	0.3	-1.2	0.3	-1.0	0.9
				SEFVVPDLELPSWLTTGNYR	2	99.2%	1																									
IPI00018246	HK1	isoform 1 of Hexokinase-1	98.8%	1.3	1	1	1	7	338,513	305,211	392,671	331,254	25,911	12,215	23,325	27,385	17.1	9.0	13.3	18.5	-1.1	0.3	1.2	0.2	-1.0	0.9	1.3	0.01	1.1	0.4	-1.2	0.1
IPI00220663	HK1	isoform 2 of Hexokinase-1	98.8%	1.3	1	1	1	7	338,513	305,211	392,671	331,254	25,911	12,215	23,325	27,385	17.1	9.0	13.3	18.5	-1.1	0.3	1.2	0.2	-1.0	0.9	1.3	0.01	1.1	0.4	-1.2	0.1
IPI00220665	HK1	isoform 3 of Hexokinase-1	98.8%	1.3	1	1	1	7	338,513	305,211	392,671	331,254	25,911	12,215	23,325	27,385	17.1	9.0	13.3	18.5	-1.1	0.3	1.2	0.2	-1.0	0.9	1.3	0.01	1.1	0.4	-1.2	0.1
IPI00220667	HK1	isoform 4 of Hexokinase-1	98.8%	1.3	1	1	1	7	338,513	305,211	392,671	331,254	25,911	12,215	23,325	27,385	17.1	9.0	13.3	18.5	-1.1	0.3	1.2	0.2	-1.0	0.9	1.3	0.01	1.1	0.4	-1.2	0.1
IPI00903226	HK1	cDNA FLJ46359 fis, clone TESTI4049786, highly similar to Hexokinase-1	98.8%	1.3	1	1	1	7	338,513	305,211	392,671	331,254	25,911	12,215	23,325	27,385	17.1	9.0	13.3	18.5	-1.1	0.3	1.2	0.2	-1.0	0.9	1.3	0.01	1.1	0.4	-1.2	0.1
IPI01008922	HK1	hexokinase-1 isoform HKI-td	98.8%	1.3	1	1	1	7	338,513	305,211	392,671	331,254	25,911	12,215	23,325	27,385	17.1	9.0	13.3	18.5	-1.1	0.3	1.2	0.2	-1.0	0.9	1.3	0.01	1.1	0.4	-1.2	0.1
IPI01014693	HK1	cDNA FLJ56506, highly similar to Hexokinase-1	98.8%	1.3	1	1	1	7	338,513	305,211	392,671	331,254	25,911	12,215	23,325	27,385	17.1	9.0	13.3	18.5	-1.1	0.3	1.2	0.2	-1.0	0.9	1.3	0.01	1.1	0.4	-1.2	0.1
				LSDETLIDIMTR	2	98.8%	1																									
IPI00018272	PNPO	Pyridoxine-5'-phosphate oxidase	100.0%	17.6	3	3	3	2	5,660,748	5,433,021	5,367,593	6,251,285	331,732	278,547	313,454	281,717	13.1	11.5	13.1	10.1	-1.0	0.6	-1.1	0.5	1.1	0.2	-1.0	0.9	1.2	0.07	1.2	0.07
IPI01013271	PNPO	cDNA FLJ59601, highly similar to Pyridoxine-5'-phosphate oxidase	100.0%	18.9	3	3	3	2	5,660,748	5,433,021	5,367,593	6,251,285	331,732	278,547	313,454	281,717	13.1	11.5	13.1	10.1	-1.0	0.6	-1.1	0.5	1.1	0.2	-1.0	0.9	1.2	0.07	1.2	0.07
				EAFEETHLTSLDPVK	2	99.9%	1																									
				GEEDWLYER	2	99.9%	1																									
				SSQIGAVVSHQSSVIPDREYLR	3	98.5%	1																									
IPI00018274	EGFR	isoform 1 of Epidermal growth factor receptor	91.2%	0.8	1	1	1	8	1,189,311	1,360,418	1,285,354	1,414,649	77,533	48,169	124,239	64,254	14.6	7.9	21.6	10.2	1.1	0.1	1.1	0.5	1.2	0.06	-1.1	0.6	1.0	0.5	1.1	0.4
IPI00221346	EGFR	isoform 2 of Epidermal growth factor receptor	91.2%	2.5	1	1	1	8	1,189,311	1,360,418	1,285,354	1,414,649	77,533	48,169	124,239	64,254	14.6	7.9	21.6	10.2	1.1	0.1	1.1	0.5	1.2	0.06	-1.1	0.6	1.0	0.5	1.1	0.4
IPI00221347	EGFR	isoform 3 of Epidermal growth factor receptor	91.2%	1.4	1	1	1	8	1,189,311	1,360,418	1,285,354	1,414,649	77,533	48,169	124,239	64,254	14.6	7.9	21.6	10.2	1.1	0.1	1.1	0.5	1.2	0.06	-1.1	0.6	1.0	0.5	1.1	0.4
IPI00221348	EGFR	isoform 4 of Epidermal growth factor receptor	91.2%	1.6	1	1	1	8	1,189,311	1,360,418	1,285,354	1,414,649	77,533	48,169	124,239	64,254	14.6	7.9	21.6	10.2	1.1	0.1	1.1	0.5	1.2	0.06	-1.1	0.6	1.0	0.5	1.1	0.4
IPI00915452	EGFR	Cell growth inhibiting protein 40	91.2%	0.8	1	1	1	8	1,189,311	1,360,418	1,285,354	1,414,649	77,533	48,169	124,239	64,254	14.6	7.9	21.6	10.2	1.1	0.1	1.1	0.5	1.2	0.06	-1.1	0.6	1.0	0.5	1.1	0.4
IPI00924546	EGFR	EGFR protein	91.2%	0.9	1	1	1	8	1,189,311	1,360,418	1,285,354	1,414,649	77,533	48,169	124,239	64,254	14.6	7.9	21.6	10.2	1.1	0.1	1.1	0.5	1.2	0.06	-1.1	0.6	1.0	0.5	1.1	0.4
IPI00926683	EGFR	Uncharacterized protein	91.2%	7.8	1	1	1	8	1,189,311	1,360,418	1,285,354	1,414,649	77,533	48,169	124,239	64,254	14.6	7.9	21.6	10.2	1.1	0.1	1.1	0.5	1.2	0.06	-1.1	0.6	1.0	0.5	1.1	0.4
IPI00943104	EGFR	72 kDa protein	91.2%	1.5	1	1	1	8	1,189,311	1,360,418	1,285,354	1,414,649	77,533	48,169	124,239	64,254	14.6	7.9	21.6	10.2	1.1	0.1	1.1	0.5	1.2	0.06	-1.1	0.6	1.0	0.5	1.1	0.4
				IPLENLQIIR	2	91.2%	1																									
IPI00018278	H2AFV	Histone H2A.V	98.2%	10.9	1	1	1	4	575,555	604,053	591,545	637,553	62,939	55,237	76,831	62,874	24.5	20.5	29.0	22.1	1.0	0.7	1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.7	1.1	0.7
IPI00398798	H2AFV	histone H2A.V isoform 3	98.2%	13.7	1	1	1	4	575,555	604,053	591,545	637,553	62,939	55,237	76,831	62,874	24.5	20.5	29.0	22.1	1.0	0.7	1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.7	1.1	0.7
IPI00398806	H2AFV	histone H2A.V isoform 5	98.2%	15.6	1	1	1	4	575,555	604,053	591,545	637,553	62,939	55,237	76,831	62,874	24.5	20.5	29.0	22.1	1.0	0.7	1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.7	1.1	0.7
IPI00218448	H2AFZ	Histone H2A.Z	98.2%	10.9	1	1	1	4	575,555	604,053	591,545	637,553	62,939	55,237	76,831	62,874	24.5	20.5	29.0	22.1	1.0	0.7	1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.7	1.1	0.7
				ATIAGGGVIPHIHK	2	98.2%	1																									
IPI00018288	POLR2C	DNA-directed RNA polymerase II subunit RPB3	99.6%	12.0	2	2	2	2	4,870,012	4,774,088	4,732,523	4,901,134	363,051	207,974	211,412	69,624	16.7	9.7	10.0	3.2	-1.0	0.8	-1.0	0.8	1.0	0.9	-1.0	0.9	1.0	0.6	1.0	0.5
IPI00922383	POLR2C	cDNA FLJ57430, highly similar to DNA-directed RNA polymerase II 33 kDa polypept	99.6%	7.8	2	2	2	2	4,870,012	4,774,088	4,732,523	4,901,134	363,051	207,974	211,412	69,624	16.7	9.7	10.0	3.2	-1.0	0.8	-1.0	0.8	1.0	0.9	-1.0	0.9	1.0	0.6	1.0	0.5
				FIIENTDLAVANSIR	2	93.8%	1																									
				WNPTAGVAFEYDPDNALR	2	99.6%	1																									
IPI00018331	SNAPIN	SNARE-associated protein Snapin	98.0%	7.4	1	1	1	1	5,801,790	3,903,320	4,914,400	5,440,090	1,687,020	195,261	271,171	510,528	65.0	11.2	12.3	21.0	-1.5	0.3	-1.2	0.6	-1.1	0.8	1.3	0.02	1.4	0.04	1.1	0.4
				VALDLDPYVK	2	98.0%	1																									
IPI00018342	AK1	Adenylate kinase isoenzyme 1	100.0%	29.9	4	5	5	2	9,006,590	9,515,197	9,137,187	10,753,691	954,167	348,612	619,490	274,368	23.7	8.2	15.2	5.7	1.1	0.6	1.0	0.9	1.2	0.1	-1.0	0.6	1.1	0.02	1.2	0.04
IPI00640817	AK1	Adenylate kinase 1	100.0%	27.6	4	5	5	2	9,006,590	9,515,197	9,137,187	10,753,691	954,167	348,612	619,490	274,368	23.7	8.2	15.2	5.7	1.1	0.6	1.0	0.9	1.2	0.1	-1.0	0.6	1.1	0.02	1.2	0.04
				ATEPVIAFYEK	2	86.8%	1																									
				GQLVPLETVLDMLR	2	100.0%	1																									
				GQLVPLETVLDMLR	3	99.5%	1																									
				IGQPTLLLYVDAGPETMTQR	2	99.3%	1																									
				YGYTHLSTGDLLR	3	99.7%	1																									
IPI00018349	MCM4	DNA replication licensing factor MCM4	99.5%	2.2	1	1	1	4	657,523	685,240	852,780	785,330	96,598	69,648	97,151	44,127	32.9	22.7	25.5	12.6	1.0	0.8	1.3	0.2	1.2	0.3	1.2	0.2	1.1	0.3	-1.1	0.5
IPI00795318	MCM4	cDNA FLJ54365, highly similar to DNA replication licensing factor MCM4	99.5%	2.3	1	1	1	4	657,523	685,240	852,780	785,330	96,598	69,648	97,151	44,127	32.9	22.7	25.5	12.6	1.0	0.8	1.3	0.2	1.2	0.3	1.2	0.2	1.1	0.3	-1.1	0.5
IPI00797037	MCM4	95 kDa protein	99.5%	2.2	1	1	1	4	657,523	685,240	852,780	785,330	96,598	69,648	97,151	44,127	32.9	22.7	25.5	12.6	1.0	0.8	1.3	0.2	1.2	0.3	1.2	0.2	1.1	0.3	-1.1	0.5
IPI00974419	MCM4	Uncharacterized protein	99.5%	6.8	1	1	1	4	657,523	685,240	852,780	785,330	96,598	69,648	97,151	44,127	32.9	22.7	25.5	12.6	1.0	0.8	1.3	0.2	1.2	0.3	1.2	0.2	1.1	0.3	-1.1	0.5
				NLNPEDIDQLITISGMVIR	2	99.5%	1																									
IPI00018370	SVIL	isoform 2 of Supervillin	95.6%	0.7	1	1	1	2	1,067,365	1,372,040	1,127,290	1,675,700	154,889	70,720	114,144	113,299	32.5	11.5	22.6	15.1	1.3	0.1	1.1	0.8	1.6	0.01	-1.2	0.1	1.2	0.05	1.5	0.009
IPI00412650	SVIL	isoform 1 of Supervillin	95.6%	0.6	1	1	1	2	1,067,365	1,372,040	1,127,290	1,675,700	154,889	70,720	114,144	113,299	32.5	11.5	22.6	15.1	1.3	0.1	1.1	0.8	1.6	0.01	-1.2	0.1	1.2	0.05	1.5	0.009
				ANPPITHLGDEPK	2	84.8%	1																									
IPI00018398	PSMC3	26S protease regulatory subunit 6A	100.0%	41.9	12	12	13	2	24,501,023	24,997,518	25,344,744	27,151,494	1,970,547	770,256	1,368,518	1,130,467	18.0	6.9	12.1	9.3	1.0	0.8	1.0	0.7	1.1	0.3	1.0	0.8	1.1	0.2	1.1	0.3
IPI00979423	PSMC3	Uncharacterized protein	100.0%	46.4	12	12	13	2	24,501,023	24,997,518	25,344,744	27,151,494	1,970,547	770,256	1,368,518	1,130,467	18.0	6.9	12.1	9.3	1.0	0.8	1.0	0.7	1.1	0.3	1.0	0.8	1.1	0.2	1.1	0.3
				AMEVDERPTEQYSDIGGLDK	3	100.0%	1																									
				AVCVEAGMIALR	2	98.8%	1																									
				DSYLILETLPTEYDSR	2	100.0%	1																									
				EKAPSIIFIDELDAIGTK	3	100.0%	1																									
				GATELTHEDYMEGILEVQAK	3	97.8%	1																									
				GVLMYGPPGTGK	2	100.0%	1																									
				KMNVSPDVNYEELAR	3	100.0%	1																									
				LAGPQLVQMFIGDGAK	2	100.0%	2																									
				LKPGDLVGVNK	3	99.5%	1																									
				MSTEEIIQR	2	100.0%	1																									
				QIQELVEAIVLPMNHK	3	99.8%	1																									
				TMLELLNQLDGFQPNTQVK	3	100.0%	1																									
IPI00018402	TBCE	Tubulin-specific chaperone E	95.5%	5.9	2	2	2	2	6,162,106	5,294,992	7,164,845	5,967,966	374,055	634,262	417,388	657,472	13.6	26.8	13.0	24.6	-1.2	0.3	1.2	0.1	-1.0	0.8	1.4	0.04	1.1	0.5	-1.2	0.2
IPI00922443	TBCE	cDNA FLJ59210, highly similar to Tubulin-specific chaperone E	95.5%	5.4	2	2	2	2	6,162,106	5,294,992	7,164,845	5,967,966	374,055	634,262	417,388	657,472	13.6	26.8	13.0	24.6	-1.2	0.3	1.2	0.1	-1.0	0.8	1.4	0.04	1.1	0.5	-1.2	0.2
				NLLSSWDEVIHIADQLR	3	95.5%	1																									
				VPVSDLLLSYESPK	2	90.6%	1																									
IPI00018451	CIB1	Calcium and integrin-binding protein 1	100.0%	7.3	1	1	1	1	22,175,500	21,943,300	21,662,500	24,864,900	2,004,938	889,880	1,535,103	895,969	20.2	9.1	15.9	8.1	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.05	1.1	0.1
				ELLAEYQDLTFLTK	2	99.5%	1																									
IPI00018452	CPNE1	Copine-1	100.0%	16.0	6	8	11	4	3,852,281	4,347,198	3,903,691	4,686,172	199,897	150,086	264,019	225,646	11.6	7.7	15.1	10.8	1.1	0.08	1.0	0.9	1.2	0.02	-1.1	0.2	1.1	0.2	1.2	0.05
IPI00852917	CPNE1	Copine I	100.0%	17.9	6	8	11	4	3,852,281	4,347,198	3,903,691	4,686,172	199,897	150,086	264,019	225,646	11.6	7.7	15.1	10.8	1.1	0.08	1.0	0.9	1.2	0.02	-1.1	0.2	1.1	0.2	1.2	0.05
IPI00894409	CPNE1	copine-1 isoform b	100.0%	15.9	6	8	11	4	3,852,281	4,347,198	3,903,691	4,686,172	199,897	150,086	264,019	225,646	11.6	7.7	15.1	10.8	1.1	0.08	1.0	0.9	1.2	0.02	-1.1	0.2	1.1	0.2	1.2	0.05
IPI00917016	CPNE1	copine-1 isoform c	100.0%	16.0	6	8	11	4	3,852,281	4,347,198	3,903,691	4,686,172	199,897	150,086	264,019	225,646	11.6	7.7	15.1	10.8	1.1	0.08	1.0	0.9	1.2	0.02	-1.1	0.2	1.1	0.2	1.2	0.05
				EALAQTVLAEVPTQLVSYFR	2	100.0%	2																									
				EALAQTVLAEVPTQLVSYFR	3	100.0%	1																									
				FGIYDIDNK	2	98.5%	1																									
				GTITVSAQELK	2	94.3%	1																									
				LYGPTNFAPIINHVAR	3	100.0%	1																									
				SDPFLEFFR	2	100.0%	2																									
				SDPLCVLLQDVGGGSWAELGR	2	100.0%	2																									
				SDPLCVLLQDVGGGSWAELGR	3	100.0%	1																									
IPI00018465	CCT7	T-complex protein 1 subunit eta	100.0%	38.7	14	14	16	2	27,003,429	26,111,144	26,541,946	29,329,992	1,563,238	893,421	1,798,398	884,421	12.9	7.7	15.2	6.7	-1.0	0.6	-1.0	0.9	1.1	0.2	1.0	0.8	1.1	0.03	1.1	0.2
IPI00952607	CCT7	T-complex protein 1 subunit eta isoform d	100.0%	42.1	14	14	16	2	27,003,429	26,111,144	26,541,946	29,329,992	1,563,238	893,421	1,798,398	884,421	12.9	7.7	15.2	6.7	-1.0	0.6	-1.0	0.9	1.1	0.2	1.0	0.8	1.1	0.03	1.1	0.2
				ATISNDGATILK	2	99.8%	1																									
				CAMTALSSK	2	99.3%	1																									
				GGAEQFMEETER	2	100.0%	1																									
				INALTAASEAACLIVSVDETIKNPR	3	100.0%	1																									
				LLDVVHPAAK	2	99.4%	1																									
				LPIGDVATQYFADR	2	99.9%	1																									
				QLCDNAGFDATNILNK	2	100.0%	1																									
				QVKPYVEEGLHPQIIIR	3	95.3%	1																									
				SLHDAIMIVR	2	96.7%	1																									
				SQDAEVGDGTTSVTLLAAEFLK	2	100.0%	2																									
				TATQLAVNK	2	99.9%	1																									
				TFSYAGFEMQPK	2	100.0%	2																									
				VHTVEDYQAIVDAEWNILYDKLEK	3	97.4%	1																									
				VQGGALEDSQLVAGVAFK	2	100.0%	1																									
IPI00018500	ARID3A	AT-rich interactive domain-containing protein 3A	100.0%	6.4	3	4	4	1	13,225,174	12,569,953	12,719,878	15,357,152	780,564	811,020	778,650	895,931	13.2	14.4	13.7	13.1	-1.1	0.6	-1.0	0.7	1.2	0.1	1.0	0.9	1.2	0.05	1.2	0.06
				ALQQNFLAMAAQLPMSIR	2	99.8%	1																									
				ALQQNFLAMAAQLPMSIR	3	98.4%	1																									
				AQMAALAAMR	2	99.8%	1																									
				QLYELDGDPK	2	98.5%	1																									
IPI00018511	TUBB4Q	Putative tubulin beta-4q chain	97.3%	7.4	1	1	1	3	1,645,583	1,953,573	1,567,753	2,343,380	332,264	212,450	272,527	201,526	45.2	24.3	38.9	19.2	1.2	0.5	-1.0	0.9	1.4	0.1	-1.2	0.3	1.2	0.2	1.5	0.05
IPI00514047	TUBB8	Tubulin, beta 8, isoform CRA_c	97.3%	7.8	1	1	1	3	1,645,583	1,953,573	1,567,753	2,343,380	332,264	212,450	272,527	201,526	45.2	24.3	38.9	19.2	1.2	0.5	-1.0	0.9	1.4	0.1	-1.2	0.3	1.2	0.2	1.5	0.05
IPI01013807	TUBB8	tubulin beta-8 chain isoform 2	97.3%	7.9	1	1	1	3	1,645,583	1,953,573	1,567,753	2,343,380	332,264	212,450	272,527	201,526	45.2	24.3	38.9	19.2	1.2	0.5	-1.0	0.9	1.4	0.1	-1.2	0.3	1.2	0.2	1.5	0.05
				EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK	3	89.7%	1																									
IPI00018522	PRMT1	isoform 1 of Protein arginine N-methyltransferase 1	96.0%	4.4	1	1	1	5	730,966	752,392	761,466	844,912	62,736	64,216	75,098	34,065	19.2	19.1	22.1	9.0	1.0	0.8	1.0	0.8	1.2	0.1	1.0	0.9	1.1	0.2	1.1	0.3
IPI00215734	PRMT1	isoform 2 of Protein arginine N-methyltransferase 1	96.0%	4.6	1	1	1	5	730,966	752,392	761,466	844,912	62,736	64,216	75,098	34,065	19.2	19.1	22.1	9.0	1.0	0.8	1.0	0.8	1.2	0.1	1.0	0.9	1.1	0.2	1.1	0.3
IPI00382516	PRMT1	protein arginine N-methyltransferase 1 isoform 3	96.0%	4.5	1	1	1	5	730,966	752,392	761,466	844,912	62,736	64,216	75,098	34,065	19.2	19.1	22.1	9.0	1.0	0.8	1.0	0.8	1.2	0.1	1.0	0.9	1.1	0.2	1.1	0.3
IPI00984352	PRMT1	Uncharacterized protein	96.0%	4.9	1	1	1	5	730,966	752,392	761,466	844,912	62,736	64,216	75,098	34,065	19.2	19.1	22.1	9.0	1.0	0.8	1.0	0.8	1.2	0.1	1.0	0.9	1.1	0.2	1.1	0.3
IPI01014546	PRMT1	protein arginine N-methyltransferase 1 isoform 1	96.0%	4.3	1	1	1	5	730,966	752,392	761,466	844,912	62,736	64,216	75,098	34,065	19.2	19.1	22.1	9.0	1.0	0.8	1.0	0.8	1.2	0.1	1.0	0.9	1.1	0.2	1.1	0.3
				TGEEIFGTIGMRPNAK	3	96.0%	1																									
IPI00477495	H2BFS	Histone H2B type F-S	100.0%	32.5	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00152906	HIST1H2BD	Histone H2B type 1-D	100.0%	32.5	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00930570	HIST1H2BD	Histone H2B	100.0%	32.5	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00020101	2BF;HIST1H2BG;HIS	Histone H2B type 1-C/E/F/G/I	100.0%	32.5	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00815755	2BF;HIST1H2BG;HIS	HIST1H2BC protein	100.0%	32.5	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00303133	HIST1H2BH	Histone H2B type 1-H	100.0%	32.5	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00419833	HIST1H2BK	Histone H2B type 1-K	100.0%	32.5	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00018534	HIST1H2BL	Histone H2B type 1-L	100.0%	32.5	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00554798	HIST1H2BM	Histone H2B type 1-M	100.0%	32.5	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00794461	HIST1H2BN	Histone H2B type 1-N	100.0%	24.7	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00329665	HIST2H2BF	Histone H2B type 2-F	100.0%	32.5	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00646240	HIST2H2BF	Histone H2B	100.0%	24.7	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009
IPI00930174	HIST2H2BF	histone H2B type 2-F isoform b	100.0%	30.6	4	6	9	13	4,425,550	4,459,520	4,606,538	5,715,717	306,863	156,615	168,167	277,561	15.5	7.9	8.2	10.9	1.0	0.9	1.0	0.6	1.3	0.01	1.0	0.5	1.3	0.004	1.2	0.009

				AMGIMNSFVNDIFER	2	100.0%	4																									
				AMGIMNSFVNDIFER	3	100.0%	1																									
				EIQTAVR	1	87.0%	1																									
				EIQTAVR	2	94.1%	1																									
				KESYSVYVYK	2	92.5%	1																									
				LLLPGELAK	1	84.1%	1																									
IPI00018671	DUSP3	Dual specificity protein phosphatase 3	100.0%	24.3	3	3	4	2	3,904,880	3,624,083	3,577,928	4,299,378	480,153	181,440	332,143	200,215	27.5	11.2	20.8	10.4	-1.1	0.6	-1.1	0.6	1.1	0.5	-1.0	0.9	1.2	0.04	1.2	0.1
IPI00790757	DUSP3	23 kDa protein	100.0%	21.4	3	3	4	2	3,904,880	3,624,083	3,577,928	4,299,378	480,153	181,440	332,143	200,215	27.5	11.2	20.8	10.4	-1.1	0.6	-1.1	0.6	1.1	0.5	-1.0	0.9	1.2	0.04	1.2	0.1
				AADFIDQALAQK	2	99.9%	2																									
				ANDTQEFNLSAYFER	2	99.6%	1																									
				EIGPNDGFLAQLCQLNDR	3	97.4%	1																									
IPI00018755	-	24 kDa protein	100.0%	20.4	4	5	7	3	3,514,329	3,474,496	3,428,076	3,671,124	291,788	187,011	143,738	72,818	18.6	12.0	9.4	4.4	-1.0	0.9	-1.0	0.8	1.0	0.6	-1.0	0.8	1.1	0.4	1.1	0.2
IPI00742929	-	Similar to High mobility group protein B1	100.0%	25.2	4	5	7	3	3,514,329	3,474,496	3,428,076	3,671,124	291,788	187,011	143,738	72,818	18.6	12.0	9.4	4.4	-1.0	0.9	-1.0	0.8	1.0	0.6	-1.0	0.8	1.1	0.4	1.1	0.2
IPI00903004	-	cDNA FLJ32558 fis, clone SPLEN1000143, highly similar to High mobility group prot	100.0%	24.4	4	5	7	3	3,514,329	3,474,496	3,428,076	3,671,124	291,788	187,011	143,738	72,818	18.6	12.0	9.4	4.4	-1.0	0.9	-1.0	0.8	1.0	0.6	-1.0	0.8	1.1	0.4	1.1	0.2
				GEHPGLSIGDVAK	2	99.4%	1																									
				IKGEHPGLSIGDVAK	3	100.0%	2																									
				LGEMWNNTAADDKQPYEK	2	99.9%	1																									
				LGEMWNNTAADDKQPYEK	3	100.0%	2																									
				TYIPPKGETK	3	98.9%	1																									
IPI00018768	TSN	Translin	100.0%	13.2	2	2	2	4	2,327,318	2,472,628	2,686,020	2,878,738	115,416	84,121	166,349	140,891	11.1	7.6	13.9	10.9	1.1	0.3	1.2	0.1	1.2	0.02	1.1	0.3	1.2	0.04	1.1	0.4
IPI00916061	TSN	Protein	100.0%	16.2	2	2	2	4	2,327,318	2,472,628	2,686,020	2,878,738	115,416	84,121	166,349	140,891	11.1	7.6	13.9	10.9	1.1	0.3	1.2	0.1	1.2	0.02	1.1	0.3	1.2	0.04	1.1	0.4
IPI00917623	TSN	Uncharacterized protein	100.0%	13.5	2	2	2	4	2,327,318	2,472,628	2,686,020	2,878,738	115,416	84,121	166,349	140,891	11.1	7.6	13.9	10.9	1.1	0.3	1.2	0.1	1.2	0.02	1.1	0.3	1.2	0.04	1.1	0.4
IPI00922875	TSN	cDNA FLJ55086, highly similar to Translin	100.0%	20.3	2	2	2	4	2,327,318	2,472,628	2,686,020	2,878,738	115,416	84,121	166,349	140,891	11.1	7.6	13.9	10.9	1.1	0.3	1.2	0.1	1.2	0.02	1.1	0.3	1.2	0.04	1.1	0.4
				EILTLLQGVHQGAGFQDIPK	3	99.9%	1																									
				VVQSLEQTAR	2	99.8%	1																									
IPI00018780	CDK5RAP3	isoform 2 of CDK5 regulatory subunit-associated protein 3	98.6%	5.7	2	2	2	2	6,057,648	5,999,532	5,839,407	6,259,312	306,102	348,918	319,745	307,904	11.3	13.0	12.2	11.0	-1.0	0.9	-1.0	0.6	1.0	0.7	-1.0	0.7	1.0	0.6	1.1	0.4
IPI00414442	CDK5RAP3	isoform 1 of CDK5 regulatory subunit-associated protein 3	98.6%	4.7	2	2	2	2	6,057,648	5,999,532	5,839,407	6,259,312	306,102	348,918	319,745	307,904	11.3	13.0	12.2	11.0	-1.0	0.9	-1.0	0.6	1.0	0.7	-1.0	0.7	1.0	0.6	1.1	0.4
				GPDALTLLEYTETR	2	98.6%	1																									
				NVNYEIPSLK	2	98.0%	1																									
IPI00018783	ITPA	Inosine triphosphate pyrophosphatase	100.0%	16.0	2	2	2	2	1,311,186	1,214,934	1,344,788	1,478,970	132,670	78,123	123,788	56,365	22.6	14.4	20.6	8.5	-1.1	0.5	1.0	0.9	1.1	0.3	1.1	0.4	1.2	0.03	1.1	0.4
IPI00375446	ITPA	inosine triphosphate pyrophosphatase isoform b	100.0%	17.5	2	2	2	2	1,311,186	1,214,934	1,344,788	1,478,970	132,670	78,123	123,788	56,365	22.6	14.4	20.6	8.5	-1.1	0.5	1.0	0.9	1.1	0.3	1.1	0.4	1.2	0.03	1.1	0.4
				ALLELQEYFGSLAA	2	99.9%	1																									
				IDLPEYQGEPDEISIQK	2	100.0%	1																									
IPI00018804	TRIP10	isoform 2 of Cdc42-interacting protein 4	100.0%	9.4	3	4	4	5	1,111,312	1,052,338	1,230,446	1,224,859	93,560	53,842	97,996	49,099	18.8	11.4	17.8	9.0	-1.1	0.6	1.1	0.4	1.1	0.3	1.2	0.1	1.2	0.05	-1.0	1
IPI00168849	TRIP10	isoform 1 of Cdc42-interacting protein 4	100.0%	8.5	3	4	4	5	1,111,312	1,052,338	1,230,446	1,224,859	93,560	53,842	97,996	49,099	18.8	11.4	17.8	9.0	-1.1	0.6	1.1	0.4	1.1	0.3	1.2	0.1	1.2	0.05	-1.0	1
IPI00395401	TRIP10	isoform 3 of Cdc42-interacting protein 4	100.0%	8.6	3	4	4	5	1,111,312	1,052,338	1,230,446	1,224,859	93,560	53,842	97,996	49,099	18.8	11.4	17.8	9.0	-1.1	0.6	1.1	0.4	1.1	0.3	1.2	0.1	1.2	0.05	-1.0	1
IPI00645818	TRIP10	isoform 5 of Cdc42-interacting protein 4	100.0%	15.0	3	4	4	5	1,111,312	1,052,338	1,230,446	1,224,859	93,560	53,842	97,996	49,099	18.8	11.4	17.8	9.0	-1.1	0.6	1.1	0.4	1.1	0.3	1.2	0.1	1.2	0.05	-1.0	1
IPI00807460	TRIP10	isoform 4 of Cdc42-interacting protein 4	100.0%	11.2	3	4	4	5	1,111,312	1,052,338	1,230,446	1,224,859	93,560	53,842	97,996	49,099	18.8	11.4	17.8	9.0	-1.1	0.6	1.1	0.4	1.1	0.3	1.2	0.1	1.2	0.05	-1.0	1
				FSQQQSFVQILQEVNDFAGQR	2	91.1%	1																									
				FSQQQSFVQILQEVNDFAGQR	3	82.2%	1																									
				LGAGYGLLSEAELEVVPIIAK	2	99.8%	1																									
				TEVEQAYAK	2	98.5%	1																									
IPI00018808	C12orf35	Uncharacterized protein C12orf35	99.6%	1.8	2	2	2	1	4,002,591	4,371,920	4,174,880	4,490,750	447,597	271,156	357,994	214,477	25.0	13.9	19.2	10.7	1.1	0.5	1.0	0.8	1.1	0.4	-1.0	0.7	1.0	0.7	1.1	0.5
				KLDQGNVLDMEVKK	2	93.4%	1																									
				SDSSCSMEVLATCLSLWK	2	93.2%	1																									
IPI00018813	COPS2	isoform 2 of COP9 signalosome complex subunit 2	99.4%	2.2	1	1	1	3	1,508,597	1,422,013	1,429,403	1,508,713	129,762	121,913	96,198	90,473	19.2	19.2	15.1	13.4	-1.1	0.6	-1.1	0.6	1.0	1	1.0	1	1.1	0.6	1.1	0.6
IPI00743825	COPS2	isoform 1 of COP9 signalosome complex subunit 2	99.4%	2.3	1	1	1	3	1,508,597	1,422,013	1,429,403	1,508,713	129,762	121,913	96,198	90,473	19.2	19.2	15.1	13.4	-1.1	0.6	-1.1	0.6	1.0	1	1.0	1	1.1	0.6	1.1	0.6
IPI01010035	COPS2	cDNA FLJ52928, highly similar to COP9 signalosome complex subunit 2	99.4%	2.6	1	1	1	3	1,508,597	1,422,013	1,429,403	1,508,713	129,762	121,913	96,198	90,473	19.2	19.2	15.1	13.4	-1.1	0.6	-1.1	0.6	1.0	1	1.0	1	1.1	0.6	1.1	0.6
				YLVLANMLMK	2	97.6%	1																									
IPI00018829	SPTBN4	isoform 1 of Spectrin beta chain, brain 3	99.1%	0.5	1	1	1	6	812,845	797,088	821,365	842,888	86,673	76,249	109,386	53,302	23.8	21.4	29.8	14.1	-1.0	0.9	1.0	1	1.0	0.8	1.0	0.9	1.1	0.6	1.0	0.9
IPI00217044	SPTBN4	isoform 2 of Spectrin beta chain, brain 3	99.1%	1.0	1	1	1	6	812,845	797,088	821,365	842,888	86,673	76,249	109,386	53,302	23.8	21.4	29.8	14.1	-1.0	0.9	1.0	1	1.0	0.8	1.0	0.9	1.1	0.6	1.0	0.9
IPI00217047	SPTBN4	Uncharacterized protein	99.1%	0.5	1	1	1	6	812,845	797,088	821,365	842,888	86,673	76,249	109,386	53,302	23.8	21.4	29.8	14.1	-1.0	0.9	1.0	1	1.0	0.8	1.0	0.9	1.1	0.6	1.0	0.9
IPI00217048	SPTBN4	isoform 4 of Spectrin beta chain, brain 3	99.1%	0.6	1	1	1	6	812,845	797,088	821,365	842,888	86,673	76,249	109,386	53,302	23.8	21.4	29.8	14.1	-1.0	0.9	1.0	1	1.0	0.8	1.0	0.9	1.1	0.6	1.0	0.9
IPI00953672	SPTBN4	Uncharacterized protein	99.1%	1.0	1	1	1	6	812,845	797,088	821,365	842,888	86,673	76,249	109,386	53,302	23.8	21.4	29.8	14.1	-1.0	0.9	1.0	1	1.0	0.8	1.0	0.9	1.1	0.6	1.0	0.9
IPI01015691	SPTBN4	Non-erythrocytic beta-spectrin 4	99.1%	0.5	1	1	1	6	812,845	797,088	821,365	842,888	86,673	76,249	109,386	53,302	23.8	21.4	29.8	14.1	-1.0	0.9	1.0	1	1.0	0.8	1.0	0.9	1.1	0.6	1.0	0.9
				MQVAVQAAEGLLR	2	99.1%	1																									
IPI00018873	NAMPT	Nicotinamide phosphoribosyltransferase	100.0%	14.9	4	5	5	1	10,848,962	10,262,335	10,807,993	12,378,107	652,592	874,469	956,584	392,549	13.5	19.1	19.8	7.1	-1.1	0.6	-1.0	1	1.1	0.08	1.1	0.7	1.2	0.06	1.1	0.2
				GVSSQETAGIGASAHLVNFK	3	98.4%	1																									
				MWSIENIAFGSGGGLLQK	2	98.7%	1																									
				MWSIENIAFGSGGGLLQK	3	96.9%	1																									
				VIQGDGVDINTLQEIVEGMK	2	100.0%	1																									
				YLLETSGNLDGLEYK	2	100.0%	1																									
IPI00018889	GLI3	Transcriptional activator GLI3	95.9%	1.2	1	1	1	1	2,637,900	2,656,770	1,835,243	2,275,110	480,487	189,505	202,310	180,979	40.7	16.0	24.7	17.8	1.0	1	-1.4	0.2	-1.2	0.5	-1.4	0.02	-1.2	0.2	1.2	0.1
				FSSLSSCNPPAMATSAEKR	2	83.6%	1																									
IPI00018907	TWIST1	Twist-related protein 1	90.9%	14.9	1	1	1	1	3,678,770	4,523,510	3,936,660	4,452,890	479,038	232,324	411,003	368,766	29.1	11.5	23.4	18.5	1.2	0.2	1.1	0.7	1.2	0.2	-1.1	0.2	-1.0	0.9	1.1	0.4
				SAGGGAGPGGAAGGGVGGGDEPGSPAQGKR	3	90.9%	1																									
IPI00018931	VPS35	Vacuolar protein sorting-associated protein 35	100.0%	11.3	6	6	6	1	15,340,175	15,951,240	15,856,531	17,659,425	1,169,257	759,190	1,359,419	602,558	17.0	10.6	19.2	7.6	1.0	0.7	1.0	0.8	1.2	0.1	-1.0	1	1.1	0.1	1.1	0.3
				IREDLPNLESSEETEQINK	3	90.7%	1																									
				LFDIFSQQVATVIQSR	2	100.0%	1																									
				LNLEHIATSSAVSK	2	96.7%	1																									
				QIVLTGILEQVVNCR	2	98.8%	1																									
				SEDPDQQYLILNTAR	2	99.9%	1																									
				VLETTVEIFNK	2	99.9%	1																									
IPI00018934	SCN1A	isoform 1 of Sodium channel protein type 1 subunit alpha	98.7%	0.5	1	1	1	3	1,217,240	1,582,687	1,232,483	1,794,263	197,088	65,440	136,582	155,379	36.2	9.3	24.8	19.4	1.3	0.1	1.0	1	1.5	0.05	-1.3	0.05	1.1	0.2	1.5	0.03
IPI00748990	SCN1A	Sodium channel, voltage-gated, type I, alpha	98.7%	0.5	1	1	1	3	1,217,240	1,582,687	1,232,483	1,794,263	197,088	65,440	136,582	155,379	36.2	9.3	24.8	19.4	1.3	0.1	1.0	1	1.5	0.05	-1.3	0.05	1.1	0.2	1.5	0.03
IPI00917812	SCN1A	sodium channel protein type 1 subunit alpha isoform 3	98.7%	0.5	1	1	1	3	1,217,240	1,582,687	1,232,483	1,794,263	197,088	65,440	136,582	155,379	36.2	9.3	24.8	19.4	1.3	0.1	1.0	1	1.5	0.05	-1.3	0.05	1.1	0.2	1.5	0.03
				CCQINVEEGR	2	98.0%	1																									
IPI00018953	DPP4	Dipeptidyl peptidase 4	100.0%	38.9	24	28	33	1	220,852,890	235,160,086	211,682,239	261,938,626	########	########	########	8,086,253	23.6	11.5	14.5	6.9	1.1	0.6	-1.0	0.7	1.2	0.2	-1.1	0.2	1.1	0.1	1.2	0.01
				CGIAVAPVSR	2	99.9%	1																									
				CQYYSVSFSK	2	93.5%	1																									
				CSGPGLPLYTLHSSVNDK	3	91.1%	1																									
				FRPSEPHFTLDGNSFYK	3	100.0%	1																									
				FWYQMILPPHFDK	3	99.9%	1																									
				HSYTASYDIYDLNKR	3	100.0%	2																									
				IAIWGWSYGGYVTSMVLGSGSGVFK	2	100.0%	1																									
				IAIWGWSYGGYVTSMVLGSGSGVFK	3	100.0%	1																									
				IISNEEGYR	2	99.9%	1																									
				IQLSDYTK	2	99.9%	1																									
				KTYTLTDYLK	2	99.6%	1																									
				KYPLLLDVYAGPCSQK	2	98.6%	1																									
				LAYVWNNDIYVK	2	100.0%	2																									
				LGTFEVEDQIEAAR	2	100.0%	2																									
				MGFVDNKR	2	81.1%	1																									
				MLQNVQMPSK	2	94.7%	1																									
				QHIEMSTTGWVGR	2	99.2%	1																									
				QHIEMSTTGWVGR	3	98.5%	1																									
				QVEYLLIHGTADDNVHFQQSAQISK	3	100.0%	1																									
				VLEDNSALDK	2	99.9%	2																									
				VTCLSCELNPER	2	97.5%	1																									
				WEYYDSVYTER	2	99.6%	1																									
				WISDHEYLYK	2	99.0%	1																									
				WISDHEYLYK	3	83.3%	1																									
				WNCLVAR	2	95.1%	1																									
				YMGLPTPEDNLDHYR	2	98.7%	1																									
				YMGLPTPEDNLDHYR	3	99.8%	1																									
				YPLLLDVYAGPCSQK	2	100.0%	2																									
IPI00018963	PARVA	alpha-parvin	99.6%	3.4	1	1	1	5	238,640	217,650	311,830	304,534	45,778	33,763	45,517	22,739	42.9	34.7	32.6	16.7	-1.1	0.7	1.3	0.3	1.3	0.2	1.4	0.1	1.4	0.07	-1.0	0.9
IPI00386908	PARVA	isoform 2 of Alpha-parvin	99.6%	7.7	1	1	1	5	238,640	217,650	311,830	304,534	45,778	33,763	45,517	22,739	42.9	34.7	32.6	16.7	-1.1	0.7	1.3	0.3	1.3	0.2	1.4	0.1	1.4	0.07	-1.0	0.9
IPI00922277	PARVA	cDNA FLJ54827, highly similar to Alpha-parvin	99.6%	4.8	1	1	1	5	238,640	217,650	311,830	304,534	45,778	33,763	45,517	22,739	42.9	34.7	32.6	16.7	-1.1	0.7	1.3	0.3	1.3	0.2	1.4	0.1	1.4	0.07	-1.0	0.9
IPI00982663	PARVA	Uncharacterized protein	99.6%	6.7	1	1	1	5	238,640	217,650	311,830	304,534	45,778	33,763	45,517	22,739	42.9	34.7	32.6	16.7	-1.1	0.7	1.3	0.3	1.3	0.2	1.4	0.1	1.4	0.07	-1.0	0.9
IPI01009766	PARVA	42 kDa protein	99.6%	3.8	1	1	1	5	238,640	217,650	311,830	304,534	45,778	33,763	45,517	22,739	42.9	34.7	32.6	16.7	-1.1	0.7	1.3	0.3	1.3	0.2	1.4	0.1	1.4	0.07	-1.0	0.9
				VLIDWINDVLVGER	2	99.6%	1																									
IPI00019025	PARD6B	Partitioning defective 6 homolog beta	99.2%	3.8	1	1	1	1	7,159,990	8,146,750	6,768,250	7,082,660	875,396	886,710	424,355	266,483	27.3	24.3	14.0	8.4	1.1	0.5	-1.1	0.7	-1.0	0.9	-1.2	0.2	-1.2	0.3	1.0	0.5
				SLDQVTDMMIANSR	2	99.2%	1																									
IPI00019046	RBM22	isoform 1 of Pre-mRNA-splicing factor RBM22	97.7%	4.5	1	1	1	3	1,079,877	1,117,183	1,334,673	1,229,430	134,904	103,962	51,771	91,080	27.9	20.8	8.7	16.6	1.0	0.8	1.2	0.1	1.1	0.4	1.2	0.1	1.1	0.4	-1.1	0.3
IPI00973998	RBM22	Uncharacterized protein	97.7%	7.8	1	1	1	3	1,079,877	1,117,183	1,334,673	1,229,430	134,904	103,962	51,771	91,080	27.9	20.8	8.7	16.6	1.0	0.8	1.2	0.1	1.1	0.4	1.2	0.1	1.1	0.4	-1.1	0.3
IPI00979459	RBM22	Uncharacterized protein	97.7%	10.6	1	1	1	3	1,079,877	1,117,183	1,334,673	1,229,430	134,904	103,962	51,771	91,080	27.9	20.8	8.7	16.6	1.0	0.8	1.2	0.1	1.1	0.4	1.2	0.1	1.1	0.4	-1.1	0.3
				NVCQTCLLDLEYGLPIQVR	2	97.7%	1																									
IPI00019090	COL19A1	Collagen alpha-1(XIX) chain	98.4%	1.3	1	1	1	1	5,882,330	6,715,910	8,228,740	7,804,610	783,097	418,258	1,861,362	666,589	29.8	13.9	50.6	19.1	1.1	0.4	1.4	0.3	1.3	0.1	1.2	0.5	1.2	0.2	-1.1	0.8
				GEAGLPGAPGSPGQK	2	97.3%	1																									
IPI00019146	CXADR	isoform 1 of Coxsackievirus and adenovirus receptor	99.0%	4.7	1	1	1	2	2,261,585	2,273,435	2,332,515	2,678,125	220,675	398,362	180,249	195,852	21.8	39.2	17.3	16.4	1.0	1	1.0	0.8	1.2	0.2	1.0	0.9	1.2	0.4	1.1	0.2
IPI00607658	CXADR	Uncharacterized protein	99.0%	4.8	1	1	1	2	2,261,585	2,273,435	2,332,515	2,678,125	220,675	398,362	180,249	195,852	21.8	39.2	17.3	16.4	1.0	1	1.0	0.8	1.2	0.2	1.0	0.9	1.2	0.4	1.1	0.2
				MPTSWLAEMTSSVISVK	2	99.0%	1																									
IPI00019148	IGBP1	Immunoglobulin-binding protein 1	100.0%	11.5	3	3	3	1	10,211,505	10,160,097	12,525,870	10,829,157	526,284	454,364	567,822	374,354	11.5	10.0	10.1	7.7	-1.0	0.9	1.2	0.02	1.1	0.4	1.2	0.01	1.1	0.3	-1.2	0.04
				AAEMLSQLDLFSR	2	98.6%	1																									
				LPELFETGR	2	99.2%	1																									
				WIDISLEEIESIDQEIK	2	100.0%	1																									
IPI00019169	SH3GL1	endophilin-A2 isoform 1	99.2%	13.3	3	3	3	1	6,285,903	6,412,204	5,870,062	6,838,558	510,313	293,826	314,808	242,781	18.2	10.3	12.0	7.9	1.0	0.8	-1.1	0.5	1.1	0.4	-1.1	0.2	1.1	0.3	1.2	0.04
				ELGGESNFGDALLDAGESMK	2	99.2%	1																									
				NPGYPQSEGLLGECMIR	2	90.9%	1																									
				TIEYLQPNPASR	2	94.2%	1																									
IPI00644418	SH3GL1	endophilin-A2 isoform 3	94.2%	4.0	1	1	1	4	298,713	358,054	298,002	476,858	32,790	25,052	36,157	73,832	24.6	15.7	27.1	34.6	1.2	0.2	-1.0	1	1.6	0.06	-1.2	0.2	1.3	0.2	1.6	0.06
IPI00019171	SH3GL2	Endophilin-A1	94.2%	3.4	1	1	1	4	298,713	358,054	298,002	476,858	32,790	25,052	36,157	73,832	24.6	15.7	27.1	34.6	1.2	0.2	-1.0	1	1.6	0.06	-1.2	0.2	1.3	0.2	1.6	0.06
IPI00922749	SH3GL2	cDNA FLJ52909, highly similar to SH3-containing GRB2-like protein 2	94.2%	6.3	1	1	1	4	298,713	358,054	298,002	476,858	32,790	25,052	36,157	73,832	24.6	15.7	27.1	34.6	1.2	0.2	-1.0	1	1.6	0.06	-1.2	0.2	1.3	0.2	1.6	0.06
IPI01009303	SH3GL2	SH3-domain GRB2-like 2, isoform CRA_b	94.2%	3.8	1	1	1	4	298,713	358,054	298,002	476,858	32,790	25,052	36,157	73,832	24.6	15.7	27.1	34.6	1.2	0.2	-1.0	1	1.6	0.06	-1.2	0.2	1.3	0.2	1.6	0.06
				TIEYLQPNPASR	2	94.2%	1																									
IPI00019178	PSPH	Phosphoserine phosphatase	100.0%	16.0	3	3	4	2	11,860,660	12,056,700	12,387,035	15,012,800	1,124,497	543,634	950,573	654,702	21.2	10.1	17.2	9.8	1.0	0.9	1.0	0.7	1.3	0.04	1.0	0.8	1.2	0.008	1.2	0.05
IPI00925737	PSPH	Uncharacterized protein	100.0%	19.3	3	3	4	2	11,860,660	12,056,700	12,387,035	15,012,800	1,124,497	543,634	950,573	654,702	21.2	10.1	17.2	9.8	1.0	0.9	1.0	0.7	1.3	0.04	1.0	0.8	1.2	0.008	1.2	0.05
				ICGVEDAVSEMTR	2	99.9%	2																									
				LIAEQPPHLTPGIR	2	95.6%	1																									
				SIVEHVASK	2	99.7%	1																									
IPI00019242	MMP15	Matrix metalloproteinase-15	98.6%	3.1	1	1	1	1	3,705,830	4,206,910	4,020,940	5,431,920	800,896	623,887	666,379	539,393	48.3	33.2	37.1	22.2	1.1	0.6	1.1	0.8	1.5	0.1	-1.0	0.8	1.3	0.2	1.4	0.1
				MGSDPSAPGRPGWTGSLLGDR	2	98.6%	1																									
IPI00019269	WDR61	WD repeat-containing protein 61	100.0%	23.0	3	3	3	1	3,571,601	3,930,250	4,041,398	4,558,827	319,542	265,870	386,337	133,435	20.0	15.1	21.4	6.5	1.1	0.4	1.1	0.4	1.3	0.02	1.0	0.8	1.2	0.07	1.1	0.3
				SIDAGPVDAWTLAFSPDSQYLATGTHVGK	3	99.9%	1																									
				SLTFSPDSQLLVTASDDGYIK	2	100.0%	1																									
				YLASGAIDGIINIFDIATGK	2	99.6%	1																									

IPI00019276	UBXN6	isoform 1 of UBX domain-containing protein 6	95.9%	3.9	1	1	1	1	2,418,820	2,490,570	2,628,880	3,166,270	174,452	244,606	356,826	241,144	16.1	22.0	30.4	17.0	1.0	0.8	1.1	0.6	1.3	0.04	1.1	0.8	1.3	0.08	1.2	0.2
				QGPTNEAQMAAAAALAR	2	95.9%	1																									
IPI00019329	DYNLL1	Dynein light chain 1, cytoplasmic	99.6%	24.7	1	1	1	1	797,141	1,041,215	857,771	1,132,856	80,171	97,424	81,906	80,853	22.5	20.9	21.4	16.0	1.3	0.09	1.1	0.6	1.4	0.02	-1.2	0.2	1.1	0.5	1.3	0.04
				NADMSEEMQQDSVECATQALEK	2	99.6%	1																									
IPI00019355	TSC22D1	isoform 2 of TSC22 domain family protein 1	99.5%	8.3	1	1	2	3	3,018,433	3,122,520	2,717,190	3,621,713	275,477	246,584	306,507	185,715	20.4	17.7	25.2	11.5	1.0	0.8	-1.1	0.5	1.2	0.1	-1.1	0.3	1.2	0.1	1.3	0.04
IPI00301610	TSC22D1	isoform 1 of TSC22 domain family protein 1	99.5%	1.1	1	1	2	3	3,018,433	3,122,520	2,717,190	3,621,713	275,477	246,584	306,507	185,715	20.4	17.7	25.2	11.5	1.0	0.8	-1.1	0.5	1.2	0.1	-1.1	0.3	1.2	0.1	1.3	0.04
IPI00942808	TSC22D1	TSC22 domain family protein 1 isoform 1	99.5%	1.1	1	1	2	3	3,018,433	3,122,520	2,717,190	3,621,713	275,477	246,584	306,507	185,715	20.4	17.7	25.2	11.5	1.0	0.8	-1.1	0.5	1.2	0.1	-1.1	0.3	1.2	0.1	1.3	0.04
				NSQLEQENNLLK	2	99.5%	2																									
IPI00019359	KRT9	Keratin, type I cytoskeletal 9	100.0%	25.7	10	10	10	1	29,823,822	31,755,489	30,815,937	34,556,086	2,342,262	1,204,862	1,553,013	945,750	17.6	8.5	11.3	6.1	1.1	0.5	1.0	0.7	1.2	0.1	-1.0	0.6	1.1	0.1	1.1	0.07
				DIENQYETQITQIEHEVSSSGQEVQSSAK	3	100.0%	1																									
				FEMEQNLRQGVDADINGLRQVLDNLTMEK	3	88.6%	1																									
				GGSGGSYGGGGSGGGYGGGSGSR	2	99.9%	1																									
				HGVQELEIELQSQLSK	2	100.0%	1																									
				QGVDADINGLR	2	99.9%	1																									
				SGGGGGGGLGSGGSIR	2	100.0%	1																									
				STMQELNSR	2	99.7%	1																									
				TLLDIDNTR	2	99.9%	1																									
				TLNDMRQEYEQLIAK	3	99.7%	1																									
				VQALEEANNDLENK	2	99.5%	1																									
IPI00019376	SEP11	isoform 2 of Septin-11	100.0%	18.2	5	5	5	4	10,212,164	11,540,597	10,316,110	12,277,852	794,565	452,432	694,560	373,479	17.4	8.8	15.1	6.8	1.1	0.2	1.0	0.9	1.2	0.05	-1.1	0.2	1.1	0.2	1.2	0.04
IPI00952909	SEP11	isoform 1 of Septin-11	100.0%	18.7	5	5	5	4	10,212,164	11,540,597	10,316,110	12,277,852	794,565	452,432	694,560	373,479	17.4	8.8	15.1	6.8	1.1	0.2	1.0	0.9	1.2	0.05	-1.1	0.2	1.1	0.2	1.2	0.04
IPI00964937	SEP11	Uncharacterized protein	100.0%	18.8	5	5	5	4	10,212,164	11,540,597	10,316,110	12,277,852	794,565	452,432	694,560	373,479	17.4	8.8	15.1	6.8	1.1	0.2	1.0	0.9	1.2	0.05	-1.1	0.2	1.1	0.2	1.2	0.04
IPI00967716	SEP11	Uncharacterized protein	100.0%	18.5	5	5	5	4	10,212,164	11,540,597	10,316,110	12,277,852	794,565	452,432	694,560	373,479	17.4	8.8	15.1	6.8	1.1	0.2	1.0	0.9	1.2	0.05	-1.1	0.2	1.1	0.2	1.2	0.04
				AAAQLLQSQAQQSGAQQTK	3	100.0%	1																									
				ELEEEVNNFQK	2	99.6%	1																									
				NLSLSGHVGFDSLPDQLVNK	3	98.1%	1																									
				RNEFLGELQK	3	95.2%	1																									
				VNIIPIIAKADTIAKNELHK	2	85.8%	1																									
IPI00019383	GALK1	cDNA FLJ56840, highly similar to Galactokinase	100.0%	19.4	5	5	5	3	8,146,524	8,595,907	8,017,143	9,033,120	770,557	357,979	693,268	279,854	21.2	9.3	19.3	6.9	1.1	0.6	-1.0	0.9	1.1	0.3	-1.1	0.5	1.1	0.4	1.1	0.2
IPI00747722	GALK1	Uncharacterized protein	100.0%	20.5	5	5	5	3	8,146,524	8,595,907	8,017,143	9,033,120	770,557	357,979	693,268	279,854	21.2	9.3	19.3	6.9	1.1	0.6	-1.0	0.9	1.1	0.3	-1.1	0.5	1.1	0.4	1.1	0.2
IPI00940264	GALK1	Galactokinase	100.0%	20.9	5	5	5	3	8,146,524	8,595,907	8,017,143	9,033,120	770,557	357,979	693,268	279,854	21.2	9.3	19.3	6.9	1.1	0.6	-1.0	0.9	1.1	0.3	-1.1	0.5	1.1	0.4	1.1	0.2
				AFREEFGAEPELAVSAPGR	3	99.3%	1																									
				AQVCQQAEHSFAGMPCGIMDQFISLMGQK	3	85.9%	1																									
				EVQLEELEAAR	2	100.0%	1																									
				HSLASSEYPVR	2	92.2%	1																									
				QPQVAELLAEAR	2	99.9%	1																									
IPI00019385	SSR4	Translocon-associated protein subunit delta	100.0%	6.4	1	1	1	5	1,637,560	1,460,302	2,027,658	1,669,634	93,652	90,016	124,446	87,425	12.8	13.8	13.7	11.7	-1.1	0.2	1.2	0.04	1.0	0.8	1.4	0.006	1.1	0.1	-1.2	0.05
IPI00646864	SSR4	Protein	100.0%	9.2	1	1	1	5	1,637,560	1,460,302	2,027,658	1,669,634	93,652	90,016	124,446	87,425	12.8	13.8	13.7	11.7	-1.1	0.2	1.2	0.04	1.0	0.8	1.4	0.006	1.1	0.1	-1.2	0.05
IPI00647421	SSR4	Uncharacterized protein	100.0%	7.4	1	1	1	5	1,637,560	1,460,302	2,027,658	1,669,634	93,652	90,016	124,446	87,425	12.8	13.8	13.7	11.7	-1.1	0.2	1.2	0.04	1.0	0.8	1.4	0.006	1.1	0.1	-1.2	0.05
IPI01008877	SSR4	translocon-associated protein subunit delta isoform 3 precursor	100.0%	6.1	1	1	1	5	1,637,560	1,460,302	2,027,658	1,669,634	93,652	90,016	124,446	87,425	12.8	13.8	13.7	11.7	-1.1	0.2	1.2	0.04	1.0	0.8	1.4	0.006	1.1	0.1	-1.2	0.05
IPI01009057	SSR4	translocon-associated protein subunit delta isoform 1 precursor	100.0%	6.0	1	1	1	5	1,637,560	1,460,302	2,027,658	1,669,634	93,652	90,016	124,446	87,425	12.8	13.8	13.7	11.7	-1.1	0.2	1.2	0.04	1.0	0.8	1.4	0.006	1.1	0.1	-1.2	0.05
				FFDEESYSLLR	2	97.6%	1																									
IPI00019407	NSDHL	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	99.5%	5.1	1	1	1	2	1,216,215	1,354,340	1,505,890	1,403,380	100,118	93,802	54,973	49,390	18.4	15.5	8.2	7.9	1.1	0.3	1.2	0.03	1.2	0.1	1.1	0.2	1.0	0.7	-1.1	0.2
IPI00646262	NSDHL	Uncharacterized protein	99.5%	7.5	1	1	1	2	1,216,215	1,354,340	1,505,890	1,403,380	100,118	93,802	54,973	49,390	18.4	15.5	8.2	7.9	1.1	0.3	1.2	0.03	1.2	0.1	1.1	0.2	1.0	0.7	-1.1	0.2
				GYAVNVFDIQQGFDNPQVR	2	99.5%	1																									
IPI00902796	-	cDNA FLJ13982 fis, clone Y79AA1001711, highly similar to 60 kDa SS-A/Ro ribonuc	92.3%	2.3	1	1	1	5	3,085,300	2,933,280	3,121,780	3,493,800	236,821	190,903	268,469	131,345	17.2	14.6	19.2	8.4	-1.1	0.6	1.0	0.9	1.1	0.2	1.1	0.6	1.2	0.04	1.1	0.2
IPI00019450	TROVE2	isoform Long of 60 kDa SS-A/Ro ribonucleoprotein	92.3%	2.4	1	1	1	5	3,085,300	2,933,280	3,121,780	3,493,800	236,821	190,903	268,469	131,345	17.2	14.6	19.2	8.4	-1.1	0.6	1.0	0.9	1.1	0.2	1.1	0.6	1.2	0.04	1.1	0.2
IPI00642416	TROVE2	60 kDa SS-A/Ro ribonucleoprotein isoform 4	92.3%	2.5	1	1	1	5	3,085,300	2,933,280	3,121,780	3,493,800	236,821	190,903	268,469	131,345	17.2	14.6	19.2	8.4	-1.1	0.6	1.0	0.9	1.1	0.2	1.1	0.6	1.2	0.04	1.1	0.2
IPI00646322	TROVE2	60 kDa SS-A/Ro ribonucleoprotein isoform 3	92.3%	2.4	1	1	1	5	3,085,300	2,933,280	3,121,780	3,493,800	236,821	190,903	268,469	131,345	17.2	14.6	19.2	8.4	-1.1	0.6	1.0	0.9	1.1	0.2	1.1	0.6	1.2	0.04	1.1	0.2
IPI00646813	TROVE2	60 kDa SS-A/Ro ribonucleoprotein isoform 1	92.3%	2.5	1	1	1	5	3,085,300	2,933,280	3,121,780	3,493,800	236,821	190,903	268,469	131,345	17.2	14.6	19.2	8.4	-1.1	0.6	1.0	0.9	1.1	0.2	1.1	0.6	1.2	0.04	1.1	0.2
				ALLQEMPLTALLR	2	92.3%	1																									
IPI00019463	EIF2AK2	Interferon-induced, double-stranded RNA-activated protein kinase	98.3%	2.2	1	1	1	3	321,511	292,364	390,732	455,636	32,577	32,584	68,851	47,615	22.7	24.9	39.4	23.4	-1.1	0.5	1.2	0.4	1.4	0.05	1.3	0.2	1.6	0.02	1.2	0.5
IPI00385404	EIF2AK2	interferon-induced, double-stranded RNA-activated protein kinase isoform b	98.3%	2.4	1	1	1	3	321,511	292,364	390,732	455,636	32,577	32,584	68,851	47,615	22.7	24.9	39.4	23.4	-1.1	0.5	1.2	0.4	1.4	0.05	1.3	0.2	1.6	0.02	1.2	0.5
IPI00807398	EIF2AK2	EIF2AK2 protein (Fragment)	98.3%	3.3	1	1	1	3	321,511	292,364	390,732	455,636	32,577	32,584	68,851	47,615	22.7	24.9	39.4	23.4	-1.1	0.5	1.2	0.4	1.4	0.05	1.3	0.2	1.6	0.02	1.2	0.5
				VLALELFEQITK	2	98.3%	1																									
IPI00019472	SLC1A5	Neutral amino acid transporter B(0)	100.0%	11.1	4	4	5	2	4,569,731	4,966,090	4,627,944	5,297,648	532,110	337,055	557,369	166,901	26.0	15.2	26.9	7.0	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.6	1.1	0.4	1.1	0.3
IPI01010276	SLC1A5	Neutral amino acid transporter	100.0%	11.1	4	4	5	2	4,569,731	4,966,090	4,627,944	5,297,648	532,110	337,055	557,369	166,901	26.0	15.2	26.9	7.0	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.6	1.1	0.4	1.1	0.3
				EVLDSFLDLAR	2	98.8%	1																									
				GPAGDATVASEKESVM	2	100.0%	1																									
				NIFPSNLVSAAFR	2	99.9%	1																									
				SELPLDPLPVPTEEGNPLLK	2	100.0%	2																									
IPI00019495	DYNLT1	Dynein light chain Tctex-type 1	99.5%	15.9	1	1	1	2	6,856,295	7,530,500	9,327,150	7,607,340	634,822	400,426	359,687	548,985	20.7	11.9	8.6	16.1	1.1	0.4	1.4	0.01	1.1	0.4	1.2	0.01	1.0	0.9	-1.2	0.03
IPI00479503	DYNLT1	Dynein, light chain, Tctex-type 1, isoform CRA_a	99.5%	19.6	1	1	1	2	6,856,295	7,530,500	9,327,150	7,607,340	634,822	400,426	359,687	548,985	20.7	11.9	8.6	16.1	1.1	0.4	1.4	0.01	1.1	0.4	1.2	0.01	1.0	0.9	-1.2	0.03
				VNQWTTNVVEQTLSQLTK	2	99.5%	1																									
IPI00019502	MYH9	isoform 1 of Myosin-9	100.0%	35.7	54	60	73	1	269,875,636	278,377,764	265,305,332	308,127,896	########	7,037,390	########	8,059,499	16.4	5.7	15.3	5.9	1.0	0.7	-1.0	0.9	1.1	0.1	-1.0	0.5	1.1	0.02	1.2	0.06
				ADEWLMK	2	99.5%	1																									
				AKQTLENERGELANEVK	3	96.5%	1																									
				ALELDSNLYR	2	99.9%	1																									
				ALEQQVEEMK	2	100.0%	1																									
				ALEQQVEEMKTQLEELEDELQATEDAK	3	100.0%	1																									
				ANLQIDQINTDLNLER	2	100.0%	1																									
				ASITALEAK	2	92.9%	1																									
				ASREEILAQAK	2	99.3%	1																									
				DELADEIANSSGKGALALEEK	2	99.7%	1																									
				DFSALESQLQDTQELLQEENR	2	100.0%	1																									
				DFSALESQLQDTQELLQEENR	3	100.0%	1																									
				DFSALESQLQDTQELLQEENRQK	3	80.5%	1																									
				DLEAHIDSANK	2	100.0%	1																									
				DLEGLSQR	2	98.3%	1																									
				DLGEELEALKTELEDTLDSTAAQQELR	3	100.0%	1																									
				DLKITDVIIGFQACCR	3	99.1%	1																									
				DVLLQVDDER	2	92.1%	1																									
				ELEDATETADAMNR	2	100.0%	2																									
				ELESQISELQEDLESER	3	100.0%	1																									
				GALALEEKR	2	86.8%	1																									
				HSQAVEELAEQLEQTKR	3	100.0%	1																									
				IAEFTTNLTEEEEK	2	100.0%	2																									
				IAQLEEELEEEQGNTELINDR	2	100.0%	1																									
				IAQLEEQLDNETKER	2	98.4%	1																									
				IAQLEEQLDNETKER	3	99.3%	1																									
				IIGLDQVAGMSETALPGAFK	2	100.0%	1																									
				IIGLDQVAGMSETALPGAFK	3	100.0%	1																									
				IMGIPEEEQMGLLR	2	100.0%	1																									
				IRELESQISELQEDLESER	3	100.0%	1																									
				KANLQIDQINTDLNLER	3	95.7%	1																									
				KEEELQAALAR	2	99.9%	2																									
				KLEEEQIILEDQNCK	3	99.3%	1																									
				KLVWVPSDK	2	93.4%	1																									
				KQELEEICHDLEAR	3	99.7%	1																									
				KVEAQLQELQVK	2	99.9%	2																									
				LEVNLQAMK	2	99.5%	1																									
				LQQELDDLLVDLDHQR	3	100.0%	1																									
				LQVELDNVTGLLSQSDSK	3	97.8%	1																									
				LTEMETLQSQLMAEK	2	100.0%	2																									
				MQQNIQELEEQLEEEESAR	2	100.0%	1																									
				MQQNIQELEEQLEEEESAR	3	100.0%	1																									
				NFINNPLAQADWAAK	2	99.9%	1																									
				NLPIYSEEIVEMYK	2	100.0%	2																									
				QAQQERDELADEIANSSGK	3	100.0%	1																									
				QIATLHAQVADMK	2	100.0%	1																									
				QLLQANPILEAFGNAK	2	100.0%	2																									
				QTLENERGELANEVK	3	99.4%	1																									
				RGDLPFVVPR	2	100.0%	2																									
				RGDLPFVVPR	3	100.0%	1																									
				RQQQLTAMK	2	98.7%	1																									
				SGFEPASLKEEVGEEAIVELVENGKK	3	100.0%	1																									
				SMEAEMIQLQEELAAAER	2	100.0%	2																									
				SMMQDREDQSILCTGESGAGK	3	94.6%	1																									
				TDLLLEPYNK	2	100.0%	2																									
				TEMEDLMSSKDDVGK	3	100.0%	1																									
				VEAQLQELQVK	2	100.0%	2																									
				VISGVLQLGNIVFK	2	100.0%	2																									
				VSHLLGINVTDFTR	2	100.0%	2																									
				VSHLLGINVTDFTR	3	100.0%	1																									
				YEILTPNSIPK	2	100.0%	1																									
IPI00019540	PPP6R3	isoform 4 of Serine/threonine-protein phosphatase 6 regulatory subunit 3	100.0%	1.4	1	1	1	9	893,433	908,507	915,210	1,052,055	53,288	37,270	61,709	124,757	13.3	9.2	15.1	26.5	1.0	0.8	1.0	0.8	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.4
IPI00030624	PPP6R3	isoform 6 of Serine/threonine-protein phosphatase 6 regulatory subunit 3	100.0%	1.3	1	1	1	9	893,433	908,507	915,210	1,052,055	53,288	37,270	61,709	124,757	13.3	9.2	15.1	26.5	1.0	0.8	1.0	0.8	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.4
IPI00719345	PPP6R3	isoform 3 of Serine/threonine-protein phosphatase 6 regulatory subunit 3	100.0%	1.4	1	1	1	9	893,433	908,507	915,210	1,052,055	53,288	37,270	61,709	124,757	13.3	9.2	15.1	26.5	1.0	0.8	1.0	0.8	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.4
IPI00719725	PPP6R3	isoform 5 of Serine/threonine-protein phosphatase 6 regulatory subunit 3	100.0%	1.3	1	1	1	9	893,433	908,507	915,210	1,052,055	53,288	37,270	61,709	124,757	13.3	9.2	15.1	26.5	1.0	0.8	1.0	0.8	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.4
IPI00719821	PPP6R3	isoform 1 of Serine/threonine-protein phosphatase 6 regulatory subunit 3	100.0%	1.3	1	1	1	9	893,433	908,507	915,210	1,052,055	53,288	37,270	61,709	124,757	13.3	9.2	15.1	26.5	1.0	0.8	1.0	0.8	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.4
IPI00909546	PPP6R3	cDNA FLJ59366, highly similar to SAPS domain family member 3	100.0%	4.4	1	1	1	9	893,433	908,507	915,210	1,052,055	53,288	37,270	61,709	124,757	13.3	9.2	15.1	26.5	1.0	0.8	1.0	0.8	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.4
IPI00983215	PPP6R3	Uncharacterized protein	100.0%	1.3	1	1	1	9	893,433	908,507	915,210	1,052,055	53,288	37,270	61,709	124,757	13.3	9.2	15.1	26.5	1.0	0.8	1.0	0.8	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.4
IPI00985128	PPP6R3	Uncharacterized protein	100.0%	1.3	1	1	1	9	893,433	908,507	915,210	1,052,055	53,288	37,270	61,709	124,757	13.3	9.2	15.1	26.5	1.0	0.8	1.0	0.8	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.4
IPI01015850	PPP6R3	98 kDa protein	100.0%	1.3	1	1	1	9	893,433	908,507	915,210	1,052,055	53,288	37,270	61,709	124,757	13.3	9.2	15.1	26.5	1.0	0.8	1.0	0.8	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.4
				QDVLNWLNEEK	2	99.9%	1																									
IPI00019599	UBE2V1	isoform 1 of Ubiquitin-conjugating enzyme E2 variant 1	100.0%	17.8	5	5	6	4	7,254,524	6,948,905	7,050,579	7,988,912	498,787	299,744	231,913	261,652	15.4	9.7	7.4	7.3	-1.0	0.6	-1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.03	1.1	0.03
IPI00030962	UBE2V1	isoform 5 of Ubiquitin-conjugating enzyme E2 variant 1	100.0%	38.8	5	5	6	4	7,254,524	6,948,905	7,050,579	7,988,912	498,787	299,744	231,913	261,652	15.4	9.7	7.4	7.3	-1.0	0.6	-1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.03	1.1	0.03
IPI00447356	UBE2V1	isoform 2 of Ubiquitin-conjugating enzyme E2 variant 1	100.0%	38.8	5	5	6	4	7,254,524	6,948,905	7,050,579	7,988,912	498,787	299,744	231,913	261,652	15.4	9.7	7.4	7.3	-1.0	0.6	-1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.03	1.1	0.03
IPI00472498	UBE2V1	isoform 3 of Ubiquitin-conjugating enzyme E2 variant 1	100.0%	44.9	5	5	6	4	7,254,524	6,948,905	7,050,579	7,988,912	498,787	299,744	231,913	261,652	15.4	9.7	7.4	7.3	-1.0	0.6	-1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.03	1.1	0.03
				GVGDGTVSWGLEDDEDMTLTR	2	100.0%	1																									
				INMNGVNSSNGVVDPR	2	100.0%	2																									
				LLEELEEGQK	2	99.9%	1																									
				WTGMIIGPPR	2	100.0%	1																									
				YPEAPPFVR	2	98.2%	1																									
IPI00019600	UBE2V2	Ubiquitin-conjugating enzyme E2 variant 2	100.0%	39.3	4	4	4	1	4,433,537	4,209,053	4,312,133	4,753,887	333,848	155,575	105,730	186,488	16.8	8.3	5.5	8.8	-1.1	0.6	-1.0	0.7	1.1	0.4	1.0	0.6	1.1	0.06	1.1	0.07
				GVGDGTVSWGLEDDEDMTLTR	2	100.0%	1																									
				INMNGINNSSGMVDAR	2	100.0%	1																									

				LLEELEEGQK	2	99.9%	1																									
				WTGMIIGPPR	2	100.0%	1																									
IPI00019733	RAE1	mRNA export factor	100.0%	9.2	2	2	2	3	3,324,020	3,170,000	3,349,040	3,773,427	397,897	223,794	205,743	254,977	26.8	15.8	13.7	15.1	-1.0	0.7	1.0	1	1.1	0.4	1.1	0.6	1.2	0.1	1.1	0.2
IPI00982313	RAE1	Uncharacterized protein	100.0%	7.8	2	2	2	3	3,324,020	3,170,000	3,349,040	3,773,427	397,897	223,794	205,743	254,977	26.8	15.8	13.7	15.1	-1.0	0.7	1.0	1	1.1	0.4	1.1	0.6	1.2	0.1	1.1	0.2
IPI01010974	RAE1	Uncharacterized protein	100.0%	15.7	2	2	2	3	3,324,020	3,170,000	3,349,040	3,773,427	397,897	223,794	205,743	254,977	26.8	15.8	13.7	15.1	-1.0	0.7	1.0	1	1.1	0.4	1.1	0.6	1.2	0.1	1.1	0.2
				APNYSCVMTGSWDK	2	99.6%	1																									
				MWDLSSNQAIQIAQHDAPVK	3	99.7%	1																									
IPI00019755	GSTO1	Glutathione S-transferase omega-1	100.0%	33.2	7	7	9	1	25,579,277	26,799,330	25,498,350	29,250,368	2,301,873	1,379,882	1,802,855	1,037,182	20.1	11.5	15.8	7.9	1.0	0.7	-1.0	1	1.1	0.2	-1.1	0.6	1.1	0.2	1.1	0.1
				EDPTVSALLTSEK	2	99.1%	1																									
				GSAPPGPVPEGSIR	2	99.8%	2																									
				KLLPDDPYEK	2	97.1%	1																									
				LNECVDHTPK	2	99.9%	1																									
				MILELFSK	2	91.1%	1																									
				SQNKEDYAGLKEEFR	3	100.0%	1																									
				VPSLVGSFIR	2	100.0%	2																									
IPI00019812	PPP5C	Serine/threonine-protein phosphatase 5	100.0%	9.0	4	4	4	4	6,109,103	6,844,243	6,128,873	7,134,923	320,777	246,588	242,196	350,424	11.7	8.1	8.8	11.0	1.1	0.1	1.0	1	1.2	0.06	-1.1	0.07	1.0	0.5	1.2	0.05
IPI00793942	PPP5C	serine/threonine-protein phosphatase 5 isoform 2	100.0%	9.4	4	4	4	4	6,109,103	6,844,243	6,128,873	7,134,923	320,777	246,588	242,196	350,424	11.7	8.1	8.8	11.0	1.1	0.1	1.0	1	1.2	0.06	-1.1	0.07	1.0	0.5	1.2	0.05
IPI00984299	PPP5C	Serine/threonine-protein phosphatase	100.0%	9.3	4	4	4	4	6,109,103	6,844,243	6,128,873	7,134,923	320,777	246,588	242,196	350,424	11.7	8.1	8.8	11.0	1.1	0.1	1.0	1	1.2	0.06	-1.1	0.07	1.0	0.5	1.2	0.05
IPI01014578	PPP5C	Serine/threonine-protein phosphatase (Fragment)	100.0%	9.3	4	4	4	4	6,109,103	6,844,243	6,128,873	7,134,923	320,777	246,588	242,196	350,424	11.7	8.1	8.8	11.0	1.1	0.1	1.0	1	1.2	0.06	-1.1	0.07	1.0	0.5	1.2	0.05
				AASNMALGK	2	80.1%	1																									
				AEGYEVAHGGR	2	85.8%	1																									
				AFLEENNLDYIIR	2	100.0%	1																									
				GVSCQFGPDVTK	2	97.3%	1																									
IPI00019848	HCFC1	isoform 1 of Host cell factor 1	99.6%	4.2	5	5	5	3	7,209,752	7,048,771	6,934,078	7,657,174	786,071	200,498	311,989	311,774	24.4	6.4	10.1	9.1	-1.0	0.9	-1.0	0.8	1.1	0.6	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00219326	HCFC1	isoform 2 of Host cell factor 1	99.6%	4.3	5	5	5	3	7,209,752	7,048,771	6,934,078	7,657,174	786,071	200,498	311,989	311,774	24.4	6.4	10.1	9.1	-1.0	0.9	-1.0	0.8	1.1	0.6	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00641743	HCFC1	Uncharacterized protein	99.6%	4.1	5	5	5	3	7,209,752	7,048,771	6,934,078	7,657,174	786,071	200,498	311,989	311,774	24.4	6.4	10.1	9.1	-1.0	0.9	-1.0	0.8	1.1	0.6	-1.0	0.8	1.1	0.1	1.1	0.1
				ENQWFDVGVIK	2	94.0%	1																									
				GPFSEISAFKTCLPGFPGAPCAIK	3	84.1%	1																									
				IATGHGQQGVTQVVLK	3	90.2%	1																									
				MYVFGGWVPLVMDDVK	2	99.6%	1																									
				SPDGAHLTWEPPSVTSGK	3	88.6%	1																									
IPI00019884	ACTN2	Alpha-actinin-2	99.7%	1.5	1	1	1	3	871,837	930,077	1,063,493	868,987	113,286	80,344	182,444	95,197	29.1	19.3	38.4	24.5	1.1	0.7	1.2	0.4	-1.0	1	1.1	0.5	-1.1	0.6	-1.2	0.4
IPI01009258	ACTN2	Actinin, alpha 2 variant (Fragment)	99.7%	2.0	1	1	1	3	871,837	930,077	1,063,493	868,987	113,286	80,344	182,444	95,197	29.1	19.3	38.4	24.5	1.1	0.7	1.2	0.4	-1.0	1	1.1	0.5	-1.1	0.6	-1.2	0.4
IPI01010507	ACTN2	cDNA, FLJ96254, highly similar to Homo sapiens actinin, alpha 2 (ACTN2), mRNA	99.7%	1.5	1	1	1	3	871,837	930,077	1,063,493	868,987	113,286	80,344	182,444	95,197	29.1	19.3	38.4	24.5	1.1	0.7	1.2	0.4	-1.0	1	1.1	0.5	-1.1	0.6	-1.2	0.4
				ISNRPAFMPSEGK	2	97.2%	1																									
IPI00019888	ALDH5A1	Succinate-semialdehyde dehydrogenase, mitochondrial	99.2%	1.9	1	1	1	4	1,716,228	1,751,480	1,703,885	1,776,775	68,649	50,510	93,611	47,298	8.9	6.5	12.3	6.0	1.0	0.7	-1.0	0.9	1.0	0.5	-1.0	0.7	1.0	0.7	1.0	0.5
IPI00336008	ALDH5A1	succinate-semialdehyde dehydrogenase, mitochondrial isoform 1 precursor	99.2%	1.8	1	1	1	4	1,716,228	1,751,480	1,703,885	1,776,775	68,649	50,510	93,611	47,298	8.9	6.5	12.3	6.0	1.0	0.7	-1.0	0.9	1.0	0.5	-1.0	0.7	1.0	0.7	1.0	0.5
IPI00946558	ALDH5A1	Uncharacterized protein	99.2%	2.0	1	1	1	4	1,716,228	1,751,480	1,703,885	1,776,775	68,649	50,510	93,611	47,298	8.9	6.5	12.3	6.0	1.0	0.7	-1.0	0.9	1.0	0.5	-1.0	0.7	1.0	0.7	1.0	0.5
IPI01012747	ALDH5A1	48 kDa protein	99.2%	2.2	1	1	1	4	1,716,228	1,751,480	1,703,885	1,776,775	68,649	50,510	93,611	47,298	8.9	6.5	12.3	6.0	1.0	0.7	-1.0	0.9	1.0	0.5	-1.0	0.7	1.0	0.7	1.0	0.5
				YGIDEYLELK	2	99.2%	1																									
IPI00019899	SC4MOL	C-4 methylsterol oxidase	99.1%	4.8	1	1	1	2	461,535	508,722	512,800	483,352	34,327	32,221	34,696	21,877	16.6	14.2	15.1	10.1	1.1	0.3	1.1	0.3	1.0	0.6	1.0	0.9	-1.1	0.5	-1.1	0.5
IPI00556210	SC4MOL	C-4 methylsterol oxidase isoform 2	99.1%	8.6	1	1	1	2	461,535	508,722	512,800	483,352	34,327	32,221	34,696	21,877	16.6	14.2	15.1	10.1	1.1	0.3	1.1	0.3	1.0	0.6	1.0	0.9	-1.1	0.5	-1.1	0.5
				IFGTDSQYNAYNEK	2	99.1%	1																									
IPI00019901	ADD1	isoform 1 of Alpha-adducin	100.0%	11.7	6	6	8	3	6,695,160	7,383,707	6,195,020	6,916,595	519,490	386,039	520,365	314,146	17.4	11.7	18.8	10.2	1.1	0.3	-1.1	0.5	1.0	0.7	-1.2	0.1	-1.1	0.4	1.1	0.3
IPI00220158	ADD1	isoform 3 of Alpha-adducin	100.0%	11.2	6	6	8	3	6,695,160	7,383,707	6,195,020	6,916,595	519,490	386,039	520,365	314,146	17.4	11.7	18.8	10.2	1.1	0.3	-1.1	0.5	1.0	0.7	-1.2	0.1	-1.1	0.4	1.1	0.3
IPI00376220	ADD1	alpha-adducin isoform d	100.0%	13.0	6	6	8	3	6,695,160	7,383,707	6,195,020	6,916,595	519,490	386,039	520,365	314,146	17.4	11.7	18.8	10.2	1.1	0.3	-1.1	0.5	1.0	0.7	-1.2	0.1	-1.1	0.4	1.1	0.3
				INLQGDIVDR	2	99.9%	1																									
				NMAPDLRQDFNMMEQKK	3	97.6%	1																									
				SLVQGELVTASK	2	99.7%	2																									
				TAGPQSQVLCGVVMDR	2	99.9%	1																									
				TLASAGGPDNLVLLNPEK	2	100.0%	1																									
				WQIGEQEFEALMR	2	100.0%	2																									
IPI00019906	BSG	isoform 2 of Basigin	100.0%	12.6	2	2	2	4	3,434,390	3,659,985	3,308,255	3,935,818	315,061	211,727	206,990	342,337	20.5	12.9	14.0	19.5	1.1	0.6	-1.0	0.7	1.1	0.3	-1.1	0.3	1.1	0.5	1.2	0.2
IPI00218019	BSG	isoform 1 of Basigin	100.0%	8.8	2	2	2	4	3,434,390	3,659,985	3,308,255	3,935,818	315,061	211,727	206,990	342,337	20.5	12.9	14.0	19.5	1.1	0.6	-1.0	0.7	1.1	0.3	-1.1	0.3	1.1	0.5	1.2	0.2
IPI00394877	BSG	basigin isoform 4	100.0%	16.6	2	2	2	4	3,434,390	3,659,985	3,308,255	3,935,818	315,061	211,727	206,990	342,337	20.5	12.9	14.0	19.5	1.1	0.6	-1.0	0.7	1.1	0.3	-1.1	0.3	1.1	0.5	1.2	0.2
IPI01010766	BSG	Basigin isoform 3	100.0%	19.3	2	2	2	4	3,434,390	3,659,985	3,308,255	3,935,818	315,061	211,727	206,990	342,337	20.5	12.9	14.0	19.5	1.1	0.6	-1.0	0.7	1.1	0.3	-1.1	0.3	1.1	0.5	1.2	0.2
				SELHIENLNMEADPGQYR	3	99.9%	1																									
				SSEHINEGETAMLVCK	3	97.8%	1																									
IPI00019907	GPC3	Glypican-3	99.5%	2.6	1	1	1	2	3,089,135	3,143,135	2,917,890	3,162,545	294,160	112,467	297,643	204,020	21.3	8.0	22.8	14.4	1.0	0.9	-1.1	0.7	1.0	0.8	-1.1	0.5	1.0	0.9	1.1	0.5
IPI00719135	GPC3	glypican-3 isoform 1 precursor	99.5%	2.5	1	1	1	2	3,089,135	3,143,135	2,917,890	3,162,545	294,160	112,467	297,643	204,020	21.3	8.0	22.8	14.4	1.0	0.9	-1.1	0.7	1.0	0.8	-1.1	0.5	1.0	0.9	1.1	0.5
				LNMEQLLQSASMELK	2	99.5%	1																									
IPI00019912	HSD17B4	Peroxisomal multifunctional enzyme type 2	100.0%	15.9	8	8	10	1	12,588,807	14,225,734	13,643,816	15,276,143	1,029,272	643,323	1,204,278	540,583	18.3	10.1	19.7	7.9	1.1	0.2	1.1	0.5	1.2	0.05	-1.0	0.7	1.1	0.2	1.1	0.3
				AYALAFAER	2	87.2%	1																									
				FAKPVYPGQTLQTEMWK	3	100.0%	1																									
				GALVVVNDLGGDFK	2	100.0%	2																									
				IDVVVNNAGILR	2	100.0%	1																									
				LGLLGLANSLAIEGR	2	100.0%	2																									
				LPPFSYAYTELEAIMYALGVGASIK	3	88.6%	1																									
				VLQQFADNDVSR	2	100.0%	1																									
				VVLVTGAGAGLGR	2	100.0%	1																									
IPI00019927	PSMD7	26S proteasome non-ATPase regulatory subunit 7	100.0%	6.8	2	2	2	2	4,298,365	4,221,370	4,344,285	4,748,515	421,927	239,067	379,822	321,696	22.0	12.7	19.6	15.2	-1.0	0.9	1.0	0.9	1.1	0.4	1.0	0.8	1.1	0.2	1.1	0.4
IPI01009629	PSMD7	cDNA FLJ51373, highly similar to 26S proteasome non-ATPase regulatory subunit 7	100.0%	8.9	2	2	2	2	4,298,365	4,221,370	4,344,285	4,748,515	421,927	239,067	379,822	321,696	22.0	12.7	19.6	15.2	-1.0	0.9	1.0	0.9	1.1	0.4	1.0	0.8	1.1	0.2	1.1	0.4
				NDIAINELMK	2	98.7%	1																									
				SVVALHNLINNK	2	91.6%	1																									
IPI00019977	GTF2E1	General transcription factor IIE subunit 1	98.3%	3.0	1	1	1	2	3,339,750	3,469,820	3,252,200	3,820,865	323,283	254,098	231,137	185,409	21.6	16.4	15.9	10.9	1.0	0.8	-1.0	0.8	1.1	0.2	-1.1	0.5	1.1	0.3	1.2	0.09
IPI00946947	GTF2E1	Uncharacterized protein	98.3%	10.1	1	1	1	2	3,339,750	3,469,820	3,252,200	3,820,865	323,283	254,098	231,137	185,409	21.6	16.4	15.9	10.9	1.0	0.8	-1.0	0.8	1.1	0.2	-1.1	0.5	1.1	0.3	1.2	0.09
				FNEQIEPIYALLR	2	98.3%	1																									
IPI00019983	BCL2L1	isoform Bcl-X(L) of Bcl-2-like protein 1	98.1%	4.3	1	1	1	7	851,693	830,024	995,656	611,110	174,768	145,074	182,873	101,114	45.9	39.1	41.1	37.0	-1.0	0.9	1.2	0.6	-1.4	0.3	1.2	0.5	-1.4	0.3	-1.6	0.1
IPI00219133	BCL2L1	isoform Bcl-X(S) of Bcl-2-like protein 1	98.1%	5.9	1	1	1	7	851,693	830,024	995,656	611,110	174,768	145,074	182,873	101,114	45.9	39.1	41.1	37.0	-1.0	0.9	1.2	0.6	-1.4	0.3	1.2	0.5	-1.4	0.3	-1.6	0.1
IPI00219134	BCL2L1	isoform Bcl-X(beta) of Bcl-2-like protein 1	98.1%	4.4	1	1	1	7	851,693	830,024	995,656	611,110	174,768	145,074	182,873	101,114	45.9	39.1	41.1	37.0	-1.0	0.9	1.2	0.6	-1.4	0.3	1.2	0.5	-1.4	0.3	-1.6	0.1
IPI00644343	BCL2L1	BCL2-like 1	98.1%	5.5	1	1	1	7	851,693	830,024	995,656	611,110	174,768	145,074	182,873	101,114	45.9	39.1	41.1	37.0	-1.0	0.9	1.2	0.6	-1.4	0.3	1.2	0.5	-1.4	0.3	-1.6	0.1
IPI00646118	BCL2L1	BCL2-like 1	98.1%	5.3	1	1	1	7	851,693	830,024	995,656	611,110	174,768	145,074	182,873	101,114	45.9	39.1	41.1	37.0	-1.0	0.9	1.2	0.6	-1.4	0.3	1.2	0.5	-1.4	0.3	-1.6	0.1
IPI00646996	BCL2L1	BCL2-like 1	98.1%	4.9	1	1	1	7	851,693	830,024	995,656	611,110	174,768	145,074	182,873	101,114	45.9	39.1	41.1	37.0	-1.0	0.9	1.2	0.6	-1.4	0.3	1.2	0.5	-1.4	0.3	-1.6	0.1
IPI00647529	BCL2L1	BCL2-like 1	98.1%	20.8	1	1	1	7	851,693	830,024	995,656	611,110	174,768	145,074	182,873	101,114	45.9	39.1	41.1	37.0	-1.0	0.9	1.2	0.6	-1.4	0.3	1.2	0.5	-1.4	0.3	-1.6	0.1
				ELVVDFLSYK	2	98.1%	1																									
IPI00019997	LIN7C	Protein lin-7 homolog C	99.0%	10.7	2	2	2	2	7,024,125	7,568,250	6,827,225	8,456,065	783,883	371,103	704,113	270,224	25.0	11.0	23.1	7.2	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.09	1.2	0.08
IPI00983405	LIN7C	19 kDa protein	99.0%	12.1	2	2	2	2	7,024,125	7,568,250	6,827,225	8,456,065	783,883	371,103	704,113	270,224	25.0	11.0	23.1	7.2	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.09	1.2	0.08
				EQNSPIYISR	2	96.8%	1																									
				VLQSEFCNAVR	2	95.3%	1																									
IPI00979485	NEDD8-MDP1	Uncharacterized protein	94.3%	16.7	1	1	1	4	273,875	326,669	296,051	341,910	15,202	16,483	41,170	14,572	12.4	11.3	31.1	9.5	1.2	0.05	1.1	0.6	1.2	0.01	-1.1	0.5	1.0	0.5	1.2	0.3
IPI00980337	NEDD8-MDP1	NEDD8-MDP1 protein	94.3%	7.3	1	1	1	4	273,875	326,669	296,051	341,910	15,202	16,483	41,170	14,572	12.4	11.3	31.1	9.5	1.2	0.05	1.1	0.6	1.2	0.01	-1.1	0.5	1.0	0.5	1.2	0.3
IPI00020008	NEDD8	NEDD8	94.3%	17.3	1	1	1	4	273,875	326,669	296,051	341,910	15,202	16,483	41,170	14,572	12.4	11.3	31.1	9.5	1.2	0.05	1.1	0.6	1.2	0.01	-1.1	0.5	1.0	0.5	1.2	0.3
IPI00873768	NEDD8	6 kDa protein	94.3%	28.0	1	1	1	4	273,875	326,669	296,051	341,910	15,202	16,483	41,170	14,572	12.4	11.3	31.1	9.5	1.2	0.05	1.1	0.6	1.2	0.01	-1.1	0.5	1.0	0.5	1.2	0.3
				EIEIDIEPTDKVER	2	94.3%	1																									
IPI00020021	DEK	Protein DEK	100.0%	9.3	3	3	3	1	19,761,845	19,747,959	17,514,619	21,192,075	1,767,163	1,161,654	1,911,726	1,297,606	20.0	13.2	24.4	13.7	-1.0	1	-1.1	0.4	1.1	0.5	-1.1	0.3	1.1	0.4	1.2	0.2
				LLASANLEEVTMK	2	100.0%	1																									
				LTMQVSSLQR	2	92.7%	1																									
				NVGQFSGFPFEK	2	99.0%	1																									
IPI00738042	LOC652826	26S protease regulatory subunit 6B-like	100.0%	23.0	6	7	7	2	18,133,540	17,985,312	17,000,001	20,790,009	1,481,539	328,360	1,068,867	304,087	18.3	4.1	14.1	3.3	-1.0	0.9	-1.1	0.6	1.1	0.1	-1.1	0.4	1.2	0.0002	1.2	0.02
IPI00020042	PSMC4	isoform 1 of 26S protease regulatory subunit 6B	100.0%	22.7	6	7	7	2	18,133,540	17,985,312	17,000,001	20,790,009	1,481,539	328,360	1,068,867	304,087	18.3	4.1	14.1	3.3	-1.0	0.9	-1.1	0.6	1.1	0.1	-1.1	0.4	1.2	0.0002	1.2	0.02
				ENAPAIIFIDEIDAIATK	3	99.9%	1																									
				ENAPAIIFIDEIDAIATKR	3	99.9%	1																									
				ILLELLNQMDGFDQNVNVK	2	100.0%	1																									
				ILLELLNQMDGFDQNVNVK	3	100.0%	1																									
				ISGADINSICQESGMLAVR	2	100.0%	1																									
				LQQELEFLEVQEEYIKDEQK	3	100.0%	1																									
				MNLSEEVDLEDYVARPDK	3	99.3%	1																									
IPI00337460	C14orf153	cDNA FLJ55519, highly similar to Kinesin light chain 1	99.6%	1.8	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956197	C14orf153	Kinesin light chain 1D	99.6%	2.1	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956248	C14orf153	Kinesin light chain 1E	99.6%	2.1	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956278	C14orf153	Kinesin light chain 1J	99.6%	2.1	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956285	C14orf153	Kinesin light chain 1K	99.6%	2.1	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956501	C14orf153	Kinesin light chain 1F	99.6%	2.4	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956542	C14orf153	Kinesin light chain 1M	99.6%	2.1	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956585	C14orf153	Kinesin light chain 1	99.6%	2.3	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956606	C14orf153	Kinesin light chain 1N	99.6%	2.1	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956709	C14orf153	Kinesin light chain 1A	99.6%	2.4	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956746	C14orf153	Kinesin light chain 1O	99.6%	2.1	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00020096	KLC1	isoform A of Kinesin light chain 1	99.6%	2.3	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00337465	KLC1	isoform P of Kinesin light chain 1	99.6%	2.2	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00394906	KLC1	isoform K of Kinesin light chain 1	99.6%	2.1	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00397666	KLC1	isoform S of Kinesin light chain 1	99.6%	2.4	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00398708	KLC1	isoform I of Kinesin light chain 1	99.6%	2.0	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00412642	KLC1	isoform G of Kinesin light chain 1	99.6%	2.3	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00472303	KLC1	isoform N of Kinesin light chain 1	99.6%	2.1	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00479424	KLC1	isoform J of Kinesin light chain 1	99.6%	2.0	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00921532	KLC1	isoform C of Kinesin light chain 1	99.6%	2.3	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI00956296	KLC1	Uncharacterized protein	99.6%	1.8	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI01009541	KLC1	Protein	99.6%	7.3	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI01010793	KLC1	cDNA FLJ61233, highly similar to Kinesin light chain 1	99.6%	2.3	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
IPI01015701	KLC1	Protein	99.6%	11.9	1	1	1	24	648,213	685,296	657,333	686,304	64,045	27,857	42,613	16,074	22.1	9.1	14.5	5.2	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.6	1.0	1	1.0	0.6
				FEAAETLEEAAMR	2	99.6%	1																									
IPI00020127	RPA1	Replication protein A 70 kDa DNA-binding subunit	100.0%	11.5	5	5	5	1	26,082,449	28,873,475	32,136,512	29,024,847	2,504,107	1,374,763	1,623,204	1,108,432	21.5	10.7	11.3	8.5	1.1	0.4	1.2	0.08	1.1	0.3	1.1	0.2	1.0	0.9	-1.1	0.2
				ATAFNEQVDKFFPLIEVNK	3	98.7%	1																									
				GWFDAEGQALDGVSISDLK	2	100.0%	1																									
				SGGVGGSNTNWK	2	99.1%	1																									
				VIDQQNGLYR	2	99.5%	1																									
				VKVETYNDESR	2	98.7%	1																									
IPI00020178	STAM	isoform 1 of Signal transducing adapter molecule 1	100.0%	5.4	2	2	3	2	2,145,593	2,249,517	2,383,165	2,320,592	115,617	157,447	96,762	29,634	12.1	15.7	9.1	2.9	1.0	0.6	1.1	0.2	1.1	0.2	1.1	0.5	1.0	0.7	-1.0	0.6
IPI00607769	STAM	isoform 2 of Signal transducing adapter molecule 1	100.0%	7.2	2	2	3	2	2,145,593	2,249,517	2,383,165	2,320,592	115,617	157,447	96,762	29,634	12.1	15.7	9.1	2.9	1.0	0.6	1.1	0.2	1.1	0.2	1.1	0.5	1.0	0.7	-1.0	0.6
				AGEIITVLDDSDPNWWK	2	99.8%	1																									
				DFASEVSNVLNK	2	99.9%	2																									
IPI00020194	TAF15	isoform Short of TATA-binding protein-associated factor 2N	100.0%	12.9	5	5	6	2	4,369,032	4,557,702	4,366,753	5,023,040	470,529	191,111	302,027	228,324	24.1	9.4	15.5	10.2	1.0	0.7	-1.0	1	1.1	0.2	-1.0	0.6	1.1	0.2	1.2	0.1
IPI00294426	TAF15	isoform Long of TATA-binding protein-associated factor 2N	100.0%	12.8	5	5	6	2	4,369,032	4,557,702	4,366,753	5,023,040	470,529	191,111	302,027	228,324	24.1	9.4	15.5	10.2	1.0	0.7	-1.0	1	1.1	0.2	-1.0	0.6	1.1	0.2	1.2	0.1
				AAIDWFDGK	2	98.2%	1																									
				AAIDWFDGKEFHGNIIK	3	99.9%	1																									
				GEATVSFDDPPSAK	2	100.0%	2																									

				QSSYSQQPYNNQGQQQNMESSGSQGGR	3	100.0%	1																									
				SGDWVCPNPSCGNMNFAR	2	100.0%	1																									
IPI00020210	DYSF	isoform 14 of Dysferlin	96.9%	1.2	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00793867	DYSF	isoform 8 of Dysferlin	96.9%	1.1	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00871702	DYSF	isoform 1 of Dysferlin	96.9%	1.2	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00890768	DYSF	isoform 10 of Dysferlin	96.9%	1.1	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00890779	DYSF	isoform 13 of Dysferlin	96.9%	1.1	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00908443	DYSF	isoform 2 of Dysferlin	96.9%	1.1	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00908579	DYSF	isoform 3 of Dysferlin	96.9%	1.2	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00908658	DYSF	isoform 5 of Dysferlin	96.9%	1.1	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00908764	DYSF	isoform 6 of Dysferlin	96.9%	1.2	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00908826	DYSF	isoform 7 of Dysferlin	96.9%	1.1	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00908936	DYSF	isoform 4 of Dysferlin	96.9%	1.1	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00910445	DYSF	isoform 12 of Dysferlin	96.9%	1.2	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00910624	DYSF	isoform 11 of Dysferlin	96.9%	1.1	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00911101	DYSF	isoform 9 of Dysferlin	96.9%	1.2	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
IPI00915417	DYSF	isoform 15 of Dysferlin	96.9%	1.2	1	1	1	15	111,550	102,384	124,642	139,325	23,149	13,641	20,955	12,077	46.4	29.8	37.6	19.4	-1.1	0.7	1.1	0.7	1.2	0.3	1.2	0.4	1.4	0.08	1.1	0.6
				FIFPFDYLPAEQVCTIAKKDAFWR	3	86.6%	1																									
IPI00020319	BLOC1S1	isoform 1 of Biogenesis of lysosome-related organelles complex 1 subunit 1	98.4%	7.2	1	1	1	2	4,280,720	4,415,105	4,045,290	4,340,465	442,538	222,877	234,039	194,764	23.1	11.3	12.9	10.0	1.0	0.8	-1.1	0.7	1.0	0.9	-1.1	0.3	-1.0	0.8	1.1	0.4
IPI01015745	BLOC1S1	isoform 2 of Biogenesis of lysosome-related organelles complex 1 subunit 1	98.4%	8.8	1	1	1	2	4,280,720	4,415,105	4,045,290	4,340,465	442,538	222,877	234,039	194,764	23.1	11.3	12.9	10.0	1.0	0.8	-1.1	0.7	1.0	0.9	-1.1	0.3	-1.0	0.8	1.1	0.4
				TIATALEYVYK	2	98.4%	1																									
IPI00020418	RRAS	Ras-related protein R-Ras	99.5%	5.5	1	1	1	1	3,470,630	3,504,030	3,808,840	3,848,690	460,548	487,824	529,800	393,214	29.7	31.1	31.1	22.9	1.0	1	1.1	0.6	1.1	0.5	1.1	0.7	1.1	0.6	1.0	1
				LNVDEAFEQLVR	2	99.5%	1																									
IPI00020436	RAB11B	Ras-related protein Rab-11B	100.0%	19.7	4	4	5	2	8,919,587	8,958,708	8,863,025	9,793,710	494,975	666,187	402,472	249,346	12.4	16.6	10.2	5.7	1.0	1	-1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.3	1.1	0.08
IPI00930720	RAB11B	cDNA FLJ61134, highly similar to Ras-related protein Rab-11B	100.0%	24.0	4	4	5	2	8,919,587	8,958,708	8,863,025	9,793,710	494,975	666,187	402,472	249,346	12.4	16.6	10.2	5.7	1.0	1	-1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.3	1.1	0.08
				GAVGALLVYDIAK	2	100.0%	1																									
				HLTYENVER	2	100.0%	2																									
				STIGVEFATR	2	100.0%	1																									
				VVLIGDSGVGK	2	98.1%	1																									
IPI00020501	MYH11	Myosin-11	99.8%	0.9	1	1	1	5	508,792	550,474	450,696	642,608	87,698	61,069	75,669	96,498	38.5	24.8	37.5	33.6	1.1	0.7	-1.1	0.6	1.3	0.3	-1.2	0.3	1.2	0.4	1.4	0.2
IPI00024870	MYH11	myosin-11 isoform SM2A	99.8%	0.9	1	1	1	5	508,792	550,474	450,696	642,608	87,698	61,069	75,669	96,498	38.5	24.8	37.5	33.6	1.1	0.7	-1.1	0.6	1.3	0.3	-1.2	0.3	1.2	0.4	1.4	0.2
IPI00743857	MYH11	myosin-11 isoform SM1B	99.8%	0.9	1	1	1	5	508,792	550,474	450,696	642,608	87,698	61,069	75,669	96,498	38.5	24.8	37.5	33.6	1.1	0.7	-1.1	0.6	1.3	0.3	-1.2	0.3	1.2	0.4	1.4	0.2
IPI00744256	MYH11	myosin-11 isoform SM2B	99.8%	0.9	1	1	1	5	508,792	550,474	450,696	642,608	87,698	61,069	75,669	96,498	38.5	24.8	37.5	33.6	1.1	0.7	-1.1	0.6	1.3	0.3	-1.2	0.3	1.2	0.4	1.4	0.2
IPI00873982	MYH11	Myosin heavy chain 11 smooth muscle isoform	99.8%	0.8	1	1	1	5	508,792	550,474	450,696	642,608	87,698	61,069	75,669	96,498	38.5	24.8	37.5	33.6	1.1	0.7	-1.1	0.6	1.3	0.3	-1.2	0.3	1.2	0.4	1.4	0.2
				KATQQAEQLSNELATER	2	99.8%	1																									
IPI00020524	CLCN7	Putative chloride channel protein 7	96.3%	3.8	1	1	1	2	551,454	560,727	621,213	619,660	34,786	36,198	53,517	54,343	14.1	14.4	19.3	19.6	1.0	0.9	1.1	0.3	1.1	0.3	1.1	0.4	1.1	0.4	-1.0	1
IPI00641148	CLCN7	H(+)/Cl(-) exchange transporter 7 isoform b	96.3%	4.0	1	1	1	2	551,454	560,727	621,213	619,660	34,786	36,198	53,517	54,343	14.1	14.4	19.3	19.6	1.0	0.9	1.1	0.3	1.1	0.3	1.1	0.4	1.1	0.4	-1.0	1
				VGVIVDVLSDTASNHNGFPVVEHADDTQPAR	3	93.4%	1																									
IPI00020530	ACOT13	Acyl-coenzyme A thioesterase 13	99.9%	21.4	2	2	2	2	5,710,050	5,938,325	5,802,950	6,843,770	396,836	287,114	409,663	272,010	15.5	10.8	15.8	8.9	1.0	0.7	1.0	0.9	1.2	0.05	-1.0	0.8	1.2	0.05	1.2	0.07
IPI00930594	ACOT13	acyl-coenzyme A thioesterase 13 isoform 2	99.9%	25.6	2	2	2	2	5,710,050	5,938,325	5,802,950	6,843,770	396,836	287,114	409,663	272,010	15.5	10.8	15.8	8.9	1.0	0.7	1.0	0.9	1.2	0.05	-1.0	0.8	1.2	0.05	1.2	0.07
				GAPGVSVDMNITYMSPAK	2	99.6%	1																									
				TLAFTSVDLTNK	2	99.8%	1																									
IPI00020546	ASH1L	isoform 1 of Probable histone-lysine N-methyltransferase ASH1L	95.4%	0.4	1	1	1	2	365,900	385,943	445,730	422,967	34,364	22,586	46,162	37,137	21.0	13.1	23.2	19.6	1.1	0.6	1.2	0.2	1.2	0.3	1.2	0.3	1.1	0.4	-1.1	0.7
IPI00642422	ASH1L	isoform 2 of Probable histone-lysine N-methyltransferase ASH1L	95.4%	0.4	1	1	1	2	365,900	385,943	445,730	422,967	34,364	22,586	46,162	37,137	21.0	13.1	23.2	19.6	1.1	0.6	1.2	0.2	1.2	0.3	1.2	0.3	1.1	0.4	-1.1	0.7
				QALAAPLLNLPPK	2	92.9%	1																									
IPI00020557	LRP1	Prolow-density lipoprotein receptor-related protein 1	100.0%	0.9	3	3	3	1	8,780,250	10,378,910	10,408,000	9,921,140	516,285	408,633	961,586	323,246	13.2	8.8	20.7	7.3	1.2	0.04	1.2	0.2	1.1	0.1	1.0	1	-1.0	0.4	-1.0	0.7
				ITWPNGLTLDYVTER	2	93.9%	1																									
				IVFPHGITLDLVSR	3	97.8%	1																									
				WTGHNVTVVQR	3	95.7%	1																									
IPI00020567	ARHGAP1	Rho GTPase-activating protein 1	100.0%	16.4	4	4	4	1	16,797,472	19,049,279	18,833,072	20,767,507	1,776,264	672,888	1,645,564	1,018,530	23.7	7.9	19.5	11.0	1.1	0.3	1.1	0.4	1.2	0.09	-1.0	0.9	1.1	0.2	1.1	0.3
				ELPEPLLTFDLYPHVVGFLNIDESQR	3	98.2%	1																									
				FLLDHQGELFPSPDPSGL	2	99.9%	1																									
				MTNTNLAVVFGPNLLWAK	2	100.0%	1																									
				WDDPYYDIAR	2	97.9%	1																									
IPI00020599	CALR	Calreticulin	100.0%	49.4	13	15	20	1	105,641,785	110,473,952	107,055,336	125,104,006	7,674,693	4,677,588	8,532,315	3,726,395	16.2	9.5	17.8	6.7	1.0	0.6	1.0	0.9	1.2	0.05	-1.0	0.7	1.1	0.04	1.2	0.09
				EQFLDGDGWTSR	2	100.0%	2																									
				FVLSSGK	1	94.4%	1																									
				FYALSASFEPFSNK	2	100.0%	1																									
				FYGDEEKDKGLQTSQDAR	3	100.0%	1																									
				HEQNIDCGGGYVK	2	100.0%	2																									
				IDNSQVESGSLEDDWDFLPPKK	3	100.0%	1																									
				IKDPDASKPEDWDER	2	100.0%	2																									
				KPEDWDEEMDGEWEPPVIQNPEYK	3	100.0%	2																									
				LFPNSLDQTDMHGDSEYNIMFGPDICGPGTK	3	100.0%	1																									
				QIDNPDYK	1	83.2%	1																									
				QIDNPDYK	2	95.4%	1																									
				SGTIFDNFLITNDEAYAEEFGNETWGVTK	2	100.0%	2																									
				SGTIFDNFLITNDEAYAEEFGNETWGVTK	3	100.0%	1																									
				VHVIFNYK	2	98.4%	1																									
				WIESK	1	92.9%	1																									
IPI00956400	BBS1	Putative uncharacterized protein DKFZp686O1117	100.0%	11.7	5	6	6	6	2,152,629	2,111,556	2,217,542	2,455,812	211,401	85,807	156,089	63,416	22.0	9.1	15.7	5.8	-1.0	0.9	1.0	0.8	1.1	0.2	1.1	0.6	1.2	0.01	1.1	0.2
IPI00020672	DPP3	isoform 1 of Dipeptidyl peptidase 3	100.0%	11.7	5	6	6	6	2,152,629	2,111,556	2,217,542	2,455,812	211,401	85,807	156,089	63,416	22.0	9.1	15.7	5.8	-1.0	0.9	1.0	0.8	1.1	0.2	1.1	0.6	1.2	0.01	1.1	0.2
IPI00975587	DPP3	84 kDa protein	100.0%	11.4	5	6	6	6	2,152,629	2,111,556	2,217,542	2,455,812	211,401	85,807	156,089	63,416	22.0	9.1	15.7	5.8	-1.0	0.9	1.0	0.8	1.1	0.2	1.1	0.6	1.2	0.01	1.1	0.2
IPI00976265	DPP3	Uncharacterized protein	100.0%	13.5	5	6	6	6	2,152,629	2,111,556	2,217,542	2,455,812	211,401	85,807	156,089	63,416	22.0	9.1	15.7	5.8	-1.0	0.9	1.0	0.8	1.1	0.2	1.1	0.6	1.2	0.01	1.1	0.2
IPI00976779	DPP3	84 kDa protein	100.0%	11.4	5	6	6	6	2,152,629	2,111,556	2,217,542	2,455,812	211,401	85,807	156,089	63,416	22.0	9.1	15.7	5.8	-1.0	0.9	1.0	0.8	1.1	0.2	1.1	0.6	1.2	0.01	1.1	0.2
IPI00979514	DPP3	79 kDa protein	100.0%	12.2	5	6	6	6	2,152,629	2,111,556	2,217,542	2,455,812	211,401	85,807	156,089	63,416	22.0	9.1	15.7	5.8	-1.0	0.9	1.0	0.8	1.1	0.2	1.1	0.6	1.2	0.01	1.1	0.2
				AGLLALEFYTPEAFNWR	2	100.0%	1																									
				GDYAPILQK	2	96.7%	1																									
				GPIVESYIGFIESYR	2	99.6%	1																									
				LEGSDVQLLEYEASAAGLIR	2	100.0%	1																									
				LEGSDVQLLEYEASAAGLIR	3	87.7%	1																									
				VLLEAGEGLVTITPTTGSDGRPDAR	3	100.0%	1																									
IPI00020701	ERI3	isoform 1 of ERI1 exoribonuclease 3	99.4%	9.2	2	2	2	5	987,403	989,861	1,072,238	1,220,474	100,001	58,517	136,514	35,638	22.7	13.2	28.5	6.5	1.0	1	1.1	0.6	1.2	0.08	1.1	0.6	1.2	0.01	1.1	0.3
IPI00641679	ERI3	Uncharacterized protein	99.4%	13.4	2	2	2	5	987,403	989,861	1,072,238	1,220,474	100,001	58,517	136,514	35,638	22.7	13.2	28.5	6.5	1.0	1	1.1	0.6	1.2	0.08	1.1	0.6	1.2	0.01	1.1	0.3
IPI00644349	ERI3	cDNA FLJ60449, highly similar to Homo sapiens prion protein interacting protein (PF	99.4%	19.4	2	2	2	5	987,403	989,861	1,072,238	1,220,474	100,001	58,517	136,514	35,638	22.7	13.2	28.5	6.5	1.0	1	1.1	0.6	1.2	0.08	1.1	0.6	1.2	0.01	1.1	0.3
IPI00888358	ERI3	isoform 2 of ERI1 exoribonuclease 3	99.4%	14.0	2	2	2	5	987,403	989,861	1,072,238	1,220,474	100,001	58,517	136,514	35,638	22.7	13.2	28.5	6.5	1.0	1	1.1	0.6	1.2	0.08	1.1	0.6	1.2	0.01	1.1	0.3
IPI00943355	ERI3	Prion protein interacting protein	99.4%	14.2	2	2	2	5	987,403	989,861	1,072,238	1,220,474	100,001	58,517	136,514	35,638	22.7	13.2	28.5	6.5	1.0	1	1.1	0.6	1.2	0.08	1.1	0.6	1.2	0.01	1.1	0.3
				SIFVTCGDWDLK	2	97.0%	1																									
				VMLPGQCQYLGLPVADYFK	2	99.4%	1																									
IPI00020771	MAP7	Uncharacterized protein	94.8%	2.2	1	1	1	5	1,022,518	959,648	1,160,365	1,303,722	100,269	59,058	104,931	79,482	21.9	13.8	20.2	13.6	-1.1	0.6	1.1	0.4	1.3	0.06	1.2	0.1	1.4	0.008	1.1	0.3
IPI00022628	MAP7	ensconsin isoform 2	94.8%	1.9	1	1	1	5	1,022,518	959,648	1,160,365	1,303,722	100,269	59,058	104,931	79,482	21.9	13.8	20.2	13.6	-1.1	0.6	1.1	0.4	1.3	0.06	1.2	0.1	1.4	0.008	1.1	0.3
IPI00976733	MAP7	ensconsin isoform 1	94.8%	2.0	1	1	1	5	1,022,518	959,648	1,160,365	1,303,722	100,269	59,058	104,931	79,482	21.9	13.8	20.2	13.6	-1.1	0.6	1.1	0.4	1.3	0.06	1.2	0.1	1.4	0.008	1.1	0.3
IPI00982359	MAP7	ensconsin isoform 8	94.8%	2.5	1	1	1	5	1,022,518	959,648	1,160,365	1,303,722	100,269	59,058	104,931	79,482	21.9	13.8	20.2	13.6	-1.1	0.6	1.1	0.4	1.3	0.06	1.2	0.1	1.4	0.008	1.1	0.3
IPI00985007	MAP7	ensconsin isoform 5	94.8%	2.0	1	1	1	5	1,022,518	959,648	1,160,365	1,303,722	100,269	59,058	104,931	79,482	21.9	13.8	20.2	13.6	-1.1	0.6	1.1	0.4	1.3	0.06	1.2	0.1	1.4	0.008	1.1	0.3
				RLSSSSATLLNSPDR	2	94.8%	1																									
IPI00020850	PPP2R2B	isoform 1 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B b	100.0%	5.0	2	2	3	6	924,469	921,272	964,862	1,060,286	122,310	37,942	112,654	56,037	29.6	9.2	26.1	11.8	-1.0	1	1.0	0.8	1.1	0.3	1.0	0.7	1.2	0.07	1.1	0.5
IPI00376972	PPP2R2B	isoform 2 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B b	100.0%	4.9	2	2	3	6	924,469	921,272	964,862	1,060,286	122,310	37,942	112,654	56,037	29.6	9.2	26.1	11.8	-1.0	1	1.0	0.8	1.1	0.3	1.0	0.7	1.2	0.07	1.1	0.5
IPI00376973	PPP2R2B	isoform 5 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B b	100.0%	4.3	2	2	3	6	924,469	921,272	964,862	1,060,286	122,310	37,942	112,654	56,037	29.6	9.2	26.1	11.8	-1.0	1	1.0	0.8	1.1	0.3	1.0	0.7	1.2	0.07	1.1	0.5
IPI00944548	PPP2R2B	isoform 4 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B b	100.0%	4.4	2	2	3	6	924,469	921,272	964,862	1,060,286	122,310	37,942	112,654	56,037	29.6	9.2	26.1	11.8	-1.0	1	1.0	0.8	1.1	0.3	1.0	0.7	1.2	0.07	1.1	0.5
IPI00944557	PPP2R2B	isoform 3 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B b	100.0%	4.9	2	2	3	6	924,469	921,272	964,862	1,060,286	122,310	37,942	112,654	56,037	29.6	9.2	26.1	11.8	-1.0	1	1.0	0.8	1.1	0.3	1.0	0.7	1.2	0.07	1.1	0.5
IPI00973360	PPP2R2B	serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform is	100.0%	5.1	2	2	3	6	924,469	921,272	964,862	1,060,286	122,310	37,942	112,654	56,037	29.6	9.2	26.1	11.8	-1.0	1	1.0	0.8	1.1	0.3	1.0	0.7	1.2	0.07	1.1	0.5
				RPEGYNLK	2	87.7%	1																									
				SFFSEIISSISDVK	2	100.0%	2																									
IPI00020873	TBL1Y	F-box-like/WD repeat-containing protein TBL1Y	100.0%	1.3	1	1	1	2	247,891	271,242	231,548	294,587	13,172	31,310	19,924	14,917	11.9	25.8	19.2	11.3	1.1	0.5	-1.1	0.5	1.2	0.05	-1.2	0.3	1.1	0.5	1.3	0.04
IPI01012500	TBL1Y	40 kDa protein	100.0%	1.9	1	1	1	2	247,891	271,242	231,548	294,587	13,172	31,310	19,924	14,917	11.9	25.8	19.2	11.3	1.1	0.5	-1.1	0.5	1.2	0.05	-1.2	0.3	1.1	0.5	1.3	0.04
				GPIFALK	2	97.3%	1																									
IPI00020898	RPS6KA3	Ribosomal protein S6 kinase alpha-3	98.3%	7.0	4	4	4	4	4,117,087	4,817,084	3,846,091	5,085,348	600,280	354,495	143,864	251,227	32.6	16.5	8.4	11.1	1.2	0.3	-1.1	0.7	1.2	0.2	-1.3	0.03	1.1	0.6	1.3	0.003
IPI00552941	RPS6KA3	cDNA FLJ56653, highly similar to Ribosomal protein S6 kinase alpha-3	98.3%	7.3	4	4	4	4	4,117,087	4,817,084	3,846,091	5,085,348	600,280	354,495	143,864	251,227	32.6	16.5	8.4	11.1	1.2	0.3	-1.1	0.7	1.2	0.2	-1.3	0.03	1.1	0.6	1.3	0.003
IPI00641592	RPS6KA3	cDNA FLJ56618, highly similar to Ribosomal protein S6 kinase alpha-3	98.3%	7.3	4	4	4	4	4,117,087	4,817,084	3,846,091	5,085,348	600,280	354,495	143,864	251,227	32.6	16.5	8.4	11.1	1.2	0.3	-1.1	0.7	1.2	0.2	-1.3	0.03	1.1	0.6	1.3	0.003
IPI01015791	RPS6KA3	cDNA, FLJ79381, highly similar to Ribosomal protein S6 kinase alpha-3	98.3%	7.3	4	4	4	4	4,117,087	4,817,084	3,846,091	5,085,348	600,280	354,495	143,864	251,227	32.6	16.5	8.4	11.1	1.2	0.3	-1.1	0.7	1.2	0.2	-1.3	0.03	1.1	0.6	1.3	0.003
				ATNMEFAVK	2	86.6%	1																									
				DLKPENILLDEEGHIK	3	93.2%	1																									
				LGMPQFLSPEAQSLLR	2	96.2%	1																									
				NQSPVLEPVGR	2	93.0%	1																									
IPI00020904	PRKX	Serine/threonine-protein kinase PRKX	99.2%	5.3	1	1	1	2	1,321,785	1,117,155	1,165,895	1,396,555	213,275	85,875	154,508	108,593	36.1	17.2	29.6	17.4	-1.2	0.4	-1.1	0.6	1.1	0.8	1.0	0.8	1.3	0.08	1.2	0.3
IPI00288889	PRKY	Serine/threonine-protein kinase PRKY	99.2%	6.9	1	1	1	2	1,321,785	1,117,155	1,165,895	1,396,555	213,275	85,875	154,508	108,593	36.1	17.2	29.6	17.4	-1.2	0.4	-1.1	0.6	1.1	0.8	1.0	0.8	1.3	0.08	1.2	0.3
				TWTLCGTPEYLAPEVIQSK	2	99.2%	1																									
IPI00020906	IMPA1	Inositol monophosphatase 1	99.4%	4.0	1	1	1	5	765,240	1,011,558	981,854	1,193,138	110,029	68,934	88,124	43,463	32.2	15.2	20.1	8.2	1.3	0.09	1.3	0.2	1.6	0.01	-1.0	0.8	1.2	0.06	1.2	0.06
IPI00921428	IMPA1	inositol monophosphatase 1 isoform 2	99.4%	3.3	1	1	1	5	765,240	1,011,558	981,854	1,193,138	110,029	68,934	88,124	43,463	32.2	15.2	20.1	8.2	1.3	0.09	1.3	0.2	1.6	0.01	-1.0	0.8	1.2	0.06	1.2	0.06
IPI00974011	IMPA1	Uncharacterized protein	99.4%	6.1	1	1	1	5	765,240	1,011,558	981,854	1,193,138	110,029	68,934	88,124	43,463	32.2	15.2	20.1	8.2	1.3	0.09	1.3	0.2	1.6	0.01	-1.0	0.8	1.2	0.06	1.2	0.06
IPI00974104	IMPA1	Uncharacterized protein	99.4%	7.2	1	1	1	5	765,240	1,011,558	981,854	1,193,138	110,029	68,934	88,124	43,463	32.2	15.2	20.1	8.2	1.3	0.09	1.3	0.2	1.6	0.01	-1.0	0.8	1.2	0.06	1.2	0.06
IPI00978875	IMPA1	Protein	99.4%	4.2	1	1	1	5	765,240	1,011,558	981,854	1,193,138	110,029	68,934	88,124	43,463	32.2	15.2	20.1	8.2	1.3	0.09	1.3	0.2	1.6	0.01	-1.0	0.8	1.2	0.06	1.2	0.06
				SLLVTELGSSR	2	99.4%	1																									
IPI00020944	FDFT1	Squalene synthase	100.0%	15.4	5	5	5	1	3,241,423	3,361,766	3,386,807	3,838,760	243,427	159,838	226,454	180,674	16.8	10.6	15.0	10.5	1.0	0.7	1.0	0.7	1.2	0.08	1.0	0.9	1.1	0.08	1.1	0.2
				DYLEDQQGGR	2	100.0%	1																									
				LFSASEFEDPLVGEDTER	2	100.0%	1																									
				MDQDSLSSSLK	2	100.0%	1																									
				MGIGMAEFLDK	2	100.0%	1																									
				SFAAVIQALDGEMR	2	100.0%	1																									
IPI00020950	PPM1A	isoform Alpha-1 of Protein phosphatase 1A	99.9%	2.6	1	1	1	10	628,679	564,756	641,045	695,782	63,718	36,303	35,399	32,898	22.7	14.4	12.4	10.6	-1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.2	1.2	0.03	1.1	0.3
IPI00216196	PPM1A	isoform Alpha-2 of Protein phosphatase 1A	99.9%	3.1	1	1	1	10	628,679	564,756	641,045	695,782	63,718	36,303	35,399	32,898	22.7	14.4	12.4	10.6	-1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.2	1.2	0.03	1.1	0.3
IPI00900291	PPM1A	protein phosphatase 1A isoform 3	99.9%	2.2	1	1	1	10	628,679	564,756	641,045	695,782	63,718	36,303	35,399	32,898	22.7	14.4	12.4	10.6	-1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.2	1.2	0.03	1.1	0.3
IPI00975663	PPM1A	Uncharacterized protein	99.9%	5.4	1	1	1	10	628,679	564,756	641,045	695,782	63,718	36,303	35,399	32,898	22.7	14.4	12.4	10.6	-1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.2	1.2	0.03	1.1	0.3
IPI00976248	PPM1A	Uncharacterized protein	99.9%	6.8	1	1	1	10	628,679	564,756	641,045	695,782	63,718	36,303	35,399	32,898	22.7	14.4	12.4	10.6	-1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.2	1.2	0.03	1.1	0.3
IPI00979580	PPM1A	Uncharacterized protein	99.9%	7.8	1	1	1	10	628,679	564,756	641,045	695,782	63,718	36,303	35,399	32,898	22.7	14.4	12.4	10.6	-1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.2	1.2	0.03	1.1	0.3
IPI00026612	PPM1B	isoform Beta-1 of Protein phosphatase 1B	99.9%	2.1	1	1	1	10	628,679	564,756	641,045	695,782	63,718	36,303	35,399	32,898	22.7	14.4	12.4	10.6	-1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.2	1.2	0.03	1.1	0.3
IPI00651725	PPM1B	protein phosphatase 1B isoform 5	99.9%	2.6	1	1	1	10	628,679	564,756	641,045	695,782	63,718	36,303	35,399	32,898	22.7	14.4	12.4	10.6	-1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.2	1.2	0.03	1.1	0.3
IPI00743802	PPM1B	isoform Beta-2 of Protein phosphatase 1B	99.9%	2.6	1	1	1	10	628,679	564,756	641,045	695,782	63,718	36,303	35,399	32,898	22.7	14.4	12.4	10.6	-1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.2	1.2	0.03	1.1	0.3
IPI00917979	PPM1B	Uncharacterized protein	99.9%	2.7	1	1	1	10	628,679	564,756	641,045	695,782	63,718	36,303	35,399	32,898	22.7	14.4	12.4	10.6	-1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.2	1.2	0.03	1.1	0.3
				YGLSSMQGWR	2	99.7%	1																									
IPI00020956	HDGF	Hepatoma-derived growth factor	100.0%	52.1	10	13	13	1	140,764,135	146,469,657	140,729,987	162,928,355	########	8,672,617	########	6,804,146	19.0	13.2	16.1	9.3	1.0	0.7	-1.0	1	1.2	0.1	-1.0	0.7	1.1	0.2	1.2	0.1
				CGDLVFAK	2	84.6%	1																									
				DLFPYEESK	2	85.2%	1																									
				DLFPYEESKEK	2	98.3%	1																									
				EAENPEGEEKEAATLEVERPLPMEVEK	3	100.0%	1																									
				GFSEGLWEIENNPTVK	2	100.0%	1																									
				GFSEGLWEIENNPTVK	3	100.0%	1																									

				GPPQEEEEEEDEEEEATKEDAEAPGIR	3	100.0%	1																									
				GYPHWPAR	2	99.0%	1																									
				IDEMPEAAVK	2	99.1%	1																									
				KGFSEGLWEIENNPTVK	2	100.0%	1																									
				KGFSEGLWEIENNPTVK	3	100.0%	1																									
				YQVFFFGTHETAFLGPK	2	100.0%	1																									
				YQVFFFGTHETAFLGPK	3	99.9%	1																									
IPI00020976	ADORA2B	Adenosine receptor A2b	99.6%	9.9	1	1	1	1	3,643,350	3,732,990	3,873,670	3,957,160	203,869	157,160	313,981	158,846	12.5	9.4	18.1	9.0	1.0	0.7	1.1	0.6	1.1	0.3	1.0	0.7	1.1	0.3	1.0	0.8
				SLVTGTRARGVIAVLWVLAFGIGLTPFLGWNSK	3	99.6%	1																									
IPI00982049	-	Conserved hypothetical protein	93.6%	3.7	1	1	1	7	1,422,206	1,286,601	1,541,370	1,449,759	46,349	73,506	37,143	84,752	7.3	12.8	5.4	13.1	-1.1	0.2	1.1	0.08	1.0	0.8	1.2	0.01	1.1	0.2	-1.1	0.4
IPI00020982	ABP1	isoform 1 of Amiloride-sensitive amine oxidase [copper-containing]	93.6%	1.3	1	1	1	7	1,422,206	1,286,601	1,541,370	1,449,759	46,349	73,506	37,143	84,752	7.3	12.8	5.4	13.1	-1.1	0.2	1.1	0.08	1.0	0.8	1.2	0.01	1.1	0.2	-1.1	0.4
IPI00219832	ABP1	isoform 2 of Amiloride-sensitive amine oxidase [copper-containing]	93.6%	1.3	1	1	1	7	1,422,206	1,286,601	1,541,370	1,449,759	46,349	73,506	37,143	84,752	7.3	12.8	5.4	13.1	-1.1	0.2	1.1	0.08	1.0	0.8	1.2	0.01	1.1	0.2	-1.1	0.4
IPI00908979	ABP1	Primary amine oxidase	93.6%	1.7	1	1	1	7	1,422,206	1,286,601	1,541,370	1,449,759	46,349	73,506	37,143	84,752	7.3	12.8	5.4	13.1	-1.1	0.2	1.1	0.08	1.0	0.8	1.2	0.01	1.1	0.2	-1.1	0.4
IPI00953666	ABP1	Primary amine oxidase	93.6%	1.3	1	1	1	7	1,422,206	1,286,601	1,541,370	1,449,759	46,349	73,506	37,143	84,752	7.3	12.8	5.4	13.1	-1.1	0.2	1.1	0.08	1.0	0.8	1.2	0.01	1.1	0.2	-1.1	0.4
IPI00956005	ABP1	Primary amine oxidase	93.6%	1.4	1	1	1	7	1,422,206	1,286,601	1,541,370	1,449,759	46,349	73,506	37,143	84,752	7.3	12.8	5.4	13.1	-1.1	0.2	1.1	0.08	1.0	0.8	1.2	0.01	1.1	0.2	-1.1	0.4
IPI01009159	ABP1	72 kDa protein	93.6%	1.6	1	1	1	7	1,422,206	1,286,601	1,541,370	1,449,759	46,349	73,506	37,143	84,752	7.3	12.8	5.4	13.1	-1.1	0.2	1.1	0.08	1.0	0.8	1.2	0.01	1.1	0.2	-1.1	0.4
				FYGSPEELAR	2	93.6%	1																									
IPI00020984	CANX	cDNA FLJ55574, highly similar to Calnexin	100.0%	19.1	8	10	11	2	20,692,710	23,210,866	22,630,747	24,855,900	1,683,245	1,613,296	2,268,333	726,921	18.2	15.5	22.4	6.5	1.1	0.3	1.1	0.5	1.2	0.05	-1.0	0.8	1.1	0.4	1.1	0.4
IPI00941747	CANX	Calnexin	100.0%	20.3	8	10	11	2	20,692,710	23,210,866	22,630,747	24,855,900	1,683,245	1,613,296	2,268,333	726,921	18.2	15.5	22.4	6.5	1.1	0.3	1.1	0.5	1.2	0.05	-1.0	0.8	1.1	0.4	1.1	0.4
				APVPTGEVYFADSFDR	2	100.0%	2																									
				CESAPGCGVWQRPVIDNPNYK	3	97.6%	1																									
				GTLSGWILSK	2	100.0%	1																									
				IPDPEAVKPDDWDEDAPAK	3	90.6%	1																									
				IVDDWANDGWGLK	2	98.1%	1																									
				KIPNPDFFEDLEPFR	2	89.8%	1																									
				KIPNPDFFEDLEPFR	3	100.0%	1																									
				TPELNLDQFHDK	2	99.9%	1																									
				TPELNLDQFHDK	3	100.0%	1																									
				YDGKWEVEEMKESK	3	99.6%	1																									
IPI00021129	AP3B1	isoform 1 of AP-3 complex subunit beta-1	100.0%	2.0	2	2	2	4	2,200,575	2,387,185	2,448,188	2,978,708	340,526	207,602	356,424	185,514	34.6	19.5	32.6	13.9	1.1	0.7	1.1	0.6	1.4	0.08	1.0	0.9	1.2	0.07	1.2	0.2
IPI00397887	AP3B1	cDNA FLJ51426, highly similar to Adapter-related protein complex 3 beta-1 subunit	100.0%	3.9	2	2	2	4	2,200,575	2,387,185	2,448,188	2,978,708	340,526	207,602	356,424	185,514	34.6	19.5	32.6	13.9	1.1	0.7	1.1	0.6	1.4	0.08	1.0	0.9	1.2	0.07	1.2	0.2
IPI00982231	AP3B1	Uncharacterized protein	100.0%	2.1	2	2	2	4	2,200,575	2,387,185	2,448,188	2,978,708	340,526	207,602	356,424	185,514	34.6	19.5	32.6	13.9	1.1	0.7	1.1	0.6	1.4	0.08	1.0	0.9	1.2	0.07	1.2	0.2
IPI01011395	AP3B1	90 kDa protein	100.0%	2.8	2	2	2	4	2,200,575	2,387,185	2,448,188	2,978,708	340,526	207,602	356,424	185,514	34.6	19.5	32.6	13.9	1.1	0.7	1.1	0.6	1.4	0.08	1.0	0.9	1.2	0.07	1.2	0.2
				LLDSITVPVAR	2	98.3%	1																									
				LLTQYILNLGK	2	98.5%	1																									
IPI00021187	RUVBL1	isoform 1 of RuvB-like 1	100.0%	24.1	9	9	10	1	###########	###########	###########	###########	########	########	########	########	3.3	2.2	5.4	5.0	1.1	0.004	1.0	0.2	1.1	0.02	-1.0	0.3	1.0	0.8	1.0	0.4
				AQTEGINISEEALNHLGEIGTK	3	100.0%	1																									
				EACGVIVELIK	2	94.2%	1																									
				GLGLDESGLAK	2	100.0%	1																									
				LDPSIFESLQK	2	100.0%	1																									
				QAASGLVGQENAR	2	100.0%	2																									
				TISHVIIGLK	3	100.0%	1																									
				VPFCPMVGSEVYSTEIK	2	100.0%	1																									
				VPFCPMVGSEVYSTEIKK	3	99.6%	1																									
				YSVQLLTPANLLAK	2	100.0%	1																									
IPI00910034	-	cDNA FLJ51105, highly similar to Arfaptin-2	100.0%	8.6	3	3	3	5	6,229,450	6,151,996	6,206,532	6,688,554	357,029	268,472	461,522	165,493	12.8	9.8	16.6	5.5	-1.0	0.9	-1.0	1	1.1	0.3	1.0	0.9	1.1	0.1	1.1	0.4
IPI00021257	ARFIP2	Arfaptin-2	100.0%	9.4	3	3	3	5	6,229,450	6,151,996	6,206,532	6,688,554	357,029	268,472	461,522	165,493	12.8	9.8	16.6	5.5	-1.0	0.9	-1.0	1	1.1	0.3	1.0	0.9	1.1	0.1	1.1	0.4
IPI00908576	ARFIP2	cDNA FLJ51194, highly similar to Arfaptin-2	100.0%	12.5	3	3	3	5	6,229,450	6,151,996	6,206,532	6,688,554	357,029	268,472	461,522	165,493	12.8	9.8	16.6	5.5	-1.0	0.9	-1.0	1	1.1	0.3	1.0	0.9	1.1	0.1	1.1	0.4
IPI00909529	ARFIP2	cDNA FLJ51138, highly similar to Arfaptin-2	100.0%	10.0	3	3	3	5	6,229,450	6,151,996	6,206,532	6,688,554	357,029	268,472	461,522	165,493	12.8	9.8	16.6	5.5	-1.0	0.9	-1.0	1	1.1	0.3	1.0	0.9	1.1	0.1	1.1	0.4
IPI01013199	ARFIP2	34 kDa protein	100.0%	10.6	3	3	3	5	6,229,450	6,151,996	6,206,532	6,688,554	357,029	268,472	461,522	165,493	12.8	9.8	16.6	5.5	-1.0	0.9	-1.0	1	1.1	0.3	1.0	0.9	1.1	0.1	1.1	0.4
				QLEQTLQQFNIK	2	99.3%	1																									
				TDLEELSLGPR	2	97.8%	1																									
				YESVLQLGR	2	99.2%	1																									
IPI00021258	ARFIP1	isoform B of Arfaptin-1	100.0%	7.0	2	2	3	2	1,884,113	1,905,065	1,795,548	2,094,368	208,908	169,080	129,051	61,328	24.8	19.9	16.1	6.6	1.0	0.9	-1.0	0.7	1.1	0.4	-1.1	0.6	1.1	0.3	1.2	0.07
IPI00216520	ARFIP1	isoform A of Arfaptin-1	100.0%	7.6	2	2	3	2	1,884,113	1,905,065	1,795,548	2,094,368	208,908	169,080	129,051	61,328	24.8	19.9	16.1	6.6	1.0	0.9	-1.0	0.7	1.1	0.4	-1.1	0.6	1.1	0.3	1.2	0.07
				LKTPGVDAPSWLEEQ	2	99.2%	1																									
				TDLEELNLGPR	2	99.9%	2																									
IPI00021263	YWHAZ	14-3-3 protein zeta/delta	100.0%	55.5	13	15	23	1	82,490,232	84,608,764	85,680,970	95,396,045	5,849,406	3,144,830	4,809,316	2,272,138	15.9	8.3	12.6	5.3	1.0	0.8	1.0	0.7	1.2	0.09	1.0	0.9	1.1	0.02	1.1	0.1
				DICNDVLSLLEK	2	100.0%	2																									
				DNLTLWTSDTQGDEAEAGEGGEN	2	100.0%	2																									
				FLIPNASQAESK	2	100.0%	2																									
				GIVDQSQQAYQEAFEISK	2	100.0%	2																									
				GIVDQSQQAYQEAFEISKK	2	100.0%	1																									
				GIVDQSQQAYQEAFEISKK	3	100.0%	2																									
				IETELRDICNDVLSLLEK	2	100.0%	1																									
				IETELRDICNDVLSLLEK	3	100.0%	1																									
				KGIVDQSQQAYQEAFEISKK	3	99.2%	1																									
				SVTEQGAELSNEER	2	100.0%	2																									
				TAFDEAIAELDTLSEESYK	2	100.0%	2																									
				TAFDEAIAELDTLSEESYKDSTLIMQLLR	3	97.9%	1																									
				YDDMAACMK	2	100.0%	2																									
				YLAEVAAGDDK	2	97.5%	1																									
				YLAEVAAGDDKK	3	100.0%	1																									
IPI00923578	-	Putative uncharacterized protein	99.9%	8.3	1	1	2	3	816,110	805,538	908,552	960,916	92,846	49,894	67,400	55,647	25.4	13.9	16.6	13.0	-1.0	0.9	1.1	0.4	1.2	0.2	1.1	0.3	1.2	0.07	1.1	0.6
IPI00021266	RPL23A	60S ribosomal protein L23a	99.9%	8.3	1	1	2	3	816,110	805,538	908,552	960,916	92,846	49,894	67,400	55,647	25.4	13.9	16.6	13.0	-1.0	0.9	1.1	0.4	1.2	0.2	1.1	0.3	1.2	0.07	1.1	0.6
IPI00794894	RPL23A	Protein	99.9%	8.2	1	1	2	3	816,110	805,538	908,552	960,916	92,846	49,894	67,400	55,647	25.4	13.9	16.6	13.0	-1.0	0.9	1.1	0.4	1.2	0.2	1.1	0.3	1.2	0.07	1.1	0.6
				LAPDYDALDVANK	2	99.8%	2																									
IPI00021290	ACLY	ATP-citrate synthase	100.0%	11.3	9	9	10	3	9,690,897	9,701,182	10,564,022	10,572,198	759,914	245,202	727,124	424,920	17.5	5.7	15.4	9.0	1.0	1	1.1	0.4	1.1	0.3	1.1	0.3	1.1	0.1	1.0	1
IPI00394838	ACLY	cDNA FLJ56442, highly similar to ATP-citrate synthase	100.0%	10.8	9	9	10	3	9,690,897	9,701,182	10,564,022	10,572,198	759,914	245,202	727,124	424,920	17.5	5.7	15.4	9.0	1.0	1	1.1	0.4	1.1	0.3	1.1	0.3	1.1	0.1	1.0	1
IPI00983296	ACLY	ACLY variant protein	100.0%	10.7	9	9	10	3	9,690,897	9,701,182	10,564,022	10,572,198	759,914	245,202	727,124	424,920	17.5	5.7	15.4	9.0	1.0	1	1.1	0.4	1.1	0.3	1.1	0.3	1.1	0.1	1.0	1
				AFDSGIIPMEFVNK	2	100.0%	1																									
				DLVSSLTSGLLTIGDR	2	99.6%	1																									
				FICTTSAIQNR	2	100.0%	1																									
				IGNTGGMLDNILASK	2	100.0%	1																									
				LGLVGVNLTLDGVK	2	99.9%	1																									
				QHFPATPLLDYALEVEK	3	98.5%	1																									
				SGGMSNELNNIISR	2	100.0%	2																									
				TIAIIAEGIPEALTR	2	100.0%	1																									
				TILSLMTR	2	99.6%	1																									
IPI00021298	KRT20	Keratin, type I cytoskeletal 20	100.0%	67.9	27	35	46	1	356,337,644	365,082,856	342,739,359	398,126,833	########	########	########	########	13.8	7.8	12.4	8.7	1.0	0.7	-1.0	0.7	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.05
				CVLQIDNAK	2	100.0%	1																									
				DYSAYYR	2	99.7%	1																									
				ESLEHTLEETK	2	99.4%	1																									
				ESLEHTLEETK	3	95.4%	1																									
				GTEVQLTELRR	3	91.1%	1																									
				HTVNYGSDLTGGGDLFVGNEK	2	100.0%	2																									
				HTVNYGSDLTGGGDLFVGNEK	3	100.0%	1																									
				LAAEDFR	2	99.7%	2																									
				LEQEIATYR	2	100.0%	2																									
				LGTTPSVYGGAGGR	2	100.0%	1																									
				LLEGEDVKTTEYQLSTLEER	3	100.0%	1																									
				LTVEADLQGLNK	2	100.0%	2																									
				MAMQNLNDR	2	100.0%	2																									
				QKYEVMAQK	2	99.4%	2																									
				QKYEVMAQK	3	99.8%	2																									
				QNNEYHILLDIK	2	100.0%	1																									
				QNNEYHILLDIK	3	82.3%	1																									
				QTAVLQQQVTVNTEELK	2	100.0%	1																									
				QWYETNAPR	2	99.9%	1																									
				RLLEGEDVK	2	97.7%	1																									
				SLSSSLQAPVVSTVGMQR	2	100.0%	1																									
				SQIKDAQLQNAR	2	100.0%	2																									
				SQIKDAQLQNAR	3	99.9%	1																									
				TDLEIQIEELNK	2	99.9%	1																									
				TDLEIQIEELNKDLALLK	2	98.4%	1																									
				TDLEIQIEELNKDLALLK	3	100.0%	1																									
				TLEQSNSKLEVQIK	2	99.3%	1																									
				TSQSLEIELQSHLSMK	2	100.0%	1																									
				TTEYQLSTLEER	2	100.0%	2																									
				TVVQEVVDGK	1	100.0%	1																									
				TVVQEVVDGK	2	100.0%	2																									
				VFDDLTLHK	2	98.6%	1																									
				VFDDLTLHK	3	100.0%	2																									
				VVSSEVKEVEENI	2	99.7%	1																									
				YEVMAQK	2	99.0%	1																									
IPI00021302	SUSD2	Sushi domain-containing protein 2	95.3%	1.5	1	1	1	1	5,300,830	5,800,320	5,040,360	6,169,580	623,452	319,594	574,526	651,571	26.3	12.3	25.5	23.6	1.1	0.5	-1.1	0.8	1.2	0.4	-1.2	0.3	1.1	0.6	1.2	0.2
				MSSPTDASVICR	2	95.3%	1																									
IPI00021304	KRT2	Keratin, type II cytoskeletal 2 epidermal	100.0%	10.5	5	5	6	1	45,529,780	48,140,370	49,041,850	50,269,165	4,677,970	3,520,248	3,214,470	2,327,172	23.0	16.4	14.7	10.4	1.1	0.7	1.1	0.6	1.1	0.4	1.0	0.9	1.0	0.6	1.0	0.8
				AQYEEIAQR	2	87.0%	1																									
				FLEQQNQVLQTK	2	99.3%	2																									
				HGGGGGGFGGGGFGSR	2	99.8%	1																									
				NKLNDLEEALQQAKEDLAR	3	99.5%	1																									
				VDLLNQEIEFLK	2	100.0%	1																									
IPI00021327	GRB2	isoform 1 of Growth factor receptor-bound protein 2	100.0%	35.5	7	8	8	1	24,231,158	23,372,293	24,567,302	27,552,857	1,450,307	855,431	1,806,217	1,638,085	13.4	8.2	16.4	13.3	-1.0	0.6	1.0	0.9	1.1	0.2	1.1	0.6	1.2	0.05	1.1	0.3
				FGNDVQHFK	3	99.8%	1																									
				FNSLNELVDYHR	3	98.1%	1																									
				GACHGQTGMFPR	2	97.0%	1																									
				HDGAFLIR	2	99.9%	1																									
				NQQIFLR	2	89.4%	1																									
				RGDFIHVMDNSDPNWWK	3	100.0%	1																									
				VLNEECDQNWYK	2	100.0%	1																									
				VLNEECDQNWYK	3	80.4%	1																									
IPI00021338	DLAT	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase	100.0%	6.8	3	3	4	3	7,210,674	7,156,627	7,154,070	8,041,038	463,198	249,123	651,192	349,692	14.4	7.8	20.4	9.7	-1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	1	1.1	0.07	1.1	0.3
IPI00788836	DLAT	Uncharacterized protein	100.0%	8.1	3	3	4	3	7,210,674	7,156,627	7,154,070	8,041,038	463,198	249,123	651,192	349,692	14.4	7.8	20.4	9.7	-1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	1	1.1	0.07	1.1	0.3
IPI00908638	DLAT	cDNA FLJ57320, highly similar to Dihydrolipoyllysine-residue acetyltransferase com	100.0%	10.3	3	3	4	3	7,210,674	7,156,627	7,154,070	8,041,038	463,198	249,123	651,192	349,692	14.4	7.8	20.4	9.7	-1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	1	1.1	0.07	1.1	0.3
				GVETIANDVVSLATK	2	100.0%	2																									
				VPEANSSWMDTVIR	3	81.0%	1																									

				VVDGAVGAQWLAEFR	2	100.0%	1																									
IPI00021347	UBE2L3	Ubiquitin-conjugating enzyme E2 L3	100.0%	24.0	2	2	2	3	4,714,159	4,451,354	4,731,833	5,133,228	320,253	280,381	372,418	166,809	15.2	14.1	17.6	7.3	-1.1	0.6	1.0	1	1.1	0.3	1.1	0.6	1.2	0.07	1.1	0.4
IPI00909773	UBE2L3	Ubiquitin carrier protein	100.0%	17.5	2	2	2	3	4,714,159	4,451,354	4,731,833	5,133,228	320,253	280,381	372,418	166,809	15.2	14.1	17.6	7.3	-1.1	0.6	1.0	1	1.1	0.3	1.1	0.6	1.2	0.07	1.1	0.4
IPI00909975	UBE2L3	Ubiquitin carrier protein	100.0%	30.3	2	2	2	3	4,714,159	4,451,354	4,731,833	5,133,228	320,253	280,381	372,418	166,809	15.2	14.1	17.6	7.3	-1.1	0.6	1.0	1	1.1	0.3	1.1	0.6	1.2	0.07	1.1	0.4
				IEINFPAEYPFKPPK	3	100.0%	1																									
				TDQVIQSLIALVNDPQPEHPLR	3	100.0%	1																									
IPI00021362	ZNF335	isoform 1 of Zinc finger protein 335	92.1%	0.7	1	1	1	3	1,311,043	1,481,043	1,545,430	1,656,473	105,192	103,030	163,994	116,893	17.9	15.6	23.7	15.8	1.1	0.3	1.2	0.3	1.3	0.06	1.0	0.7	1.1	0.3	1.1	0.6
IPI00181856	ZNF335	ZNF335 protein (Fragment)	92.1%	0.8	1	1	1	3	1,311,043	1,481,043	1,545,430	1,656,473	105,192	103,030	163,994	116,893	17.9	15.6	23.7	15.8	1.1	0.3	1.2	0.3	1.3	0.06	1.0	0.7	1.1	0.3	1.1	0.6
IPI00915023	ZNF335	isoform 2 of Zinc finger protein 335	92.1%	0.8	1	1	1	3	1,311,043	1,481,043	1,545,430	1,656,473	105,192	103,030	163,994	116,893	17.9	15.6	23.7	15.8	1.1	0.3	1.2	0.3	1.3	0.06	1.0	0.7	1.1	0.3	1.1	0.6
				CPDCPFSAR	2	86.8%	1																									
IPI00021370	UBE2K	isoform 1 of Ubiquitin-conjugating enzyme E2 K	100.0%	11.5	2	2	2	2	3,281,090	3,393,217	3,782,665	3,414,645	183,421	113,975	135,522	377,601	12.5	7.5	8.0	24.7	1.0	0.6	1.2	0.06	1.0	0.8	1.1	0.06	1.0	1	-1.1	0.4
IPI00910176	UBE2K	cDNA FLJ57995, moderately similar to Ubiquitin-conjugating enzyme E2-25 kDa	100.0%	16.6	2	2	2	2	3,281,090	3,393,217	3,782,665	3,414,645	183,421	113,975	135,522	377,601	12.5	7.5	8.0	24.7	1.0	0.6	1.2	0.06	1.0	0.8	1.1	0.06	1.0	1	-1.1	0.4
				IENLCAMGFDR	2	98.6%	1																									
				VDLVDENFTELR	2	99.9%	1																									
IPI00021389	CCS	Copper chaperone for superoxide dismutase	99.9%	9.9	2	2	2	2	2,589,563	2,681,842	2,879,773	2,805,060	157,221	58,590	175,649	79,884	13.6	4.9	13.6	6.4	1.0	0.6	1.1	0.3	1.1	0.3	1.1	0.3	1.0	0.2	-1.0	0.7
IPI00980505	CCS	27 kDa protein	99.9%	10.6	2	2	2	2	2,589,563	2,681,842	2,879,773	2,805,060	157,221	58,590	175,649	79,884	13.6	4.9	13.6	6.4	1.0	0.6	1.1	0.3	1.1	0.3	1.1	0.3	1.0	0.2	-1.0	0.7
				QICSCDGLTIWEER	2	92.7%	1																									
				SLIIDEGEDDLGR	2	100.0%	1																									
IPI00021405	LMNA	isoform A of Prelamin-A/C	100.0%	58.0	36	51	72	1	501,662,841	513,317,104	496,131,578	571,297,388	########	########	########	########	16.7	8.8	13.2	7.9	1.0	0.8	-1.0	0.9	1.1	0.1	-1.0	0.6	1.1	0.08	1.2	0.07
				AAYEAELGDAR	2	100.0%	1																									
				AAYEAELGDARK	2	99.9%	1																									
				AGQVVTIWAAGAGATHSPPTDLVWK	3	100.0%	1																									
				AQNTWGCGNSLR	2	100.0%	2																									
				ASASGSGAQVGGPISSGSSASSVTVTR	2	100.0%	2																									
				ASASGSGAQVGGPISSGSSASSVTVTR	3	100.0%	2																									
				EAALSTALSEK	2	100.0%	1																									
				EAALSTALSEKR	2	100.0%	1																									
				EGDLIAAQAR	2	100.0%	1																									
				IDSLSAQLSQLQK	2	100.0%	2																									
				IRIDSLSAQLSQLQK	2	100.0%	1																									
				IRIDSLSAQLSQLQK	3	99.7%	1																									
				ITESEEVVSR	1	98.4%	1																									
				ITESEEVVSR	2	100.0%	2																									
				KEGDLIAAQAR	2	98.9%	1																									
				KQLQDEMLR	2	99.8%	1																									
				KQLQDEMLR	3	99.0%	2																									
				LADALQELR	2	100.0%	2																									
				LALDMEIHAYR	2	99.8%	1																									
				LALDMEIHAYR	3	99.9%	1																									
				LAVYIDR	2	99.1%	1																									
				LEAALGEAK	1	98.9%	1																									
				LEAALGEAK	2	99.9%	1																									
				LKDLEALLNSK	2	100.0%	2																									
				LKDLEALLNSK	3	100.0%	1																									
				LQEKEDLQELNDR	2	100.0%	2																									
				LQEKEDLQELNDR	3	99.9%	2																									
				LQLELSK	1	84.6%	1																									
				LQLELSK	2	94.5%	1																									
				LQTMKEELDFQK	2	100.0%	2																									
				LQTMKEELDFQK	3	100.0%	1																									
				LRDLEDSLAR	2	99.9%	1																									
				LRDLEDSLAR	3	98.2%	1																									
				LVEIDNGK	1	100.0%	1																									
				LVEIDNGK	2	98.6%	1																									
				MQQQLDEYQELLDIK	2	100.0%	2																									
				MQQQLDEYQELLDIK	3	100.0%	1																									
				NIYSEELR	2	99.9%	2																									
				NSNLVGAAHEELQQSR	2	100.0%	2																									
				NSNLVGAAHEELQQSR	3	100.0%	1																									
				QLQDEMLR	2	99.3%	2																									
				QNGDDPLLTYR	2	100.0%	1																									
				SGAQASSTPLSPTR	2	100.0%	3																									
				SLETENAGLR	2	99.9%	1																									
				SNEDQSMGNWQIK	2	100.0%	2																									
				SVGGSGGGSFGDNLVTR	2	100.0%	2																									
				TALINSTGEEVAMR	2	100.0%	2																									
				TLEGELHDLR	2	100.0%	1																									
				TVLCGTCGQPADK	2	100.0%	1																									
				VAVEEVDEEGKFVR	2	100.0%	2																									
				VAVEEVDEEGKFVR	3	100.0%	1																									
IPI00021435	PSMC2	26S protease regulatory subunit 7	100.0%	21.9	7	7	7	1	20,733,990	22,139,360	21,402,530	24,935,985	1,443,703	826,520	1,536,084	711,453	15.6	8.4	16.1	6.4	1.1	0.4	1.0	0.8	1.2	0.03	-1.0	0.7	1.1	0.03	1.2	0.07
				ACLIFFDEIDAIGGAR	2	93.9%	1																									
				FVNLGIEPPK	2	91.8%	1																									
				FVVDLSDQVAPTDIEEGMR	2	100.0%	1																									
				LCPNSTGAEIR	2	99.4%	1																									
				QTLQSEQPLQVAR	2	99.7%	1																									
				QVEDDIQQLLK	2	100.0%	1																									
				TMLELINQLDGFDPR	2	100.0%	1																									
IPI00455339	-	42 kDa protein	96.4%	5.5	2	2	2	5	2,592,048	2,640,479	2,621,774	2,667,945	140,017	209,776	233,440	137,518	12.1	17.8	19.9	11.5	1.0	0.9	1.0	0.9	1.0	0.7	-1.0	1	1.0	0.9	1.0	0.9
IPI00021466	PAIP1	isoform 1 of Polyadenylate-binding protein-interacting protein 1	96.4%	4.2	2	2	2	5	2,592,048	2,640,479	2,621,774	2,667,945	140,017	209,776	233,440	137,518	12.1	17.8	19.9	11.5	1.0	0.9	1.0	0.9	1.0	0.7	-1.0	1	1.0	0.9	1.0	0.9
IPI00337775	PAIP1	isoform 2 of Polyadenylate-binding protein-interacting protein 1	96.4%	5.0	2	2	2	5	2,592,048	2,640,479	2,621,774	2,667,945	140,017	209,776	233,440	137,518	12.1	17.8	19.9	11.5	1.0	0.9	1.0	0.9	1.0	0.7	-1.0	1	1.0	0.9	1.0	0.9
IPI00386299	PAIP1	polyadenylate-binding protein-interacting protein 1 isoform 3	96.4%	5.5	2	2	2	5	2,592,048	2,640,479	2,621,774	2,667,945	140,017	209,776	233,440	137,518	12.1	17.8	19.9	11.5	1.0	0.9	1.0	0.9	1.0	0.7	-1.0	1	1.0	0.9	1.0	0.9
IPI00967955	PAIP1	Uncharacterized protein	96.4%	5.7	2	2	2	5	2,592,048	2,640,479	2,621,774	2,667,945	140,017	209,776	233,440	137,518	12.1	17.8	19.9	11.5	1.0	0.9	1.0	0.9	1.0	0.7	-1.0	1	1.0	0.9	1.0	0.9
				ADILQVGLR	2	96.0%	1																									
				LTGSVLEDAWK	2	96.4%	1																									
IPI00021537	OGFR	isoform 1 of Opioid growth factor receptor	97.7%	2.4	1	1	1	5	1,616,168	1,836,478	1,671,448	2,069,266	171,383	162,512	167,926	203,430	23.7	19.8	22.5	22.0	1.1	0.4	1.0	0.8	1.3	0.1	-1.1	0.5	1.1	0.4	1.2	0.2
IPI00216130	OGFR	isoform 2 of Opioid growth factor receptor	97.7%	2.4	1	1	1	5	1,616,168	1,836,478	1,671,448	2,069,266	171,383	162,512	167,926	203,430	23.7	19.8	22.5	22.0	1.1	0.4	1.0	0.8	1.3	0.1	-1.1	0.5	1.1	0.4	1.2	0.2
IPI00449112	OGFR	OGFR protein	97.7%	3.1	1	1	1	5	1,616,168	1,836,478	1,671,448	2,069,266	171,383	162,512	167,926	203,430	23.7	19.8	22.5	22.0	1.1	0.4	1.0	0.8	1.3	0.1	-1.1	0.5	1.1	0.4	1.2	0.2
IPI00642693	OGFR	67 kDa protein	97.7%	2.6	1	1	1	5	1,616,168	1,836,478	1,671,448	2,069,266	171,383	162,512	167,926	203,430	23.7	19.8	22.5	22.0	1.1	0.4	1.0	0.8	1.3	0.1	-1.1	0.5	1.1	0.4	1.2	0.2
IPI00937682	OGFR	Opioid growth factor receptor	97.7%	3.5	1	1	1	5	1,616,168	1,836,478	1,671,448	2,069,266	171,383	162,512	167,926	203,430	23.7	19.8	22.5	22.0	1.1	0.4	1.0	0.8	1.3	0.1	-1.1	0.5	1.1	0.4	1.2	0.2
				SLGELGLEHFQAPLVR	3	97.7%	1																									
IPI00021626	RBM42	isoform 1 of RNA-binding protein 42	99.3%	4.4	1	1	1	4	245,004	234,310	271,091	231,808	14,664	12,048	23,936	10,324	13.4	11.5	19.7	10.0	-1.0	0.6	1.1	0.4	-1.1	0.5	1.2	0.2	-1.0	0.9	-1.2	0.2
IPI00074329	RBM42	isoform 3 of RNA-binding protein 42	99.3%	4.7	1	1	1	4	245,004	234,310	271,091	231,808	14,664	12,048	23,936	10,324	13.4	11.5	19.7	10.0	-1.0	0.6	1.1	0.4	-1.1	0.5	1.2	0.2	-1.0	0.9	-1.2	0.2
IPI00550442	RBM42	isoform 2 of RNA-binding protein 42	99.3%	4.7	1	1	1	4	245,004	234,310	271,091	231,808	14,664	12,048	23,936	10,324	13.4	11.5	19.7	10.0	-1.0	0.6	1.1	0.4	-1.1	0.5	1.2	0.2	-1.0	0.9	-1.2	0.2
IPI00929470	RBM42	isoform 4 of RNA-binding protein 42	99.3%	4.7	1	1	1	4	245,004	234,310	271,091	231,808	14,664	12,048	23,936	10,324	13.4	11.5	19.7	10.0	-1.0	0.6	1.1	0.4	-1.1	0.5	1.2	0.2	-1.0	0.9	-1.2	0.2
				TAAGSSWEDPSLLEWDADDFR	2	99.3%	1																									
IPI00021700	PCNA;PCNA-AS1	Proliferating cell nuclear antigen	100.0%	47.1	10	11	14	1	94,052,250	89,763,390	83,923,992	105,543,110	7,862,045	5,045,589	6,376,510	5,728,498	18.7	12.6	17.0	12.1	-1.0	0.7	-1.1	0.3	1.1	0.3	-1.1	0.5	1.2	0.07	1.3	0.04
				AEDNADTLALVFEAPNQEK	2	100.0%	1																									
				AEDNADTLALVFEAPNQEK	3	100.0%	1																									
				ATPLSSTVTLSMSADVPLVVEYK	2	100.0%	1																									
				CAGNEDIITLR	2	99.9%	1																									
				DLSHIGDAVVISCAK	2	99.9%	1																									
				FSASGELGNGNIK	2	100.0%	2																									
				MPSGEFAR	2	99.6%	1																									
				NLAMGVNLTSMSK	2	100.0%	2																									
				SEGFDTYR	2	99.9%	1																									
				YLNFFTK	2	99.8%	2																									
				YYLAPK	2	97.9%	1																									
IPI00021728	EIF2S2	Eukaryotic translation initiation factor 2 subunit 2	100.0%	4.5	2	2	2	1	11,167,845	11,021,970	9,573,830	12,757,925	1,340,741	951,136	758,558	701,456	26.8	19.3	17.7	12.3	-1.0	0.9	-1.2	0.3	1.1	0.3	-1.2	0.3	1.2	0.2	1.3	0.02
				TGFQAVTGK	2	99.8%	1																									
				VFNIMR	2	94.1%	1																									
IPI00021759	-	Similar to Oncogene	99.7%	7.1	1	2	2	3	6,188,970	5,883,510	6,141,900	6,831,133	316,036	314,566	341,605	253,104	11.4	12.0	12.4	8.3	-1.1	0.5	-1.0	0.9	1.1	0.2	1.0	0.6	1.2	0.05	1.1	0.1
IPI00423562	USP6	isoform 1 of Ubiquitin carboxyl-terminal hydrolase 6	99.7%	1.0	1	2	2	3	6,188,970	5,883,510	6,141,900	6,831,133	316,036	314,566	341,605	253,104	11.4	12.0	12.4	8.3	-1.1	0.5	-1.0	0.9	1.1	0.2	1.0	0.6	1.2	0.05	1.1	0.1
IPI00423563	USP6	isoform 2 of Ubiquitin carboxyl-terminal hydrolase 6	99.7%	1.3	1	2	2	3	6,188,970	5,883,510	6,141,900	6,831,133	316,036	314,566	341,605	253,104	11.4	12.0	12.4	8.3	-1.1	0.5	-1.0	0.9	1.1	0.2	1.0	0.6	1.2	0.05	1.1	0.1
				RFQFVNDQWIKSQK	2	96.0%	1																									
				RFQFVNDQWIKSQK	3	93.9%	1																									
IPI00021766	RTN4	isoform 1 of Reticulon-4	99.5%	2.9	1	1	1	4	756,840	804,520	783,370	866,485	109,047	60,325	69,010	45,820	32.2	16.8	19.7	11.8	1.1	0.7	1.0	0.8	1.1	0.4	-1.0	0.8	1.1	0.4	1.1	0.3
IPI00298289	RTN4	isoform 2 of Reticulon-4	99.5%	9.1	1	1	1	4	756,840	804,520	783,370	866,485	109,047	60,325	69,010	45,820	32.2	16.8	19.7	11.8	1.1	0.7	1.0	0.8	1.1	0.4	-1.0	0.8	1.1	0.4	1.1	0.3
IPI00478442	RTN4	isoform 5 of Reticulon-4	99.5%	8.7	1	1	1	4	756,840	804,520	783,370	866,485	109,047	60,325	69,010	45,820	32.2	16.8	19.7	11.8	1.1	0.7	1.0	0.8	1.1	0.4	-1.0	0.8	1.1	0.4	1.1	0.3
IPI01011809	RTN4	RTN4 protein	99.5%	9.9	1	1	1	4	756,840	804,520	783,370	866,485	109,047	60,325	69,010	45,820	32.2	16.8	19.7	11.8	1.1	0.7	1.0	0.8	1.1	0.4	-1.0	0.8	1.1	0.4	1.1	0.3
				KPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPR	3	99.5%	1																									
IPI00021785	COX5B	Cytochrome c oxidase subunit 5B, mitochondrial	99.2%	9.3	2	2	2	1	11,959,440	11,687,480	11,313,920	12,165,270	886,020	762,147	640,885	291,933	16.6	14.6	12.7	5.4	-1.0	0.8	-1.1	0.6	1.0	0.8	-1.0	0.7	1.0	0.6	1.1	0.3
				GLDPYNVLAPK	2	99.2%	1																									
				KGLDPYNVLAPK	2	95.5%	1																									
IPI00021794	CTSA	Lysosomal protective protein	100.0%	7.3	2	2	3	3	2,463,083	2,303,107	2,888,157	2,857,017	359,521	108,046	209,268	126,848	32.6	10.5	16.2	9.9	-1.1	0.7	1.2	0.3	1.2	0.3	1.3	0.04	1.2	0.01	-1.0	0.9
IPI00640525	CTSA	lysosomal protective protein isoform a precursor	100.0%	7.0	2	2	3	3	2,463,083	2,303,107	2,888,157	2,857,017	359,521	108,046	209,268	126,848	32.6	10.5	16.2	9.9	-1.1	0.7	1.2	0.3	1.2	0.3	1.3	0.04	1.2	0.01	-1.0	0.9
IPI00641157	CTSA	lysosomal protective protein isoform c precursor	100.0%	7.3	2	2	3	3	2,463,083	2,303,107	2,888,157	2,857,017	359,521	108,046	209,268	126,848	32.6	10.5	16.2	9.9	-1.1	0.7	1.2	0.3	1.2	0.3	1.3	0.04	1.2	0.01	-1.0	0.9
				MDPPCTNTTAASTYLNNPYVRK	3	97.9%	1																									
				YGDSGEQIAGFVK	2	100.0%	2																									
IPI00021808	HARS	Histidyl-tRNA synthetase, cytoplasmic	100.0%	19.7	8	8	8	2	6,458,782	6,766,571	6,321,895	7,418,515	557,237	256,615	438,099	176,271	19.3	8.5	15.5	5.3	1.0	0.6	-1.0	0.9	1.1	0.2	-1.1	0.4	1.1	0.07	1.2	0.05
IPI00967106	HARS	Uncharacterized protein	100.0%	20.5	8	8	8	2	6,458,782	6,766,571	6,321,895	7,418,515	557,237	256,615	438,099	176,271	19.3	8.5	15.5	5.3	1.0	0.6	-1.0	0.9	1.1	0.2	-1.1	0.4	1.1	0.07	1.2	0.05
				ASAELIEEEVAK	2	100.0%	1																									
				HGAEVIDTPVFELK	2	96.7%	1																									
				IFSIVEQR	2	90.1%	1																									
				IGDYVQQHGGVSLVEQLLQDPK	3	99.9%	1																									
				LLFEYLTLFGIDDK	2	89.3%	1																									
				QALEGLGDLK	2	96.4%	1																									
				YDGLVGMFDPK	2	98.9%	1																									
				YDLTVPFAR	2	86.3%	1																									
IPI00021812	AHNAK	Neuroblast differentiation-associated protein AHNAK	100.0%	30.6	129	138	168	1	###########	###########	###########	###########	########	########	########	########	17.2	8.8	14.4	6.7	1.0	0.7	1.0	0.9	1.1	0.1	-1.0	0.8	1.1	0.08	1.1	0.1
				ADIDVSGPK	1	96.9%	1																									
				ADIDVSGPK	2	82.7%	1																									
				ADIDVSGPKVDIDTPDIDIHGPEGK	3	91.5%	1																									
				ADIDVSGPSVDTDAPDLDIEGPEGK	2	100.0%	1																									
				ADLDVSGPK	1	95.2%	1																									
				ADLGVSGPK	2	98.8%	2																									
				ADVDISGPK	1	84.6%	1																									

				ADVDISGPK	2	97.9%	1																									
				ADVDVSGPK	2	99.8%	1																									
				ADVDVSGPKVDVEGPDVNIEGPEGK	3	100.0%	1																									
				ADVVVSGPK	2	99.4%	1																									
				AEASIQAGAGDGEWEESEVK	2	100.0%	1																									
				AEGPDVAVDLPK	2	100.0%	2																									
				AEGPEVDVNLPK	2	100.0%	2																									
				AGAISASGPELQGAGHSK	3	100.0%	1																									
				APDVEGQGLDWSLK	2	100.0%	2																									
				APEVNLNAPDVDVHGPDWNLK	3	100.0%	1																									
				APNISMPDVDLNLK	2	83.5%	1																									
				DDGVFVQEVTQNSPAAR	2	100.0%	2																									
				DIDISSPEFK	2	99.8%	1																									
				ELLLPNWQGSGSHGLTIAQR	3	99.8%	1																									
				FGTFGGLGSK	2	99.7%	1																									
				FKMPDMHFK	3	92.0%	1																									
				FKMPEMHFK	3	99.8%	1																									
				FKMPEMNIK	3	99.9%	2																									
				FSMPGFKGEGPEVDVNLPK	3	92.4%	1																									
				FSVPGFK	2	95.3%	1																									
				GEGPDVDVNLPK	2	100.0%	2																									
				GEGPDVDVSLPK	2	99.8%	1																									
				GEGPDVDVTLPK	2	99.9%	2																									
				GEGPEFDVNLSK	2	100.0%	1																									
				GEGPEVDVNLPK	2	100.0%	2																									
				GEGPEVDVTLPK	2	100.0%	2																									
				GEYDVTMPK	2	99.9%	1																									
				GGQIGLQAPGLSVSGPQGHLESGSGK	3	100.0%	1																									
				GGVQVPAVDISSSLGGR	2	100.0%	2																									
				GGVTGSPEASISGSK	2	100.0%	1																									
				GKGGVTGSPEASISGSK	3	99.9%	1																									
				GNVDISAPK	2	99.7%	1																									
				GPAFNMASPESDFGINLK	2	100.0%	2																									
				GPFVEAEVPDVDLECPDAK	2	100.0%	1																									
				GPGVDLPSVNLSMPK	2	98.2%	1																									
				GPHVDVSGPDIDIEGPEGK	3	99.8%	1																									
				GPQITGPSLEGDLGLK	2	100.0%	1																									
				GPQVSGELKGPGVDVNLK	3	99.7%	1																									
				GPQVSSALNLDTSK	2	100.0%	2																									
				GPSLDIDTPDVNIEGPEGK	2	100.0%	1																									
				GSEVGFHGAAPDISVK	2	100.0%	1																									
				GSEVGFHGAAPDISVK	3	99.8%	1																									
				GSLGATGEIKGPTVGGGLPGIGVQGLEGNLQMPGIK	3	100.0%	1																									
				IDVDAPDIDIHGPDAK	2	99.8%	1																									
				IDVTAPDVSIEEPEGK	2	100.0%	2																									
				IEGEMQVPDVDIR	2	100.0%	2																									
				IGFSGPK	2	86.2%	1																									
				IKGGADVSGGVSAPDISLGEGHLSVK	3	99.8%	1																									
				IPMPDFDLHLK	3	96.6%	1																									
				ISAPNVDFNLEGPK	2	100.0%	2																									
				ISIPDVGLHLK	3	100.0%	1																									
				ISMPDFDLHLK	2	99.9%	1																									
				ISMPDFDLHLK	3	100.0%	1																									
				ISMPDFDLNLK	2	99.1%	1																									
				ISMPDVDLHLK	2	99.9%	1																									
				ISMPDVDLHLK	3	100.0%	1																									
				ISMPDVDLHLKGPKVK	3	87.7%	1																									
				ISMPEIDLNLK	2	97.5%	1																									
				ISMPGFK	2	81.1%	1																									
				ISMPGFKGEGPEVDVNLPK	3	99.9%	1																									
				ISMQDVDLSLGSPK	2	100.0%	2																									
				ISMSEVDLNVAAPK	2	99.9%	1																									
				LDADMPEVAVEGPNGK	2	100.0%	1																									
				LEGDLTGPSVDVEVPDVELECPDAK	2	100.0%	1																									
				LEGELQAPDLELSLPAIHVEGLDIK	3	100.0%	1																									
				LKGEIDASVPELEGDLRGPQVDVK	3	91.7%	1																									
				LKGPQITGPSLEGDLGLK	3	100.0%	1																									
				LKSEDGVEGDLGETQSR	3	98.9%	1																									
				LNVGAPDVTLR	2	99.9%	1																									
				LPQFGISTPGSDLHVNAK	3	100.0%	1																									
				LPSGSGAASPTGSAVDIR	2	100.0%	1																									
				LPTGQISGPEIK	2	100.0%	2																									
				MDIDAPDVDVHGPDWHLK	3	94.8%	1																									
				MDIDAPDVEVQGPDWHLK	2	99.7%	1																									
				MDIDAPDVEVQGPDWHLK	3	100.0%	2																									
				MDIDVPDVEVQGPDWHLK	2	99.9%	1																									
				MDIDVPDVEVQGPDWHLK	3	100.0%	1																									
				MDVNVGDIDIEGPEGK	2	100.0%	2																									
				MEGDLKAPEVDIK	3	97.4%	1																									
				MKGNVDISAPK	2	99.3%	1																									
				MPDVDISVPK	2	99.6%	1																									
				MPEMHFK	2	95.7%	1																									
				MPFLSISSPK	2	99.6%	1																									
				MPSLEISAPK	2	97.6%	1																									
				MPSLEISAPKVTAPDVDLHLKAPK	3	97.0%	1																									
				MSLPDVDLDLKGPK	3	98.7%	1																									
				MYFPDVEFDIK	2	99.9%	1																									
				SEDGVEGDLGETQSR	3	98.4%	1																									
				SPSLDVTVPEAELNLETPEISVGGK	2	100.0%	1																									
				TPSFGISAPQVSIPDVNVNLK	2	100.0%	1																									
				TPSFGISAPQVSIPDVNVNLKGPK	3	99.4%	1																									
				VDIDAPDVDVHGPDWHLK	3	100.0%	1																									
				VDIDAPDVEVHDPDWHLK	3	99.9%	1																									
				VDIDAPDVSIEGPDAK	2	100.0%	1																									
				VDIDTPDIDIHGPEGK	3	100.0%	1																									
				VDIDTPDINIEGSEGK	2	100.0%	1																									
				VDIDVPDVDVQGPDWHLK	3	100.0%	1																									
				VDIDVPDVNIEGPDAK	2	90.1%	1																									
				VDIDVPDVNIEGPEGK	2	95.9%	1																									
				VDIDVPDVNLEAPEGK	2	100.0%	2																									
				VDIEAPDVSLEGPEGK	2	99.8%	1																									
				VDIEGPDVNIEGPEGK	2	100.0%	2																									
				VDIETPNLEGTLTGPR	2	100.0%	1																									
				VDINAPDVDVQGPDWHLK	3	100.0%	1																									
				VDINAPDVDVR	2	90.8%	1																									
				VDINAPDVEVQGK	2	100.0%	2																									
				VDINAPDVGVQGPDWHLK	3	100.0%	1																									
				VDTNAPDLSLEGPEGK	2	100.0%	2																									
				VDVDVPDVNIEGPDAK	2	100.0%	2																									
				VDVEGPDVNIEGPEGK	2	100.0%	1																									
				VDVNAPDVQAPDWHLK	3	100.0%	1																									
				VDVSAPDVEAHGPEWNLK	3	99.6%	1																									
				VDVSAPDVEMQGPDWNLK	2	100.0%	2																									
				VEGDLKGPEVDIR	3	84.5%	1																									
				VEGDMQVPDLDIK	2	100.0%	1																									
				VEGDMQVPDLDIKGPK	3	97.9%	1																									
				VGGSGVNVNAK	2	100.0%	1																									
				VGVEVPDVNIEGPEGK	2	100.0%	2																									
				VKGDMDVSVPK	3	98.5%	1																									
				VKGDVDVSLPK	2	100.0%	1																									
				VKGDVDVSLPK	3	99.7%	1																									
				VKGDVDVSVPK	2	99.0%	1																									
				VQANLGAPDINIEGLDAK	2	100.0%	1																									
				VSAPEVSVGHK	2	98.6%	2																									
				VSAPEVSVGHK	3	100.0%	1																									
				VSAPGVQGDVK	2	99.9%	1																									
				VSGPDLDLNLK	2	99.8%	1																									
				VSMPDVDLNLK	2	98.6%	1																									
				VSMPDVELNLK	2	100.0%	2																									
				VSVGAPDLSLEASEGSIK	2	100.0%	1																									
				VTAYTVDVTGR	2	100.0%	2																									
IPI00021828	CSTB	Cystatin-B	100.0%	45.9	3	4	8	1	49,315,610	47,890,560	46,713,840	56,082,680	5,090,043	2,759,426	3,397,801	2,917,831	23.1	12.9	16.3	11.6	-1.0	0.8	-1.1	0.7	1.1	0.3	-1.0	0.8	1.2	0.08	1.2	0.07
				SQVVAGTNYFIK	2	100.0%	2																									
				VFQSLPHENKPLTLSNYQTNK	3	100.0%	2																									
				VHVGDEDFVHLR	2	100.0%	2																									
				VHVGDEDFVHLR	3	100.0%	2																									
IPI00021841	APOA1	Apolipoprotein A-I	100.0%	24.7	5	5	5	1	12,209,540	13,126,985	12,487,990	14,141,990	1,322,801	278,280	675,730	320,666	24.2	4.7	12.1	5.1	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.04	1.1	0.06
				DYVSQFEGSALGK	2	98.5%	1																									
				EQLGPVTQEFWDNLEK	2	93.2%	1																									
				LLDNWDSVTSTFSK	2	100.0%	1																									
				QGLLPVLESFK	2	97.6%	1																									
				VSFLSALEEYTK	2	100.0%	1																									
IPI00021842	APOE	Apolipoprotein E	100.0%	33.8	7	7	8	1	19,753,834	20,669,445	19,711,449	23,946,428	1,791,519	901,351	1,286,940	721,996	20.3	9.8	14.6	6.7	1.0	0.7	-1.0	1	1.2	0.06	-1.0	0.6	1.2	0.02	1.2	0.02
				AKLEEQAQQIR	2	99.8%	2																									
				AYKSELEEQLTPVAEETR	3	98.4%	1																									
				DRLDEVKEQVAEVR	3	99.8%	1																									
				GEVQAMLGQSTEELR	2	100.0%	1																									

				LGPLVEQGR	2	89.4%	1																									
				VQAAVGTSAAPVPSDNH	2	100.0%	1																									
				WVQTLSEQVQEELLSSQVTQELR	2	100.0%	1																									
IPI00021926	PSMC6	26S protease regulatory subunit 10B	100.0%	32.7	9	10	11	2	29,086,711	28,597,938	32,486,018	32,782,122	1,412,718	1,052,291	1,060,356	857,425	10.9	8.2	7.3	5.9	-1.0	0.8	1.1	0.09	1.1	0.06	1.1	0.03	1.1	0.02	1.0	0.8
IPI00926977	PSMC6	26S protease regulatory subunit 10B	100.0%	31.5	9	10	11	2	29,086,711	28,597,938	32,486,018	32,782,122	1,412,718	1,052,291	1,060,356	857,425	10.9	8.2	7.3	5.9	-1.0	0.8	1.1	0.09	1.1	0.06	1.1	0.03	1.1	0.02	1.0	0.8
				ALQSVGQIVGEVLK	2	100.0%	2																									
				AVASQLDCNFLK	2	99.9%	1																									
				EVDPLVYNMSHEDPGNVSYSEIGGLSEQIR	3	100.0%	1																									
				GCLLYGPPGTGK	2	99.7%	1																									
				HGEIDYEAIVK	2	100.0%	1																									
				IHAGPITK	2	86.4%	1																									
				LSDGFNGADLR	2	96.3%	1																									
				TLMELLNQMDGFDTLHR	2	100.0%	1																									
				TLMELLNQMDGFDTLHR	3	100.0%	1																									
				VALDMTTLTIMR	2	98.4%	1																									
IPI00021954	GBF1	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	99.9%	2.0	2	2	2	3	820,639	775,111	874,999	896,944	47,693	60,716	64,414	72,178	13.0	17.5	16.5	18.0	-1.1	0.6	1.1	0.5	1.1	0.4	1.1	0.3	1.2	0.2	1.0	0.8
IPI00983220	GBF1	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 3	99.9%	2.1	2	2	2	3	820,639	775,111	874,999	896,944	47,693	60,716	64,414	72,178	13.0	17.5	16.5	18.0	-1.1	0.6	1.1	0.5	1.1	0.4	1.1	0.3	1.2	0.2	1.0	0.8
IPI00983896	GBF1	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 2	99.9%	2.1	2	2	2	3	820,639	775,111	874,999	896,944	47,693	60,716	64,414	72,178	13.0	17.5	16.5	18.0	-1.1	0.6	1.1	0.5	1.1	0.4	1.1	0.3	1.2	0.2	1.0	0.8
				EVLNSITELSEIEPNVFLRPFLEVIR	3	99.7%	1																									
				KLMEIITVENPK	2	92.3%	1																									
IPI00021983	NCSTN	isoform 1 of Nicastrin	91.7%	1.7	1	1	1	7	472,409	413,869	465,273	486,516	56,754	26,243	28,124	49,135	26.9	14.2	13.5	22.6	-1.1	0.4	-1.0	0.9	1.0	0.9	1.1	0.2	1.2	0.2	1.0	0.7
IPI00375688	NCSTN	isoform 2 of Nicastrin	91.7%	1.7	1	1	1	7	472,409	413,869	465,273	486,516	56,754	26,243	28,124	49,135	26.9	14.2	13.5	22.6	-1.1	0.4	-1.0	0.9	1.0	0.9	1.1	0.2	1.2	0.2	1.0	0.7
IPI00513841	NCSTN	Nicastrin	91.7%	5.5	1	1	1	7	472,409	413,869	465,273	486,516	56,754	26,243	28,124	49,135	26.9	14.2	13.5	22.6	-1.1	0.4	-1.0	0.9	1.0	0.9	1.1	0.2	1.2	0.2	1.0	0.7
IPI00514793	NCSTN	Uncharacterized protein	91.7%	3.9	1	1	1	7	472,409	413,869	465,273	486,516	56,754	26,243	28,124	49,135	26.9	14.2	13.5	22.6	-1.1	0.4	-1.0	0.9	1.0	0.9	1.1	0.2	1.2	0.2	1.0	0.7
IPI00514877	NCSTN	Nicastrin	91.7%	3.8	1	1	1	7	472,409	413,869	465,273	486,516	56,754	26,243	28,124	49,135	26.9	14.2	13.5	22.6	-1.1	0.4	-1.0	0.9	1.0	0.9	1.1	0.2	1.2	0.2	1.0	0.7
IPI00515093	NCSTN	cDNA FLJ60331, highly similar to Nicastrin	91.7%	2.1	1	1	1	7	472,409	413,869	465,273	486,516	56,754	26,243	28,124	49,135	26.9	14.2	13.5	22.6	-1.1	0.4	-1.0	0.9	1.0	0.9	1.1	0.2	1.2	0.2	1.0	0.7
IPI01010317	NCSTN	50 kDa protein	91.7%	2.7	1	1	1	7	472,409	413,869	465,273	486,516	56,754	26,243	28,124	49,135	26.9	14.2	13.5	22.6	-1.1	0.4	-1.0	0.9	1.0	0.9	1.1	0.2	1.2	0.2	1.0	0.7
				NQVEDLLATLEK	2	91.7%	1																									
IPI00021985	TM9SF4	Transmembrane 9 superfamily member 4	99.6%	5.1	2	2	2	2	3,949,867	3,938,463	3,919,443	4,394,483	305,917	173,726	181,459	206,891	17.3	9.9	10.4	10.5	-1.0	1	-1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00885106	TM9SF4	Similar to Transmembrane 9 superfamily member 4 precursor	99.6%	5.3	2	2	2	2	3,949,867	3,938,463	3,919,443	4,394,483	305,917	173,726	181,459	206,891	17.3	9.9	10.4	10.5	-1.0	1	-1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.1	1.1	0.1
				ITEDYYVHLIADNLPVATR	3	99.6%	1																									
				IVNTPFQVLMNSEK	2	99.3%	1																									
IPI00022058	ASAP2	isoform 1 of Arf-GAP with SH3 domain, ANK repeat and PH domain-containing prote	95.6%	1.8	1	1	1	2	155,268	218,388	198,172	188,881	14,547	45,605	33,454	12,388	21.0	46.7	37.8	14.7	1.4	0.2	1.3	0.3	1.2	0.1	-1.1	0.7	-1.2	0.6	-1.0	0.8
IPI00409613	ASAP2	isoform 2 of Arf-GAP with SH3 domain, ANK repeat and PH domain-containing prote	95.6%	1.9	1	1	1	2	155,268	218,388	198,172	188,881	14,547	45,605	33,454	12,388	21.0	46.7	37.8	14.7	1.4	0.2	1.3	0.3	1.2	0.1	-1.1	0.7	-1.2	0.6	-1.0	0.8
				DIFGLLQAYADGVDLTEK	2	95.6%	1																									
IPI00022078	NDRG1	Protein NDRG1	100.0%	38.3	8	11	16	3	19,820,101	21,934,352	21,515,133	24,255,539	1,631,871	972,582	1,629,960	363,797	18.4	9.9	16.9	3.4	1.1	0.3	1.1	0.5	1.2	0.05	-1.0	0.8	1.1	0.07	1.1	0.2
IPI00923597	NDRG1	Uncharacterized protein	100.0%	42.3	8	11	16	3	19,820,101	21,934,352	21,515,133	24,255,539	1,631,871	972,582	1,629,960	363,797	18.4	9.9	16.9	3.4	1.1	0.3	1.1	0.5	1.2	0.05	-1.0	0.8	1.1	0.07	1.1	0.2
IPI01015869	NDRG1	cDNA FLJ38330 fis, clone FCBBF3025280, highly similar to NDRG1 PROTEIN	100.0%	46.6	8	11	16	3	19,820,101	21,934,352	21,515,133	24,255,539	1,631,871	972,582	1,629,960	363,797	18.4	9.9	16.9	3.4	1.1	0.3	1.1	0.5	1.2	0.05	-1.0	0.8	1.1	0.07	1.1	0.2
				EEMQSNVEVVHTYR	2	100.0%	1																									
				EEMQSNVEVVHTYR	3	95.5%	1																									
				EMQDVDLAEVKPLVEK	2	100.0%	1																									
				EMQDVDLAEVKPLVEK	3	89.2%	1																									
				FALNNPEMVEGLVLINVNPCAEGWMDWAASK	3	96.9%	1																									
				GNRPVILTYHDIGMNHK	3	100.0%	2																									
				ISGWTQALPDMVVSHLFGK	2	100.0%	1																									
				ISGWTQALPDMVVSHLFGK	3	100.0%	2																									
				MADCGGLPQISQPAK	2	100.0%	2																									
				SHTSEGAHLDITPNSGAAGNSAGPK	3	100.0%	2																									
				TASGSSVTSLDGTR	2	100.0%	2																									
IPI00022095	PEG10	isoform RF1/RF2 of Retrotransposon-derived protein PEG10	98.4%	3.8	2	2	2	3	1,805,730	1,786,712	1,726,152	2,170,698	144,446	89,864	140,331	146,838	17.9	11.3	18.2	15.1	-1.0	0.9	-1.0	0.7	1.2	0.1	-1.0	0.7	1.2	0.06	1.3	0.06
IPI00955846	PEG10	retrotransposon-derived protein PEG10 isoform 3	98.4%	3.4	2	2	2	3	1,805,730	1,786,712	1,726,152	2,170,698	144,446	89,864	140,331	146,838	17.9	11.3	18.2	15.1	-1.0	0.9	-1.0	0.7	1.2	0.1	-1.0	0.7	1.2	0.06	1.3	0.06
IPI00976384	PEG10	retrotransposon-derived protein PEG10 isoform 5	98.4%	3.6	2	2	2	3	1,805,730	1,786,712	1,726,152	2,170,698	144,446	89,864	140,331	146,838	17.9	11.3	18.2	15.1	-1.0	0.9	-1.0	0.7	1.2	0.1	-1.0	0.7	1.2	0.06	1.3	0.06
				LPGPAVEGPSATGPEIIR	2	92.8%	1																									
				LTEENTTLR	2	97.1%	1																									
IPI00022134	RAB1B	Putative small GTP-binding protein	100.0%	11.7	1	1	2	2	479,191	513,950	522,023	527,207	41,753	25,418	61,962	17,414	19.5	11.1	26.5	7.4	1.1	0.5	1.1	0.6	1.1	0.3	1.0	0.9	1.0	0.7	1.0	0.9
IPI01009517	RAB1B	Small GTP-binding protein	100.0%	16.0	1	1	2	2	479,191	513,950	522,023	527,207	41,753	25,418	61,962	17,414	19.5	11.1	26.5	7.4	1.1	0.5	1.1	0.6	1.1	0.3	1.0	0.9	1.0	0.7	1.0	0.9
				FADDTYTESYISTIGVDFK	2	100.0%	2																									
IPI00022143	ESYT1	isoform 1 of Extended synaptotagmin-1	97.8%	3.2	2	2	2	2	5,335,292	6,126,168	5,439,788	6,124,905	219,517	226,243	376,917	226,362	9.2	8.3	15.5	8.3	1.1	0.04	1.0	0.8	1.1	0.04	-1.1	0.2	-1.0	1	1.1	0.2
IPI00746655	ESYT1	isoform 2 of Extended synaptotagmin-1	97.8%	3.1	2	2	2	2	5,335,292	6,126,168	5,439,788	6,124,905	219,517	226,243	376,917	226,362	9.2	8.3	15.5	8.3	1.1	0.04	1.0	0.8	1.1	0.04	-1.1	0.2	-1.0	1	1.1	0.2
				QLLDDEEQLTAK	2	91.9%	1																									
				VLQASVLDDWFPLQGGQGQVHLR	3	97.7%	1																									
IPI00022202	SLC25A3	isoform A of Phosphate carrier protein, mitochondrial	100.0%	3.3	1	1	1	2	1,676,950	1,786,910	2,330,485	1,651,225	150,012	111,990	248,205	124,447	20.0	14.0	23.8	16.9	1.1	0.6	1.4	0.05	-1.0	0.9	1.3	0.08	-1.1	0.4	-1.4	0.04
IPI00215777	SLC25A3	isoform B of Phosphate carrier protein, mitochondrial	100.0%	3.3	1	1	1	2	1,676,950	1,786,910	2,330,485	1,651,225	150,012	111,990	248,205	124,447	20.0	14.0	23.8	16.9	1.1	0.6	1.4	0.05	-1.0	0.9	1.3	0.08	-1.1	0.4	-1.4	0.04
				IQTQPGYANTLR	2	100.0%	1																									
IPI00022228	HDLBP	Vigilin	100.0%	19.2	18	19	23	1	66,085,940	67,536,223	62,469,185	76,003,793	6,135,912	2,989,237	4,352,745	2,407,300	20.8	9.9	15.6	7.1	1.0	0.8	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.06	1.2	0.03
				APDMSSSEEFPSFGAQVAPK	2	90.1%	1																									
				ASVITQVFHVPLEER	2	97.2%	1																									
				DKFPEVIINFPDPAQK	3	98.9%	1																									
				DLANIAEVEVSIPAK	2	93.0%	1																									
				DQGLSIMVSGK	2	99.8%	1																									
				EALEALVPVTIEVEVPFDLHR	3	100.0%	1																									
				EIAEEYGGVMVSFPR	2	100.0%	2																									
				FPEVIINFPDPAQKSDIVQLR	2	97.6%	1																									
				GNSLQEILER	2	89.0%	1																									
				HEVLLISAEQDKR	3	99.3%	1																									
				ICLEIMQR	2	92.7%	1																									
				IDLPAENSNSETIIITGK	2	100.0%	1																									
				IVGELEQMVSEDVPLDHR	3	100.0%	2																									
				LGQALTEVYAK	2	100.0%	1																									
				LQTQASATVAIPK	2	100.0%	2																									
				LVGEIMQETGTR	2	100.0%	2																									
				RCDIIIISGR	2	99.2%	1																									
				TGAHLELSLAK	2	99.4%	1																									
				TGAHLELSLAK	3	99.5%	1																									
IPI00022254	ATG3	isoform 1 of Ubiquitin-like-conjugating enzyme ATG3	99.4%	6.7	2	2	2	2	2,738,745	2,958,020	3,347,140	3,510,915	379,071	175,643	252,456	244,432	31.0	13.3	16.9	15.6	1.1	0.6	1.2	0.2	1.3	0.1	1.1	0.2	1.2	0.1	1.0	0.7
IPI00449201	ATG3	isoform 2 of Ubiquitin-like-conjugating enzyme ATG3	99.4%	6.8	2	2	2	2	2,738,745	2,958,020	3,347,140	3,510,915	379,071	175,643	252,456	244,432	31.0	13.3	16.9	15.6	1.1	0.6	1.2	0.2	1.3	0.1	1.1	0.2	1.2	0.1	1.0	0.7
				IVEACKAKTDAGGEDAILQTR	3	98.4%	1																									
				TDAGGEDAILQTR	2	99.4%	1																									
IPI00022256	AP2M1	isoform 1 of AP-2 complex subunit mu	99.6%	3.7	1	1	1	6	391,417	398,623	425,370	413,747	38,101	33,791	45,313	25,606	21.8	19.0	23.8	13.8	1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.6	1.0	0.7	-1.0	0.8
IPI00619900	AP2M1	isoform 2 of AP-2 complex subunit mu	99.6%	3.7	1	1	1	6	391,417	398,623	425,370	413,747	38,101	33,791	45,313	25,606	21.8	19.0	23.8	13.8	1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.6	1.0	0.7	-1.0	0.8
IPI00790642	AP2M1	cDNA FLJ50581, highly similar to AP-2 complex subunit mu-1	99.6%	5.0	1	1	1	6	391,417	398,623	425,370	413,747	38,101	33,791	45,313	25,606	21.8	19.0	23.8	13.8	1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.6	1.0	0.7	-1.0	0.8
IPI00909772	AP2M1	cDNA FLJ53069, highly similar to AP-2 complex subunit mu-1	99.6%	3.5	1	1	1	6	391,417	398,623	425,370	413,747	38,101	33,791	45,313	25,606	21.8	19.0	23.8	13.8	1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.6	1.0	0.7	-1.0	0.8
IPI01009864	AP2M1	cDNA FLJ53962, highly similar to AP-2 complex subunit mu-1	99.6%	3.8	1	1	1	6	391,417	398,623	425,370	413,747	38,101	33,791	45,313	25,606	21.8	19.0	23.8	13.8	1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.6	1.0	0.7	-1.0	0.8
IPI01015530	AP2M1	cDNA FLJ53049, highly similar to AP-2 complex subunit mu-1	99.6%	4.3	1	1	1	6	391,417	398,623	425,370	413,747	38,101	33,791	45,313	25,606	21.8	19.0	23.8	13.8	1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.6	1.0	0.7	-1.0	0.8
				IPTPLNTSGVQVICMK	2	99.6%	1																									
IPI00022283	TFF1	Trefoil factor 1	100.0%	32.1	3	3	4	1	42,139,492	40,394,970	37,429,876	45,526,830	2,682,842	2,178,714	2,624,679	2,257,253	14.2	12.1	15.7	11.1	-1.0	0.6	-1.1	0.2	1.1	0.4	-1.1	0.4	1.1	0.1	1.2	0.05
				ERQNCGFPGVTPSQCANK	3	89.5%	1																									
				GCCFDDTVR	2	98.1%	1																									
				QNCGFPGVTPSQCANK	2	100.0%	2																									
IPI00022314	SOD2	Superoxide dismutase [Mn], mitochondrial	100.0%	16.2	3	3	4	3	9,121,312	9,683,196	8,827,369	10,366,597	581,414	457,646	282,817	260,350	14.3	10.6	7.2	5.6	1.1	0.5	-1.0	0.7	1.1	0.09	-1.1	0.2	1.1	0.2	1.2	0.004
IPI00847322	SOD2	superoxide dismutase [Mn], mitochondrial isoform A precursor	100.0%	16.2	3	3	4	3	9,121,312	9,683,196	8,827,369	10,366,597	581,414	457,646	282,817	260,350	14.3	10.6	7.2	5.6	1.1	0.5	-1.0	0.7	1.1	0.09	-1.1	0.2	1.1	0.2	1.2	0.004
IPI01011075	SOD2	Superoxide dismutase	100.0%	22.2	3	3	4	3	9,121,312	9,683,196	8,827,369	10,366,597	581,414	457,646	282,817	260,350	14.3	10.6	7.2	5.6	1.1	0.5	-1.0	0.7	1.1	0.09	-1.1	0.2	1.1	0.2	1.2	0.004
				AIWNVINWENVTER	2	100.0%	2																									
				GDVTAQIALQPALK	2	98.8%	1																									
				NVRPDYLK	2	92.6%	1																									
IPI00022334	OAT	Ornithine aminotransferase, mitochondrial	100.0%	19.1	6	6	7	1	25,502,311	32,921,752	28,050,545	35,360,804	2,796,988	2,919,029	1,831,424	2,079,581	24.5	19.8	14.6	13.2	1.3	0.1	1.1	0.5	1.4	0.02	-1.2	0.2	1.1	0.5	1.3	0.03
				AFYNNVLGEYEEYITK	2	100.0%	1																									
				GIYLWDVEGR	2	99.8%	2																									
				LPSDVVTAVR	2	99.9%	1																									
				TVQGPPTSDDIFER	2	99.1%	1																									
				VLPMNTGVEAGETACK	2	99.9%	1																									
				WLAVDYENVRPDIVLLGK	3	97.4%	1																									
IPI00022370	CUX2	Homeobox protein cut-like 2	100.0%	3.4	3	3	3	1	23,877,255	23,401,318	21,414,301	26,613,036	1,723,703	1,129,196	1,717,369	1,205,262	16.1	10.8	17.9	10.1	-1.0	0.8	-1.1	0.3	1.1	0.2	-1.1	0.4	1.1	0.09	1.2	0.04
				KYDEEAASKADEVGLIMTNLEK	3	95.5%	1																									
				QLTAKSEAIEKLEEK	3	81.4%	1																									
				SSPSPPPSPTEPEK	2	99.8%	1																									
IPI00022388	DPYSL4	Dihydropyrimidinase-related protein 4	99.6%	2.8	1	1	1	2	939,915	885,630	1,059,020	1,069,425	60,219	57,915	156,273	95,126	14.3	14.6	33.0	19.9	-1.1	0.5	1.1	0.5	1.1	0.3	1.2	0.3	1.2	0.1	1.0	1
IPI00514623	DPYSL4	Dihydropyrimidinase-like 4	99.6%	3.9	1	1	1	2	939,915	885,630	1,059,020	1,069,425	60,219	57,915	156,273	95,126	14.3	14.6	33.0	19.9	-1.1	0.5	1.1	0.5	1.1	0.3	1.2	0.3	1.2	0.1	1.0	1
				MDENEFVAVTSTNAAK	2	99.6%	1																									
IPI00022418	FN1	isoform 1 of Fibronectin	100.0%	0.7	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00339223	FN1	isoform 3 of Fibronectin	100.0%	0.7	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00339224	FN1	isoform 4 of Fibronectin	100.0%	0.8	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00339225	FN1	isoform 5 of Fibronectin	100.0%	0.8	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00339226	FN1	isoform 6 of Fibronectin	100.0%	0.8	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00339227	FN1	isoform 7 of Fibronectin	100.0%	0.7	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00339228	FN1	isoform 8 of Fibronectin	100.0%	0.7	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00414283	FN1	isoform 9 of Fibronectin	100.0%	0.8	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00479723	FN1	isoform 10 of Fibronectin	100.0%	0.8	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00845263	FN1	fibronectin isoform 4 preproprotein	100.0%	0.7	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00855777	FN1	isoform 14 of Fibronectin	100.0%	0.8	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00855785	FN1	isoform 15 of Fibronectin	100.0%	0.7	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00867588	FN1	isoform 13 of Fibronectin	100.0%	0.8	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00339319	FN1	isoform 11 of Fibronectin	100.0%	0.7	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00556632	FN1	isoform 12 of Fibronectin	100.0%	0.9	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00873210	FN1	Uncharacterized protein	100.0%	0.7	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
IPI00922213	FN1	cDNA FLJ53292, highly similar to Homo sapiens fibronectin 1 (FN1), transcript varia	100.0%	1.7	1	1	1	17	317,499	317,176	320,888	331,394	19,288	14,516	19,181	20,306	13.6	10.2	13.4	13.7	-1.0	1	1.0	0.9	1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
				FLATTPNSLLVSWQPPR	2	99.1%	1																									
IPI00022431	AHSG	cDNA FLJ55606, highly similar to Alpha-2-HS-glycoprotein	99.9%	4.4	3	3	3	2	11,673,156	14,284,495	11,770,761	17,027,065	2,280,433	1,731,735	832,823	1,113,387	43.7	27.1	15.8	14.6	1.2	0.4	1.0	1	1.5	0.07	-1.2	0.2	1.2	0.2	1.4	0.005
IPI00953689	AHSG	Alpha-2-HS-glycoprotein	99.9%	5.2	3	3	3	2	11,673,156	14,284,495	11,770,761	17,027,065	2,280,433	1,731,735	832,823	1,113,387	43.7	27.1	15.8	14.6	1.2	0.4	1.0	1	1.5	0.07	-1.2	0.2	1.2	0.2	1.4	0.005
				AHYDLR	1	87.6%	1																									
				CNLLAEK	1	95.5%	1																									
				QYGFCK	2	86.5%	1																									
IPI00022434	ALB	Uncharacterized protein	100.0%	8.0	6	8	12	5	8,339,894	11,094,575	8,672,628	13,625,148	2,318,685	1,539,022	620,359	952,837	62.2	31.0	16.0	15.6	1.3	0.4	1.0	0.9	1.6	0.07	-1.3	0.2	1.2	0.2	1.6	0.002
IPI00745872	ALB	isoform 1 of Serum albumin	100.0%	8.2	6	8	12	5	8,339,894	11,094,575	8,672,628	13,625,148	2,318,685	1,539,022	620,359	952,837	62.2	31.0	16.0	15.6	1.3	0.4	1.0	0.9	1.6	0.07	-1.3	0.2	1.2	0.2	1.6	0.002
IPI00908876	ALB	cDNA FLJ50830, highly similar to Serum albumin	100.0%	9.6	6	8	12	5	8,339,894	11,094,575	8,672,628	13,625,148	2,318,685	1,539,022	620,359	952,837	62.2	31.0	16.0	15.6	1.3	0.4	1.0	0.9	1.6	0.07	-1.3	0.2	1.2	0.2	1.6	0.002
IPI00965913	ALB	Protein	100.0%	11.0	6	8	12	5	8,339,894	11,094,575	8,672,628	13,625,148	2,318,685	1,539,022	620,359	952,837	62.2	31.0	16.0	15.6	1.3	0.4	1.0	0.9	1.6	0.07	-1.3	0.2	1.2	0.2	1.6	0.002
IPI00966829	ALB	69 kDa protein	100.0%	8.3	6	8	12	5	8,339,894	11,094,575	8,672,628	13,625,148	2,318,685	1,539,022	620,359	952,837	62.2	31.0	16.0	15.6	1.3	0.4	1.0	0.9	1.6	0.07	-1.3	0.2	1.2	0.2	1.6	0.002

				CCTESLVNR	2	100.0%	1																									
				KVPQVSTPTLVEVSR	2	100.0%	2																									
				KVPQVSTPTLVEVSR	3	100.0%	2																									
				LVTDLTK	1	99.5%	1																									
				LVTDLTK	2	99.9%	1																									
				VPQVSTPTLVEVSR	2	100.0%	2																									
				YICENQDSISSK	2	100.0%	2																									
				YLYEIAR	2	98.7%	1																									
IPI00022443	AFP	Alpha-fetoprotein	99.6%	2.6	1	1	1	3	797,297	800,737	991,437	952,840	59,130	92,541	107,972	104,065	16.6	25.8	24.4	24.4	1.0	1	1.2	0.2	1.2	0.2	1.2	0.2	1.2	0.3	-1.0	0.8
IPI00968077	AFP	70 kDa protein	99.6%	2.6	1	1	1	3	797,297	800,737	991,437	952,840	59,130	92,541	107,972	104,065	16.6	25.8	24.4	24.4	1.0	1	1.2	0.2	1.2	0.2	1.2	0.2	1.2	0.3	-1.0	0.8
IPI01009043	AFP	cDNA FLJ51509, highly similar to Alpha-fetoprotein	99.6%	3.3	1	1	1	3	797,297	800,737	991,437	952,840	59,130	92,541	107,972	104,065	16.6	25.8	24.4	24.4	1.0	1	1.2	0.2	1.2	0.2	1.2	0.2	1.2	0.3	-1.0	0.8
				LGEYYLQNAFLVAYTK	2	99.6%	1																									
IPI00022462	TFRC	Transferrin receptor protein 1	100.0%	24.5	15	15	17	1	53,714,878	53,103,504	56,046,437	61,017,352	5,308,102	3,052,604	3,914,602	2,043,176	22.1	12.9	15.6	7.5	-1.0	0.9	1.0	0.7	1.1	0.3	1.1	0.6	1.1	0.06	1.1	0.3
				AAAEVAGQFVIK	2	100.0%	1																									
				AFTYINLDK	2	96.5%	1																									
				DSAQNSVIIVDK	2	100.0%	1																									
				HPVTGQFLYQDSNWASK	3	100.0%	1																									
				ILNIFGVIK	2	99.8%	1																									
				IPELNK	1	86.7%	1																									
				LAQMFSDMVLK	2	100.0%	2																									
				LFGNMEGDCPSDWK	2	100.0%	1																									
				LTTDFGNAEK	2	95.2%	1																									
				LVYLVENPGGYVAYSK	2	82.1%	1																									
				SAFSNLFGGEPLSYTR	2	100.0%	1																									
				SGVGTALLLK	2	83.0%	1																									
				SSGLPNIPVQTISR	2	99.5%	2																									
				VANAESLNAIGVLIYMDQTK	3	99.9%	1																									
				YNSQLLSFVR	2	100.0%	1																									
IPI00022501	DNAJC27	isoform 1 of DnaJ homolog subfamily C member 27	94.3%	7.0	1	1	1	2	1,849,905	1,797,415	1,818,360	1,962,930	177,880	52,407	177,018	60,072	21.5	6.5	21.8	6.8	-1.0	0.8	-1.0	0.9	1.1	0.6	1.0	0.9	1.1	0.07	1.1	0.5
IPI00892589	DNAJC27	isoform 3 of DnaJ homolog subfamily C member 27	94.3%	10.7	1	1	1	2	1,849,905	1,797,415	1,818,360	1,962,930	177,880	52,407	177,018	60,072	21.5	6.5	21.8	6.8	-1.0	0.8	-1.0	0.9	1.1	0.6	1.0	0.9	1.1	0.07	1.1	0.5
				NEFYKDTQGVILVYDVGQK	3	94.3%	1																									
IPI00022597	UBE2M	NEDD8-conjugating enzyme Ubc12	100.0%	19.7	3	3	3	1	12,153,690	11,678,980	11,569,780	13,363,270	911,968	319,058	886,056	370,519	16.8	6.1	17.1	6.2	-1.0	0.6	-1.1	0.7	1.1	0.3	-1.0	0.9	1.1	0.009	1.2	0.1
				DINELNLPK	2	99.9%	1																									
				GGYIGSTYFER	2	97.2%	1																									
				TCDISFSDPDDLLNFK	2	100.0%	1																									
IPI00022608	SORL1	Sortilin-related receptor	99.8%	0.9	1	1	1	1	1,781,316	1,682,808	1,862,670	1,966,170	311,346	322,251	223,990	208,609	39.1	42.8	26.9	23.7	-1.1	0.8	1.0	0.8	1.1	0.6	1.1	0.7	1.2	0.5	1.1	0.7
				YSGSQMEILANQLTGLMDMK	2	99.8%	1																									
IPI00022648	EIF5	Eukaryotic translation initiation factor 5	100.0%	13.9	5	5	7	1	27,840,992	30,454,609	30,979,472	33,598,897	2,662,044	1,243,710	2,369,847	1,444,878	21.4	9.1	17.1	9.6	1.1	0.4	1.1	0.4	1.2	0.09	1.0	0.8	1.1	0.1	1.1	0.4
				AMGPLVLTEVLFNEK	2	100.0%	2																									
				TVIVNMVDVAK	2	100.0%	1																									
				VLTLSDDLER	2	99.9%	2																									
				VNILFDFVK	2	99.9%	1																									
				YFGCELGAQTQFDVK	2	99.1%	1																									
IPI00022649	SLC12A2	isoform 1 of Solute carrier family 12 member 2	99.6%	1.0	1	1	1	3	1,055,413	1,127,537	1,124,023	1,173,837	44,513	47,358	43,785	50,615	9.4	9.4	8.7	9.6	1.1	0.3	1.1	0.3	1.1	0.1	-1.0	1	1.0	0.5	1.0	0.5
IPI00220844	SLC12A2	isoform 2 of Solute carrier family 12 member 2	99.6%	1.0	1	1	1	3	1,055,413	1,127,537	1,124,023	1,173,837	44,513	47,358	43,785	50,615	9.4	9.4	8.7	9.6	1.1	0.3	1.1	0.3	1.1	0.1	-1.0	1	1.0	0.5	1.0	0.5
IPI00966284	SLC12A2	Solute carrier family 12 (Sodium/potassium/chloride transporters), member 2 variant	99.6%	1.0	1	1	1	3	1,055,413	1,127,537	1,124,023	1,173,837	44,513	47,358	43,785	50,615	9.4	9.4	8.7	9.6	1.1	0.3	1.1	0.3	1.1	0.1	-1.0	1	1.0	0.5	1.0	0.5
				FQVDLVSENAGR	2	99.6%	1																									
IPI00022661	PVRL2	isoform Delta of Poliovirus receptor-related protein 2	94.0%	2.2	1	1	1	2	2,732,550	2,727,345	2,636,895	3,137,320	133,090	109,962	90,827	163,853	10.9	9.0	7.7	11.7	-1.0	1	-1.0	0.6	1.1	0.09	-1.0	0.5	1.2	0.07	1.2	0.03
IPI00215980	PVRL2	isoform Alpha of Poliovirus receptor-related protein 2	94.0%	2.5	1	1	1	2	2,732,550	2,727,345	2,636,895	3,137,320	133,090	109,962	90,827	163,853	10.9	9.0	7.7	11.7	-1.0	1	-1.0	0.6	1.1	0.09	-1.0	0.5	1.2	0.07	1.2	0.03
				ISWLSSLDWEAK	2	94.0%	1																									
IPI00022694	PSMD4	isoform Rpn10A of 26S proteasome non-ATPase regulatory subunit 4	100.0%	19.9	5	5	7	1	10,005,048	10,889,818	10,103,077	12,332,141	814,949	524,536	701,740	559,366	18.2	10.8	15.5	10.1	1.1	0.4	1.0	0.9	1.2	0.05	-1.1	0.4	1.1	0.1	1.2	0.04
				AAAASAAEAGIATTGTEDSDDALLK	3	99.8%	1																									
				LTAFVNTLNGK	2	99.9%	2																									
				MTISQQEFGR	2	99.9%	2																									
				NAMGSLASQATK	2	97.4%	1																									
				VNVDIINFGEEEVNTEK	2	100.0%	1																									
IPI00910508	-	cDNA FLJ52694, moderately similar to Developmentally-regulated GTP-binding prot	90.4%	9.2	1	1	1	5	421,106	473,548	476,572	528,060	39,414	52,066	35,440	30,216	20.9	24.6	16.6	12.8	1.1	0.4	1.1	0.3	1.3	0.06	1.0	1	1.1	0.4	1.1	0.3
IPI00022697	DRG2	Developmentally-regulated GTP-binding protein 2	90.4%	5.5	1	1	1	5	421,106	473,548	476,572	528,060	39,414	52,066	35,440	30,216	20.9	24.6	16.6	12.8	1.1	0.4	1.1	0.3	1.3	0.06	1.0	1	1.1	0.4	1.1	0.3
IPI00794194	DRG2	Uncharacterized protein	90.4%	5.8	1	1	1	5	421,106	473,548	476,572	528,060	39,414	52,066	35,440	30,216	20.9	24.6	16.6	12.8	1.1	0.4	1.1	0.3	1.3	0.06	1.0	1	1.1	0.4	1.1	0.3
IPI00794224	DRG2	18 kDa protein	90.4%	11.6	1	1	1	5	421,106	473,548	476,572	528,060	39,414	52,066	35,440	30,216	20.9	24.6	16.6	12.8	1.1	0.4	1.1	0.3	1.3	0.06	1.0	1	1.1	0.4	1.1	0.3
IPI00797141	DRG2	27 kDa protein	90.4%	8.2	1	1	1	5	421,106	473,548	476,572	528,060	39,414	52,066	35,440	30,216	20.9	24.6	16.6	12.8	1.1	0.4	1.1	0.3	1.3	0.06	1.0	1	1.1	0.4	1.1	0.3
				GANIQLLDLPGIIEGAAQGK	2	90.5%	1																									
IPI00022744	CSE1L	isoform 1 of Exportin-2	100.0%	22.1	16	18	22	2	30,086,646	31,344,384	29,522,272	34,407,314	2,534,684	1,489,328	2,002,118	1,150,048	18.8	10.6	15.2	7.5	1.0	0.7	-1.0	0.9	1.1	0.2	-1.1	0.5	1.1	0.1	1.2	0.07
IPI00219994	CSE1L	isoform 3 of Exportin-2	100.0%	22.8	16	18	22	2	30,086,646	31,344,384	29,522,272	34,407,314	2,534,684	1,489,328	2,002,118	1,150,048	18.8	10.6	15.2	7.5	1.0	0.7	-1.0	0.9	1.1	0.2	-1.1	0.5	1.1	0.1	1.2	0.07
				AADEEAFEDNSEEYIR	2	99.4%	1																									
				AADEEAFEDNSEEYIRR	3	98.5%	1																									
				ALTLPGSSENEYIMK	2	99.9%	1																									
				EDFPQKWPDLLTEMVNR	3	96.9%	1																									
				FFEGPVTGIFSGYVNSMLQEYAK	2	100.0%	2																									
				FFEGPVTGIFSGYVNSMLQEYAK	3	100.0%	1																									
				FLESVEGNQNYPLLLLTLLEK	2	100.0%	2																									
				FLESVEGNQNYPLLLLTLLEK	3	100.0%	2																									
				GLCKFFEGPVTGIFSGYVNSMLQEYAK	3	95.9%	1																									
				GSNTIASAAADKIPGLLGVFQK	3	100.0%	1																									
				LLQAFLER	2	99.9%	1																									
				LLQTDDEEEAGLLELLK	2	100.0%	1																									
				LVLDAFALPLTNLFK	2	100.0%	2																									
				QLSDAISIIGR	2	94.5%	1																									
				SANVNEFPVLK	2	96.6%	1																									
				TLDPDPAIR	2	98.9%	1																									
				VIVPNMEFR	2	99.6%	1																									
				YGALALQEIFDGIQPK	2	96.9%	1																									
IPI00022745	MVD	Diphosphomevalonate decarboxylase	98.0%	3.3	1	1	1	3	1,169,080	1,037,293	1,039,123	1,102,393	115,449	66,134	88,210	64,375	22.1	14.3	19.0	13.1	-1.1	0.4	-1.1	0.4	-1.1	0.6	1.0	1	1.1	0.5	1.1	0.6
IPI00556625	MVD	Diphosphomevalonate decarboxylase variant (Fragment)	98.0%	5.6	1	1	1	3	1,169,080	1,037,293	1,039,123	1,102,393	115,449	66,134	88,210	64,375	22.1	14.3	19.0	13.1	-1.1	0.4	-1.1	0.4	-1.1	0.6	1.0	1	1.1	0.5	1.1	0.6
IPI00640007	MVD	29 kDa protein	98.0%	4.8	1	1	1	3	1,169,080	1,037,293	1,039,123	1,102,393	115,449	66,134	88,210	64,375	22.1	14.3	19.0	13.1	-1.1	0.4	-1.1	0.4	-1.1	0.6	1.0	1	1.1	0.5	1.1	0.6
				VYGVESDLSEVAR	2	98.0%	1																									
IPI00022774	VCP	Transitional endoplasmic reticulum ATPase	100.0%	40.7	30	36	48	1	322,702,806	337,337,460	321,633,238	368,839,533	########	########	########	########	16.7	7.3	16.2	6.4	1.0	0.6	-1.0	1	1.1	0.1	-1.0	0.6	1.1	0.07	1.1	0.1
				AIANECQANFISIK	2	100.0%	2																									
				AIGVKPPR	2	95.1%	1																									
				DVDLEFLAK	2	100.0%	1																									
				ELQELVQYPVEHPDK	3	98.0%	1																									
				ERQTNPSAMEVEEDDPVPEIR	3	100.0%	1																									
				FGMTPSK	2	86.1%	1																									
				GDDLSTAILK	2	99.9%	1																									
				GVLFYGPPGCGK	2	100.0%	2																									
				HPALFK	2	98.3%	2																									
				IVSQLLTLMDGLK	2	100.0%	2																									
				KGDIFLVR	2	100.0%	2																									
				KQLAQIK	2	88.8%	1																									
				KYEMFAQTLQQSR	2	100.0%	1																									
				KYEMFAQTLQQSR	3	99.9%	1																									
				LAGESESNLR	2	100.0%	1																									
				LAGESESNLRK	2	100.0%	1																									
				LDQLIYIPLPDEK	2	100.0%	2																									
				LEILQIHTK	2	100.0%	1																									
				LEILQIHTK	3	94.4%	1																									
				LGDVISIQPCPDVK	2	99.5%	1																									
				LIVDEAINEDNSVVSLSQPK	2	100.0%	2																									
				LIVDEAINEDNSVVSLSQPK	3	100.0%	1																									
				MDELQLFR	2	100.0%	1																									
				MTNGFSGADLTEICQR	2	100.0%	2																									
				NAPAIIFIDELDAIAPK	2	100.0%	3																									
				NAPAIIFIDELDAIAPK	3	99.9%	1																									
				NVFIIGATNRPDIIDPAILRPGR	3	100.0%	1																									
				QAAPCVLFFDELDSIAK	2	100.0%	2																									
				QAAPCVLFFDELDSIAK	3	100.0%	1																									
				QTNPSAMEVEEDDPVPEIR	2	82.2%	1																									
				QTNPSAMEVEEDDPVPEIR	3	99.5%	1																									
				QTNPSAMEVEEDDPVPEIRR	3	95.0%	1																									
				RDHFEEAMR	2	98.8%	1																									
				VINQILTEMDGMSTK	2	100.0%	1																									
				VINQILTEMDGMSTKK	3	94.9%	1																									
				WALSQSNPSALR	2	100.0%	2																									
IPI00022790	MFAP1	Microfibrillar-associated protein 1	96.9%	5.7	1	1	1	1	1,272,901	1,446,562	1,328,485	1,607,268	202,651	164,862	147,653	155,778	35.6	25.5	24.9	21.7	1.1	0.5	1.0	0.8	1.3	0.2	-1.1	0.6	1.1	0.5	1.2	0.2
				YTHLVDQDTTSFDSAWGQESAQNTK	3	96.9%	1																									
IPI00022793	HADHB	Trifunctional enzyme subunit beta, mitochondrial	100.0%	8.4	3	3	3	1	6,111,313	5,513,268	5,797,149	6,081,328	570,301	188,533	305,934	127,246	20.9	7.7	11.8	4.7	-1.1	0.4	-1.1	0.6	-1.0	1	1.1	0.5	1.1	0.04	1.0	0.4
				FNNWGGSLSLGHPFGATGCR	3	80.9%	1																									
				LEQDEYALR	2	99.1%	1																									
				TPFLLSGTSYK	2	99.8%	1																									
IPI00022796	-	Putative high mobility group protein B1-like 1	100.0%	7.1	1	2	3	1	1,810,941	1,775,458	1,714,552	1,839,513	179,461	126,031	79,926	101,413	22.2	15.9	10.4	12.3	-1.0	0.9	-1.1	0.6	1.0	0.9	-1.0	0.7	1.0	0.7	1.1	0.4
				IKGEHPGLSIGDVAK	2	100.0%	1																									
				IKGEHPGLSIGDVAK	3	100.0%	2																									
IPI00022810	CTSC	isoform 1 of Dipeptidyl peptidase 1	99.5%	3.0	1	1	1	2	3,252,665	3,161,205	3,291,415	3,674,910	389,863	110,305	293,750	354,449	26.8	7.8	20.0	21.6	-1.0	0.8	1.0	0.9	1.1	0.4	1.0	0.7	1.2	0.2	1.1	0.4
IPI01013193	CTSC	cDNA FLJ55694, highly similar to Dipeptidyl-peptidase 1	99.5%	3.1	1	1	1	2	3,252,665	3,161,205	3,291,415	3,674,910	389,863	110,305	293,750	354,449	26.8	7.8	20.0	21.6	-1.0	0.8	1.0	0.9	1.1	0.4	1.0	0.7	1.2	0.2	1.1	0.4
				NSWGTGWGENGYFR	2	99.5%	1																									
IPI00022827	SLK	isoform 1 of STE20-like serine/threonine-protein kinase	100.0%	1.8	2	2	2	2	6,859,360	7,228,225	6,197,205	7,551,625	465,403	169,262	426,828	467,071	15.2	5.2	15.4	13.8	1.1	0.5	-1.1	0.3	1.1	0.3	-1.2	0.05	1.0	0.5	1.2	0.06
IPI00247439	SLK	isoform 2 of STE20-like serine/threonine-protein kinase	100.0%	1.8	2	2	2	2	6,859,360	7,228,225	6,197,205	7,551,625	465,403	169,262	426,828	467,071	15.2	5.2	15.4	13.8	1.1	0.5	-1.1	0.3	1.1	0.3	-1.2	0.05	1.0	0.5	1.2	0.06
				AGNILFTLDGDIK	2	89.5%	1																									
				RFEQEMMSK	2	91.7%	1																									
IPI00022830	NSFL1C	isoform 2 of NSFL1 cofactor p47	100.0%	20.1	5	5	5	1	9,610,220	10,407,640	9,552,535	11,643,763	783,880	368,071	716,852	484,714	18.2	7.9	16.8	9.3	1.1	0.4	-1.0	1	1.2	0.06	-1.1	0.3	1.1	0.08	1.2	0.04
				ASSSILIDESEPTTNIQIR	2	100.0%	1																									
				EANLLNAVIVQR	2	100.0%	1																									
				SGFSLDNGELR	2	99.9%	1																									
				SPNELVDDLFK	2	99.7%	1																									
				SYQDPSNAQFLESIR	2	99.5%	1																									
IPI00022881	CLTCL1	isoform 1 of Clathrin heavy chain 2	97.5%	0.7	1	1	1	3	753,970	726,767	737,453	800,383	107,511	30,148	45,310	33,249	31.9	9.3	13.7	9.3	-1.0	0.8	-1.0	0.9	1.1	0.7	1.0	0.8	1.1	0.1	1.1	0.3
IPI00300446	CLTCL1	isoform 2 of Clathrin heavy chain 2	97.5%	0.7	1	1	1	3	753,970	726,767	737,453	800,383	107,511	30,148	45,310	33,249	31.9	9.3	13.7	9.3	-1.0	0.8	-1.0	0.9	1.1	0.7	1.0	0.8	1.1	0.1	1.1	0.3

IPI01010066	CLTCL1	CLTCL1 protein	97.5%	0.9	1	1	1	3	753,970	726,767	737,453	800,383	107,511	30,148	45,310	33,249	31.9	9.3	13.7	9.3	-1.0	0.8	-1.0	0.9	1.1	0.7	1.0	0.8	1.1	0.1	1.1	0.3
				CYEEGMYEAAK	2	97.9%	1																									
IPI00022891	SLC25A4	ADP/ATP translocase 1	100.0%	6.4	2	2	3	1	2,211,972	2,071,365	2,622,617	2,600,712	213,194	106,766	111,300	238,079	21.6	11.5	9.5	20.5	-1.1	0.6	1.2	0.1	1.2	0.3	1.3	0.007	1.3	0.08	-1.0	0.9
				MMMQSGR	2	98.9%	1																									
				YFPTQALNFAFK	2	100.0%	2																									
IPI00022977	CKB	Creatine kinase B-type	100.0%	62.5	22	31	52	1	428,781,236	422,292,868	438,473,237	497,606,754	########	########	########	########	19.5	9.7	17.4	6.1	-1.0	0.9	1.0	0.9	1.2	0.1	1.0	0.7	1.2	0.01	1.1	0.2
				AIEKLAVEALSSLDGDLAGR	2	84.1%	1																									
				DLFDPIIEDR	2	100.0%	2																									
				DYEFMWNPHLGYILTCPSNLGTGLR	3	100.0%	1																									
				FCTGLTQIETLFK	2	100.0%	3																									
				FCTGLTQIETLFK	3	99.0%	1																									
				FPAEDEFPDLSAHNNHMAK	3	100.0%	2																									
				FSEVLKR	2	98.4%	1																									
				GGNMKEVFTR	2	99.9%	2																									
				GIWHNDNK	1	100.0%	2																									
				GIWHNDNK	2	87.1%	1																									
				GTGGVDTAAVGGVFDVSNADR	2	100.0%	2																									
				GTGGVDTAAVGGVFDVSNADR	3	100.0%	2																									
				LAVEALSSLDGDLAGR	2	100.0%	4																									
				LEQGQAIDDLMPAQK	2	100.0%	3																									
				LEQGQAIDDLMPAQK	3	99.9%	1																									
				LGFSEVELVQMVVDGVK	2	100.0%	3																									
				LGFSEVELVQMVVDGVK	3	100.0%	1																									
				LGYILTCPSNLGTGLR	2	100.0%	1																									
				LLIEMEQR	1	93.2%	1																									
				LLIEMEQR	2	100.0%	3																									
				LPNLGK	1	98.9%	1																									
				LPNLGKHEK	2	99.3%	1																									
				RGTGGVDTAAVGGVFDVSNADR	2	100.0%	1																									
				RGTGGVDTAAVGGVFDVSNADR	3	100.0%	1																									
				SKDYEFMWNPHLGYILTCPSNLGTGLR	3	100.0%	1																									
				TDLNPDNLQGGDDLDPNYVLSSR	2	100.0%	2																									
				TDLNPDNLQGGDDLDPNYVLSSR	3	91.8%	1																									
				TFLVWVNEEDHLR	2	100.0%	1																									
				TFLVWVNEEDHLR	3	100.0%	2																									
				VISMQK	1	98.7%	2																									
				VLTPELYAELR	2	100.0%	2																									
IPI00023001	FAM162A	Protein FAM162A	99.6%	7.1	1	1	1	2	3,208,600	2,913,630	3,116,610	3,382,365	267,126	192,288	131,830	138,886	18.6	14.8	9.5	9.2	-1.1	0.4	-1.0	0.8	1.1	0.6	1.1	0.4	1.2	0.08	1.1	0.2
IPI00945585	FAM162A	Uncharacterized protein	99.6%	7.6	1	1	1	2	3,208,600	2,913,630	3,116,610	3,382,365	267,126	192,288	131,830	138,886	18.6	14.8	9.5	9.2	-1.1	0.4	-1.0	0.8	1.1	0.6	1.1	0.4	1.2	0.08	1.1	0.2
				HETLTSLNLEK	2	99.6%	1																									
IPI00232533	EIF1AX	Eukaryotic translation initiation factor 1A, X-chromosomal	100.0%	53.5	5	6	7	2	9,836,798	9,657,388	8,426,843	10,852,258	899,425	443,019	630,006	699,819	20.5	10.3	16.7	14.4	-1.0	0.9	-1.2	0.2	1.1	0.4	-1.1	0.1	1.1	0.2	1.3	0.03
IPI00023004	EIF1AY	Eukaryotic translation initiation factor 1A, Y-chromosomal	100.0%	53.5	5	6	7	2	9,836,798	9,657,388	8,426,843	10,852,258	899,425	443,019	630,006	699,819	20.5	10.3	16.7	14.4	-1.0	0.9	-1.2	0.2	1.1	0.4	-1.1	0.1	1.1	0.2	1.3	0.03
				AYGELPEHAK	2	99.3%	1																									
				AYGELPEHAK	3	84.5%	1																									
				DYQDNKADVILK	2	99.8%	1																									
				EDGQEYAQVIK	2	97.6%	1																									
				INETDTFGPGDDDEIQFDDIGDDDEDIDDI	3	97.6%	1																									
				VWINTSDIILVGLR	2	100.0%	2																									
IPI00023048	EEF1D	isoform 1 of Elongation factor 1-delta	100.0%	34.9	7	7	11	5	4,118,253	4,099,939	3,859,803	4,495,167	290,711	149,569	218,130	183,197	15.8	8.2	12.6	9.1	-1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.4	1.1	0.1	1.2	0.06
IPI00642971	EEF1D	isoform 2 of Elongation factor 1-delta	100.0%	15.2	7	7	11	5	4,118,253	4,099,939	3,859,803	4,495,167	290,711	149,569	218,130	183,197	15.8	8.2	12.6	9.1	-1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.4	1.1	0.1	1.2	0.06
IPI00975963	EEF1D	Uncharacterized protein	100.0%	37.6	7	7	11	5	4,118,253	4,099,939	3,859,803	4,495,167	290,711	149,569	218,130	183,197	15.8	8.2	12.6	9.1	-1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.4	1.1	0.1	1.2	0.06
IPI00982982	EEF1D	69 kDa protein	100.0%	15.5	7	7	11	5	4,118,253	4,099,939	3,859,803	4,495,167	290,711	149,569	218,130	183,197	15.8	8.2	12.6	9.1	-1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.4	1.1	0.1	1.2	0.06
IPI00985353	EEF1D	Uncharacterized protein	100.0%	14.1	7	7	11	5	4,118,253	4,099,939	3,859,803	4,495,167	290,711	149,569	218,130	183,197	15.8	8.2	12.6	9.1	-1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.4	1.1	0.1	1.2	0.06
				ATAPQTQHVSPMR	3	92.1%	1																									
				FYEQMNGPVAGASR	2	100.0%	2																									
				GVVQELQQAISK	2	100.0%	2																									
				IASLEVENQSLR	2	100.0%	2																									
				QENGASVILR	2	99.9%	1																									
				SIQLDGLVWGASK	2	100.0%	2																									
				SLAGSSGPGASSGTSGDHGELVVR	3	99.9%	1																									
IPI00023097	PBRM1	isoform 5 of Protein polybromo-1	94.8%	0.4	1	1	1	8	379,123	394,089	477,334	445,888	36,983	71,184	43,344	87,290	21.8	40.4	20.3	43.8	1.0	0.9	1.3	0.1	1.2	0.5	1.2	0.3	1.1	0.7	-1.1	0.8
IPI00301041	PBRM1	isoform 2 of Protein polybromo-1	94.8%	0.4	1	1	1	8	379,123	394,089	477,334	445,888	36,983	71,184	43,344	87,290	21.8	40.4	20.3	43.8	1.0	0.9	1.3	0.1	1.2	0.5	1.2	0.3	1.1	0.7	-1.1	0.8
IPI00334894	PBRM1	isoform 3 of Protein polybromo-1	94.8%	0.4	1	1	1	8	379,123	394,089	477,334	445,888	36,983	71,184	43,344	87,290	21.8	40.4	20.3	43.8	1.0	0.9	1.3	0.1	1.2	0.5	1.2	0.3	1.1	0.7	-1.1	0.8
IPI00384176	PBRM1	isoform 1 of Protein polybromo-1	94.8%	0.4	1	1	1	8	379,123	394,089	477,334	445,888	36,983	71,184	43,344	87,290	21.8	40.4	20.3	43.8	1.0	0.9	1.3	0.1	1.2	0.5	1.2	0.3	1.1	0.7	-1.1	0.8
IPI00640304	PBRM1	isoform 4 of Protein polybromo-1	94.8%	0.4	1	1	1	8	379,123	394,089	477,334	445,888	36,983	71,184	43,344	87,290	21.8	40.4	20.3	43.8	1.0	0.9	1.3	0.1	1.2	0.5	1.2	0.3	1.1	0.7	-1.1	0.8
IPI00873041	PBRM1	isoform 7 of Protein polybromo-1	94.8%	0.4	1	1	1	8	379,123	394,089	477,334	445,888	36,983	71,184	43,344	87,290	21.8	40.4	20.3	43.8	1.0	0.9	1.3	0.1	1.2	0.5	1.2	0.3	1.1	0.7	-1.1	0.8
IPI00909142	PBRM1	isoform 9 of Protein polybromo-1	94.8%	0.4	1	1	1	8	379,123	394,089	477,334	445,888	36,983	71,184	43,344	87,290	21.8	40.4	20.3	43.8	1.0	0.9	1.3	0.1	1.2	0.5	1.2	0.3	1.1	0.7	-1.1	0.8
IPI00910435	PBRM1	isoform 8 of Protein polybromo-1	94.8%	0.4	1	1	1	8	379,123	394,089	477,334	445,888	36,983	71,184	43,344	87,290	21.8	40.4	20.3	43.8	1.0	0.9	1.3	0.1	1.2	0.5	1.2	0.3	1.1	0.7	-1.1	0.8
				DTLNIR	1	80.1%	1																									
IPI00023098	FOXP1	isoform 1 of Forkhead box protein P1	93.7%	1.9	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00182980	FOXP1	cDNA FLJ35064 fis, clone PEBLM1000147, moderately similar to Glutamine (Q)-rich	93.7%	2.2	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00220201	FOXP1	isoform 2 of Forkhead box protein P1	93.7%	2.7	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00220203	FOXP1	Uncharacterized protein	93.7%	1.9	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00748383	FOXP1	isoform 3 of Forkhead box protein P1	93.7%	2.2	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00946520	FOXP1	FOXP1 protein	93.7%	2.3	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00947112	FOXP1	75 kDa protein	93.7%	1.9	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00947506	FOXP1	Uncharacterized protein	93.7%	2.1	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00386277	FOXP4	FOXP4 protein (Fragment)	93.7%	3.4	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00395554	FOXP4	Forkhead box protein P4	93.7%	1.9	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00554470	FOXP4	forkhead box protein P4 isoform 3	93.7%	1.9	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00554643	FOXP4	forkhead box protein P4 isoform 2	93.7%	2.0	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
IPI00915788	FOXP4	Forkhead box P4	93.7%	2.0	1	1	1	13	45,690	44,003	43,506	55,306	3,221	3,506	4,515	4,637	15.8	17.8	23.2	18.8	-1.0	0.7	-1.1	0.7	1.2	0.1	-1.0	0.9	1.3	0.09	1.3	0.1
				QLTLNEIYNWFTR	2	93.7%	1																									
IPI00023188	ENC1	Ectoderm-neural cortex protein 1	94.7%	3.1	1	1	1	2	2,322,105	2,247,685	2,361,070	2,334,660	256,961	228,894	226,141	174,380	24.7	22.8	21.4	16.7	-1.0	0.8	1.0	0.9	1.0	1	1.1	0.7	1.0	0.8	-1.0	0.9
IPI00968218	ENC1	Uncharacterized protein	94.7%	3.5	1	1	1	2	2,322,105	2,247,685	2,361,070	2,334,660	256,961	228,894	226,141	174,380	24.7	22.8	21.4	16.7	-1.0	0.8	1.0	0.9	1.0	1	1.1	0.7	1.0	0.8	-1.0	0.9
				LKLFAFGGTSVSHDKLPK	3	94.7%	1																									
IPI00023191	TOM1	cDNA FLJ54710, highly similar to Target of Myb protein 1	99.5%	2.6	1	1	1	8	91,854	97,887	91,486	99,795	9,492	11,335	10,633	4,485	23.1	25.9	26.0	10.1	1.1	0.7	-1.0	1	1.1	0.5	-1.1	0.7	1.0	0.9	1.1	0.5
IPI00879576	TOM1	Target of myb1	99.5%	3.9	1	1	1	8	91,854	97,887	91,486	99,795	9,492	11,335	10,633	4,485	23.1	25.9	26.0	10.1	1.1	0.7	-1.0	1	1.1	0.5	-1.1	0.7	1.0	0.9	1.1	0.5
IPI00879680	TOM1	isoform 4 of Target of Myb protein 1	99.5%	2.8	1	1	1	8	91,854	97,887	91,486	99,795	9,492	11,335	10,633	4,485	23.1	25.9	26.0	10.1	1.1	0.7	-1.0	1	1.1	0.5	-1.1	0.7	1.0	0.9	1.1	0.5
IPI00903336	TOM1	cDNA FLJ40607 fis, clone THYMU2012273, highly similar to Target of Myb protein 1	99.5%	4.9	1	1	1	8	91,854	97,887	91,486	99,795	9,492	11,335	10,633	4,485	23.1	25.9	26.0	10.1	1.1	0.7	-1.0	1	1.1	0.5	-1.1	0.7	1.0	0.9	1.1	0.5
IPI00910932	TOM1	cDNA FLJ54716, highly similar to Target of Myb protein 1	99.5%	2.9	1	1	1	8	91,854	97,887	91,486	99,795	9,492	11,335	10,633	4,485	23.1	25.9	26.0	10.1	1.1	0.7	-1.0	1	1.1	0.5	-1.1	0.7	1.0	0.9	1.1	0.5
IPI00913835	TOM1	isoform 1 of Target of Myb protein 1	99.5%	2.6	1	1	1	8	91,854	97,887	91,486	99,795	9,492	11,335	10,633	4,485	23.1	25.9	26.0	10.1	1.1	0.7	-1.0	1	1.1	0.5	-1.1	0.7	1.0	0.9	1.1	0.5
IPI00941588	TOM1	isoform 2 of Target of Myb protein 1	99.5%	2.6	1	1	1	8	91,854	97,887	91,486	99,795	9,492	11,335	10,633	4,485	23.1	25.9	26.0	10.1	1.1	0.7	-1.0	1	1.1	0.5	-1.1	0.7	1.0	0.9	1.1	0.5
IPI00942537	TOM1	Uncharacterized protein	99.5%	6.2	1	1	1	8	91,854	97,887	91,486	99,795	9,492	11,335	10,633	4,485	23.1	25.9	26.0	10.1	1.1	0.7	-1.0	1	1.1	0.5	-1.1	0.7	1.0	0.9	1.1	0.5
				VLNLIQSWADAFR	2	99.5%	1																									
IPI00023234	UBA2	SUMO-activating enzyme subunit 2	100.0%	4.2	2	2	3	1	7,702,120	6,733,865	8,087,625	8,355,860	365,031	374,785	383,083	233,317	10.6	12.5	10.6	6.2	-1.1	0.1	1.1	0.5	1.1	0.2	1.2	0.04	1.2	0.006	1.0	0.6
				QFILVMNALDNR	2	99.8%	1																									
				VLVVGAGGIGCELLK	2	100.0%	2																									
IPI00023283	TTN	isoform 2 of Titin	99.8%	0.4	10	10	10	3	6,869,462	6,868,848	7,381,271	7,913,884	604,680	305,406	570,472	216,816	19.7	9.9	17.3	6.1	-1.0	1	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.02	1.1	0.4
IPI00759542	TTN	isoform 8 of Titin	99.8%	0.4	10	10	10	3	6,869,462	6,868,848	7,381,271	7,913,884	604,680	305,406	570,472	216,816	19.7	9.9	17.3	6.1	-1.0	1	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.02	1.1	0.4
IPI00759754	TTN	isoform 1 of Titin	99.8%	0.4	10	10	10	3	6,869,462	6,868,848	7,381,271	7,913,884	604,680	305,406	570,472	216,816	19.7	9.9	17.3	6.1	-1.0	1	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.02	1.1	0.4
				AEDLSATVTDVVEGQEYSFR	3	97.1%	1																									
				ITQFLKAEASKEIAK	2	84.0%	1																									
				KAEAVATVVAAVDQAR	3	93.8%	1																									
				MPDDDGGDR	1	92.2%	1																									
				PKVPVPAPVPEIK	3	94.2%	1																									
				STVTIVDSKR	2	89.8%	1																									
				VLDTPGPPVNVTVK	2	90.2%	1																									
				VNTEDHQGEYVCEALNDSGK	3	87.7%	1																									
				VTGLSEGCEYFFR	3	94.3%	1																									
				YLISTEEVSYFNVQSR	3	85.6%	1																									
IPI00023461	MLLT4	isoform 4 of Afadin	100.0%	1.6	2	2	2	8	877,884	776,185	739,155	861,973	56,267	40,121	83,619	53,887	14.3	11.6	25.3	14.0	-1.1	0.2	-1.2	0.2	-1.0	0.8	-1.1	0.7	1.1	0.2	1.2	0.3
IPI00216505	MLLT4	isoform 3 of Afadin	100.0%	1.7	2	2	2	8	877,884	776,185	739,155	861,973	56,267	40,121	83,619	53,887	14.3	11.6	25.3	14.0	-1.1	0.2	-1.2	0.2	-1.0	0.8	-1.1	0.7	1.1	0.2	1.2	0.3
IPI00398718	MLLT4	isoform 2 of Afadin	100.0%	1.6	2	2	2	8	877,884	776,185	739,155	861,973	56,267	40,121	83,619	53,887	14.3	11.6	25.3	14.0	-1.1	0.2	-1.2	0.2	-1.0	0.8	-1.1	0.7	1.1	0.2	1.2	0.3
IPI00479469	MLLT4	Myeloid/lymphoid or mixed-lineage leukemia	100.0%	1.7	2	2	2	8	877,884	776,185	739,155	861,973	56,267	40,121	83,619	53,887	14.3	11.6	25.3	14.0	-1.1	0.2	-1.2	0.2	-1.0	0.8	-1.1	0.7	1.1	0.2	1.2	0.3
IPI00759546	MLLT4	isoform 5 of Afadin	100.0%	1.6	2	2	2	8	877,884	776,185	739,155	861,973	56,267	40,121	83,619	53,887	14.3	11.6	25.3	14.0	-1.1	0.2	-1.2	0.2	-1.0	0.8	-1.1	0.7	1.1	0.2	1.2	0.3
IPI00953593	MLLT4	Uncharacterized protein	100.0%	1.7	2	2	2	8	877,884	776,185	739,155	861,973	56,267	40,121	83,619	53,887	14.3	11.6	25.3	14.0	-1.1	0.2	-1.2	0.2	-1.0	0.8	-1.1	0.7	1.1	0.2	1.2	0.3
IPI00965424	MLLT4	208 kDa protein	100.0%	1.6	2	2	2	8	877,884	776,185	739,155	861,973	56,267	40,121	83,619	53,887	14.3	11.6	25.3	14.0	-1.1	0.2	-1.2	0.2	-1.0	0.8	-1.1	0.7	1.1	0.2	1.2	0.3
IPI01014668	MLLT4	afadin	100.0%	1.8	2	2	2	8	877,884	776,185	739,155	861,973	56,267	40,121	83,619	53,887	14.3	11.6	25.3	14.0	-1.1	0.2	-1.2	0.2	-1.0	0.8	-1.1	0.7	1.1	0.2	1.2	0.3
				SMDAETYVEGQR	2	97.4%	1																									
				TPAAIPATPVAVSQPIR	2	99.2%	1																									
IPI00910170	-	cDNA FLJ59582, highly similar to Ras-related protein Rab-3A	100.0%	6.5	1	1	1	2	682,263	724,470	887,600	828,847	85,372	61,291	106,584	106,152	28.0	18.9	26.9	28.6	1.1	0.7	1.3	0.2	1.2	0.3	1.2	0.2	1.1	0.4	-1.1	0.7
IPI00023504	RAB3A	Ras-related protein Rab-3A	100.0%	8.6	1	1	1	2	682,263	724,470	887,600	828,847	85,372	61,291	106,584	106,152	28.0	18.9	26.9	28.6	1.1	0.7	1.3	0.2	1.2	0.3	1.2	0.2	1.1	0.4	-1.1	0.7
				YADDSFTPAFVSTVGIDFK	2	100.0%	1																									
IPI00023532	SPATS2L	cDNA FLJ59751, weakly similar to Mus musculus spermatogenesis associated, seri	99.6%	6.0	2	2	2	5	395,970	416,932	457,586	448,127	46,819	5,320	31,118	18,088	26.4	2.9	15.2	9.0	1.1	0.7	1.2	0.3	1.1	0.3	1.1	0.3	1.1	0.2	-1.0	0.8
IPI00103027	SPATS2L	isoform 2 of SPATS2-like protein	99.6%	7.2	2	2	2	5	395,970	416,932	457,586	448,127	46,819	5,320	31,118	18,088	26.4	2.9	15.2	9.0	1.1	0.7	1.2	0.3	1.1	0.3	1.1	0.3	1.1	0.2	-1.0	0.8
IPI00916831	SPATS2L	isoform 1 of SPATS2-like protein	99.6%	6.3	2	2	2	5	395,970	416,932	457,586	448,127	46,819	5,320	31,118	18,088	26.4	2.9	15.2	9.0	1.1	0.7	1.2	0.3	1.1	0.3	1.1	0.3	1.1	0.2	-1.0	0.8
IPI00926880	SPATS2L	Uncharacterized protein	99.6%	13.2	2	2	2	5	395,970	416,932	457,586	448,127	46,819	5,320	31,118	18,088	26.4	2.9	15.2	9.0	1.1	0.7	1.2	0.3	1.1	0.3	1.1	0.3	1.1	0.2	-1.0	0.8
IPI00956176	SPATS2L	cDNA FLJ59743, weakly similar to Mus musculus spermatogenesis associated, seri	99.6%	6.2	2	2	2	5	395,970	416,932	457,586	448,127	46,819	5,320	31,118	18,088	26.4	2.9	15.2	9.0	1.1	0.7	1.2	0.3	1.1	0.3	1.1	0.3	1.1	0.2	-1.0	0.8
				LTDLASQMAEMQLAELR	2	97.0%	1																									
				SNNEIVLVLQQFDFNVDK	2	99.6%	1																									
IPI00023542	TMED9	Transmembrane emp24 domain-containing protein 9	99.9%	11.9	2	3	3	1	11,712,730	12,958,280	11,204,588	13,021,628	1,891,397	1,368,620	645,122	673,839	36.1	23.6	12.9	11.6	1.1	0.6	-1.0	0.8	1.1	0.5	-1.2	0.3	1.0	1	1.2	0.09
				CFIEEIPDETMVIGNYR	2	99.9%	1																									
				CFIEEIPDETMVIGNYR	3	91.6%	1																									
				QLVEQVEQIQK	2	90.3%	1																									
IPI00023591	PURA	Transcriptional activator protein Pur-alpha	100.0%	28.9	5	5	5	1	33,496,110	33,089,000	33,235,460	37,364,800	1,904,362	1,047,252	1,739,642	1,167,462	12.7	7.1	11.7	7.0	-1.0	0.9	-1.0	0.9	1.1	0.1	1.0	0.9	1.1	0.03	1.1	0.08
				DYLGDFIEHYAQLGPSQPPDLAQAQDEPR	3	99.7%	1																									
				FFFDVGSNK	2	96.9%	1																									
				GPGLGSTQGQTIALPAQGLIEFR	3	95.6%	1																									
				LIDDYGVEEEPAELPEGTSLTVDNKR	3	100.0%	1																									
				YGVFMR	2	99.2%	1																									
IPI00023640	PDCD5	Programmed cell death protein 5	100.0%	28.0	3	3	3	1	15,929,520	15,909,900	16,170,165	18,663,675	1,105,794	667,484	845,311	380,060	15.5	9.4	11.7	4.6	-1.0	1	1.0	0.9	1.2	0.07	1.0	0.8	1.2	0.007	1.2	0.03
				LSNLALVKPEK	2	91.9%	1																									
				NSILAQVLDQSAR	2	100.0%	1																									
				VSEQGLIEILK	2	99.5%	1																									
IPI00023647	UBA6	isoform 1 of Ubiquitin-like modifier-activating enzyme 6	96.2%	1.2	1	1	1	2	622,342	775,386	670,697	742,090	104,911	57,142	105,119	53,444	37.7	16.5	35.1	16.1	1.2	0.2	1.1	0.8	1.2	0.3	-1.2	0.4	-1.0	0.7	1.1	0.6
IPI00827491	UBA6	isoform 2 of Ubiquitin-like modifier-activating enzyme 6	96.2%	2.3	1	1	1	2	622,342	775,386	670,697	742,090	104,911	57,142	105,119	53,444	37.7	16.5	35.1	16.1	1.2	0.2	1.1	0.8	1.2	0.3	-1.2	0.4	-1.0	0.7	1.1	0.6

				EDFTLLDFINAVK	2	96.2%	1																									
IPI00023672	EZH1	isoform 1 of Histone-lysine N-methyltransferase EZH1	99.3%	2.3	1	1	1	3	508,986	486,607	570,157	563,752	56,220	47,331	49,127	60,861	24.7	21.8	19.3	24.1	-1.0	0.8	1.1	0.4	1.1	0.5	1.2	0.3	1.2	0.3	-1.0	0.9
IPI00921284	EZH1	isoform 3 of Histone-lysine N-methyltransferase EZH1	99.3%	2.4	1	1	1	3	508,986	486,607	570,157	563,752	56,220	47,331	49,127	60,861	24.7	21.8	19.3	24.1	-1.0	0.8	1.1	0.4	1.1	0.5	1.2	0.3	1.2	0.3	-1.0	0.9
IPI00921311	EZH1	isoform 2 of Histone-lysine N-methyltransferase EZH1	99.3%	2.3	1	1	1	3	508,986	486,607	570,157	563,752	56,220	47,331	49,127	60,861	24.7	21.8	19.3	24.1	-1.0	0.8	1.1	0.4	1.1	0.5	1.2	0.3	1.2	0.3	-1.0	0.9
				VQPVQSMKPVSGHPFLK	2	99.1%	1																									
IPI00023673	LGALS3BP	Galectin-3-binding protein	100.0%	21.7	10	10	13	2	40,355,269	38,842,811	37,751,683	45,562,826	3,171,134	1,632,474	2,361,440	755,941	17.6	9.4	14.0	3.7	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.7	1.2	0.006	1.2	0.03
IPI01010990	LGALS3BP	cDNA FLJ53478, highly similar to Galectin-3-binding protein	100.0%	22.2	10	10	13	2	40,355,269	38,842,811	37,751,683	45,562,826	3,171,134	1,632,474	2,361,440	755,941	17.6	9.4	14.0	3.7	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.7	1.2	0.006	1.2	0.03
				ALMLCEGLFVADVTDFEGWK	2	100.0%	1																									
				ASHEEVEGLVEK	3	100.0%	1																									
				AVDTWSWGER	2	100.0%	2																									
				ELSEALGQIFDSQR	2	100.0%	2																									
				RIDITLSSVK	2	100.0%	2																									
				SDLAVPSELALLK	2	99.9%	1																									
				STHTLDLSR	2	99.6%	1																									
				STSSFPCPAGHFNGFR	3	98.6%	1																									
				TLQALEFHTVPFQLLAR	3	99.1%	1																									
				VEIFYR	2	80.7%	1																									
IPI00023704	LPP	Lipoma-preferred partner	99.3%	2.0	1	1	1	10	505,943	465,861	534,883	549,126	30,577	32,628	38,981	21,669	13.5	15.7	16.3	8.8	-1.1	0.4	1.1	0.6	1.1	0.3	1.1	0.2	1.2	0.07	1.0	0.8
IPI00793907	LPP	lipoma-preferred partner isoform b	99.3%	2.6	1	1	1	10	505,943	465,861	534,883	549,126	30,577	32,628	38,981	21,669	13.5	15.7	16.3	8.8	-1.1	0.4	1.1	0.6	1.1	0.3	1.1	0.2	1.2	0.07	1.0	0.8
IPI00794013	LPP	Uncharacterized protein	99.3%	25.5	1	1	1	10	505,943	465,861	534,883	549,126	30,577	32,628	38,981	21,669	13.5	15.7	16.3	8.8	-1.1	0.4	1.1	0.6	1.1	0.3	1.1	0.2	1.2	0.07	1.0	0.8
IPI00797120	LPP	Uncharacterized protein	99.3%	2.8	1	1	1	10	505,943	465,861	534,883	549,126	30,577	32,628	38,981	21,669	13.5	15.7	16.3	8.8	-1.1	0.4	1.1	0.6	1.1	0.3	1.1	0.2	1.2	0.07	1.0	0.8
IPI00924594	LPP	Uncharacterized protein	99.3%	22.6	1	1	1	10	505,943	465,861	534,883	549,126	30,577	32,628	38,981	21,669	13.5	15.7	16.3	8.8	-1.1	0.4	1.1	0.6	1.1	0.3	1.1	0.2	1.2	0.07	1.0	0.8
IPI00926750	LPP	Uncharacterized protein	99.3%	21.1	1	1	1	10	505,943	465,861	534,883	549,126	30,577	32,628	38,981	21,669	13.5	15.7	16.3	8.8	-1.1	0.4	1.1	0.6	1.1	0.3	1.1	0.2	1.2	0.07	1.0	0.8
IPI00927168	LPP	Uncharacterized protein	99.3%	10.8	1	1	1	10	505,943	465,861	534,883	549,126	30,577	32,628	38,981	21,669	13.5	15.7	16.3	8.8	-1.1	0.4	1.1	0.6	1.1	0.3	1.1	0.2	1.2	0.07	1.0	0.8
IPI00927466	LPP	Uncharacterized protein	99.3%	18.2	1	1	1	10	505,943	465,861	534,883	549,126	30,577	32,628	38,981	21,669	13.5	15.7	16.3	8.8	-1.1	0.4	1.1	0.6	1.1	0.3	1.1	0.2	1.2	0.07	1.0	0.8
IPI00927693	LPP	Uncharacterized protein	99.3%	18.5	1	1	1	10	505,943	465,861	534,883	549,126	30,577	32,628	38,981	21,669	13.5	15.7	16.3	8.8	-1.1	0.4	1.1	0.6	1.1	0.3	1.1	0.2	1.2	0.07	1.0	0.8
IPI00927909	LPP	Uncharacterized protein	99.3%	12.9	1	1	1	10	505,943	465,861	534,883	549,126	30,577	32,628	38,981	21,669	13.5	15.7	16.3	8.8	-1.1	0.4	1.1	0.6	1.1	0.3	1.1	0.2	1.2	0.07	1.0	0.8
				STGEPLGHVPAR	2	99.3%	1																									
IPI00023728	GGH	Gamma-glutamyl hydrolase	99.6%	8.2	2	2	2	1	9,461,418	10,697,217	11,575,580	10,153,983	789,032	414,304	562,040	551,789	18.7	8.7	10.9	12.2	1.1	0.2	1.2	0.06	1.1	0.5	1.1	0.2	-1.1	0.5	-1.1	0.1
				FFNVLTTNTDGK	2	99.1%	1																									
				TAFYLAEFFVNEAR	2	99.6%	1																									
IPI00023729	FN3K	Fructosamine-3-kinase	90.8%	4.5	1	1	1	3	943,983	906,450	1,005,080	1,196,830	43,331	47,247	65,986	90,899	10.3	11.7	14.7	17.0	-1.0	0.6	1.1	0.5	1.3	0.04	1.1	0.3	1.3	0.02	1.2	0.1
IPI00902629	FN3K	cDNA FLJ30276 fis, clone BRACE2002736, highly similar to Fructosamine-3-kinase	90.8%	7.9	1	1	1	3	943,983	906,450	1,005,080	1,196,830	43,331	47,247	65,986	90,899	10.3	11.7	14.7	17.0	-1.0	0.6	1.1	0.5	1.3	0.04	1.1	0.3	1.3	0.02	1.2	0.1
IPI00909077	FN3K	cDNA FLJ60514, highly similar to Fructosamine-3-kinase	90.8%	6.9	1	1	1	3	943,983	906,450	1,005,080	1,196,830	43,331	47,247	65,986	90,899	10.3	11.7	14.7	17.0	-1.0	0.6	1.1	0.5	1.3	0.04	1.1	0.3	1.3	0.02	1.2	0.1
				QMFEGEVASLEALR	2	90.8%	1																									
IPI00023736	CORO2A	Coronin-2A	97.0%	2.3	1	1	1	1	3,210,190	3,046,690	3,206,270	2,961,180	300,316	200,630	275,209	142,888	20.9	14.7	19.2	10.8	-1.1	0.7	-1.0	1	-1.1	0.5	1.1	0.7	-1.0	0.7	-1.1	0.5
				SLIEPISMIVPR	2	97.0%	1																									
IPI00909970	-	cDNA FLJ53704, moderately similar to Nascent polypeptide-associated complex sub	100.0%	33.7	4	4	8	2	5,118,673	5,544,921	5,051,356	5,891,951	432,538	186,125	314,468	212,494	18.9	7.5	13.9	8.1	1.1	0.4	-1.0	0.9	1.2	0.1	-1.1	0.2	1.1	0.3	1.2	0.06
IPI00023748	NACA	Nascent polypeptide-associated complex subunit alpha	100.0%	26.5	4	4	8	2	5,118,673	5,544,921	5,051,356	5,891,951	432,538	186,125	314,468	212,494	18.9	7.5	13.9	8.1	1.1	0.4	-1.0	0.9	1.2	0.1	-1.1	0.2	1.1	0.3	1.2	0.06
				DIELVMSQANVSR	2	99.6%	2																									
				IEDLSQQAQLAAAEK	2	99.2%	2																									
				NNSNDIVNAIMELTM	2	100.0%	2																									
				SPASDTYIVFGEAK	2	100.0%	2																									
IPI00023845	KLK6	isoform 1 of Kallikrein-6	97.4%	4.9	1	1	1	2	3,413,885	3,081,615	3,860,470	3,406,385	291,255	304,232	358,416	221,542	19.1	22.1	20.8	14.5	-1.1	0.5	1.1	0.4	-1.0	1	1.3	0.1	1.1	0.4	-1.1	0.3
IPI00554738	KLK6	isoform 2 of Kallikrein-6	97.4%	8.8	1	1	1	2	3,413,885	3,081,615	3,860,470	3,406,385	291,255	304,232	358,416	221,542	19.1	22.1	20.8	14.5	-1.1	0.5	1.1	0.4	-1.0	1	1.3	0.1	1.1	0.4	-1.1	0.3
				LSELIQPLPLER	2	97.4%	1																									
IPI00023860	NAP1L1	Nucleosome assembly protein 1-like 1	100.0%	22.0	6	7	9	2	6,043,562	5,789,273	6,185,122	6,473,701	538,454	177,087	338,919	297,398	19.9	6.8	12.3	10.3	-1.0	0.7	1.0	0.8	1.1	0.5	1.1	0.3	1.1	0.08	1.0	0.5
IPI00797545	NAP1L1	cDNA FLJ60539, highly similar to Nucleosome assembly protein 1-like 1	100.0%	22.5	6	7	9	2	6,043,562	5,789,273	6,185,122	6,473,701	538,454	177,087	338,919	297,398	19.9	6.8	12.3	10.3	-1.0	0.7	1.0	0.8	1.1	0.5	1.1	0.3	1.1	0.08	1.0	0.5
				FYEEVHDLER	2	100.0%	1																									
				GIPEFWLTVFK	2	100.0%	2																									
				LDGLVETPTGYIESLPR	2	100.0%	2																									
				NVDLLSDMVQEHDEPILK	3	99.9%	1																									
				QLTVQMMQNPQILAALQER	2	100.0%	1																									
				QLTVQMMQNPQILAALQER	3	100.0%	1																									
				YAVLYQPLFDK	2	99.9%	1																									
IPI00023876	CASP6	isoform Alpha of Caspase-6	92.2%	3.8	1	1	1	3	704,247	840,953	772,613	815,047	96,242	78,034	66,864	30,556	30.6	20.8	19.4	8.4	1.2	0.3	1.1	0.6	1.2	0.3	-1.1	0.5	-1.0	0.8	1.1	0.6
IPI00217208	CASP6	isoform Beta of Caspase-6	92.2%	5.4	1	1	1	3	704,247	840,953	772,613	815,047	96,242	78,034	66,864	30,556	30.6	20.8	19.4	8.4	1.2	0.3	1.1	0.6	1.2	0.3	-1.1	0.5	-1.0	0.8	1.1	0.6
IPI00966602	CASP6	Uncharacterized protein	92.2%	7.7	1	1	1	3	704,247	840,953	772,613	815,047	96,242	78,034	66,864	30,556	30.6	20.8	19.4	8.4	1.2	0.3	1.1	0.6	1.2	0.3	-1.1	0.5	-1.0	0.8	1.1	0.6
				IEIQTLTGLFK	2	92.2%	1																									
IPI00023919	PSMC5	26S protease regulatory subunit 8	100.0%	24.9	7	7	8	2	9,342,529	9,755,931	9,382,613	10,670,498	954,578	508,528	695,010	409,025	22.9	11.7	16.6	8.6	1.0	0.7	1.0	1	1.1	0.2	-1.0	0.7	1.1	0.2	1.1	0.1
IPI00745502	PSMC5	26S protease regulatory subunit 8 isoform 2	100.0%	25.4	7	7	8	2	9,342,529	9,755,931	9,382,613	10,670,498	954,578	508,528	695,010	409,025	22.9	11.7	16.6	8.6	1.0	0.7	1.0	1	1.1	0.2	-1.0	0.7	1.1	0.2	1.1	0.1
				FVVDVDKNIDINDVTPNCR	3	99.9%	1																									
				IAELMPGASGAEVK	2	99.9%	1																									
				IEELQLIVNDK	2	100.0%	2																									
				IEFPPPNEEAR	2	90.7%	1																									
				LLREELQLLQEQGSYVGEVVR	3	100.0%	1																									
				TMLELLNQLDGFEATK	2	100.0%	1																									
				VSGSELVQK	2	99.1%	1																									
IPI00023987	PPCS	Phosphopantothenate--cysteine ligase	99.6%	5.5	2	2	2	1	25,707,290	25,940,410	24,266,560	30,109,140	2,004,652	1,261,816	1,898,198	2,158,086	17.4	10.9	17.5	16.0	1.0	0.9	-1.1	0.6	1.2	0.2	-1.1	0.5	1.2	0.1	1.2	0.08
				FLDNFSSGR	2	90.4%	1																									
				IVDNLQSR	2	95.3%	1																									
IPI00024067	CLTC	isoform 1 of Clathrin heavy chain 1	100.0%	37.0	41	45	54	2	105,654,686	106,999,095	105,963,498	119,334,569	7,417,651	3,584,661	6,027,236	3,895,374	15.7	7.5	12.7	7.3	1.0	0.9	1.0	1	1.1	0.1	-1.0	0.9	1.1	0.05	1.1	0.1
IPI00455383	CLTC	isoform 2 of Clathrin heavy chain 1	100.0%	37.8	41	45	54	2	105,654,686	106,999,095	105,963,498	119,334,569	7,417,651	3,584,661	6,027,236	3,895,374	15.7	7.5	12.7	7.3	1.0	0.9	1.0	1	1.1	0.1	-1.0	0.9	1.1	0.05	1.1	0.1
				ADDPSSYMEVVQAANTSGNWEELVK	2	100.0%	1																									
				AFMTADLPNELIELLEK	2	100.0%	2																									
				AFMTADLPNELIELLEK	3	100.0%	1																									
				AHIAQLCEK	2	93.0%	1																									
				CNEPAVWSQLAK	2	100.0%	1																									
				DAMQYASESK	2	100.0%	1																									
				DTELAEELLQWFLQEEKR	3	100.0%	1																									
				ESYVETELIFALAK	2	100.0%	1																									
				FDFVHDLVLYLYR	3	85.0%	1																									
				FDVNTSAVQVLIEHIGNLDR	3	99.9%	1																									
				FQSVPAQPGQTSPLLQYFGILLDQGQLNK	3	100.0%	1																									
				GQCDLELINVCNENSLFK	2	100.0%	1																									
				GQFSTDELVAEVEKR	2	100.0%	1																									
				GQFSTDELVAEVEKR	3	99.4%	1																									
				HELIEFR	2	98.6%	1																									
				HSSLAGCQIINYR	2	88.8%	1																									
				ISGETIFVTAPHEATAGIIGVNR	3	100.0%	1																									
				IYIDSNNNPER	2	99.9%	1																									
				KAVDVFFPPEAQNDFPVAMQISEK	3	100.0%	1																									
				KFDVNTSAVQVLIEHIGNLDR	3	100.0%	2																									
				KFNALFAQGNYSEAAK	3	99.9%	1																									
				LAELEEFINGPNNAHIQQVGDR	3	99.6%	1																									
				LASTLVHLGEYQAAVDGAR	3	100.0%	1																									
				LHIIEVGTPPTGNQPFPK	3	99.8%	1																									
				LLEMNLMHAPQVADAILGNQMFTHYDR	3	80.8%	1																									
				LLLPWLEAR	2	99.8%	1																									
				LLYNNVSNFGR	2	99.9%	2																									
				LPVVIGGLLDVDCSEDVIK	2	100.0%	2																									
				NLQNLLILTAIK	2	100.0%	2																									
				NNLAGAEELFAR	2	100.0%	2																									
				NNRPSEGPLQTR	2	100.0%	1																									
				QLPLVKPYLR	3	99.6%	1																									
				SVDPTLALSVYLR	2	100.0%	1																									
				TLQIFNIEMK	2	100.0%	2																									
				TSIDAYDNFDNISLAQR	2	100.0%	1																									
				TSIDAYDNFDNISLAQR	3	99.8%	1																									
				VANVELYYR	2	100.0%	1																									
				VDKLDASESLR	2	87.5%	1																									
				VDKLDASESLR	3	93.9%	1																									
				VGEQAQVVIIDMNDPSNPIR	3	90.8%	1																									
				VGYTPDWIFLLR	2	100.0%	1																									
				VIQCFAETGQVQK	2	100.0%	2																									
				WISLNTVALVTDNAVYHWSMEGESQPVK	3	100.0%	1																									
				WLLLTGISAQQNR	2	100.0%	2																									
				YIEIYVQK	2	93.5%	1																									
IPI00024087	PDHA2	Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochor	100.0%	2.8	1	1	1	1	2,907,280	2,577,400	2,745,980	2,825,720	174,903	43,712	133,707	123,446	13.5	3.8	10.9	9.8	-1.1	0.1	-1.1	0.5	-1.0	0.7	1.1	0.3	1.1	0.1	1.0	0.7
				GPILMELQTYR	2	99.7%	1																									
IPI00024095	ANXA3	Annexin A3	100.0%	45.8	13	15	21	1	53,231,066	57,878,341	54,524,793	61,961,142	4,734,232	3,036,819	4,904,861	2,033,183	19.9	11.7	20.1	7.3	1.1	0.4	1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.3	1.1	0.2
				DESLKVDEHLAK	2	85.4%	1																									
				DYPDFSPSVDAEAIQK	2	100.0%	2																									
				GAGTNEDALIEILTTR	2	100.0%	2																									
				GAGTNEDALIEILTTR	3	87.4%	1																									
				GELSGHFEDLLLAIVNCVR	2	99.9%	1																									
				GELSGHFEDLLLAIVNCVR	3	100.0%	1																									
				GIGTDEFTLNR	2	100.0%	2																									
				HYGYSLYSAIK	2	99.9%	1																									
				MLISILTER	2	100.0%	2																									
				RDESLKVDEHLAK	3	97.5%	1																									
				SDTSGDYEITLLK	2	100.0%	2																									
				SEIDLLDIR	2	99.9%	1																									
				SLGDDISSETSGDFR	2	100.0%	2																									
				SLGDDISSETSGDFRK	2	100.0%	1																									
				WGTDEDKFTEILCLR	3	100.0%	1																									
IPI00024097	TES	isoform 1 of Testin	100.0%	15.4	5	5	5	3	7,653,586	7,610,770	7,346,852	8,100,290	494,513	290,196	378,081	358,177	14.5	8.5	11.5	9.9	-1.0	0.9	-1.0	0.6	1.1	0.5	-1.0	0.6	1.1	0.3	1.1	0.2
IPI00216425	TES	isoform 2 of Testin	100.0%	15.8	5	5	5	3	7,653,586	7,610,770	7,346,852	8,100,290	494,513	290,196	378,081	358,177	14.5	8.5	11.5	9.9	-1.0	0.9	-1.0	0.6	1.1	0.5	-1.0	0.6	1.1	0.3	1.1	0.2
IPI01015717	TES	48 kDa protein	100.0%	15.4	5	5	5	3	7,653,586	7,610,770	7,346,852	8,100,290	494,513	290,196	378,081	358,177	14.5	8.5	11.5	9.9	-1.0	0.9	-1.0	0.6	1.1	0.5	-1.0	0.6	1.1	0.3	1.1	0.2
				LPCEMDAQGPK	2	94.4%	1																									
				NVMILTNPVAAK	2	100.0%	1																									
				NVSINTVTYEWAPPVQNQALAR	2	89.6%	1																									
				QYMQMLPK	2	98.3%	1																									
				STPAAVGAMEDK	2	99.9%	1																									
IPI00024145	VDAC2	isoform 2 of Voltage-dependent anion-selective channel protein 2	100.0%	27.2	6	6	8	5	7,381,040	7,442,197	6,995,972	8,339,088	601,286	352,947	587,670	217,527	18.2	10.6	18.8	5.8	1.0	0.9	-1.1	0.7	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.08
IPI00216026	VDAC2	isoform 3 of Voltage-dependent anion-selective channel protein 2	100.0%	26.2	6	6	8	5	7,381,040	7,442,197	6,995,972	8,339,088	601,286	352,947	587,670	217,527	18.2	10.6	18.8	5.8	1.0	0.9	-1.1	0.7	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.08
IPI00455531	VDAC2	Voltage-dependent anion-selective channel protein 2	100.0%	26.3	6	6	8	5	7,381,040	7,442,197	6,995,972	8,339,088	601,286	352,947	587,670	217,527	18.2	10.6	18.8	5.8	1.0	0.9	-1.1	0.7	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.08

IPI00902560	VDAC2	isoform 1 of Voltage-dependent anion-selective channel protein 2	100.0%	24.9	6	6	8	5	7,381,040	7,442,197	6,995,972	8,339,088	601,286	352,947	587,670	217,527	18.2	10.6	18.8	5.8	1.0	0.9	-1.1	0.7	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.08
IPI00917420	VDAC2	30 kDa protein	100.0%	27.3	6	6	8	5	7,381,040	7,442,197	6,995,972	8,339,088	601,286	352,947	587,670	217,527	18.2	10.6	18.8	5.8	1.0	0.9	-1.1	0.7	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.08
				LTFDTTFSPNTGK	2	98.8%	1																									
				LTLSALVDGK	2	100.0%	1																									
				NNFAVGYR	2	99.2%	1																									
				TGDFQLHTNVNDGTEFGGSIYQK	3	100.0%	2																									
				WCEYGLTFTEK	2	99.3%	1																									
				YQLDPTASISAK	2	100.0%	2																									
IPI00024157	FKBP3	Peptidyl-prolyl cis-trans isomerase FKBP3	100.0%	21.0	5	5	6	1	43,847,190	50,109,650	44,286,810	54,791,830	4,909,084	2,561,521	3,085,715	1,030,475	25.0	11.4	15.6	4.2	1.1	0.3	1.0	0.9	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
				ARLEIEPEWAYGKK	3	87.7%	1																									
				AWTVEQLR	2	96.9%	1																									
				DHLVTAYNHLFETK	3	97.3%	1																									
				GWDEALLTMSK	2	100.0%	2																									
				LEIEPEWAYGK	2	85.5%	1																									
IPI00024163	POLR3A	Similar to DNA-directed RNA polymerase	99.7%	1.7	2	2	2	2	9,216,545	9,339,780	9,177,360	9,946,580	1,443,807	814,839	741,699	401,211	35.0	19.5	18.1	9.0	1.0	0.9	-1.0	1	1.1	0.6	-1.0	0.9	1.1	0.5	1.1	0.4
IPI01015730	POLR3A	DNA-directed RNA polymerase	99.7%	1.7	2	2	2	2	9,216,545	9,339,780	9,177,360	9,946,580	1,443,807	814,839	741,699	401,211	35.0	19.5	18.1	9.0	1.0	0.9	-1.0	1	1.1	0.6	-1.0	0.9	1.1	0.5	1.1	0.4
				RHVMLLSDLMTYK	2	97.6%	1																									
				TVISPDPNLR	2	89.4%	1																									
IPI00024175	PSMA7	isoform 1 of Proteasome subunit alpha type-7	100.0%	24.2	4	4	5	1	12,017,643	13,136,687	11,107,330	13,556,760	1,169,002	436,188	775,105	654,218	21.8	7.4	15.6	10.8	1.1	0.4	-1.1	0.5	1.1	0.3	-1.2	0.05	1.0	0.6	1.2	0.04
				GRDIVVLGVEK	2	99.7%	1																									
				ICALDDNVCMAFAGLTADAR	2	97.8%	1																									
				LTVEDPVTVEYITR	2	100.0%	1																									
				NYTDEAIETDDLTIK	2	100.0%	2																									
IPI00024255	GPKOW	G patch domain and KOW motifs-containing protein	100.0%	6.9	2	2	2	1	6,601,976	5,847,551	6,607,103	7,442,075	787,314	675,750	427,097	271,390	26.7	25.8	14.5	8.2	-1.1	0.5	1.0	1	1.1	0.4	1.1	0.4	1.3	0.06	1.1	0.1
				QDGPAAK	1	96.9%	1																									
				QPPARPPGPSTDTGALADGVVSQAVK	3	85.3%	1																									
IPI00024266	MGST3	Microsomal glutathione S-transferase 3	99.8%	8.6	1	1	1	3	1,151,963	1,190,363	1,083,913	1,292,343	113,132	96,289	117,867	43,426	22.0	18.1	24.3	7.5	1.0	0.8	-1.1	0.7	1.1	0.3	-1.1	0.5	1.1	0.4	1.2	0.2
IPI00639812	MGST3	Microsomal glutathione S-transferase 3	99.8%	7.8	1	1	1	3	1,151,963	1,190,363	1,083,913	1,292,343	113,132	96,289	117,867	43,426	22.0	18.1	24.3	7.5	1.0	0.8	-1.1	0.7	1.1	0.3	-1.1	0.5	1.1	0.4	1.2	0.2
IPI00647044	MGST3	Microsomal glutathione S-transferase 3	99.8%	10.1	1	1	1	3	1,151,963	1,190,363	1,083,913	1,292,343	113,132	96,289	117,867	43,426	22.0	18.1	24.3	7.5	1.0	0.8	-1.1	0.7	1.1	0.3	-1.1	0.5	1.1	0.4	1.2	0.2
				IASGLGLAWIVGR	2	99.6%	1																									
IPI00024284	HSPG2	Basement membrane-specific heparan sulfate proteoglycan core protein	100.0%	0.7	2	2	2	1	6,223,203	6,812,840	7,238,867	7,517,110	404,512	412,602	266,402	343,986	14.5	13.5	8.2	10.2	1.1	0.3	1.2	0.07	1.2	0.04	1.1	0.4	1.1	0.2	1.0	0.5
				AMDFNGILTIR	2	99.7%	1																									
				FLVHDSFWALPEQFLGNK	3	81.2%	1																									
IPI00024307	EFNB1	Ephrin-B1	96.7%	5.2	1	1	1	2	4,265,430	4,142,775	3,971,305	4,786,385	379,819	203,648	314,921	341,551	19.9	11.0	17.7	16.0	-1.0	0.8	-1.1	0.6	1.1	0.3	-1.0	0.7	1.2	0.1	1.2	0.1
IPI00976219	EFNB1	Conserved hypothetical protein	96.7%	25.0	1	1	1	2	4,265,430	4,142,775	3,971,305	4,786,385	379,819	203,648	314,921	341,551	19.9	11.0	17.7	16.0	-1.0	0.8	-1.1	0.6	1.1	0.3	-1.0	0.7	1.2	0.1	1.2	0.1
				GGSGTAGTEPSDIIIPLR	2	96.7%	1																									
IPI00024320	RBM3	Putative RNA-binding protein 3	100.0%	47.8	4	4	4	1	32,680,877	34,796,480	32,021,120	40,202,620	1,892,089	774,029	1,573,597	1,403,143	13.0	5.0	11.0	7.8	1.1	0.3	-1.0	0.8	1.2	0.01	-1.1	0.2	1.2	0.01	1.3	0.005
				AMNGESLDGR	2	98.8%	1																									
				GFGFITFTNPEHASVAMR	3	99.9%	1																									
				LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	3	100.0%	1																									
				YYDSRPGGYGYGYGR	3	99.0%	1																									
IPI00024364	TNPO1	isoform 1 of Transportin-1	100.0%	7.6	6	6	7	3	14,070,977	14,985,752	15,260,412	16,849,815	1,604,821	492,856	1,419,968	1,129,656	25.5	7.4	20.8	15.0	1.1	0.6	1.1	0.6	1.2	0.2	1.0	0.9	1.1	0.2	1.1	0.4
IPI00843876	TNPO1	isoform 2 of Transportin-1	100.0%	7.6	6	6	7	3	14,070,977	14,985,752	15,260,412	16,849,815	1,604,821	492,856	1,419,968	1,129,656	25.5	7.4	20.8	15.0	1.1	0.6	1.1	0.6	1.2	0.2	1.0	0.9	1.1	0.2	1.1	0.4
IPI00908817	TNPO1	isoform 3 of Transportin-1	100.0%	8.0	6	6	7	3	14,070,977	14,985,752	15,260,412	16,849,815	1,604,821	492,856	1,419,968	1,129,656	25.5	7.4	20.8	15.0	1.1	0.6	1.1	0.6	1.2	0.2	1.0	0.9	1.1	0.2	1.1	0.4
				ALVMLLEVR	2	84.3%	1																									
				FSDQFPLPLK	2	99.9%	1																									
				ILHGFKNQVGDENWR	3	84.2%	1																									
				QSSFALLGDLTK	2	99.6%	1																									
				TLLENTAITIGR	2	100.0%	2																									
				YSDIDIILLK	2	99.9%	1																									
IPI00024403	CPNE3	Copine-3	93.4%	1.7	1	1	1	4	1,271,620	1,335,498	1,291,265	1,322,288	94,031	66,483	73,731	74,433	16.5	11.1	12.8	12.6	1.1	0.6	1.0	0.9	1.0	0.7	-1.0	0.7	-1.0	0.9	1.0	0.8
IPI00975515	CPNE3	Uncharacterized protein	93.4%	3.9	1	1	1	4	1,271,620	1,335,498	1,291,265	1,322,288	94,031	66,483	73,731	74,433	16.5	11.1	12.8	12.6	1.1	0.6	1.0	0.9	1.0	0.7	-1.0	0.7	-1.0	0.9	1.0	0.8
IPI00981530	CPNE3	Uncharacterized protein	93.4%	5.9	1	1	1	4	1,271,620	1,335,498	1,291,265	1,322,288	94,031	66,483	73,731	74,433	16.5	11.1	12.8	12.6	1.1	0.6	1.0	0.9	1.0	0.7	-1.0	0.7	-1.0	0.9	1.0	0.8
IPI00982238	CPNE3	Protein	93.4%	3.4	1	1	1	4	1,271,620	1,335,498	1,291,265	1,322,288	94,031	66,483	73,731	74,433	16.5	11.1	12.8	12.6	1.1	0.6	1.0	0.9	1.0	0.7	-1.0	0.7	-1.0	0.9	1.0	0.8
				VVLFEMEAR	2	93.4%	1																									
IPI00024466	UGGT1	isoform 1 of UDP-glucose:glycoprotein glucosyltransferase 1	100.0%	15.9	15	15	15	1	27,482,747	27,206,666	27,456,259	31,097,389	2,607,693	855,281	1,987,095	807,080	21.2	7.0	16.2	5.8	-1.0	0.9	-1.0	1	1.1	0.2	1.0	0.9	1.1	0.01	1.1	0.1
				AIWAALQTQTSNAAK	2	100.0%	1																									
				DYLDLTASNNFFVDDYAR	2	100.0%	1																									
				EGETYFDVVAVVDPVTR	2	99.8%	1																									
				EISYENTQISR	2	100.0%	1																									
				FLDMPQSPLFTLNLNTPESWMVESVR	3	97.8%	1																									
				GDASGACAAGALPVTGVCYK	2	99.6%	1																									
				IIGPLEDSELFNQDDFHLLENIILK	3	100.0%	1																									
				ILETTTFFQR	2	98.0%	1																									
				IVPEWQDYDQEIK	2	99.6%	1																									
				LNIQPSEADYAVDIR	2	100.0%	1																									
				TAAVANSMNYLTK	2	90.1%	1																									
				VDALLSAQPK	2	84.6%	1																									
				VEEDVASDLVMK	2	99.8%	1																									
				WFSTPLLLEASEFLAEDSQEK	2	85.7%	1																									
				YNSWPSSLQELLRPTFPGVIR	3	98.5%	1																									
IPI00024502	UBQLN4	Ubiquilin-4	100.0%	6.5	2	2	2	2	1,151,412	1,084,133	1,103,238	1,287,258	124,341	72,044	76,834	36,397	24.2	14.9	15.6	6.3	-1.1	0.7	-1.0	0.8	1.1	0.3	1.0	0.9	1.2	0.04	1.2	0.06
IPI00744359	UBQLN4	cDNA FLJ13292 fis, clone OVARC1001180, weakly similar to UBIQUITIN-LIKE PRO	100.0%	12.4	2	2	2	2	1,151,412	1,084,133	1,103,238	1,287,258	124,341	72,044	76,834	36,397	24.2	14.9	15.6	6.3	-1.1	0.7	-1.0	0.8	1.1	0.3	1.0	0.9	1.2	0.04	1.2	0.06
				NPAMMQEMMR	2	100.0%	1																									
				QLMSNPEMLSQIMENPLVQDMMSNPDLMR	3	99.5%	1																									
IPI00024540	SH3GLB2	isoform 1 of Endophilin-B2	99.1%	6.6	2	2	2	5	2,234,732	2,282,216	2,340,311	2,295,624	112,175	49,277	57,852	99,606	11.2	4.8	5.5	9.7	1.0	0.7	1.0	0.4	1.0	0.7	1.0	0.5	1.0	0.9	-1.0	0.7
IPI00398828	SH3GLB2	isoform 2 of Endophilin-B2	99.1%	6.4	2	2	2	5	2,234,732	2,282,216	2,340,311	2,295,624	112,175	49,277	57,852	99,606	11.2	4.8	5.5	9.7	1.0	0.7	1.0	0.4	1.0	0.7	1.0	0.5	1.0	0.9	-1.0	0.7
IPI00435916	SH3GLB2	PP9455	99.1%	10.2	2	2	2	5	2,234,732	2,282,216	2,340,311	2,295,624	112,175	49,277	57,852	99,606	11.2	4.8	5.5	9.7	1.0	0.7	1.0	0.4	1.0	0.7	1.0	0.5	1.0	0.9	-1.0	0.7
IPI00922456	SH3GLB2	SH3-domain GRB2-like endophilin B2	99.1%	7.0	2	2	2	5	2,234,732	2,282,216	2,340,311	2,295,624	112,175	49,277	57,852	99,606	11.2	4.8	5.5	9.7	1.0	0.7	1.0	0.4	1.0	0.7	1.0	0.5	1.0	0.9	-1.0	0.7
IPI00925205	SH3GLB2	SH3-domain GRB2-like endophilin B2	99.1%	6.4	2	2	2	5	2,234,732	2,282,216	2,340,311	2,295,624	112,175	49,277	57,852	99,606	11.2	4.8	5.5	9.7	1.0	0.7	1.0	0.4	1.0	0.7	1.0	0.5	1.0	0.9	-1.0	0.7
				CLHEFVKSQTTYYAQCYR	2	81.8%	1																									
				VAQTEFDR	2	95.0%	1																									
IPI00024572	ASPH	isoform Junctin-1 of Aspartyl/asparaginyl beta-hydroxylase	99.9%	8.0	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00032449	ASPH	isoform Junctate of Aspartyl/asparaginyl beta-hydroxylase	99.9%	5.8	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00032450	ASPH	isoform Junctin-2 of Aspartyl/asparaginyl beta-hydroxylase	99.9%	8.6	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00032453	ASPH	aspartyl/asparaginyl beta-hydroxylase isoform b	99.9%	6.0	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00396582	ASPH	aspartyl/asparaginyl beta-hydroxylase isoform k	99.9%	6.7	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00433478	ASPH	aspartyl/asparaginyl beta-hydroxylase isoform l	99.9%	8.9	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00746217	ASPH	aspartyl/asparaginyl beta-hydroxylase isoform j	99.9%	4.2	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00909538	ASPH	cDNA FLJ54075, highly similar to Aspartyl/asparaginyl beta-hydroxylase	99.9%	6.3	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00910043	ASPH	aspartyl/asparaginyl beta-hydroxylase isoform i	99.9%	7.0	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00921959	ASPH	aspartyl/asparaginyl beta-hydroxylase isoform h	99.9%	6.5	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00944646	ASPH	aspartyl/asparaginyl beta-hydroxylase isoform g	99.9%	6.0	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00974367	ASPH	Uncharacterized protein	99.9%	13.2	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00976292	ASPH	19 kDa protein	99.9%	10.3	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00979367	ASPH	Uncharacterized protein	99.9%	9.1	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00980037	ASPH	Uncharacterized protein	99.9%	5.5	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
IPI00982358	ASPH	Uncharacterized protein	99.9%	15.9	1	1	1	16	323,272	312,725	334,813	318,465	16,685	16,350	7,639	11,389	11.5	11.7	5.1	8.0	-1.0	0.7	1.0	0.5	-1.0	0.8	1.1	0.3	1.0	0.8	-1.1	0.3
				LGIYDADGDGDFDVDDAK	2	100.0%	1																									
IPI00024623	ACADSB	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	99.7%	3.0	1	1	1	2	982,180	898,365	1,117,345	1,131,695	185,617	76,509	41,192	112,507	42.3	19.0	8.2	22.2	-1.1	0.7	1.1	0.5	1.2	0.5	1.2	0.04	1.3	0.1	1.0	0.9
IPI01012473	ACADSB	cDNA FLJ57418, highly similar to Short/branched chain specific acyl-CoAdehydroge	99.7%	3.9	1	1	1	2	982,180	898,365	1,117,345	1,131,695	185,617	76,509	41,192	112,507	42.3	19.0	8.2	22.2	-1.1	0.7	1.1	0.5	1.2	0.5	1.2	0.04	1.3	0.1	1.0	0.9
				YYASEIAGQTTSK	2	99.5%	1																									
IPI00908823	-	cDNA FLJ52122, moderately similar to Creatine kinase, ubiquitous mitochondrial	100.0%	22.2	1	1	1	6	36,811	36,590	37,211	47,224	5,591	6,046	7,527	5,410	34.0	37.0	45.2	25.6	-1.0	1	1.0	1	1.3	0.2	1.0	1	1.3	0.2	1.3	0.3
IPI00024638	CKMT1B;CKMT1A	Uncharacterized protein	100.0%	17.6	1	1	1	6	36,811	36,590	37,211	47,224	5,591	6,046	7,527	5,410	34.0	37.0	45.2	25.6	-1.0	1	1.0	1	1.3	0.2	1.0	1	1.3	0.2	1.3	0.3
IPI00797318	CKMT1B	cDNA FLJ51878, highly similar to Creatine kinase, ubiquitous mitochondrial	100.0%	14.1	1	1	1	6	36,811	36,590	37,211	47,224	5,591	6,046	7,527	5,410	34.0	37.0	45.2	25.6	-1.0	1	1.0	1	1.3	0.2	1.0	1	1.3	0.2	1.3	0.3
IPI00852728	CKMT1B;CKMT1A	Uncharacterized protein	100.0%	10.8	1	1	1	6	36,811	36,590	37,211	47,224	5,591	6,046	7,527	5,410	34.0	37.0	45.2	25.6	-1.0	1	1.0	1	1.3	0.2	1.0	1	1.3	0.2	1.3	0.3
IPI00853566	CKMT1B;CKMT1A	Uncharacterized protein	100.0%	20.2	1	1	1	6	36,811	36,590	37,211	47,224	5,591	6,046	7,527	5,410	34.0	37.0	45.2	25.6	-1.0	1	1.0	1	1.3	0.2	1.0	1	1.3	0.2	1.3	0.3
IPI00922077	CKMT1B;CKMT1A	Uncharacterized protein	100.0%	12.8	1	1	1	6	36,811	36,590	37,211	47,224	5,591	6,046	7,527	5,410	34.0	37.0	45.2	25.6	-1.0	1	1.0	1	1.3	0.2	1.0	1	1.3	0.2	1.3	0.3
				TVGMVAGDEETYEVFADLFDPVIQER	2	100.0%	1																									
IPI00024642	CCDC47	isoform 1 of Coiled-coil domain-containing protein 47	99.5%	5.0	1	1	1	2	210,137	236,927	284,599	280,014	26,216	11,030	34,488	14,371	27.9	10.4	27.1	11.5	1.1	0.4	1.4	0.1	1.3	0.05	1.2	0.2	1.2	0.04	-1.0	0.9
IPI00743775	CCDC47	isoform 2 of Coiled-coil domain-containing protein 47	99.5%	5.0	1	1	1	2	210,137	236,927	284,599	280,014	26,216	11,030	34,488	14,371	27.9	10.4	27.1	11.5	1.1	0.4	1.4	0.1	1.3	0.05	1.2	0.2	1.2	0.04	-1.0	0.9
				YGLPDSLAILSEMGEVTDGMMDTK	2	99.5%	1																									
IPI00024661	SEC24C	Protein transport protein Sec24C	100.0%	4.9	3	3	3	2	6,903,586	6,717,469	6,538,980	7,840,362	363,433	495,896	247,628	408,395	11.8	16.5	8.5	11.7	-1.0	0.8	-1.1	0.4	1.1	0.1	-1.0	0.8	1.2	0.1	1.2	0.03
IPI01015489	SEC24C	cDNA FLJ60345, highly similar to Protein transport protein Sec24C	100.0%	5.5	3	3	3	2	6,903,586	6,717,469	6,538,980	7,840,362	363,433	495,896	247,628	408,395	11.8	16.5	8.5	11.7	-1.0	0.8	-1.1	0.4	1.1	0.1	-1.0	0.8	1.2	0.1	1.2	0.03
				AVITSLLDQIPEMFADTR	2	100.0%	1																									
				GPQSNYGGPYPAAPTFGSQPGPPQPLPPK	3	98.6%	1																									
				HFLVEDK	2	96.9%	1																									
IPI00024662	CBX5	Chromobox protein homolog 5	100.0%	27.2	4	4	5	1	13,682,895	12,918,125	13,126,920	14,419,220	1,027,722	639,576	593,740	465,294	16.8	11.1	10.1	7.2	-1.1	0.5	-1.0	0.7	1.1	0.5	1.0	0.8	1.1	0.09	1.1	0.1
				CPQIVIAFYEER	2	99.9%	2																									
				IIGATDSCGDLMFLMK	2	99.9%	1																									
				NLDCPELISEFMK	2	98.4%	1																									
				SNFSNSADDIK	2	90.1%	1																									
IPI00024664	USP5	isoform Long of Ubiquitin carboxyl-terminal hydrolase 5	100.0%	20.4	11	13	13	2	20,051,375	19,469,171	21,032,613	22,317,421	1,305,858	500,043	1,808,451	377,590	14.6	5.7	19.2	3.8	-1.0	0.7	1.0	0.7	1.1	0.2	1.1	0.4	1.1	0.002	1.1	0.5
IPI00375145	USP5	isoform Short of Ubiquitin carboxyl-terminal hydrolase 5	100.0%	21.0	11	13	13	2	20,051,375	19,469,171	21,032,613	22,317,421	1,305,858	500,043	1,808,451	377,590	14.6	5.7	19.2	3.8	-1.0	0.7	1.0	0.7	1.1	0.2	1.1	0.4	1.1	0.002	1.1	0.5
				ENLWLNLTDGSILCGR	2	97.6%	1																									
				IFQNAPTDPTQDFSTQVAK	2	100.0%	1																									
				IGEWELIQESGVPLKPLFGPGYTGIR	3	100.0%	1																									
				IVILPDYLEIAR	2	100.0%	1																									
				KLDVSIEMPEELDISQLR	2	100.0%	1																									
				KLDVSIEMPEELDISQLR	3	100.0%	1																									
				LEKIFQNAPTDPTQDFSTQVAK	3	97.4%	1																									
				QQDAQEFFLHLINMVER	2	99.9%	1																									
				QQDAQEFFLHLINMVER	3	100.0%	1																									
				SSENPNEVFR	2	99.3%	1																									
				TMTELEIDMNQR	2	94.8%	1																									
				VDYIMQLPVPMDAALNKEELLEYEEK	3	97.1%	1																									
				VTSAVEALLSADSASR	2	100.0%	1																									
IPI00922290	-	cDNA FLJ53094, highly similar to Receptor expression-enhancing protein 5	99.5%	6.4	1	1	1	4	630,165	739,420	744,098	683,503	103,253	100,411	79,519	74,100	36.6	30.4	23.9	24.2	1.2	0.5	1.2	0.4	1.1	0.7	1.0	1	-1.1	0.7	-1.1	0.6
IPI00024670	REEP5	Receptor expression-enhancing protein 5	99.5%	5.3	1	1	1	4	630,165	739,420	744,098	683,503	103,253	100,411	79,519	74,100	36.6	30.4	23.9	24.2	1.2	0.5	1.2	0.4	1.1	0.7	1.0	1	-1.1	0.7	-1.1	0.6
IPI00852934	REEP5	Uncharacterized protein	99.5%	6.1	1	1	1	4	630,165	739,420	744,098	683,503	103,253	100,411	79,519	74,100	36.6	30.4	23.9	24.2	1.2	0.5	1.2	0.4	1.1	0.7	1.0	1	-1.1	0.7	-1.1	0.6
IPI00922887	REEP5	cDNA FLJ59876, highly similar to Receptor expression-enhancing protein 5	99.5%	6.2	1	1	1	4	630,165	739,420	744,098	683,503	103,253	100,411	79,519	74,100	36.6	30.4	23.9	24.2	1.2	0.5	1.2	0.4	1.1	0.7	1.0	1	-1.1	0.7	-1.1	0.6
				HESQMDSVVK	2	99.5%	1																									
IPI00024705	GIPC1	PDZ domain-containing protein GIPC1	99.1%	3.6	1	1	1	2	2,233,045	2,039,080	2,166,770	2,265,955	128,960	80,992	217,099	123,019	12.9	8.9	22.4	12.1	-1.1	0.2	-1.0	0.8	1.0	0.9	1.1	0.6	1.1	0.2	1.0	0.7
IPI00401971	GIPC1	PDZ domain-containing protein GIPC1 isoform 2	99.1%	5.1	1	1	1	2	2,233,045	2,039,080	2,166,770	2,265,955	128,960	80,992	217,099	123,019	12.9	8.9	22.4	12.1	-1.1	0.2	-1.0	0.8	1.0	0.9	1.1	0.6	1.1	0.2	1.0	0.7
				NPDELAEALDER	2	99.1%	1																									
IPI00024719	HAT1	Histone acetyltransferase type B catalytic subunit	99.5%	4.3	1	1	1	2	2,475,880	2,207,495	3,094,600	2,288,830	263,608	329,925	247,736	178,523	23.8	33.4	17.9	17.4	-1.1	0.5	1.2	0.1	-1.1	0.6	1.4	0.06	1.0	0.8	-1.4	0.03
IPI00651621	HAT1	Histone acetyltransferase 1, isoform CRA_b	99.5%	5.4	1	1	1	2	2,475,880	2,207,495	3,094,600	2,288,830	263,608	329,925	247,736	178,523	23.8	33.4	17.9	17.4	-1.1	0.5	1.2	0.1	-1.1	0.6	1.4	0.06	1.0	0.8	-1.4	0.03

				YYTEFPTVLDITAEDPSK	2	99.5%	1																									
IPI00024787	SLC27A2	Very long-chain acyl-CoA synthetase	95.9%	2.6	1	1	1	3	1,848,193	1,947,297	1,737,763	2,215,803	243,344	142,922	123,912	111,024	29.4	16.4	15.9	11.2	1.1	0.7	-1.1	0.7	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.02
IPI00447606	SLC27A2	very long-chain acyl-CoA synthetase isoform 2	95.9%	2.8	1	1	1	3	1,848,193	1,947,297	1,737,763	2,215,803	243,344	142,922	123,912	111,024	29.4	16.4	15.9	11.2	1.1	0.7	-1.1	0.7	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.02
IPI01015450	SLC27A2	44 kDa protein	95.9%	4.2	1	1	1	3	1,848,193	1,947,297	1,737,763	2,215,803	243,344	142,922	123,912	111,024	29.4	16.4	15.9	11.2	1.1	0.7	-1.1	0.7	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.02
				MYVPMTEDIYNAISAK	2	95.9%	1																									
IPI00024804	ATP2A1	isoform SERCA1B of Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	99.6%	2.3	1	1	1	5	113,653	96,975	124,519	125,187	19,032	8,744	15,528	4,831	37.5	20.2	27.9	8.6	-1.2	0.4	1.1	0.7	1.1	0.6	1.3	0.2	1.3	0.02	1.0	1
IPI00396118	ATP2A1	isoform SERCA1A of Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	99.6%	2.3	1	1	1	5	113,653	96,975	124,519	125,187	19,032	8,744	15,528	4,831	37.5	20.2	27.9	8.6	-1.2	0.4	1.1	0.7	1.1	0.6	1.3	0.2	1.3	0.02	1.0	1
IPI00646947	ATP2A1	cDNA FLJ46599 fis, clone THYMU3047115, highly similar to Sarcoplasmic/endoplas	99.6%	2.7	1	1	1	5	113,653	96,975	124,519	125,187	19,032	8,744	15,528	4,831	37.5	20.2	27.9	8.6	-1.2	0.4	1.1	0.7	1.1	0.6	1.3	0.2	1.3	0.02	1.0	1
IPI00872163	ATP2A1	Similar to ATPase, Ca++ transporting, cardiac muscle, fast twitch 1 (Fragment)	99.6%	2.7	1	1	1	5	113,653	96,975	124,519	125,187	19,032	8,744	15,528	4,831	37.5	20.2	27.9	8.6	-1.2	0.4	1.1	0.7	1.1	0.6	1.3	0.2	1.3	0.02	1.0	1
IPI00983553	LOC100510514	sarcoplasmic/endoplasmic reticulum calcium ATPase 1-like, partial	99.6%	6.3	1	1	1	5	113,653	96,975	124,519	125,187	19,032	8,744	15,528	4,831	37.5	20.2	27.9	8.6	-1.2	0.4	1.1	0.7	1.1	0.6	1.3	0.2	1.3	0.02	1.0	1
				TASEMVLADDNFSTIVAAVEEGR	2	99.6%	1																									
IPI00024811	MPZL2	Myelin protein zero-like protein 2	97.1%	11.6	2	2	2	1	15,780,110	15,015,020	15,275,920	17,150,520	1,235,708	756,838	469,686	767,322	17.5	11.3	6.9	10.0	-1.1	0.6	-1.0	0.7	1.1	0.4	1.0	0.8	1.1	0.08	1.1	0.07
				LQFDDNGTYTCQVK	3	84.7%	1																									
				VLEAVNGTDAR	2	81.2%	1																									
IPI00024821	PSMD14	26S proteasome non-ATPase regulatory subunit 14	99.9%	12.6	2	2	3	1	9,089,020	9,842,480	10,505,120	11,149,120	458,335	580,526	1,626,668	1,022,145	11.3	13.2	34.6	20.5	1.1	0.3	1.2	0.4	1.2	0.1	1.1	0.7	1.1	0.3	1.1	0.7
				AVAVVVDPIQSVK	2	99.9%	2																									
				VIDVFAMPQSGTGVSVEAVDPVFQAK	3	98.9%	1																									
IPI00024900	SBNO2	protein strawberry notch homolog 2 isoform 2	96.1%	0.8	1	1	1	5	593,808	717,914	515,694	734,994	127,761	126,994	42,781	58,279	48.1	39.6	18.6	17.7	1.2	0.5	-1.2	0.6	1.2	0.3	-1.4	0.2	1.0	0.9	1.4	0.02
IPI00158514	SBNO2	isoform 1 of Protein strawberry notch homolog 2	96.1%	0.8	1	1	1	5	593,808	717,914	515,694	734,994	127,761	126,994	42,781	58,279	48.1	39.6	18.6	17.7	1.2	0.5	-1.2	0.6	1.2	0.3	-1.4	0.2	1.0	0.9	1.4	0.02
IPI00332643	SBNO2	Uncharacterized protein	96.1%	0.8	1	1	1	5	593,808	717,914	515,694	734,994	127,761	126,994	42,781	58,279	48.1	39.6	18.6	17.7	1.2	0.5	-1.2	0.6	1.2	0.3	-1.4	0.2	1.0	0.9	1.4	0.02
IPI00878948	SBNO2	isoform 2 of Protein strawberry notch homolog 2	96.1%	0.8	1	1	1	5	593,808	717,914	515,694	734,994	127,761	126,994	42,781	58,279	48.1	39.6	18.6	17.7	1.2	0.5	-1.2	0.6	1.2	0.3	-1.4	0.2	1.0	0.9	1.4	0.02
IPI01012331	SBNO2	cDNA FLJ60290, highly similar to Mus musculus strawberry notch homolog 2, mRNA	96.1%	1.4	1	1	1	5	593,808	717,914	515,694	734,994	127,761	126,994	42,781	58,279	48.1	39.6	18.6	17.7	1.2	0.5	-1.2	0.6	1.2	0.3	-1.4	0.2	1.0	0.9	1.4	0.02
				ALWFSVSNDLK	2	82.8%	1																									
IPI00024911	ERP29	Endoplasmic reticulum resident protein 29	100.0%	45.2	7	8	10	1	26,188,747	27,429,723	28,673,478	30,621,268	2,484,979	941,930	2,160,376	934,462	21.2	7.7	16.9	6.8	1.0	0.7	1.1	0.5	1.2	0.2	1.0	0.6	1.1	0.04	1.1	0.4
				DGDFENPVPYTGAVK	2	100.0%	2																									
				GALPLDTVTFYK	2	100.0%	2																									
				GQGVYLGMPGCLPVYDALAGEFIR	2	100.0%	1																									
				GQGVYLGMPGCLPVYDALAGEFIR	3	100.0%	1																									
				ILDQGEDFPASEMTR	2	100.0%	1																									
				LAENSASSDDLLVAEVGISDYGDKLNMELSEK	3	100.0%	1																									
				QGQDNLSSVK	2	82.5%	1																									
				SLNILTAFQK	2	100.0%	1																									
IPI00024915	PRDX5	isoform Mitochondrial of Peroxiredoxin-5, mitochondrial	100.0%	56.1	11	12	16	2	32,902,344	32,047,289	31,963,312	36,493,096	2,667,715	769,775	1,908,380	1,267,208	18.1	5.4	13.4	7.8	-1.0	0.8	-1.0	0.8	1.1	0.3	-1.0	1	1.1	0.02	1.1	0.08
IPI00759663	PRDX5	isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial	100.0%	74.1	11	12	16	2	32,902,344	32,047,289	31,963,312	36,493,096	2,667,715	769,775	1,908,380	1,267,208	18.1	5.4	13.4	7.8	-1.0	0.8	-1.0	0.8	1.1	0.3	-1.0	1	1.1	0.02	1.1	0.08
				ALNVEPDGTGLTCSLAPNIISQL	2	100.0%	1																									
				ETDLLLDDSLVSIFGNR	2	100.0%	1																									
				FSMVVQDGIVK	2	100.0%	2																									
				GVLFGVPGAFTPGCSK	2	100.0%	2																									
				KGVLFGVPGAFTPGCSK	2	99.5%	1																									
				LLADPTGAFGK	2	100.0%	1																									
				LLADPTGAFGKETDLLLDDSLVSIFGNR	3	89.3%	1																									
				RFSMVVQDGIVK	2	100.0%	1																									
				THLPGFVEQAEALK	2	100.0%	2																									
				THLPGFVEQAEALK	3	100.0%	1																									
				VGDAIPAVEVFEGEPGNK	2	100.0%	2																									
				VNLAELFK	2	100.0%	1																									
IPI00024919	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	100.0%	22.7	5	5	6	2	40,989,610	45,827,725	42,385,115	55,618,640	485,950	2,066,782	4,125,111	2,129,783	2.7	10.1	21.8	8.6	1.1	0.08	1.0	0.8	1.4	0.002	-1.1	0.5	1.2	0.01	1.3	0.02
IPI00374151	PRDX3	thioredoxin-dependent peroxide reductase, mitochondrial isoform b	100.0%	24.4	5	5	6	2	40,989,610	45,827,725	42,385,115	55,618,640	485,950	2,066,782	4,125,111	2,129,783	2.7	10.1	21.8	8.6	1.1	0.08	1.0	0.8	1.4	0.002	-1.1	0.5	1.2	0.01	1.3	0.02
				DLSLDDFK	2	99.5%	1																									
				GLFIIDPNGVIK	2	100.0%	1																									
				GTAVVNGEFK	2	100.0%	1																									
				HLSVNDLPVGR	2	100.0%	2																									
				NGGLGHMNIALLSDLTK	2	99.8%	1																									
IPI00024920	ATP5D	ATP synthase subunit delta, mitochondrial	100.0%	5.4	1	1	1	1	22,845,400	23,110,600	25,631,200	24,132,200	2,455,759	2,397,153	1,765,811	2,169,618	24.0	23.2	15.4	20.1	1.0	0.9	1.1	0.4	1.1	0.7	1.1	0.4	1.0	0.8	-1.1	0.6
				IEANEALVK	2	98.7%	1																									
IPI00024933	RPL12	isoform 1 of 60S ribosomal protein L12	100.0%	54.6	6	6	11	1	23,717,630	23,890,040	22,892,145	27,634,725	1,861,486	1,014,640	1,592,398	915,977	17.6	9.5	15.6	7.4	1.0	0.9	-1.0	0.7	1.2	0.1	-1.0	0.6	1.2	0.03	1.2	0.03
				CTGGEVGATSALAPK	2	100.0%	2																									
				EILGTAQSVGCNVDGR	2	100.0%	2																									
				HPHDIIDDINSGAVECPAS	3	100.0%	1																									
				HSGNITFDEIVNIAR	2	100.0%	2																									
				IGPLGLSPK	2	100.0%	2																									
				QAQIEVVPSASALIIK	2	100.0%	2																									
IPI00442146	-	101 kDa protein	99.8%	1.7	1	1	1	9	249,142	241,328	247,109	272,473	19,502	14,436	16,550	4,333	17.5	13.4	15.0	3.6	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.8	1.1	0.1	1.1	0.2
IPI00877714	OSBP2	Protein	99.8%	2.7	1	1	1	9	249,142	241,328	247,109	272,473	19,502	14,436	16,550	4,333	17.5	13.4	15.0	3.6	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.8	1.1	0.1	1.1	0.2
IPI00877892	OSBP2	Oxysterol-binding protein	99.8%	2.9	1	1	1	9	249,142	241,328	247,109	272,473	19,502	14,436	16,550	4,333	17.5	13.4	15.0	3.6	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.8	1.1	0.1	1.1	0.2
IPI00878237	OSBP2	86 kDa protein	99.8%	2.0	1	1	1	9	249,142	241,328	247,109	272,473	19,502	14,436	16,550	4,333	17.5	13.4	15.0	3.6	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.8	1.1	0.1	1.1	0.2
IPI00878859	OSBP2	50 kDa protein	99.8%	3.6	1	1	1	9	249,142	241,328	247,109	272,473	19,502	14,436	16,550	4,333	17.5	13.4	15.0	3.6	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.8	1.1	0.1	1.1	0.2
IPI00893681	OSBP2	Protein	99.8%	5.4	1	1	1	9	249,142	241,328	247,109	272,473	19,502	14,436	16,550	4,333	17.5	13.4	15.0	3.6	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.8	1.1	0.1	1.1	0.2
IPI01014439	OSBP2	Oxysterol-binding protein	99.8%	3.5	1	1	1	9	249,142	241,328	247,109	272,473	19,502	14,436	16,550	4,333	17.5	13.4	15.0	3.6	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.8	1.1	0.1	1.1	0.2
IPI00024971	OSBP	Oxysterol-binding protein 1	99.8%	2.0	1	1	1	9	249,142	241,328	247,109	272,473	19,502	14,436	16,550	4,333	17.5	13.4	15.0	3.6	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.8	1.1	0.1	1.1	0.2
IPI00976485	OSBP	Protein	99.8%	9.4	1	1	1	9	249,142	241,328	247,109	272,473	19,502	14,436	16,550	4,333	17.5	13.4	15.0	3.6	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.8	1.1	0.1	1.1	0.2
				IPMPVNFNEPLSMLQR	2	99.7%	1																									
IPI00024990	ALDH6A1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	99.3%	2.4	1	1	1	1	6,945,160	7,317,560	6,850,630	6,920,810	288,106	386,568	407,820	461,086	9.3	11.8	13.3	14.9	1.1	0.5	-1.0	0.9	-1.0	1	-1.1	0.4	-1.1	0.5	1.0	0.9
				AFPAWADTSVLSR	2	99.3%	1																									
IPI00024993	ECHS1	Enoyl-CoA hydratase, mitochondrial	100.0%	49.0	11	14	17	1	92,268,567	97,574,613	88,337,787	109,155,854	8,531,045	3,368,646	6,280,247	3,378,867	20.7	7.7	15.9	6.9	1.1	0.6	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.04	1.2	0.02
				AFAAGADIK	2	99.8%	1																									
				ALNALCDGLIDELNQALK	2	100.0%	1																									
				ALNALCDGLIDELNQALK	3	100.0%	1																									
				AQFAQPEILIGTIPGAGGTQR	2	100.0%	2																									
				EGMTAFVEK	2	100.0%	1																									
				EMQNLSFQDCYSSK	2	100.0%	2																									
				GKNNTVGLIQLNRPK	3	100.0%	1																									
				HWDHLTQVK	2	99.4%	1																									
				HWDHLTQVK	3	99.7%	1																									
				ICPVETLVEEAIQCAEK	2	100.0%	2																									
				ICPVETLVEEAIQCAEK	3	100.0%	1																									
				NNTVGLIQLNRPK	3	97.7%	1																									
				SLAMEMVLTGDR	2	100.0%	1																									
				TFEEDPAVGAIVLTGGDK	2	100.0%	1																									
IPI00025019	PSMB1	Proteasome subunit beta type-1	100.0%	12.5	2	2	2	1	6,505,805	7,116,185	6,861,895	8,042,415	888,682	424,584	525,776	413,342	30.5	13.3	17.1	11.5	1.1	0.6	1.1	0.7	1.2	0.2	-1.0	0.7	1.1	0.2	1.2	0.1
				AGGSASAMLQPLLDNQVGFK	2	100.0%	1																									
				LSEGFSIHTR	2	95.0%	1																									
IPI00025084	CAPNS1	Calpain small subunit 1	100.0%	34.3	6	9	12	1	39,500,370	39,066,198	37,860,969	43,841,122	3,220,720	1,345,512	3,043,254	1,330,964	18.2	7.7	18.0	6.8	-1.0	0.9	-1.0	0.7	1.1	0.2	-1.0	0.7	1.1	0.04	1.2	0.1
				ILGGVISAISEAAAQYNPEPPPPR	2	100.0%	1																									
				ILGGVISAISEAAAQYNPEPPPPR	3	100.0%	1																									
				LFAQLAGDDMEVSATELMNILNK	2	100.0%	2																									
				LFAQLAGDDMEVSATELMNILNK	3	100.0%	1																									
				RLFAQLAGDDMEVSATELMNILNK	3	98.0%	1																									
				TDGFGIDTCR	2	100.0%	2																									
				THYSNIEANESEEVR	2	100.0%	1																									
				THYSNIEANESEEVR	3	100.0%	1																									
				YSDESGNMDFDNFISCLVR	2	100.0%	2																									
IPI00025086	COX5A	Cytochrome c oxidase subunit 5A, mitochondrial	100.0%	26.7	3	3	4	1	15,075,880	14,081,210	14,301,040	16,410,160	1,335,187	830,630	1,084,592	366,968	19.8	13.2	17.0	5.0	-1.1	0.5	-1.1	0.7	1.1	0.4	1.0	0.9	1.2	0.03	1.1	0.1
				EIYPYVIQELRPTLNELGISTPEELGLDKV	3	100.0%	1																									
				LNDFASTVR	2	99.2%	2																									
				RLNDFASTVR	2	90.7%	1																									
IPI00025100	BCKDHA	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	99.8%	2.3	1	1	1	4	985,995	942,475	847,413	1,021,083	139,863	113,574	128,360	68,411	31.7	27.0	33.9	15.0	-1.0	0.8	-1.2	0.5	1.0	0.8	-1.1	0.6	1.1	0.6	1.2	0.3
IPI00910865	BCKDHA	cDNA FLJ55733, highly similar to 2-oxoisovalerate dehydrogenase alpha subunit, m	99.8%	2.2	1	1	1	4	985,995	942,475	847,413	1,021,083	139,863	113,574	128,360	68,411	31.7	27.0	33.9	15.0	-1.0	0.8	-1.2	0.5	1.0	0.8	-1.1	0.6	1.1	0.6	1.2	0.3
IPI00944561	BCKDHA	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial isoform 2 precursor	99.8%	2.3	1	1	1	4	985,995	942,475	847,413	1,021,083	139,863	113,574	128,360	68,411	31.7	27.0	33.9	15.0	-1.0	0.8	-1.2	0.5	1.0	0.8	-1.1	0.6	1.1	0.6	1.2	0.3
IPI00974102	BCKDHA	cDNA FLJ45695 fis, clone FEBRA2013570, highly similar to 2-oxoisovalerate dehyd	99.8%	2.1	1	1	1	4	985,995	942,475	847,413	1,021,083	139,863	113,574	128,360	68,411	31.7	27.0	33.9	15.0	-1.0	0.8	-1.2	0.5	1.0	0.8	-1.1	0.6	1.1	0.6	1.2	0.3
				VMEAFEQAER	2	99.2%	1																									
IPI00025178	BCAS2	Pre-mRNA-splicing factor SPF27	99.5%	8.9	1	1	1	1	2,114,180	2,264,280	2,421,225	2,303,990	374,919	247,414	344,622	191,360	39.7	24.4	31.8	18.6	1.1	0.7	1.1	0.6	1.1	0.7	1.1	0.7	1.0	0.9	-1.1	0.8
				NYLSYLTAPDYSAFETDIMR	2	99.5%	1																									
IPI00025244	ZNF259	Zinc finger protein ZPR1	100.0%	8.5	3	3	4	3	4,888,573	5,004,653	4,932,557	5,818,713	392,047	148,391	324,793	195,576	17.9	6.6	14.7	7.5	1.0	0.8	1.0	0.9	1.2	0.07	-1.0	0.8	1.2	0.01	1.2	0.05
IPI00657874	ZNF259	Protein	100.0%	10.1	3	3	4	3	4,888,573	5,004,653	4,932,557	5,818,713	392,047	148,391	324,793	195,576	17.9	6.6	14.7	7.5	1.0	0.8	1.0	0.9	1.2	0.07	-1.0	0.8	1.2	0.01	1.2	0.05
IPI00657912	ZNF259	Protein	100.0%	9.1	3	3	4	3	4,888,573	5,004,653	4,932,557	5,818,713	392,047	148,391	324,793	195,576	17.9	6.6	14.7	7.5	1.0	0.8	1.0	0.9	1.2	0.07	-1.0	0.8	1.2	0.01	1.2	0.05
				GALTTVEGLITR	2	97.9%	1																									
				IPELDFEIPAFSQK	2	99.9%	2																									
				ITLHITDASDMTR	3	99.9%	1																									
IPI00025252	PDIA3	Protein disulfide-isomerase A3	100.0%	62.8	30	34	49	1	290,798,811	291,309,886	282,827,758	330,050,578	########	9,942,844	########	########	16.6	7.6	12.8	7.2	1.0	1	-1.0	0.8	1.1	0.1	-1.0	0.7	1.1	0.03	1.2	0.04
				DASIVGFFDDSFSEAHSEFLK	2	100.0%	1																									
				DASIVGFFDDSFSEAHSEFLK	3	98.6%	1																									
				DGEEAGAYDGPR	2	99.9%	1																									
				ELSDFISYLQR	2	100.0%	3																									
				FAHTNVESLVNEYDDNGEGIILFR	3	100.0%	1																									
				FIQENIFGICPHMTEDNKDLIQGK	3	100.0%	1																									
				FISDKDASIVGFFDDSFSEAHSEFLK	3	100.0%	2																									
				FLDAGHK	1	88.9%	1																									
				FLDAGHKLNFAVASR	3	88.1%	1																									
				FLQDYFDGNLK	2	99.9%	2																									
				FLQDYFDGNLKR	2	100.0%	2																									
				FLQDYFDGNLKR	3	100.0%	1																									
				FVMQEEFSR	2	100.0%	2																									
				GFPTIYFSPANK	2	100.0%	2																									
				GSNYWR	2	93.2%	1																									
				IFRDGEEAGAYDGPR	3	100.0%	1																									
				ISDTGSAGLMLVEFFAPWCGHCK	3	100.0%	2																									
				KTFSHELSDFGLESTAGEIPVVAIR	3	100.0%	1																									
				LAPEYEAAATR	2	99.9%	1																									
				LNFAVASR	2	99.8%	2																									
				LSKDPNIVIAK	2	99.9%	2																									
				LSKDPNIVIAK	3	99.9%	2																									
				MDATANDVPSPYEVR	2	100.0%	2																									
				PSHLTNKFEDK	3	98.8%	1																									
				QAGPASVPLR	2	98.3%	1																									
				RLAPEYEAAATR	2	100.0%	2																									
				SEPIPESNDGPVK	2	100.0%	2																									

				TADGIVSHLK	2	88.2%	1																									
				TADGIVSHLKK	2	100.0%	1																									
				TFSHELSDFGLESTAGEIPVVAIR	2	100.0%	1																									
				TFSHELSDFGLESTAGEIPVVAIR	3	100.0%	1																									
				VMMVAK	1	99.5%	1																									
				VVVAENFDEIVNNENK	2	100.0%	1																									
				YGVSGYPTLK	2	100.0%	2																									
IPI00025273	GART	isoform Long of Trifunctional purine biosynthetic protein adenosine-3	100.0%	3.6	3	3	3	1	3,273,639	3,890,552	3,411,564	3,884,572	332,487	65,054	198,893	91,335	22.7	3.7	13.0	5.3	1.2	0.1	1.0	0.7	1.2	0.1	-1.1	0.07	-1.0	1	1.1	0.06
				AIAFLQQPR	2	96.8%	1																									
				FGDPECQVILPLLK	2	100.0%	1																									
				VDLGGFAGLFDLK	2	99.5%	1																									
IPI00025277	PDCD6	Programmed cell death protein 6	100.0%	20.4	3	3	4	2	5,811,460	5,857,610	5,547,320	6,291,707	419,425	282,409	419,209	387,066	16.1	10.8	16.9	13.8	1.0	0.9	-1.0	0.7	1.1	0.4	-1.1	0.6	1.1	0.4	1.1	0.2
IPI00930049	PDCD6	Programmed cell death 6	100.0%	20.6	3	3	4	2	5,811,460	5,857,610	5,547,320	6,291,707	419,425	282,409	419,209	387,066	16.1	10.8	16.9	13.8	1.0	0.9	-1.0	0.7	1.1	0.4	-1.1	0.6	1.1	0.4	1.1	0.2
				AGVNFSEFTGVWK	2	100.0%	2																									
				TYDRDNSGMIDKNELK	3	99.9%	1																									
				YITDWQNVFR	2	99.8%	1																									
IPI00025285	ATP6V1G1	V-type proton ATPase subunit G 1	98.2%	9.3	1	1	1	1	3,078,260	3,269,540	3,294,900	3,359,560	171,428	348,410	203,205	178,559	12.5	23.8	13.8	11.9	1.1	0.6	1.1	0.4	1.1	0.3	1.0	1	1.0	0.8	1.0	0.8
				EEAQAEIEQYR	2	98.2%	1																									
IPI00025311	BCAS1	isoform 1 of Breast carcinoma-amplified sequence 1	100.0%	13.7	4	4	6	1	6,702,253	7,267,418	6,517,532	7,796,577	769,683	600,946	543,511	200,678	25.7	18.5	18.7	5.8	1.1	0.6	-1.0	0.8	1.2	0.2	-1.1	0.4	1.1	0.4	1.2	0.08
				EDSVPTGAEENVVCESPVEIIK	3	87.5%	1																									
				MLDAQVQTDPVSIGPVGK	2	100.0%	2																									
				SKEVESALQTVDLNEGDAAPEPTEAK	3	100.0%	1																									
				TGDQAADSSLGSVK	2	100.0%	2																									
IPI00025329	RPL19	60S ribosomal protein L19	99.9%	8.7	1	1	1	1	1,134,947	1,365,861	1,519,395	1,602,500	92,241	69,872	98,542	103,382	18.2	11.4	14.5	14.4	1.2	0.08	1.3	0.02	1.4	0.01	1.1	0.2	1.2	0.09	1.1	0.6
				VWLDPNETNEIANANSR	2	99.9%	1																									
IPI00025333	CIAPIN1	isoform 3 of Anamorsin	99.5%	3.7	1	1	1	3	2,018,823	2,092,237	1,700,437	2,156,317	183,316	66,045	130,504	85,847	20.3	7.1	17.2	8.9	1.0	0.7	-1.2	0.2	1.1	0.5	-1.2	0.03	1.0	0.6	1.3	0.02
IPI00387130	CIAPIN1	isoform 1 of Anamorsin	99.5%	3.5	1	1	1	3	2,018,823	2,092,237	1,700,437	2,156,317	183,316	66,045	130,504	85,847	20.3	7.1	17.2	8.9	1.0	0.7	-1.2	0.2	1.1	0.5	-1.2	0.03	1.0	0.6	1.3	0.02
IPI00513770	CIAPIN1	isoform 2 of Anamorsin	99.5%	10.2	1	1	1	3	2,018,823	2,092,237	1,700,437	2,156,317	183,316	66,045	130,504	85,847	20.3	7.1	17.2	8.9	1.0	0.7	-1.2	0.2	1.1	0.5	-1.2	0.03	1.0	0.6	1.3	0.02
				VLLSDSNLHDA	2	99.5%	1																									
IPI00025340	PDXP	Pyridoxal phosphate phosphatase	99.5%	4.7	1	1	1	1	1,476,385	1,910,470	1,738,196	2,137,450	255,361	256,292	250,366	330,374	38.7	30.0	32.2	34.6	1.3	0.3	1.2	0.5	1.4	0.2	-1.1	0.6	1.1	0.6	1.2	0.4
				LAGDPSAGDGAAPR	2	99.5%	1																									
IPI00025347	EMG1	Ribosomal RNA small subunit methyltransferase NEP1	94.4%	4.5	1	1	1	1	6,951,880	6,656,140	6,058,960	7,498,910	439,335	215,662	403,270	299,242	14.1	7.2	14.9	8.9	-1.0	0.6	-1.1	0.2	1.1	0.3	-1.1	0.2	1.1	0.05	1.2	0.02
				NVLIEVNPQTR	2	91.6%	1																									
IPI00025366	CS	Citrate synthase, mitochondrial	96.6%	2.4	1	1	1	2	6,214,700	7,263,405	6,561,580	7,339,245	170,877	382,445	559,867	931,143	6.2	11.8	19.1	28.4	1.2	0.04	1.1	0.6	1.2	0.3	-1.1	0.3	1.0	0.9	1.1	0.5
IPI00383539	CS	Citrate synthase	96.6%	2.4	1	1	1	2	6,214,700	7,263,405	6,561,580	7,339,245	170,877	382,445	559,867	931,143	6.2	11.8	19.1	28.4	1.2	0.04	1.1	0.6	1.2	0.3	-1.1	0.3	1.0	0.9	1.1	0.5
				DYIWNTLNSGR	2	96.6%	1																									
IPI00025427	RNASE3	Eosinophil cationic protein	94.7%	16.9	1	1	1	1	2,833,190	3,030,690	2,906,220	3,312,370	428,943	126,112	197,885	190,927	33.9	9.3	15.2	12.9	1.1	0.7	1.0	0.9	1.2	0.3	-1.0	0.6	1.1	0.3	1.1	0.2
				VPLLHCDLINPGAQNISNCTYADRPGR	3	94.7%	1																									
IPI00025491	EIF4A1	Eukaryotic initiation factor 4A-I	100.0%	44.8	15	16	19	1	42,481,651	43,304,741	40,357,414	48,107,168	4,045,604	2,038,213	3,274,512	1,334,063	21.3	10.5	18.1	6.2	1.0	0.9	-1.1	0.7	1.1	0.2	-1.1	0.5	1.1	0.08	1.2	0.06
				DFTVSAMHGDMDQK	2	98.9%	1																									
				DIETFYNTSIEEMPLNVADLI	2	100.0%	1																									
				GFKDQIYDIFQK	2	99.9%	1																									
				GIDVQQVSLVINYDLPTNR	2	100.0%	2																									
				GIYAYGFEKPSAIQQR	3	99.8%	1																									
				GVAINMVTEEDKR	2	99.9%	1																									
				GYDVIAQAQSGTGK	2	100.0%	2																									
				KGVAINMVTEEDKR	3	100.0%	1																									
				LNSNTQVVLLSATMPSDVLEVTK	2	100.0%	1																									
				LNSNTQVVLLSATMPSDVLEVTKK	3	99.5%	1																									
				LQMEAPHIIVGTPGR	2	100.0%	1																									
				LQMEAPHIIVGTPGR	3	93.9%	1																									
				MFVLDEADEMLSR	2	100.0%	2																									
				TLRDIETFYNTSIEEMPLNVADLI	2	100.0%	1																									
				VDWLTEK	2	95.2%	1																									
				VLITTDLLAR	2	100.0%	1																									
IPI00025512	HSPB1	Heat shock protein beta-1	100.0%	41.5	5	6	6	1	36,345,990	37,645,605	32,444,065	39,919,875	1,944,875	1,027,193	1,526,895	1,682,316	12.0	6.1	10.5	9.4	1.0	0.6	-1.1	0.2	1.1	0.2	-1.2	0.02	1.1	0.3	1.2	0.01
				KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	3	100.0%	1																									
				LATQSNEITIPVTFESR	2	100.0%	1																									
				QLSSGVSEIR	2	99.5%	1																									
				QLSSGVSEIR	3	87.0%	1																									
				TKDGVVEITGK	2	86.6%	1																									
				VSLDVNHFAPDELTVK	2	100.0%	1																									
IPI00025721	COPS3	COP9 signalosome complex subunit 3	100.0%	6.6	2	2	2	2	2,430,762	2,498,723	2,463,333	2,788,873	298,774	185,134	219,112	103,094	27.5	16.6	19.9	8.3	1.0	0.9	1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.2	1.1	0.2
IPI00980899	COPS3	COP9 signalosome complex subunit 3 isoform 2	100.0%	7.0	2	2	2	2	2,430,762	2,498,723	2,463,333	2,788,873	298,774	185,134	219,112	103,094	27.5	16.6	19.9	8.3	1.0	0.9	1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.2	1.1	0.2
				AMDQEITVNPQFVQK	2	91.3%	1																									
				TFLTLSLQDMASR	2	100.0%	1																									
IPI00025796	NDUFS3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	99.4%	10.6	2	2	2	3	3,579,593	3,548,275	3,712,806	3,905,742	260,781	131,513	200,131	108,244	16.3	8.3	12.1	6.2	-1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.5	1.1	0.07	1.1	0.4
IPI00982902	NDUFS3	Uncharacterized protein	99.4%	17.4	2	2	2	3	3,579,593	3,548,275	3,712,806	3,905,742	260,781	131,513	200,131	108,244	16.3	8.3	12.1	6.2	-1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.5	1.1	0.07	1.1	0.4
IPI00983169	NDUFS3	cDNA FLJ57965, highly similar to NADH-ubiquinone oxidoreductase 30 kDa subunit	99.4%	21.2	2	2	2	3	3,579,593	3,548,275	3,712,806	3,905,742	260,781	131,513	200,131	108,244	16.3	8.3	12.1	6.2	-1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.5	1.1	0.07	1.1	0.4
				QLSAFGEYVAEILPK	2	99.4%	1																									
				SLVDLTAVDVPTR	2	90.4%	1																									
IPI00025815	TARDBP	isoform 2 of TAR DNA-binding protein 43	100.0%	20.7	6	6	8	2	5,280,686	5,054,951	4,958,829	5,981,278	410,019	304,028	270,701	239,426	17.4	13.5	12.2	9.0	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.04	1.2	0.02
IPI00971018	TARDBP	isoform 1 of TAR DNA-binding protein 43	100.0%	20.8	6	6	8	2	5,280,686	5,054,951	4,958,829	5,981,278	410,019	304,028	270,701	239,426	17.4	13.5	12.2	9.0	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.04	1.2	0.02
				AFAFVTFADDQIAQSLCGEDLIIK	2	100.0%	1																									
				FGGNPGGFGNQGGFGNSR	2	100.0%	2																									
				FTEYETQVK	2	85.2%	1																									
				GISVHISNAEPK	2	96.2%	1																									
				MDETDASSAVK	2	99.6%	1																									
				TSDLIVLGLPWK	2	100.0%	2																									
IPI00971061	-	HNF1 alpha A splice variant 2	99.4%	10.4	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI00025839	HNF1A	isoform A of Hepatocyte nuclear factor 1-alpha	99.4%	5.1	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI00219056	HNF1A	isoform C of Hepatocyte nuclear factor 1-alpha	99.4%	6.1	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI00411416	HNF1A	isoform B of Hepatocyte nuclear factor 1-alpha	99.4%	5.6	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI00971064	HNF1A	HNF1 alpha B splice variant 1	99.4%	11.5	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI00971187	HNF1A	Uncharacterized protein	99.4%	6.2	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI00972971	HNF1A	HNF1A homeobox A insIVS8	99.4%	4.8	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI00979621	HNF1A	Uncharacterized protein	99.4%	5.6	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI00981532	HNF1A	HNF1 alpha A splice variant 3	99.4%	6.1	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI01011057	HNF1A	HNF1 alpha A splice variant 7	99.4%	6.8	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI01012243	HNF1A	HNF1 alpha A splice variant 8	99.4%	8.1	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI01012412	HNF1A	cDNA FLJ56500, highly similar to Hepatocyte nuclear factor 1-alpha	99.4%	7.1	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI01013668	HNF1A	HNF1 alpha A splice variant 1	99.4%	5.3	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
IPI01014756	HNF1A	68 kDa protein	99.4%	5.0	2	2	2	14	684,939	659,918	643,125	689,524	39,308	32,556	39,328	15,258	12.8	11.0	13.7	5.0	-1.0	0.6	-1.1	0.5	1.0	0.9	-1.0	0.8	1.0	0.4	1.1	0.3
				AVVETLLQEDPWR	2	93.3%	1																									
				LSQLQTELLAALLESGLSK	2	99.4%	1																									
IPI00025849	ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member A	100.0%	23.7	6	8	10	2	20,640,062	20,245,283	21,945,912	23,100,127	1,368,291	534,415	1,003,577	774,170	14.8	5.9	10.2	7.5	-1.0	0.8	1.1	0.5	1.1	0.2	1.1	0.2	1.1	0.02	1.1	0.4
IPI00940656	ANP32A	ANP32A protein	100.0%	28.1	6	8	10	2	20,640,062	20,245,283	21,945,912	23,100,127	1,368,291	534,415	1,003,577	774,170	14.8	5.9	10.2	7.5	-1.0	0.8	1.1	0.5	1.1	0.2	1.1	0.2	1.1	0.02	1.1	0.4
				CPNLTHLNLSGNK	2	100.0%	1																									
				CPNLTHLNLSGNK	3	99.8%	1																									
				ELVLDNSR	2	95.1%	1																									
				SLDLFNCEVTNLNDYR	2	100.0%	2																									
				SLDLFNCEVTNLNDYR	3	100.0%	1																									
				SLDLFNCEVTNLNDYRENVFK	3	100.0%	1																									
				TPSDVKELVLDNSR	3	90.1%	1																									
				VSGGLEVLAEK	2	100.0%	2																									
IPI00025861	CDH1	Cadherin-1	100.0%	14.9	8	8	11	2	10,034,791	9,782,694	10,539,738	11,273,668	553,326	481,396	591,644	253,174	12.3	11.0	12.6	5.0	-1.0	0.7	1.1	0.6	1.1	0.08	1.1	0.4	1.2	0.03	1.1	0.3
IPI00744889	CDH1	E-cadherin	100.0%	14.5	8	8	11	2	10,034,791	9,782,694	10,539,738	11,273,668	553,326	481,396	591,644	253,174	12.3	11.0	12.6	5.0	-1.0	0.7	1.1	0.6	1.1	0.08	1.1	0.4	1.2	0.03	1.1	0.3
				DNVYYYDEEGGGEEDQDFDLSQLHR	3	99.6%	1																									
				DTANWLEINPDTGAISTR	2	100.0%	2																									
				GQVPENEANVVITTLK	2	100.0%	1																									
				ITYRIWRDTANWLEINPDTGAISTR	3	95.9%	1																									
				MALEVGDYK	2	100.0%	2																									
				NTGVISVVTTGLDR	2	100.0%	2																									
				VFYSITGQGADTPPVGVFIIER	2	99.9%	1																									
				YLPRPANPDEIGNFIDENLK	3	100.0%	1																									
IPI00025874	RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor	100.0%	10.8	5	5	5	1	22,853,027	23,797,290	22,770,498	25,835,025	2,490,563	1,610,072	1,237,628	732,417	24.4	15.1	12.2	6.3	1.0	0.8	-1.0	1	1.1	0.3	-1.0	0.6	1.1	0.3	1.1	0.07
				ATSFLLALEPELEAR	2	100.0%	1																									
				FVDHVFDEQVIDSLTVK	2	99.8%	1																									
				QPDSGISSIR	2	92.5%	1																									
				SEDLLDYGPFR	2	97.6%	1																									
				VTAEVVLAHLGGGSTSR	3	99.7%	1																									
IPI00025890	NAA25	isoform 1 of N-alpha-acetyltransferase 25, NatB auxiliary subunit	99.3%	4.8	2	2	2	1	5,493,729	5,772,492	6,011,515	6,170,317	360,348	598,714	406,224	529,619	14.7	23.2	15.1	19.2	1.1	0.7	1.1	0.4	1.1	0.3	1.0	0.7	1.1	0.6	1.0	0.8
				LEELILEDTSLSPEERK	3	91.5%	1																									
				QEEAFTLAQEVAALEPTDDNSLQALTILYR	3	92.3%	1																									
IPI00025974	CHMP4B	Charged multivesicular body protein 4b	100.0%	27.7	6	6	10	1	80,164,553	82,599,076	74,080,389	93,259,597	7,377,642	6,548,420	5,681,359	3,853,164	20.6	17.7	17.2	9.2	1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.4	1.1	0.2	1.3	0.02
				EALENANTNTEVLK	2	100.0%	2																									
				GGPTPQEAIQR	2	100.0%	2																									
				KIEQELTAAK	2	100.0%	2																									
				KIEQELTAAKK	2	95.6%	1																									
				LRDTEEMLSK	3	99.6%	1																									
				QLAQIDGTLSTIEFQR	2	100.0%	2																									
IPI00026087	BANF1	Barrier-to-autointegration factor	100.0%	48.3	3	4	5	1	22,766,215	28,920,549	22,872,976	33,384,270	5,044,822	3,667,134	2,289,224	2,478,035	49.6	28.4	22.4	16.6	1.3	0.4	1.0	1	1.5	0.1	-1.3	0.2	1.2	0.3	1.5	0.01
				AYVVLGQFLVLK	2	100.0%	2																									
				DFVAEPMGEKPVGSLAGIGEVLGK	2	100.0%	1																									
				DFVAEPMGEKPVGSLAGIGEVLGK	3	100.0%	1																									
				KDEDLFR	2	99.8%	1																									
IPI00026089	SF3B1	Splicing factor 3B subunit 1	99.9%	2.4	2	2	2	1	1,420,120	1,335,861	1,532,026	1,434,595	124,125	108,815	179,402	48,925	19.5	18.2	26.2	7.6	-1.1	0.6	1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.4	-1.1	0.6
				AFAVVASALGIPSLLPFLK	2	98.9%	1																									
				VPELNVQNGVLK	2	99.1%	1																									
IPI00026105	SCP2	isoform SCPx of Non-specific lipid-transfer protein	100.0%	16.8	9	9	11	3	8,968,856	8,784,782	9,175,901	10,413,621	894,950	305,615	649,467	467,665	22.3	7.8	15.8	10.0	-1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.6	1.2	0.02	1.1	0.2
IPI00479510	SCP2	non-specific lipid-transfer protein isoform 7 proprotein	100.0%	17.6	9	9	11	3	8,968,856	8,784,782	9,175,901	10,413,621	894,950	305,615	649,467	467,665	22.3	7.8	15.8	10.0	-1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.6	1.2	0.02	1.1	0.2
IPI00973807	SCP2	non-specific lipid-transfer protein isoform 6 proprotein	100.0%	18.3	9	9	11	3	8,968,856	8,784,782	9,175,901	10,413,621	894,950	305,615	649,467	467,665	22.3	7.8	15.8	10.0	-1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.6	1.2	0.02	1.1	0.2
				ADCTITMADSDFLALMTGK	2	100.0%	1																									
				AVEILAQEMMTDLPSSFEEK	3	87.9%	1																									
				EATWVVDVK	2	99.9%	2																									
				IGGIFAFK	2	100.0%	1																									
				KLEEEGEQFVK	2	100.0%	2																									

				KLEEEGEQFVKK	2	100.0%	1																									
				LQNLQLQPGNAK	2	100.0%	1																									
				LQNLQLQPGNAKL	2	99.5%	1																									
				MNPQSAFFQGK	2	99.4%	1																									
IPI00026154	PRKCSH	cDNA FLJ59211, highly similar to Glucosidase 2 subunit beta	100.0%	21.5	10	11	18	2	35,753,713	38,173,852	35,073,388	41,489,042	4,104,313	2,073,873	2,750,285	1,359,322	25.7	12.2	17.5	7.3	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.2	1.2	0.07
IPI00792916	PRKCSH	glucosidase 2 subunit beta isoform 2	100.0%	21.9	10	11	18	2	35,753,713	38,173,852	35,073,388	41,489,042	4,104,313	2,073,873	2,750,285	1,359,322	25.7	12.2	17.5	7.3	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.2	1.2	0.07
				AQQEQELAADAFK	2	100.0%	2																									
				ETMVTSTTEPSR	2	100.0%	3																									
				ILIEDWK	2	87.9%	1																									
				LGGSPTSLGTWGSWIGPDHDKFSAMK	3	100.0%	1																									
				LIELQAGKK	2	95.6%	1																									
				LLCGKETMVTSTTEPSR	2	95.3%	1																									
				LWEEQLAAAK	2	100.0%	2																									
				SLEDQVEMLR	2	100.0%	2																									
				SLKDMEESIR	2	99.8%	2																									
				SLKDMEESIR	3	93.5%	1																									
				YEQGTGCWQGPNR	2	100.0%	2																									
IPI00026167	NHP2L1	NHP2-like protein 1	100.0%	18.8	2	2	4	2	8,825,315	9,169,610	8,529,810	10,054,070	727,602	309,420	665,514	329,833	18.4	7.6	17.5	7.3	1.0	0.7	-1.0	0.8	1.1	0.2	-1.1	0.4	1.1	0.09	1.2	0.07
IPI00893746	NHP2L1	NHP2 non-histone chromosome protein 2-like 1	100.0%	18.2	2	2	4	2	8,825,315	9,169,610	8,529,810	10,054,070	727,602	309,420	665,514	329,833	18.4	7.6	17.5	7.3	1.0	0.7	-1.0	0.8	1.1	0.2	-1.1	0.4	1.1	0.09	1.2	0.07
				LLDLVQQSCNYK	2	100.0%	2																									
				QQIQSIQQSIER	2	100.0%	2																									
IPI00026182	CAPZA2	F-actin-capping protein subunit alpha-2	100.0%	38.5	7	7	9	1	26,234,479	26,692,538	27,402,761	30,048,040	2,029,957	1,229,388	2,745,253	575,921	17.3	10.3	22.4	4.3	1.0	0.9	1.0	0.7	1.1	0.1	1.0	0.8	1.1	0.04	1.1	0.4
				DIQDSLTVSNEVQTAK	2	99.9%	1																									
				EATDPRPCEVENAVESWR	3	99.5%	1																									
				FIIHAPPGEFNEVFNDVR	3	100.0%	1																									
				FTITPSTTQVVGILK	2	100.0%	2																									
				IVEAAENEYQTAISENYQTMSDTTFK	3	90.3%	1																									
				LLLNNDNLLR	2	100.0%	2																									
				RQLPVTR	2	99.9%	1																									
IPI00026185	CAPZB	isoform 1 of F-actin-capping protein subunit beta	100.0%	37.6	10	10	14	1	11,651,369	11,892,177	11,217,532	13,978,073	747,525	453,484	774,824	224,141	14.4	8.5	15.5	3.6	1.0	0.8	-1.0	0.7	1.2	0.03	-1.1	0.5	1.2	0.003	1.2	0.02
				DYLLCDYNR	2	100.0%	2																									
				KLEVEANNAFDQYR	2	100.0%	1																									
				LEVEANNAFDQYR	2	100.0%	1																									
				LVEDMENK	2	99.7%	1																									
				QMEKDETVSDCSPHIANIGR	3	99.9%	1																									
				RLPPQQIEK	2	99.9%	2																									
				SGSGTMNLGGSLTR	2	100.0%	2																									
				SPWSNKYDPPLEDGAMPSAR	3	100.0%	1																									
				STLNEIYFGK	2	100.0%	2																									
				YDPPLEDGAMPSAR	2	98.2%	1																									
IPI00026215	FEN1	Flap endonuclease 1	100.0%	5.3	1	1	1	1	12,562,530	11,806,660	14,188,410	12,239,510	611,262	612,117	900,749	903,957	10.9	11.6	14.2	16.5	-1.1	0.4	1.1	0.2	-1.0	0.8	1.2	0.06	1.0	0.7	-1.2	0.2
				EAHQLFLEPEVLDPESVELK	3	99.9%	1																									
IPI00026216	NPEPPS	Puromycin-sensitive aminopeptidase	100.0%	16.7	11	11	11	2	24,214,868	24,598,507	24,049,111	26,946,920	2,063,675	1,108,249	2,062,427	390,294	19.1	10.1	19.2	3.2	1.0	0.9	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00978387	NPEPPS	Uncharacterized protein	100.0%	16.7	11	11	11	2	24,214,868	24,598,507	24,049,111	26,946,920	2,063,675	1,108,249	2,062,427	390,294	19.1	10.1	19.2	3.2	1.0	0.9	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.2
				DYFNVPYPLPK	2	100.0%	1																									
				HGDGTTLDIMLK	2	99.6%	1																									
				ILMDKPEMNVVLK	2	97.4%	1																									
				LGWDPKPGEGHLDALLR	3	98.7%	1																									
				LSVEGFAVDK	2	99.7%	1																									
				NAATEDLWESLENASGKPIAAVMNTWTK	3	99.9%	1																									
				SPVYLTVLK	2	98.7%	1																									
				TIQQCCENILLNAAWLK	2	100.0%	1																									
				TQYSSAMLESLLPGIR	2	98.5%	1																									
				VALSNMNVIDR	2	99.9%	1																									
				YQGGFLISR	2	99.8%	1																									
IPI00026230	HNRNPH2	Heterogeneous nuclear ribonucleoprotein H2	100.0%	26.1	8	9	12	1	48,724,542	53,169,295	47,094,015	57,119,409	3,958,006	2,597,388	3,177,268	1,826,170	18.2	10.9	15.1	7.2	1.1	0.4	-1.0	0.8	1.2	0.09	-1.1	0.2	1.1	0.2	1.2	0.03
				ATENDIYNFFSPLNPMR	2	100.0%	2																									
				DLNYCFSGMSDHR	2	99.8%	1																									
				DLNYCFSGMSDHR	3	98.8%	1																									
				GLPWSCSADEVMR	2	100.0%	2																									
				HTGPNSPDTANDGFVR	3	100.0%	1																									
				IQNGTSGIR	2	95.7%	1																									
				SNSVEMDWVLK	2	100.0%	1																									
				STGEAFVQFASQEIAEK	2	100.0%	2																									
				VTGEADVEFATHEDAVAAMAK	3	97.6%	1																									
IPI00026260	NME1	isoform 1 of Nucleoside diphosphate kinase B	100.0%	40.1	4	4	8	1	4,091,507	3,947,831	4,414,581	4,646,319	379,079	302,751	328,440	148,194	20.7	17.2	16.6	7.1	-1.0	0.8	1.1	0.5	1.1	0.2	1.1	0.3	1.2	0.07	1.1	0.5
				EISLWFKPEELVDYK	2	100.0%	2																									
				NIIHGSDSVK	1	100.0%	1																									
				VMLGETNPADSKPGTIR	2	100.0%	2																									
				YMNSGPVVAMVWEGLNVVK	2	100.0%	3																									
IPI00026268	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	100.0%	30.3	8	9	12	1	33,602,976	33,132,893	32,930,042	38,859,504	2,759,401	806,833	1,684,441	1,225,057	18.4	5.5	11.4	7.1	-1.0	0.9	-1.0	0.8	1.2	0.1	-1.0	0.9	1.2	0.005	1.2	0.02
				ACADATLSQITNNIDPVGR	2	99.6%	1																									
				AGVLAGHDNR	2	100.0%	1																									
				IYAMHWGTDSR	2	100.0%	1																									
				KACADATLSQITNNIDPVGR	3	100.0%	1																									
				LIIWDSYTTNK	2	100.0%	2																									
				LLLAGYDDFNCNVWDALK	2	100.0%	2																									
				LLVSASQDGK	2	93.5%	1																									
				VSCLGVTDDGMAVATGSWDSFLK	2	100.0%	2																									
				VSCLGVTDDGMAVATGSWDSFLK	3	100.0%	1																									
IPI00026271	RPS14	40S ribosomal protein S14	100.0%	29.1	3	4	5	1	10,608,110	11,525,750	10,621,410	12,194,263	702,409	704,311	771,744	522,643	14.8	13.7	16.3	9.6	1.1	0.4	1.0	1	1.1	0.1	-1.1	0.4	1.1	0.5	1.1	0.1
				ADRDESSPYAAMLAAQDVAQR	3	99.9%	1																									
				ELGITALHIK	2	99.0%	1																									
				ELGITALHIK	3	99.8%	1																									
				IEDVTPIPSDSTR	2	100.0%	2																									
IPI00741894	LOC730429	e3 ubiquitin-protein ligase UBR5-like isoform 1, partial	98.6%	1.1	2	2	2	4	920,230	1,045,081	1,134,820	1,066,766	51,833	87,954	84,709	46,264	12.6	18.8	16.7	9.7	1.1	0.3	1.2	0.06	1.2	0.07	1.1	0.5	1.0	0.8	-1.1	0.5
IPI00026320	UBR5	E3 ubiquitin-protein ligase UBR5	98.6%	1.1	2	2	2	4	920,230	1,045,081	1,134,820	1,066,766	51,833	87,954	84,709	46,264	12.6	18.8	16.7	9.7	1.1	0.3	1.2	0.06	1.2	0.07	1.1	0.5	1.0	0.8	-1.1	0.5
IPI00976576	UBR5	309 kDa protein	98.6%	1.1	2	2	2	4	920,230	1,045,081	1,134,820	1,066,766	51,833	87,954	84,709	46,264	12.6	18.8	16.7	9.7	1.1	0.3	1.2	0.06	1.2	0.07	1.1	0.5	1.0	0.8	-1.1	0.5
IPI00983716	UBR5	Uncharacterized protein	98.6%	1.1	2	2	2	4	920,230	1,045,081	1,134,820	1,066,766	51,833	87,954	84,709	46,264	12.6	18.8	16.7	9.7	1.1	0.3	1.2	0.06	1.2	0.07	1.1	0.5	1.0	0.8	-1.1	0.5
				MLVVAEQPLHAMRK	2	86.8%	1																									
				NILHACVSVCFPTSNK	3	90.4%	1																									
IPI00026328	TXNDC12	Thioredoxin domain-containing protein 12	99.6%	22.1	3	3	3	1	21,870,370	23,528,120	21,841,990	24,231,220	910,316	613,350	1,311,252	500,902	9.3	5.8	13.4	4.6	1.1	0.2	-1.0	1	1.1	0.05	-1.1	0.3	1.0	0.4	1.1	0.1
				GFGDHIHWR	2	92.3%	1																									
				VHPEIINENGNPSYK	3	98.5%	1																									
				YFYVSAEQVVQGMK	2	99.6%	1																									
IPI00026496	NPM3	Nucleoplasmin-3	97.5%	11.8	1	1	1	1	3,089,100	2,937,660	3,115,740	3,345,780	435,087	140,617	370,841	248,697	31.5	10.7	26.6	16.6	-1.1	0.8	1.0	1	1.1	0.6	1.1	0.7	1.1	0.2	1.1	0.6
				VPAPVTMDSFFFGCELSGHTR	3	97.5%	1																									
IPI00026513	RPIA	Ribose-5-phosphate isomerase	100.0%	10.3	2	2	2	1	17,681,315	23,361,430	18,129,090	21,661,430	2,719,757	3,944,598	1,611,271	1,437,314	34.4	37.8	19.9	14.8	1.3	0.3	1.0	0.9	1.2	0.2	-1.3	0.3	-1.1	0.7	1.2	0.1
				NNQVLGIGSGSTIVHAVQR	3	97.8%	1																									
				VYFGMQDGSVNMR	2	99.7%	1																									
IPI00026519	PPIF	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	100.0%	18.4	2	2	2	2	3,709,420	3,713,935	3,512,770	4,120,395	198,553	143,889	255,553	322,865	12.0	8.7	16.3	17.5	1.0	1	-1.1	0.6	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.2
IPI00657779	PPIF	Peptidyl-prolyl cis-trans isomerase	100.0%	24.5	2	2	2	2	3,709,420	3,713,935	3,512,770	4,120,395	198,553	143,889	255,553	322,865	12.0	8.7	16.3	17.5	1.0	1	-1.1	0.6	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.2
				FPDENFTLK	2	83.8%	1																									
				GSGDPSSSSSSGNPLVYLDVDANGKPLGR	3	100.0%	1																									
IPI00026530	LMAN1	Protein ERGIC-53	98.7%	2.0	1	1	1	1	3,838,110	3,597,270	4,516,730	4,585,730	617,795	368,352	929,121	389,741	36.0	22.9	46.0	19.0	-1.1	0.7	1.2	0.6	1.2	0.3	1.3	0.4	1.3	0.1	1.0	0.9
				QLDMILDEQR	2	98.7%	1																									
IPI00026546	PAFAH1B2	Platelet-activating factor acetylhydrolase IB subunit beta	100.0%	28.0	5	7	7	1	11,010,685	10,373,140	11,563,985	12,169,177	980,936	533,499	846,196	575,373	19.9	11.5	16.4	10.6	-1.1	0.6	1.1	0.7	1.1	0.3	1.1	0.3	1.2	0.05	1.1	0.6
				DKEPDVLFVGDSMVQLMQQYEIWR	3	100.0%	1																									
				ELFSPLHALNFGIGGDTTR	2	100.0%	1																									
				ELFSPLHALNFGIGGDTTR	3	99.9%	1																									
				IIVLGLLPR	2	100.0%	1																									
				LKNGELENIKPK	2	99.7%	1																									
				LKNGELENIKPK	3	99.9%	1																									
				NGELENIKPK	2	99.0%	1																									
IPI00026570	COX7A2	cytochrome c oxidase subunit 7A2, mitochondrial precursor	99.3%	11.3	1	1	1	4	1,517,348	1,644,728	1,474,385	1,739,375	167,971	77,035	100,415	83,591	24.8	10.5	15.2	10.8	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.2	1.1	0.4	1.2	0.08
IPI00964894	COX7A2	Uncharacterized protein	99.3%	14.3	1	1	1	4	1,517,348	1,644,728	1,474,385	1,739,375	167,971	77,035	100,415	83,591	24.8	10.5	15.2	10.8	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.2	1.1	0.4	1.2	0.08
IPI00966054	COX7A2	Uncharacterized protein	99.3%	12.6	1	1	1	4	1,517,348	1,644,728	1,474,385	1,739,375	167,971	77,035	100,415	83,591	24.8	10.5	15.2	10.8	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.2	1.1	0.4	1.2	0.08
IPI01014268	COX7A2	Cytochrome c oxidase subunit 7A2, mitochondrial	99.3%	15.7	1	1	1	4	1,517,348	1,644,728	1,474,385	1,739,375	167,971	77,035	100,415	83,591	24.8	10.5	15.2	10.8	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.2	1.1	0.4	1.2	0.08
				LFQEDDEIPLYLK	2	99.3%	1																									
IPI00026625	NUP155	isoform 1 of Nuclear pore complex protein Nup155	100.0%	3.0	3	3	3	4	18,768,588	19,140,495	17,603,458	21,293,293	1,795,389	712,087	1,219,462	903,333	21.4	8.3	15.5	9.5	1.0	0.9	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00376609	NUP155	isoform 2 of Nuclear pore complex protein Nup155	100.0%	3.2	3	3	3	4	18,768,588	19,140,495	17,603,458	21,293,293	1,795,389	712,087	1,219,462	903,333	21.4	8.3	15.5	9.5	1.0	0.9	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00965680	NUP155	Uncharacterized protein	100.0%	3.2	3	3	3	4	18,768,588	19,140,495	17,603,458	21,293,293	1,795,389	712,087	1,219,462	903,333	21.4	8.3	15.5	9.5	1.0	0.9	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI01012167	NUP155	cDNA FLJ56637, highly similar to Nuclear pore complex protein Nup155	100.0%	3.1	3	3	3	4	18,768,588	19,140,495	17,603,458	21,293,293	1,795,389	712,087	1,219,462	903,333	21.4	8.3	15.5	9.5	1.0	0.9	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
				GVIQVYDLGQDGQGMSR	2	99.6%	1																									
				IMGNIWDASLVVER	2	98.3%	1																									
				IQLQIQETLQR	2	99.2%	1																									
IPI00026670	TCEB2	Transcription elongation factor B polypeptide 2	99.8%	21.2	1	1	1	3	903,360	956,270	976,103	948,157	125,439	82,517	110,735	86,079	31.1	19.3	25.4	20.3	1.1	0.7	1.1	0.7	1.0	0.8	1.0	0.9	-1.0	0.9	-1.0	0.8
IPI00410162	TCEB2	transcription elongation factor B polypeptide 2 isoform b	99.8%	15.5	1	1	1	3	903,360	956,270	976,103	948,157	125,439	82,517	110,735	86,079	31.1	19.3	25.4	20.3	1.1	0.7	1.1	0.7	1.0	0.8	1.0	0.9	-1.0	0.9	-1.0	0.8
IPI00917694	TCEB2	Uncharacterized protein	99.8%	22.1	1	1	1	3	903,360	956,270	976,103	948,157	125,439	82,517	110,735	86,079	31.1	19.3	25.4	20.3	1.1	0.7	1.1	0.7	1.0	0.8	1.0	0.9	-1.0	0.9	-1.0	0.8
				TLGECGFTSQTARPQAPATVGLAFR	3	99.6%	1																									
IPI00026689	CDK1	Putative uncharacterized protein DKFZp686L20222	98.1%	4.0	1	1	1	3	1,927,867	2,165,227	1,909,987	2,194,900	187,390	203,534	61,678	160,846	21.7	21.0	7.2	16.4	1.1	0.4	-1.0	0.9	1.1	0.3	-1.1	0.3	1.0	0.9	1.1	0.2
IPI00073536	CDK1	isoform 2 of Cyclin-dependent kinase 1	98.1%	5.0	1	1	1	3	1,927,867	2,165,227	1,909,987	2,194,900	187,390	203,534	61,678	160,846	21.7	21.0	7.2	16.4	1.1	0.4	-1.0	0.9	1.1	0.3	-1.1	0.3	1.0	0.9	1.1	0.2
IPI00955014	CDK1	cyclin-dependent kinase 1 isoform 1	98.1%	4.0	1	1	1	3	1,927,867	2,165,227	1,909,987	2,194,900	187,390	203,534	61,678	160,846	21.7	21.0	7.2	16.4	1.1	0.4	-1.0	0.9	1.1	0.3	-1.1	0.3	1.0	0.9	1.1	0.2
				NLDENGLDLLSK	2	97.6%	1																									
IPI00026781	FASN	Fatty acid synthase	100.0%	22.0	38	40	44	1	297,688,825	301,036,426	297,116,414	338,094,366	########	9,145,288	########	7,798,900	14.9	6.8	11.4	5.2	1.0	0.9	-1.0	1	1.1	0.1	-1.0	0.8	1.1	0.02	1.1	0.04
				ACLDTAVENMPSLK	2	99.9%	1																									
				AFEVSENGNLVVSGK	2	100.0%	1																									
				ALGLGVEQLPVVFEDVVLHQATILPK	3	100.0%	1																									
				DLVEAVAHILGIR	2	100.0%	1																									
				DLVEAVAHILGIR	3	100.0%	1																									
				DNLEFFLAGIGR	2	100.0%	1																									
				DTVTISGPQAPVFEFVEQLRK	3	98.6%	1																									
				EDGLAQQQTQLNLR	2	100.0%	1																									
				EQGVTFPSGDIQEQLIR	2	97.6%	1																									
				GILADEDSSRPVWLK	2	100.0%	1																									
				GLVQALQTK	2	98.1%	1																									
				GNAGQSNYGFANSAMER	2	100.0%	1																									

				GVDLVLNSLAEEK	2	100.0%	1																									
				GYDYGPHFQGILEASLEGDSGR	3	99.9%	1																									
				HGLYLPTR	2	99.9%	1																									
				IPGLLSPHPLLQLSYTATDR	3	100.0%	1																									
				KLQELSSK	2	98.5%	1																									
				LGMLSPEGTCK	2	98.9%	1																									
				LHLSGIDANPNALFPPVEFPAPR	3	100.0%	1																									
				LPESENLQEFWDNLIGGVDMVTDDDRR	3	100.0%	2																									
				LQVVDQPLPVR	2	100.0%	2																									
				MVVPGLDGAQIPR	2	99.8%	1																									
				QAHTMDPQLR	2	99.6%	1																									
				QEPLLIGSTK	2	92.9%	1																									
				QGVQVQVSTSNISSLEGAR	2	100.0%	2																									
				QQEQQVPILEK	2	94.2%	1																									
				QVQPEGPYR	2	99.9%	1																									
				RPTPQDSPIFLPVDDTSFR	3	93.7%	1																									
				SEGVVAVLLTK	2	100.0%	1																									
				SNMGHPEPASGLAALAK	3	95.4%	1																									
				TLLEGSGLESIISIIHSSLAEPR	3	100.0%	2																									
				VAAAVDLIIK	2	100.0%	1																									
				VGDPQELNGITR	2	100.0%	1																									
				VLFPATGYLSIVWK	2	100.0%	1																									
				VLQGDLVMNVYR	2	100.0%	1																									
				VSVHVIEGDHR	2	98.6%	1																									
				VSVHVIEGDHR	3	99.9%	1																									
				VYQWDDPDPR	2	100.0%	1																									
				WLSTSIPEAQWHSSLAR	3	100.0%	1																									
				YSGTLNLDR	2	98.9%	1																									
IPI00026813	FNTA	Farnesyltransferase, CAAX box, alpha, isoform CRA_a	100.0%	5.9	2	2	2	4	1,112,393	1,235,139	1,079,388	1,166,477	130,884	112,086	87,639	51,020	26.3	20.3	18.2	9.8	1.1	0.5	-1.0	0.8	1.0	0.7	-1.1	0.3	-1.1	0.6	1.1	0.4
IPI00607601	FNTA	isoform 2 of Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alp	100.0%	8.7	2	2	2	4	1,112,393	1,235,139	1,079,388	1,166,477	130,884	112,086	87,639	51,020	26.3	20.3	18.2	9.8	1.1	0.5	-1.0	0.8	1.0	0.7	-1.1	0.3	-1.1	0.6	1.1	0.4
IPI00789666	FNTA	26 kDa protein	100.0%	12.6	2	2	2	4	1,112,393	1,235,139	1,079,388	1,166,477	130,884	112,086	87,639	51,020	26.3	20.3	18.2	9.8	1.1	0.5	-1.0	0.8	1.0	0.7	-1.1	0.3	-1.1	0.6	1.1	0.4
IPI00976845	FNTA	Uncharacterized protein	100.0%	10.8	2	2	2	4	1,112,393	1,235,139	1,079,388	1,166,477	130,884	112,086	87,639	51,020	26.3	20.3	18.2	9.8	1.1	0.5	-1.0	0.8	1.0	0.7	-1.1	0.3	-1.1	0.6	1.1	0.4
				LWDNELQYVDQLLK	2	96.7%	1																									
				YFVISNTTGYNDR	2	99.2%	1																									
IPI00026833	ADSS	Adenylosuccinate synthetase isozyme 2	100.0%	5.5	2	2	2	2	6,237,320	5,684,830	7,283,660	6,139,105	375,029	359,003	313,171	355,433	13.4	14.1	9.6	13.0	-1.1	0.3	1.2	0.06	-1.0	0.9	1.3	0.01	1.1	0.4	-1.2	0.04
IPI00641992	ADSS	Adenylosuccinate synthetase	100.0%	5.8	2	2	2	2	6,237,320	5,684,830	7,283,660	6,139,105	375,029	359,003	313,171	355,433	13.4	14.1	9.6	13.0	-1.1	0.3	1.2	0.06	-1.0	0.9	1.3	0.01	1.1	0.4	-1.2	0.04
				ELPVNAQNYVR	2	97.5%	1																									
				MCDLVSDFDGFSER	2	100.0%	1																									
IPI00026848	LRPAP1	Alpha-2-macroglobulin receptor-associated protein	99.7%	10.6	2	2	2	1	29,610,696	29,739,940	27,752,090	33,256,320	1,660,490	2,029,451	2,060,233	1,594,392	12.5	15.3	16.6	10.7	1.0	1	-1.1	0.5	1.1	0.2	-1.1	0.5	1.1	0.2	1.2	0.07
				QVTSNSLSGTQEDGLDDPRLEK	3	99.3%	1																									
				VSHQGYSTEAEFEEPR	3	95.3%	1																									
IPI00026940	NUP50	isoform 1 of Nuclear pore complex protein Nup50	99.1%	2.8	1	1	1	3	1,955,410	2,306,027	1,910,423	2,364,347	292,079	154,169	182,259	216,229	33.4	15.0	21.3	20.5	1.2	0.3	-1.0	0.9	1.2	0.3	-1.2	0.1	1.0	0.8	1.2	0.1
IPI00170581	NUP50	isoform 2 of Nuclear pore complex protein Nup50	99.1%	3.0	1	1	1	3	1,955,410	2,306,027	1,910,423	2,364,347	292,079	154,169	182,259	216,229	33.4	15.0	21.3	20.5	1.2	0.3	-1.0	0.9	1.2	0.3	-1.2	0.1	1.0	0.8	1.2	0.1
IPI00889717	NUP50	Uncharacterized protein	99.1%	5.3	1	1	1	3	1,955,410	2,306,027	1,910,423	2,364,347	292,079	154,169	182,259	216,229	33.4	15.0	21.3	20.5	1.2	0.3	-1.0	0.9	1.2	0.3	-1.2	0.1	1.0	0.8	1.2	0.1
				NVGFESDTGGAFK	2	99.1%	1																									
IPI00026942	ERLIN2	isoform 1 of Erlin-2	100.0%	13.9	3	3	4	2	4,441,830	4,880,186	4,950,524	5,572,186	615,817	394,858	467,427	189,638	31.0	18.1	21.1	7.6	1.1	0.6	1.1	0.5	1.3	0.1	1.0	0.9	1.1	0.2	1.1	0.3
IPI01011577	ERLIN2	Uncharacterized protein	100.0%	13.9	3	3	4	2	4,441,830	4,880,186	4,950,524	5,572,186	615,817	394,858	467,427	189,638	31.0	18.1	21.1	7.6	1.1	0.6	1.1	0.5	1.3	0.1	1.0	0.9	1.1	0.2	1.1	0.3
				DIPNMFMDSAGSVSK	2	99.7%	2																									
				ISEIEDAAFLAR	2	94.3%	1																									
				LALQQDLTSMAPGLVIQAVR	2	100.0%	1																									
IPI00026952	PKP3	Plakophilin-3	100.0%	10.4	6	6	6	1	23,411,657	25,333,900	22,462,332	26,241,223	1,197,094	1,289,532	1,077,940	1,440,253	11.4	11.4	10.7	12.3	1.1	0.3	-1.0	0.6	1.1	0.2	-1.1	0.1	1.0	0.7	1.2	0.07
				GVGGAVPGAVLEPVAR	2	100.0%	1																									
				LALVEENGIFELLR	2	100.0%	1																									
				LFNHANQEVQR	3	97.6%	1																									
				LSSGFDDIDLPSAVK	2	99.9%	1																									
				SVENAVCVLR	2	99.7%	1																									
				YSLVSEQLEPAATSTYR	2	96.3%	1																									
IPI00889196	UQCRFS1P1	Putative cytochrome b-c1 complex subunit Rieske-like protein 1	94.0%	2.8	1	1	1	2	4,605,280	4,414,010	4,673,170	5,348,705	425,295	335,688	298,149	340,333	20.7	17.0	14.3	14.2	-1.0	0.7	1.0	0.9	1.2	0.2	1.1	0.6	1.2	0.09	1.1	0.2
IPI00026964	UQCRFS1	Cytochrome b-c1 complex subunit Rieske, mitochondrial	94.0%	2.9	1	1	1	2	4,605,280	4,414,010	4,673,170	5,348,705	425,295	335,688	298,149	340,333	20.7	17.0	14.3	14.2	-1.0	0.7	1.0	0.9	1.2	0.2	1.1	0.6	1.2	0.09	1.1	0.2
				VPDFSEYR	2	94.0%	1																									
IPI00026970	SUPT16H	FACT complex subunit SPT16	99.3%	1.2	1	1	1	1	3,989,830	4,241,940	3,941,780	4,802,460	337,604	116,955	188,562	332,347	18.9	6.2	10.7	15.5	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.05
				YTEGVQSLNWTK	2	99.3%	1																									
IPI00027009	PACSIN2	isoform 1 of Protein kinase C and casein kinase substrate in neurons protein 2	100.0%	12.4	5	5	6	2	17,005,220	16,423,255	16,971,490	18,472,555	1,741,232	571,615	926,970	634,691	22.9	7.8	12.2	7.7	-1.0	0.8	-1.0	1	1.1	0.5	1.0	0.6	1.1	0.04	1.1	0.2
IPI00221111	PACSIN2	isoform 2 of Protein kinase C and casein kinase substrate in neurons protein 2	100.0%	13.5	5	5	6	2	17,005,220	16,423,255	16,971,490	18,472,555	1,741,232	571,615	926,970	634,691	22.9	7.8	12.2	7.7	-1.0	0.8	-1.0	1	1.1	0.5	1.0	0.6	1.1	0.04	1.1	0.2
				AGDELTKMEDEDEQGWCK	3	90.1%	1																									
				AIYHDLEQSIR	2	99.1%	1																									
				AWMAFMSEAER	2	99.4%	1																									
				HLDLSNVAGYK	2	100.0%	2																									
				VSELHLEVK	2	87.4%	1																									
IPI00027032	LYPLA2	Acyl-protein thioesterase 2	100.0%	33.3	4	4	4	1	5,995,985	5,981,275	5,759,421	6,697,165	758,243	179,249	593,746	207,442	28.3	6.7	23.1	6.9	-1.0	1	-1.0	0.8	1.1	0.4	-1.0	0.7	1.1	0.03	1.2	0.2
				DLAILQCHGELDPMVPVR	3	100.0%	1																									
				ETAAVIFLHGLGDTGHSWADALSTIR	3	89.0%	1																									
				IPVTLNMK	2	99.6%	1																									
				MVMPSWFDLMGLSPDAPEDEAGIKK	3	100.0%	1																									
IPI00027078	CPD	Carboxypeptidase D	100.0%	2.6	3	3	3	1	9,189,631	9,525,355	7,529,393	11,475,202	922,555	675,043	689,472	861,687	22.5	15.9	20.5	16.8	1.0	0.8	-1.2	0.2	1.2	0.1	-1.3	0.07	1.2	0.1	1.5	0.007
				EAAAAGLPGLAR	2	88.8%	1																									
				ELLLNLIEYLCK	2	99.9%	1																									
				SQEGDSISVIGR	2	98.1%	1																									
IPI00027082	EPN1	isoform 1 of Epsin-1	100.0%	4.0	1	2	2	4	2,927,360	2,825,543	2,924,840	3,378,685	219,670	132,556	266,384	163,207	16.8	10.5	20.4	10.8	-1.0	0.7	-1.0	1	1.2	0.1	1.0	0.7	1.2	0.03	1.2	0.2
IPI00397365	EPN1	isoform 3 of Epsin-1	100.0%	4.2	1	2	2	4	2,927,360	2,825,543	2,924,840	3,378,685	219,670	132,556	266,384	163,207	16.8	10.5	20.4	10.8	-1.0	0.7	-1.0	1	1.2	0.1	1.0	0.7	1.2	0.03	1.2	0.2
IPI00647389	EPN1	isoform 2 of Epsin-1	100.0%	3.5	1	2	2	4	2,927,360	2,825,543	2,924,840	3,378,685	219,670	132,556	266,384	163,207	16.8	10.5	20.4	10.8	-1.0	0.7	-1.0	1	1.2	0.1	1.0	0.7	1.2	0.03	1.2	0.2
IPI01011997	EPN1	cDNA FLJ55368, highly similar to Epsin-1	100.0%	4.3	1	2	2	4	2,927,360	2,825,543	2,924,840	3,378,685	219,670	132,556	266,384	163,207	16.8	10.5	20.4	10.8	-1.0	0.7	-1.0	1	1.2	0.1	1.0	0.7	1.2	0.03	1.2	0.2
				TALPTSGSSAGELELLAGEVPAR	2	100.0%	1																									
				TALPTSGSSAGELELLAGEVPAR	3	100.0%	1																									
IPI00027107	TUFM	elongation factor Tu, mitochondrial precursor	100.0%	12.5	4	4	4	1	29,872,790	29,995,610	30,646,760	33,862,960	2,337,312	1,247,081	1,818,345	1,548,067	17.5	9.3	13.3	10.2	1.0	1	1.0	0.8	1.1	0.2	1.0	0.8	1.1	0.09	1.1	0.2
				AEAGDNLGALVR	2	99.9%	1																									
				GTVVTGTLER	2	92.9%	1																									
				IILPPEKELAMPGEDLK	3	95.2%	1																									
				TIGTGLVTNTLAMTEEEK	2	100.0%	1																									
IPI00027139	INPP1	Inositol polyphosphate 1-phosphatase	99.5%	3.0	1	1	1	8	562,833	659,171	585,693	656,398	38,348	74,774	39,939	30,522	15.2	25.4	15.3	10.4	1.2	0.3	1.0	0.7	1.2	0.09	-1.1	0.4	-1.0	1	1.1	0.2
IPI00916305	INPP1	Uncharacterized protein	99.5%	6.3	1	1	1	8	562,833	659,171	585,693	656,398	38,348	74,774	39,939	30,522	15.2	25.4	15.3	10.4	1.2	0.3	1.0	0.7	1.2	0.09	-1.1	0.4	-1.0	1	1.1	0.2
IPI00916784	INPP1	Uncharacterized protein	99.5%	8.4	1	1	1	8	562,833	659,171	585,693	656,398	38,348	74,774	39,939	30,522	15.2	25.4	15.3	10.4	1.2	0.3	1.0	0.7	1.2	0.09	-1.1	0.4	-1.0	1	1.1	0.2
IPI00916959	INPP1	Uncharacterized protein	99.5%	13.6	1	1	1	8	562,833	659,171	585,693	656,398	38,348	74,774	39,939	30,522	15.2	25.4	15.3	10.4	1.2	0.3	1.0	0.7	1.2	0.09	-1.1	0.4	-1.0	1	1.1	0.2
IPI00917132	INPP1	Uncharacterized protein	99.5%	7.7	1	1	1	8	562,833	659,171	585,693	656,398	38,348	74,774	39,939	30,522	15.2	25.4	15.3	10.4	1.2	0.3	1.0	0.7	1.2	0.09	-1.1	0.4	-1.0	1	1.1	0.2
IPI00917471	INPP1	Uncharacterized protein	99.5%	5.6	1	1	1	8	562,833	659,171	585,693	656,398	38,348	74,774	39,939	30,522	15.2	25.4	15.3	10.4	1.2	0.3	1.0	0.7	1.2	0.09	-1.1	0.4	-1.0	1	1.1	0.2
IPI00917637	INPP1	Uncharacterized protein	99.5%	5.7	1	1	1	8	562,833	659,171	585,693	656,398	38,348	74,774	39,939	30,522	15.2	25.4	15.3	10.4	1.2	0.3	1.0	0.7	1.2	0.09	-1.1	0.4	-1.0	1	1.1	0.2
IPI00917834	INPP1	Uncharacterized protein	99.5%	17.7	1	1	1	8	562,833	659,171	585,693	656,398	38,348	74,774	39,939	30,522	15.2	25.4	15.3	10.4	1.2	0.3	1.0	0.7	1.2	0.09	-1.1	0.4	-1.0	1	1.1	0.2
				TLADVLVQEVIK	2	99.5%	1																									
IPI00027146	GLUD2	Glutamate dehydrogenase 2, mitochondrial	100.0%	15.8	8	8	8	1	9,967,056	10,863,832	10,113,699	11,769,641	959,649	346,033	740,677	421,814	21.5	7.1	16.4	8.0	1.1	0.4	1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.09
				ALASLMTYK	2	99.8%	1																									
				DDGSWEVIEGYR	2	100.0%	1																									
				IIAEGANGPTTPEADKIFLER	3	100.0%	1																									
				MVEGFFDR	2	99.2%	1																									
				NLNHVSYGR	2	99.9%	1																									
				TAAYVNAIEK	2	99.7%	1																									
				YNLGLDLR	2	100.0%	1																									
				YSTDVSVDEVK	2	100.0%	1																									
IPI00027165	PKLR	isoform R-type of Pyruvate kinase isozymes R/L	95.8%	1.6	1	1	1	5	1,792,374	1,750,620	1,657,838	2,035,450	160,905	73,872	114,660	93,562	20.1	9.4	15.5	10.3	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.5	1.2	0.04	1.2	0.03
IPI00743713	PKLR	Pyruvate kinase	95.8%	1.5	1	1	1	5	1,792,374	1,750,620	1,657,838	2,035,450	160,905	73,872	114,660	93,562	20.1	9.4	15.5	10.3	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.5	1.2	0.04	1.2	0.03
IPI00871353	PKLR	Pyruvate kinase	95.8%	1.5	1	1	1	5	1,792,374	1,750,620	1,657,838	2,035,450	160,905	73,872	114,660	93,562	20.1	9.4	15.5	10.3	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.5	1.2	0.04	1.2	0.03
IPI00909829	PKLR	Pyruvate kinase	95.8%	1.8	1	1	1	5	1,792,374	1,750,620	1,657,838	2,035,450	160,905	73,872	114,660	93,562	20.1	9.4	15.5	10.3	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.5	1.2	0.04	1.2	0.03
IPI00941093	PKLR	isoform L-type of Pyruvate kinase isozymes R/L	95.8%	1.7	1	1	1	5	1,792,374	1,750,620	1,657,838	2,035,450	160,905	73,872	114,660	93,562	20.1	9.4	15.5	10.3	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.5	1.2	0.04	1.2	0.03
				VQFGIESGK	2	95.8%	1																									
IPI00027169	CIB2	cDNA FLJ59581, highly similar to Calcium and integrin-binding protein 2	98.3%	5.7	1	1	1	2	2,610,380	2,608,960	2,326,115	2,799,180	322,575	320,557	146,864	248,306	27.6	27.5	14.1	19.8	-1.0	1	-1.1	0.4	1.1	0.7	-1.1	0.4	1.1	0.7	1.2	0.1
IPI00797165	CIB2	Calcium and integrin binding family member 2, isoform CRA_a	98.3%	8.3	1	1	1	2	2,610,380	2,608,960	2,326,115	2,799,180	322,575	320,557	146,864	248,306	27.6	27.5	14.1	19.8	-1.0	1	-1.1	0.4	1.1	0.7	-1.1	0.4	1.1	0.7	1.2	0.1
				IYDFNTDNFICK	3	98.3%	1																									
IPI00027175	SRI	Sorcin	100.0%	43.4	8	8	9	3	19,785,460	20,685,730	21,863,937	24,015,587	1,342,726	537,681	980,710	884,507	15.2	5.8	10.0	8.2	1.0	0.6	1.1	0.2	1.2	0.03	1.1	0.3	1.2	0.01	1.1	0.1
IPI00946099	SRI	Uncharacterized protein	100.0%	55.5	8	8	9	3	19,785,460	20,685,730	21,863,937	24,015,587	1,342,726	537,681	980,710	884,507	15.2	5.8	10.0	8.2	1.0	0.6	1.1	0.2	1.2	0.03	1.1	0.3	1.2	0.01	1.1	0.1
IPI01013070	SRI	sorcin isoform b	100.0%	47.0	8	8	9	3	19,785,460	20,685,730	21,863,937	24,015,587	1,342,726	537,681	980,710	884,507	15.2	5.8	10.0	8.2	1.0	0.6	1.1	0.2	1.2	0.03	1.1	0.3	1.2	0.01	1.1	0.1
				DMSGTMGFNEFK	2	98.9%	1																									
				DTAQQGVVNFPYDDFIQCVMSV	2	90.1%	1																									
				ITFDDYIACCVK	2	100.0%	2																									
				LMVSMLDR	2	99.9%	1																									
				LMVSMLDRDMSGTMGFNEFK	3	99.9%	1																									
				LSPQAVNSIAK	2	99.9%	1																									
				QHFISFDTDR	3	99.8%	1																									
				SGTVDPQELQK	2	99.7%	1																									
IPI00027178	AP1G2	AP-1 complex subunit gamma-like 2	96.5%	0.8	1	1	1	3	3,977,120	4,519,773	3,515,480	4,362,333	221,142	549,983	147,027	196,449	12.4	27.2	9.4	10.1	1.1	0.4	-1.1	0.1	1.1	0.2	-1.3	0.1	-1.0	0.8	1.2	0.009
IPI00908750	AP1G2	AP1G2 protein	96.5%	0.9	1	1	1	3	3,977,120	4,519,773	3,515,480	4,362,333	221,142	549,983	147,027	196,449	12.4	27.2	9.4	10.1	1.1	0.4	-1.1	0.1	1.1	0.2	-1.3	0.1	-1.0	0.8	1.2	0.009
IPI01010653	AP1G2	cDNA FLJ56213, highly similar to Adapter-relatedprotein complex 1 gamma- 2 subu	96.5%	1.1	1	1	1	3	3,977,120	4,519,773	3,515,480	4,362,333	221,142	549,983	147,027	196,449	12.4	27.2	9.4	10.1	1.1	0.4	-1.1	0.1	1.1	0.2	-1.3	0.1	-1.0	0.8	1.2	0.009
				MPLVER	2	96.5%	1																									
IPI00981773	-	cDNA FLJ53377, highly similar to Procollagen-lysine, 2-oxoglutarate 5-dioxygenase	99.6%	3.9	2	2	2	3	2,058,348	1,867,097	2,179,559	1,908,265	135,400	120,922	103,129	137,173	14.7	14.5	10.6	16.1	-1.1	0.3	1.1	0.5	-1.1	0.5	1.2	0.08	1.0	0.8	-1.1	0.2
IPI00027192	PLOD1	cDNA, FLJ79184, highly similar to Procollagen-lysine, 2-oxoglutarate 5-dioxygenase	99.6%	3.5	2	2	2	3	2,058,348	1,867,097	2,179,559	1,908,265	135,400	120,922	103,129	137,173	14.7	14.5	10.6	16.1	-1.1	0.3	1.1	0.5	-1.1	0.5	1.2	0.08	1.0	0.8	-1.1	0.2
IPI00943008	PLOD1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	99.6%	3.7	2	2	2	3	2,058,348	1,867,097	2,179,559	1,908,265	135,400	120,922	103,129	137,173	14.7	14.5	10.6	16.1	-1.1	0.3	1.1	0.5	-1.1	0.5	1.2	0.08	1.0	0.8	-1.1	0.2
				FLLEYIAPMTEK	2	95.7%	1																									
				IFQNLDGALDEVVLK	2	99.6%	1																									
IPI00027193	CLIC5	isoform 2 of Chloride intracellular channel protein 5	100.0%	6.3	2	3	4	5	2,955,095	3,130,385	2,897,289	3,523,819	330,766	124,965	378,160	128,368	25.0	8.9	29.2	8.2	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.06	1.2	0.2
IPI00294443	CLIC5	isoform 1 of Chloride intracellular channel protein 5	100.0%	10.4	2	3	4	5	2,955,095	3,130,385	2,897,289	3,523,819	330,766	124,965	378,160	128,368	25.0	8.9	29.2	8.2	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.06	1.2	0.2
IPI00844301	CLIC5	cDNA, FLJ95199, highly similar to Homo sapiens chloride intracellular channel 5 (CL	100.0%	10.4	2	3	4	5	2,955,095	3,130,385	2,897,289	3,523,819	330,766	124,965	378,160	128,368	25.0	8.9	29.2	8.2	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.06	1.2	0.2
IPI00165936	CLIC6	isoform A of Chloride intracellular channel protein 6	100.0%	3.8	2	3	4	5	2,955,095	3,130,385	2,897,289	3,523,819	330,766	124,965	378,160	128,368	25.0	8.9	29.2	8.2	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.06	1.2	0.2
IPI00394749	CLIC6	isoform B of Chloride intracellular channel protein 6	100.0%	3.7	2	3	4	5	2,955,095	3,130,385	2,897,289	3,523,819	330,766	124,965	378,160	128,368	25.0	8.9	29.2	8.2	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.06	1.2	0.2
				FLDGDELTLADCNLLPK	2	99.4%	1																									
				FLDGDELTLADCNLLPK	3	99.6%	1																									
				IGNCPFSQR	2	100.0%	2																									
IPI00027201	MUC2	Mucin-2	96.2%	0.2	1	1	1	1	10,138,970	9,434,540	8,254,620	11,996,730	1,218,660	743,675	940,313	837,112	26.9	17.6	25.5	15.6	-1.1	0.6	-1.2	0.3	1.2	0.2	-1.1	0.4	1.3	0.05	1.5	0.02
				HETQEVLIK	2	95.0%	1																									
IPI00027223	IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	100.0%	55.3	19	23	33	1	136,330,038	134,286,751	139,377,670	153,987,574	########	4,526,866	########	4,036,133	23.1	7.5	17.3	5.9	-1.0	0.9	1.0	0.9	1.1	0.3	1.0	0.7	1.1	0.01	1.1	0.3

				ATDFVVPGPGK	2	100.0%	2																										
				CATITPDEKR	2	98.8%	1																										
				FKDIFQEIYDK	3	100.0%	1																										
				FKDIFQEIYDKQYK	3	99.7%	1																										
				GQETSTNPIASIFAWTR	2	99.9%	1																										
				HAYGDQYR	2	100.0%	1																										
				IIWELIK	2	96.9%	1																										
				ISGGSVVEMQGDEMTR	2	100.0%	3																										
				LIDDMVAQAMK	2	100.0%	2																										
				LIFPYVELDLHSYDLGIENR	2	100.0%	1																										
				LIFPYVELDLHSYDLGIENR	3	100.0%	2																										
				LVSGWVKPIIIGR	2	100.0%	2																										
				LVSGWVKPIIIGR	3	100.0%	1																										
				NILGGTVFR	2	99.3%	1																										
				SDYLNTFEFMDK	2	100.0%	2																										
				SDYLNTFEFMDKLGENLK	2	94.9%	1																										
				SDYLNTFEFMDKLGENLK	3	99.9%	1																										
				SEGGFIWACK	2	100.0%	1																										
				SIEDFAHSSFQMALSK	2	100.0%	2																										
				SIEDFAHSSFQMALSK	3	100.0%	1																										
				TVEAEAAHGTVTR	2	100.0%	2																										
				VEITYTPSDGTQK	2	100.0%	2																										
				VTYLVHNFEEGGGVAMGMYNQDK	3	100.0%	1																										
IPI00027230	HSP90B1	Endoplasmin	100.0%	44.0	32	38	51	1	291,605,415	288,700,450	285,652,768	330,366,547	########	########	########	9,154,673	17.2	7.8	16.5	6.2	-1.0	0.9	-1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.02	1.2	0.09
				DISTNYYASQK	2	100.0%	1																										
				EAESSPFVER	2	100.0%	1																										
				EAVEKEFEPLLNWMK	2	100.0%	2																										
				EAVEKEFEPLLNWMK	3	100.0%	2																										
				EEASDYLELDTIK	2	100.0%	2																										
				EGSRTDDEVVQREEEAIQLDGLNASQIR	3	100.0%	1																										
				EGVKFDESEKTK	2	99.8%	1																										
				ELISNASDALDK	2	99.9%	2																										
				ELISNASDALDKIR	2	100.0%	1																										
				FAFQAEVNR	2	100.0%	2																										
				GLFDEYGSK	2	100.0%	1																										
				GTTITLVLKEEASDYLELDTIK	3	93.9%	1																										
				GVVDSDDLPLNVSR	2	100.0%	2																										
				GYEVIYLTEPVDEYCIQALPEFDGKR	3	100.0%	1																										
				IADDKYNDTFWK	2	100.0%	1																										
				IADDKYNDTFWK	3	97.1%	1																										
				KEAESSPFVER	2	99.8%	1																										
				KYSQFINFPIYVWSSK	2	95.1%	1																										
				KYSQFINFPIYVWSSK	3	100.0%	1																										
				LGVIEDHSNR	2	100.0%	3																										
				LIINSLYK	2	99.5%	1																										
				LISLTDENALSGNEELTVK	2	100.0%	1																										
				LISLTDENALSGNEELTVK	3	100.0%	1																										
				LSLNIDPDAK	2	98.5%	1																										
				LTESPCALVASQYGWSGNMER	2	100.0%	1																										
				NLLHVTDTGVGMTR	2	100.0%	2																										
				NLLHVTDTGVGMTREELVK	3	99.8%	1																										
				RVFITDDFHDMMPK	3	100.0%	1																										
				SGTSEFLNK	2	100.0%	2																										
				SGYLLPDTK	2	100.0%	1																										
				SILFVPTSAPR	2	100.0%	2																										
				TDDEVVQREEEAIQLDGLNASQIR	2	98.9%	1																										
				TFEINPR	2	99.9%	2																										
				TVWDWELMNDIKPIWQR	3	99.3%	1																										
				VFITDDFHDMMPK	2	100.0%	1																										
				VFITDDFHDMMPK	3	99.9%	1																										
				YSQFINFPIYVWSSK	2	100.0%	2																										
				YSQFINFPIYVWSSK	3	100.0%	1																										
IPI00027252	PHB2	Prohibitin-2	100.0%	29.1	6	7	8	1	8,039,751	8,869,174	8,525,210	9,930,978	588,859	220,362	664,349	348,809	16.4	5.6	17.4	7.9	1.1	0.2	1.1	0.6	1.2	0.02	-1.0	0.6	1.1	0.03	1.2	0.1
				FNASQLITQR	2	99.9%	2																										
				IGGVQQDTILAEGLHFR	3	100.0%	1																										
				IPWFQYPIIYDIR	2	99.9%	1																										
				IVQAEGEAEAAK	2	100.0%	1																										
				IYLTADNLVLNLQDESFTR	2	100.0%	1																										
				IYLTADNLVLNLQDESFTR	3	100.0%	1																										
				VLSRPNAQELPSMYQR	3	95.0%	1																										
IPI00027255	MYL6B	Myosin light chain 6B	100.0%	14.4	3	3	4	1	16,496,960	16,910,308	15,575,770	17,889,060	1,073,155	984,073	1,121,413	738,815	14.6	13.0	16.1	9.2	1.0	0.8	-1.1	0.6	1.1	0.3	-1.1	0.4	1.1	0.4	1.1	0.1
				ALGQNPTNAEVLK	2	100.0%	2																										
				EAFELFDR	2	99.9%	1																										
				HVLTTLGEK	2	100.0%	1																										
IPI00027264	CALB2	Calretinin	100.0%	37.6	9	9	10	1	46,138,270	45,558,877	44,831,187	51,530,390	4,097,319	1,792,847	3,613,047	1,371,216	19.9	8.8	18.0	6.0	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.03	1.1	0.1
				ELENFFQELEK	2	99.9%	2																										
				EMNIQQLTNYR	2	100.0%	1																										
				HFDADGNGYIEGK	2	100.0%	1																										
				LGLSEMSR	2	99.0%	1																										
				LLPVQENFLLK	2	99.4%	1																										
				LQEYTQTILR	2	99.1%	1																										
				MFDLNGDGK	2	99.9%	1																										
				SGYIDEHELDALLKDLYEK	3	100.0%	1																										
				SGYIEANELK	2	96.6%	1																										
IPI00027285	SNRPB	isoform SM-B' of Small nuclear ribonucleoprotein-associated proteins B and B'	99.5%	10.0	2	2	2	7	1,374,847	1,370,459	1,415,637	1,633,443	94,184	63,903	94,564	137,995	15.3	10.4	14.9	18.9	-1.0	1	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.1	1.2	0.2
IPI00329512	SNRPB	isoform SM-B1 of Small nuclear ribonucleoprotein-associated proteins B and B'	99.5%	8.3	2	2	2	7	1,374,847	1,370,459	1,415,637	1,633,443	94,184	63,903	94,564	137,995	15.3	10.4	14.9	18.9	-1.0	1	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.1	1.2	0.2
IPI00384173	SNRPB	Small nuclear ribonucleoprotein B'	99.5%	9.9	2	2	2	7	1,374,847	1,370,459	1,415,637	1,633,443	94,184	63,903	94,564	137,995	15.3	10.4	14.9	18.9	-1.0	1	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.1	1.2	0.2
IPI00395674	SNRPB	isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B'	99.5%	10.4	2	2	2	7	1,374,847	1,370,459	1,415,637	1,633,443	94,184	63,903	94,564	137,995	15.3	10.4	14.9	18.9	-1.0	1	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.1	1.2	0.2
IPI00877103	SNRPB	Uncharacterized protein	99.5%	8.4	2	2	2	7	1,374,847	1,370,459	1,415,637	1,633,443	94,184	63,903	94,564	137,995	15.3	10.4	14.9	18.9	-1.0	1	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.1	1.2	0.2
IPI00220360	SNRPN	Small nuclear ribonucleoprotein-associated protein N	99.5%	10.0	2	2	2	7	1,374,847	1,370,459	1,415,637	1,633,443	94,184	63,903	94,564	137,995	15.3	10.4	14.9	18.9	-1.0	1	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.1	1.2	0.2
IPI00785142	SNRPN	cDNA FLJ41124 fis, clone BRACE2014850, highly similar to Small nuclear ribonucle	99.5%	9.8	2	2	2	7	1,374,847	1,370,459	1,415,637	1,633,443	94,184	63,903	94,564	137,995	15.3	10.4	14.9	18.9	-1.0	1	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.1	1.2	0.2
				GENLVSMTVEGPPPK	2	98.8%	1																										
				RVLGLVLLR	2	87.8%	1																										
IPI00027341	CAPG	Macrophage-capping protein	100.0%	25.3	8	9	12	2	24,177,673	23,845,932	21,257,532	26,380,205	2,686,629	1,482,024	1,551,399	2,057,612	24.9	13.9	16.3	17.4	-1.0	0.9	-1.1	0.4	1.1	0.5	-1.1	0.3	1.1	0.3	1.2	0.08
IPI00908511	CAPG	cDNA FLJ51488, highly similar to Macrophage capping protein	100.0%	26.9	8	9	12	2	24,177,673	23,845,932	21,257,532	26,380,205	2,686,629	1,482,024	1,551,399	2,057,612	24.9	13.9	16.3	17.4	-1.0	0.9	-1.1	0.4	1.1	0.5	-1.1	0.3	1.1	0.3	1.2	0.08
				ANAQAAALYK	2	99.5%	1																										
				AQVEIVTDGEEPAEMIQVLGPK	2	99.7%	1																										
				DLALAIR	2	95.0%	1																										
				EGNPEEDLTADK	2	99.9%	1																										
				EGNPEEDLTADKANAQAAALYK	3	99.9%	2																										
				QAALQVAEGFISR	2	100.0%	2																										
				VSDATGQMNLTK	2	100.0%	1																										
				YQEGGVESAFHK	2	100.0%	2																										
				YQEGGVESAFHK	3	98.9%	1																										
IPI00027350	PRDX2	Peroxiredoxin-2	100.0%	46.5	10	12	18	2	36,776,107	38,821,978	38,521,016	43,146,660	2,547,972	1,123,367	2,073,729	1,113,806	15.5	6.5	12.0	5.8	1.1	0.5	1.0	0.6	1.2	0.05	-1.0	0.9	1.1	0.03	1.1	0.08
IPI00909207	PRDX2	cDNA FLJ60461, highly similar to Peroxiredoxin-2	100.0%	50.3	10	12	18	2	36,776,107	38,821,978	38,521,016	43,146,660	2,547,972	1,123,367	2,073,729	1,113,806	15.5	6.5	12.0	5.8	1.1	0.5	1.0	0.6	1.2	0.05	-1.0	0.9	1.1	0.03	1.1	0.08
				ATAVVDGAFK	2	100.0%	2																										
				ATAVVDGAFKEVK	2	99.6%	1																										
				EGGLGPLNIPLLADVTR	2	100.0%	2																										
				EGGLGPLNIPLLADVTR	3	99.8%	1																										
				GLFIIDGK	2	98.2%	1																										
				KEGGLGPLNIPLLADVTR	2	100.0%	2																										
				KEGGLGPLNIPLLADVTR	3	100.0%	2																										
				LGCEVLGVSVDSQFTHLAWINTPR	3	100.0%	2																										
				LSEDYGVLK	2	99.9%	1																										
				QITVNDLPVGR	2	100.0%	2																										
				RLSEDYGVLK	2	99.3%	1																										
				TDEGIAYR	2	100.0%	1																										
IPI00027378	UBXN1	isoform 1 of UBX domain-containing protein 1	99.4%	4.0	1	1	1	5	1,921,896	1,898,778	1,970,852	2,066,354	111,289	134,364	97,986	41,635	13.0	15.8	11.1	4.5	-1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.3	1.0	0.4
IPI00396563	UBXN1	isoform 2 of UBX domain-containing protein 1	99.4%	3.9	1	1	1	5	1,921,896	1,898,778	1,970,852	2,066,354	111,289	134,364	97,986	41,635	13.0	15.8	11.1	4.5	-1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.3	1.0	0.4
IPI00978573	UBXN1	Uncharacterized protein	99.4%	4.1	1	1	1	5	1,921,896	1,898,778	1,970,852	2,066,354	111,289	134,364	97,986	41,635	13.0	15.8	11.1	4.5	-1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.3	1.0	0.4
IPI00982790	UBXN1	Uncharacterized protein	99.4%	4.1	1	1	1	5	1,921,896	1,898,778	1,970,852	2,066,354	111,289	134,364	97,986	41,635	13.0	15.8	11.1	4.5	-1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.3	1.0	0.4
IPI01014777	UBXN1	cDNA FLJ53007, highly similar to UBA/UBX 33.3 kDa protein	99.4%	6.0	1	1	1	5	1,921,896	1,898,778	1,970,852	2,066,354	111,289	134,364	97,986	41,635	13.0	15.8	11.1	4.5	-1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.3	1.0	0.4
				LPDGTSLTQTFR	2	99.4%	1																										
IPI00027381	LY75	isoform 4 of Lymphocyte antigen 75	98.8%	1.0	1	1	1	1	1,361,887	930,483	1,114,907	1,022,337	305,748	141,056	107,444	92,852	50.2	33.9	21.6	20.3	-1.5	0.2	-1.2	0.5	-1.3	0.3	1.2	0.3	1.1	0.6	-1.1	0.5
				FLAGLSTDGFWDIQTFK	2	98.8%	1																										
IPI00985496	PAK1	Protein	100.0%	15.6	3	3	3	6	2,341,907	2,465,028	2,555,549	2,788,429	122,942	153,506	178,457	24,712	11.7	13.9	15.6	2.0	1.1	0.5	1.1	0.4	1.2	0.02	1.0	0.7	1.1	0.1	1.1	0.3
IPI00027382	PAK3	isoform 2 of Serine/threonine-protein kinase PAK 3	100.0%	7.0	3	3	3	6	2,341,907	2,465,028	2,555,549	2,788,429	122,942	153,506	178,457	24,712	11.7	13.9	15.6	2.0	1.1	0.5	1.1	0.4	1.2	0.02	1.0	0.7	1.1	0.1	1.1	0.3
IPI00410084	PAK3	isoform 1 of Serine/threonine-protein kinase PAK 3	100.0%	6.8	3	3	3	6	2,341,907	2,465,028	2,555,549	2,788,429	122,942	153,506	178,457	24,712	11.7	13.9	15.6	2.0	1.1	0.5	1.1	0.4	1.2	0.02	1.0	0.7	1.1	0.1	1.1	0.3
IPI00896377	PAK3	serine/threonine-protein kinase PAK 3 isoform c	100.0%	6.7	3	3	3	6	2,341,907	2,465,028	2,555,549	2,788,429	122,942	153,506	178,457	24,712	11.7	13.9	15.6	2.0	1.1	0.5	1.1	0.4	1.2	0.02	1.0	0.7	1.1	0.1	1.1	0.3
IPI00930214	PAK3	PAK2	100.0%	7.0	3	3	3	6	2,341,907	2,465,028	2,555,549	2,788,429	122,942	153,506	178,457	24,712	11.7	13.9	15.6	2.0	1.1	0.5	1.1	0.4	1.2	0.02	1.0	0.7	1.1	0.1	1.1	0.3
IPI01015232	PAK3	serine/threonine-protein kinase PAK 3 isoform b	100.0%	6.6	3	3	3	6	2,341,907	2,465,028	2,555,549	2,788,429	122,942	153,506	178,457	24,712	11.7	13.9	15.6	2.0	1.1	0.5	1.1	0.4	1.2	0.02	1.0	0.7	1.1	0.1	1.1	0.3
				LTDFGFCAQITPEQSK	2	100.0%	1																										
				QMNLQQQPK	2	93.9%	1																										
				SDNILLGMDGSVK	2	99.8%	1																										
IPI00027397	HN1L	isoform 1 of Hematological and neurological expressed 1-like protein	100.0%	14.7	2	2	3	4	1,944,854	1,776,346	1,922,708	1,914,280	268,808	87,775	121,102	84,465	30.9	11.1	14.1	9.9	-1.1	0.6	-1.0	0.9	-1.0	0.9	1.1	0.4	1.1	0.3	-1.0	1
IPI00607884	HN1L	cDNA, FLJ79413, highly similar to Hematological and neurological expressed 1-like	100.0%	15.7	2	2	3	4	1,944,854	1,776,346	1,922,708	1,914,280	268,808	87,775	121,102	84,465	30.9	11.1	14.1	9.9	-1.1	0.6	-1.0	0.9	-1.0	0.9	1.1	0.4	1.1	0.3	-1.0	1
IPI00909195	HN1L	cDNA FLJ53622, highly similar to Hematological and neurological expressed1-like p	100.0%	12.8	2	2	3	4	1,944,854	1,776,346	1,922,708	1,914,280	268,808	87,775	121,102	84,465	30.9	11.1	14.1	9.9	-1.1	0.6	-1.0	0.9	-1.0	0.9	1.1	0.4	1.1	0.3	-1.0	1
IPI00909743	HN1L	Uncharacterized protein	100.0%	13.4	2	2	3	4	1,944,854	1,776,346	1,922,708	1,914,280	268,808	87,775	121,102	84,465	30.9	11.1	14.1	9.9	-1.1	0.6	-1.0	0.9	-1.0	0.9	1.1	0.4	1.1	0.3	-1.0	1
				GSGIFDESTPVQTR	2	100.0%	2																										
				TSDIFGSPVTATSR	2	100.0%	1																										
IPI00027412	CEACAM6	Carcinoembryonic antigen-related cell adhesion molecule 6	99.6%	6.1	1	1	1	1	11,571,020	15,343,100	11,806,910	16,875,500	2,029,089	1,796,835	1,639,870	1,127,984	39.2	26.2	31.1	15.0	1.3	0.2	1.0	0.9	1.5	0.05	-1.3	0.2	1.1	0.5	1.4	0.03
				SDPVTLNVLYGPDGPTISPSK	2	99.6%	1																										
IPI00027422	ITGB4	isoform Beta-4C of Integrin beta-4	100.0%	1.7	2	2	2	3	1,403,960	1,378,555	1,389,988	1,671,980	212,038	93,442	118,395	64,742	33.8	15.2	19.1	8.7	-1.0	0.9	-1.0	1	1.2	0.3	1.0	0.9	1.2	0.03	1.2	0.07
IPI00220845	ITGB4	isoform Beta-4A of Integrin beta-4	100.0%	1.7	2	2	2	3	1,403,960	1,378,555	1,389,988	1,671,980	212,038	93,442	118,395	64,742	33.8	15.2	19.1	8.7	-1.0	0.9	-1.0	1	1.2	0.3	1.0	0.9	1.2	0.03	1.2	0.07
IPI00220847	ITGB4	isoform Beta-4D of Integrin beta-4	100.0%	1.7	2	2	2	3	1,403,960	1,378,555	1,389,988	1,671,980	212,038	93,442	118,395	64,742	33.8	15.2	19.1	8.7	-1.0	0.9	-1.0	1	1.2	0.3	1.0	0.9	1.2	0.03	1.2	0.07
				DYIPVEGELLFQPGEAWK	2	100.0%	1																										

				QEVEENLNEVYR	2	99.9%	1																									
IPI00027423	PPP1CA	serine/threonine-protein phosphatase PP1-alpha catalytic subunit isoform 3	100.0%	25.2	7	7	10	3	4,233,860	4,423,630	4,582,383	5,137,484	307,811	79,553	414,728	158,589	16.3	4.0	20.2	6.9	1.0	0.6	1.1	0.5	1.2	0.03	1.0	0.7	1.2	0.004	1.1	0.3
IPI00550451	PPP1CA	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	100.0%	26.1	7	7	10	3	4,233,860	4,423,630	4,582,383	5,137,484	307,811	79,553	414,728	158,589	16.3	4.0	20.2	6.9	1.0	0.6	1.1	0.5	1.2	0.03	1.0	0.7	1.2	0.004	1.1	0.3
IPI00902512	PPP1CA	Uncharacterized protein	100.0%	20.1	7	7	10	3	4,233,860	4,423,630	4,582,383	5,137,484	307,811	79,553	414,728	158,589	16.3	4.0	20.2	6.9	1.0	0.6	1.1	0.5	1.2	0.03	1.0	0.7	1.2	0.004	1.1	0.3
				EIFLSQPILLELEAPLK	2	100.0%	2																									
				HDLDLICR	2	99.9%	2																									
				IYGFYDECK	2	99.2%	1																									
				LFEYGGFPPESNYLFLGDYVDR	2	90.7%	1																									
				NVQLTENEIR	2	100.0%	2																									
				SREIFLSQPILLELEAPLK	3	98.3%	1																									
				TFTDCFNCLPIAAIVDEK	2	100.0%	1																									
IPI00027434	RHOC	Rho-related GTP-binding protein RhoC	100.0%	26.4	4	4	5	4	3,355,413	3,286,873	3,838,776	3,541,732	134,218	126,043	135,830	96,606	8.9	8.6	7.9	6.1	-1.0	0.7	1.1	0.04	1.1	0.3	1.2	0.02	1.1	0.1	-1.1	0.1
IPI00647268	RHOC	Ras homolog gene family, member C	100.0%	27.0	4	4	5	4	3,355,413	3,286,873	3,838,776	3,541,732	134,218	126,043	135,830	96,606	8.9	8.6	7.9	6.1	-1.0	0.7	1.1	0.04	1.1	0.3	1.2	0.02	1.1	0.1	-1.1	0.1
IPI00980853	RHOC	Uncharacterized protein	100.0%	22.3	4	4	5	4	3,355,413	3,286,873	3,838,776	3,541,732	134,218	126,043	135,830	96,606	8.9	8.6	7.9	6.1	-1.0	0.7	1.1	0.04	1.1	0.3	1.2	0.02	1.1	0.1	-1.1	0.1
IPI01009702	RHOC	Uncharacterized protein	100.0%	30.2	4	4	5	4	3,355,413	3,286,873	3,838,776	3,541,732	134,218	126,043	135,830	96,606	8.9	8.6	7.9	6.1	-1.0	0.7	1.1	0.04	1.1	0.3	1.2	0.02	1.1	0.1	-1.1	0.1
				DQFPEVYVPTVFENYIADIEVDGK	2	100.0%	2																									
				HFCPNVPIILVGNK	2	99.4%	1																									
				HFCPNVPIILVGNKK	3	100.0%	1																									
				KLVIVGDGACGK	2	99.2%	1																									
IPI00027438	FLOT1	Flotillin-1	99.4%	6.8	2	2	2	1	8,977,960	7,805,700	9,423,739	8,611,430	417,503	313,034	518,273	421,445	10.4	9.0	12.3	10.9	-1.2	0.05	1.0	0.5	-1.0	0.6	1.2	0.03	1.1	0.2	-1.1	0.3
				TEAEIAHIALETLEGHQR	3	98.5%	1																									
				VTGEVLDILTR	2	99.4%	1																									
IPI00027442	AARS	Alanyl-tRNA synthetase, cytoplasmic	100.0%	36.0	22	25	32	1	90,489,745	92,604,545	84,098,772	103,024,973	6,034,767	3,768,705	4,978,660	3,442,117	14.9	9.1	13.2	7.5	1.0	0.8	-1.1	0.4	1.1	0.1	-1.1	0.2	1.1	0.08	1.2	0.01
				ASEWVQQVSGLMDGK	2	100.0%	2																									
				AVFDETYPDPVR	2	100.0%	2																									
				AVYTQDCPLAAAK	2	100.0%	1																									
				DAAHLVNQDDPNVLEIWNLVFIQYNR	3	92.0%	1																									
				DIINEEEVQFLK	2	88.4%	1																									
				EIADLGEALATAVIPQWQK	2	100.0%	2																									
				EIADLGEALATAVIPQWQK	3	100.0%	1																									
				GAGGEDLIMLDIYAIEELR	2	100.0%	1																									
				GLEVTDDSPK	2	99.4%	1																									
				GLVVDMDGFEEER	2	100.0%	2																									
				KAEEIANEMIEAAK	2	100.0%	1																									
				KDPDMVKDIINEEEVQFLK	3	99.5%	1																									
				MALELLTQEFGIPIER	2	99.8%	1																									
				MSNYDTDLFVPYFEAIQK	2	100.0%	2																									
				MSNYDTDLFVPYFEAIQK	3	99.4%	1																									
				NVGCLQEALQLATSFAQLR	2	100.0%	1																									
				NVGCLQEALQLATSFAQLR	3	100.0%	1																									
				QFIDSNPNQPLVILEMESGASAK	2	100.0%	1																									
				QIWQNLGLDDTK	2	100.0%	2																									
				RIVAVTGAEAQK	2	99.9%	1																									
				SIDTGMGLER	2	99.8%	1																									
				TITVALADGGRPDNTGR	3	81.0%	1																									
				VGAEDADGIDMAYR	2	100.0%	2																									
				VGDQVWLFIDEPR	2	100.0%	1																									
				VVSIGVPVSELLDDPSGPAGSLTSVEFCGGTHLR	3	98.8%	1																									
IPI00027443	CARS	cysteinyl-tRNA synthetase, cytoplasmic isoform c	99.9%	2.3	2	2	2	5	1,885,242	2,046,922	1,784,462	1,966,746	199,943	96,016	132,787	129,829	23.7	10.5	16.6	14.8	1.1	0.5	-1.1	0.7	1.0	0.7	-1.1	0.1	-1.0	0.6	1.1	0.4
IPI00556365	CARS	isoform 1 of Cysteinyl-tRNA synthetase, cytoplasmic	99.9%	2.5	2	2	2	5	1,885,242	2,046,922	1,784,462	1,966,746	199,943	96,016	132,787	129,829	23.7	10.5	16.6	14.8	1.1	0.5	-1.1	0.7	1.0	0.7	-1.1	0.1	-1.0	0.6	1.1	0.4
IPI00556541	CARS	cDNA FLJ38994 fis, clone NT2RI2009259, highly similar to Cysteinyl-tRNA syntheta	99.9%	2.6	2	2	2	5	1,885,242	2,046,922	1,784,462	1,966,746	199,943	96,016	132,787	129,829	23.7	10.5	16.6	14.8	1.1	0.5	-1.1	0.7	1.0	0.7	-1.1	0.1	-1.0	0.6	1.1	0.4
IPI00909763	CARS	cysteinyl-tRNA synthetase, cytoplasmic isoform e	99.9%	2.4	2	2	2	5	1,885,242	2,046,922	1,784,462	1,966,746	199,943	96,016	132,787	129,829	23.7	10.5	16.6	14.8	1.1	0.5	-1.1	0.7	1.0	0.7	-1.1	0.1	-1.0	0.6	1.1	0.4
IPI00939491	CARS	isoform 2 of Cysteinyl-tRNA synthetase, cytoplasmic	99.9%	2.6	2	2	2	5	1,885,242	2,046,922	1,784,462	1,966,746	199,943	96,016	132,787	129,829	23.7	10.5	16.6	14.8	1.1	0.5	-1.1	0.7	1.0	0.7	-1.1	0.1	-1.0	0.6	1.1	0.4
				APVDITGQFEK	2	95.7%	1																									
				FWEGDFHR	3	99.1%	1																									
IPI00027444	SERPINB1	Leukocyte elastase inhibitor	100.0%	44.3	16	17	19	2	57,185,366	55,548,212	57,667,639	63,827,059	3,719,833	1,762,320	3,365,843	1,922,782	14.6	7.1	13.1	6.7	-1.0	0.7	1.0	0.9	1.1	0.2	1.0	0.6	1.1	0.01	1.1	0.2
IPI01014238	SERPINB1	cDNA FLJ53963, highly similar to Leukocyte elastase inhibitor	100.0%	49.3	16	17	19	2	57,185,366	55,548,212	57,667,639	63,827,059	3,719,833	1,762,320	3,365,843	1,922,782	14.6	7.1	13.1	6.7	-1.0	0.7	1.0	0.9	1.1	0.2	1.0	0.6	1.1	0.01	1.1	0.2
				ADLSGMSGAR	2	100.0%	1																									
				EATTNAPFR	2	91.4%	1																									
				FAYGYIEDLK	2	99.9%	1																									
				FKLEESYTLNSDLAR	3	100.0%	1																									
				FQSLNADINKR	2	91.1%	1																									
				IEEQLTLEK	2	98.9%	1																									
				IPELLASGMVDNMTK	2	100.0%	1																									
				KIEEQLTLEK	2	99.8%	1																									
				LGVQDLFNSSK	2	100.0%	2																									
				LVLVNAIYFK	2	100.0%	2																									
				MMYQK	1	87.8%	1																									
				TFHFNTVEEVHSR	2	99.9%	1																									
				TFHFNTVEEVHSR	3	100.0%	1																									
				TYGADLASVDFQHASEDAR	3	100.0%	1																									
				TYGADLASVDFQHASEDARK	2	88.0%	1																									
				VLELPYQGEELSMVILLPDDIEDESTGLK	3	100.0%	1																									
				VLELPYQGEELSMVILLPDDIEDESTGLKK	3	100.0%	1																									
IPI00027445	HARS2	Probable histidyl-tRNA synthetase, mitochondrial	99.9%	2.2	1	1	1	7	361,683	437,410	399,545	421,391	28,573	15,341	24,117	13,025	17.7	7.8	13.5	6.9	1.2	0.05	1.1	0.3	1.2	0.09	-1.1	0.2	-1.0	0.4	1.1	0.4
IPI00908759	HARS2	Uncharacterized protein	99.9%	3.1	1	1	1	7	361,683	437,410	399,545	421,391	28,573	15,341	24,117	13,025	17.7	7.8	13.5	6.9	1.2	0.05	1.1	0.3	1.2	0.09	-1.1	0.2	-1.0	0.4	1.1	0.4
IPI00909584	HARS2	cDNA FLJ50611, highly similar to Histidyl-tRNA synthetase homolog	99.9%	3.3	1	1	1	7	361,683	437,410	399,545	421,391	28,573	15,341	24,117	13,025	17.7	7.8	13.5	6.9	1.2	0.05	1.1	0.3	1.2	0.09	-1.1	0.2	-1.0	0.4	1.1	0.4
IPI00910031	HARS2	Uncharacterized protein	99.9%	2.6	1	1	1	7	361,683	437,410	399,545	421,391	28,573	15,341	24,117	13,025	17.7	7.8	13.5	6.9	1.2	0.05	1.1	0.3	1.2	0.09	-1.1	0.2	-1.0	0.4	1.1	0.4
IPI00940266	HARS2	Uncharacterized protein	99.9%	2.8	1	1	1	7	361,683	437,410	399,545	421,391	28,573	15,341	24,117	13,025	17.7	7.8	13.5	6.9	1.2	0.05	1.1	0.3	1.2	0.09	-1.1	0.2	-1.0	0.4	1.1	0.4
IPI00942264	HARS2	Uncharacterized protein	99.9%	2.4	1	1	1	7	361,683	437,410	399,545	421,391	28,573	15,341	24,117	13,025	17.7	7.8	13.5	6.9	1.2	0.05	1.1	0.3	1.2	0.09	-1.1	0.2	-1.0	0.4	1.1	0.4
IPI00966091	HARS2	cDNA FLJ50406, highly similar to Histidyl-tRNA synthetase homolog	99.9%	2.3	1	1	1	7	361,683	437,410	399,545	421,391	28,573	15,341	24,117	13,025	17.7	7.8	13.5	6.9	1.2	0.05	1.1	0.3	1.2	0.09	-1.1	0.2	-1.0	0.4	1.1	0.4
				YDGLVGMFDPK	2	98.9%	1																									
IPI00027463	S100A6	Protein S100-A6	100.0%	32.2	5	8	20	1	352,396,740	408,845,530	430,184,660	456,880,880	########	########	########	########	20.8	12.7	15.9	6.6	1.2	0.2	1.2	0.1	1.3	0.02	1.1	0.6	1.1	0.1	1.1	0.4
				ELIQKELTIGSK	2	98.4%	1																									
				ELTIGSK	1	99.5%	4																									
				ELTIGSK	2	96.6%	2																									
				LMEDLDR	1	93.3%	1																									
				LMEDLDR	2	99.5%	2																									
				LMEDLDRNK	2	99.2%	2																									
				LQDAEIAR	1	99.0%	3																									
				LQDAEIAR	2	100.0%	5																									
IPI00788723	-	Similar to Eukaryotic translation initiation factor 4E	97.9%	5.1	1	1	2	5	621,300	512,066	558,478	673,580	58,376	37,442	92,426	61,556	21.0	16.4	37.0	20.4	-1.2	0.2	-1.1	0.6	1.1	0.6	1.1	0.7	1.3	0.06	1.2	0.3
IPI00027485	EIF4E	Eukaryotic translation initiation factor 4E	97.9%	5.1	1	1	2	5	621,300	512,066	558,478	673,580	58,376	37,442	92,426	61,556	21.0	16.4	37.0	20.4	-1.2	0.2	-1.1	0.6	1.1	0.6	1.1	0.7	1.3	0.06	1.2	0.3
IPI00873680	EIF4E	eukaryotic translation initiation factor 4E isoform 3	97.9%	4.6	1	1	2	5	621,300	512,066	558,478	673,580	58,376	37,442	92,426	61,556	21.0	16.4	37.0	20.4	-1.2	0.2	-1.1	0.6	1.1	0.6	1.1	0.7	1.3	0.06	1.2	0.3
IPI00965726	EIF4E	eukaryotic translation initiation factor 4E isoform 2	97.9%	4.4	1	1	2	5	621,300	512,066	558,478	673,580	58,376	37,442	92,426	61,556	21.0	16.4	37.0	20.4	-1.2	0.2	-1.1	0.6	1.1	0.6	1.1	0.7	1.3	0.06	1.2	0.3
IPI00966031	EIF4E	Uncharacterized protein	97.9%	4.5	1	1	2	5	621,300	512,066	558,478	673,580	58,376	37,442	92,426	61,556	21.0	16.4	37.0	20.4	-1.2	0.2	-1.1	0.6	1.1	0.6	1.1	0.7	1.3	0.06	1.2	0.3
				IAIWTTECENR	2	97.9%	2																									
IPI00908787	-	cDNA FLJ57403, moderately similar to Creatine kinase M-type	100.0%	4.8	1	1	1	3	164,763	195,341	206,871	169,085	16,786	9,614	13,479	13,724	22.8	11.0	14.6	18.2	1.2	0.2	1.3	0.09	1.0	0.8	1.1	0.5	-1.2	0.2	-1.2	0.09
IPI00027487	CKM	Creatine kinase M-type	100.0%	1.6	1	1	1	3	164,763	195,341	206,871	169,085	16,786	9,614	13,479	13,724	22.8	11.0	14.6	18.2	1.2	0.2	1.3	0.09	1.0	0.8	1.1	0.5	-1.2	0.2	-1.2	0.09
IPI00909684	CKM	cDNA FLJ57602, highly similar to Creatine kinase M-type	100.0%	2.3	1	1	1	3	164,763	195,341	206,871	169,085	16,786	9,614	13,479	13,724	22.8	11.0	14.6	18.2	1.2	0.2	1.3	0.09	1.0	0.8	1.1	0.5	-1.2	0.2	-1.2	0.09
				VISMEK	1	100.0%	1																									
IPI00027493	SLC3A2	isoform 2 of 4F2 cell-surface antigen heavy chain	100.0%	9.8	4	4	4	7	2,675,876	2,608,711	2,761,766	2,941,737	188,377	45,262	89,367	34,232	15.7	3.9	7.2	2.6	-1.0	0.7	1.0	0.7	1.1	0.2	1.1	0.2	1.1	0.0004	1.1	0.1
IPI00554481	SLC3A2	isoform 4 of 4F2 cell-surface antigen heavy chain	100.0%	7.9	4	4	4	7	2,675,876	2,608,711	2,761,766	2,941,737	188,377	45,262	89,367	34,232	15.7	3.9	7.2	2.6	-1.0	0.7	1.0	0.7	1.1	0.2	1.1	0.2	1.1	0.0004	1.1	0.1
IPI00554611	SLC3A2	4F2 cell-surface antigen heavy chain isoform b	100.0%	8.7	4	4	4	7	2,675,876	2,608,711	2,761,766	2,941,737	188,377	45,262	89,367	34,232	15.7	3.9	7.2	2.6	-1.0	0.7	1.0	0.7	1.1	0.2	1.1	0.2	1.1	0.0004	1.1	0.1
IPI00554722	SLC3A2	isoform 3 of 4F2 cell-surface antigen heavy chain	100.0%	9.2	4	4	4	7	2,675,876	2,608,711	2,761,766	2,941,737	188,377	45,262	89,367	34,232	15.7	3.9	7.2	2.6	-1.0	0.7	1.0	0.7	1.1	0.2	1.1	0.2	1.1	0.0004	1.1	0.1
IPI00604710	SLC3A2	isoform 1 of 4F2 cell-surface antigen heavy chain	100.0%	8.3	4	4	4	7	2,675,876	2,608,711	2,761,766	2,941,737	188,377	45,262	89,367	34,232	15.7	3.9	7.2	2.6	-1.0	0.7	1.0	0.7	1.1	0.2	1.1	0.2	1.1	0.0004	1.1	0.1
IPI01010400	SLC3A2	68 kDa protein	100.0%	8.2	4	4	4	7	2,675,876	2,608,711	2,761,766	2,941,737	188,377	45,262	89,367	34,232	15.7	3.9	7.2	2.6	-1.0	0.7	1.0	0.7	1.1	0.2	1.1	0.2	1.1	0.0004	1.1	0.1
IPI01013280	SLC3A2	cDNA FLJ54090, highly similar to 4F2 cell-surface antigen heavy chain	100.0%	10.2	4	4	4	7	2,675,876	2,608,711	2,761,766	2,941,737	188,377	45,262	89,367	34,232	15.7	3.9	7.2	2.6	-1.0	0.7	1.0	0.7	1.1	0.2	1.1	0.2	1.1	0.0004	1.1	0.1
				ADLLLSTQPGREEGSPLELER	3	99.9%	1																									
				GLVLGPIHK	2	87.3%	1																									
				LLTSFLPAQLLR	2	100.0%	1																									
				VILDLTPNYR	2	99.8%	1																									
IPI00027497	GPI	Glucose-6-phosphate isomerase	100.0%	46.4	19	23	35	1	143,836,710	151,759,466	147,553,254	172,497,474	########	7,830,236	########	6,950,943	24.9	11.5	18.9	9.0	1.1	0.7	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.08	1.2	0.1
				AVLHVALR	2	88.1%	1																									
				EWFLQAAK	2	99.9%	1																									
				FAAYFQQGDMESNGK	2	100.0%	2																									
				HFVALSTNTTK	2	100.0%	2																									
				IFVQGIIWDINSFDQWGVELGK	2	100.0%	1																									
				ILLANFLAQTEALMR	2	100.0%	2																									
				ILLANFLAQTEALMR	3	100.0%	2																									
				INYTEGR	2	96.5%	2																									
				KIEPELDGSAQVTSHDASTNGLINFIK	3	100.0%	2																									
				LQQWYR	2	99.8%	1																									
				MLVDLAK	2	89.3%	1																									
				SNTPILVDGK	2	99.8%	1																									
				SNTPILVDGKDVMPEVNK	2	100.0%	2																									
				SNTPILVDGKDVMPEVNK	3	100.0%	2																									
				TFTTQETITNAETAK	2	100.0%	2																									
				TFTTQETITNAETAKEWFLQAAK	3	100.0%	1																									
				TITDVINIGIGGSDLGPLMVTEALKPYSSGGPR	3	100.0%	1																									
				TLAQLNPESSLFIIASK	2	100.0%	1																									
				VFEGNRPTNSIVFTK	2	100.0%	2																									
				VFEGNRPTNSIVFTK	3	99.9%	1																									
				VKEFGIDPQNMFEFWDWVGGR	3	100.0%	1																									
				VWYVSNIDGTHIAK	2	100.0%	2																									
				VWYVSNIDGTHIAK	3	100.0%	2																									
IPI00027505	ITGAV	isoform 1 of Integrin alpha-V	99.9%	5.8	4	4	4	2	2,591,488	2,691,139	2,581,899	2,875,695	274,389	115,815	205,961	94,840	23.7	9.6	17.8	7.4	1.0	0.7	-1.0	1	1.1	0.4	-1.0	0.7	1.1	0.3	1.1	0.2
IPI00922108	ITGAV	integrin alpha-V isoform 2	99.9%	6.1	4	4	4	2	2,591,488	2,691,139	2,581,899	2,875,695	274,389	115,815	205,961	94,840	23.7	9.6	17.8	7.4	1.0	0.7	-1.0	1	1.1	0.4	-1.0	0.7	1.1	0.3	1.1	0.2
				AGTQLLAGLR	2	99.5%	1																									
				IYIGDDNPLTLIVK	2	90.9%	1																									
				LTPITIFMEYR	2	91.0%	1																									
				VLLGGPGSFYWQGQLISDQVAEIVSK	3	99.8%	1																									
IPI00027626	CCT6A	T-complex protein 1 subunit zeta	100.0%	42.6	17	19	23	1	55,122,109	57,185,682	56,351,863	62,256,695	3,394,088	1,990,808	3,758,222	1,636,331	13.8	7.8	14.9	5.9	1.0	0.6	1.0	0.8	1.1	0.09	-1.0	0.8	1.1	0.08	1.1	0.2
				AGMSSLKG	2	96.9%	2																									
				ALQFLEEVK	2	99.9%	1																									
				AQAALAVNISAAR	2	99.9%	1																									
				AQLGVQAFADALLIIPK	2	100.0%	2																									

				DGNVLLHEMQIQHPTASLIAK	3	100.0%	1																									
				EMDRETLIDVAR	2	91.2%	1																									
				GIDPFSLDALSK	2	95.1%	1																									
				HKSETDTSLIR	3	98.5%	1																									
				HTLTQIK	2	96.9%	1																									
				IITEGFEAAK	2	98.8%	1																									
				KQDEPIDLFMIEIMEMK	2	99.9%	1																									
				KQDEPIDLFMIEIMEMK	3	100.0%	1																									
				MLVSGAGDIK	2	87.7%	1																									
				NAIDDGCVVPGAGAVEVAMAEALIK	2	100.0%	1																									
				NAIDDGCVVPGAGAVEVAMAEALIK	3	100.0%	1																									
				QADLYISEGLHPR	2	97.8%	1																									
				QDEPIDLFMIEIMEMK	2	98.8%	1																									
				VATAQDDITGDGTTSNVLIIGELLK	2	100.0%	2																									
				VLAQNSGFDLQETLVK	2	100.0%	2																									
IPI00027745	GUSB	isoform Long of Beta-glucuronidase	100.0%	2.5	2	2	2	3	2,178,191	2,284,998	2,159,600	2,582,527	180,874	146,489	247,024	75,120	18.6	14.3	25.6	6.5	1.0	0.7	-1.0	1	1.2	0.07	-1.1	0.7	1.1	0.1	1.2	0.2
IPI00219516	GUSB	isoform Short of Beta-glucuronidase	100.0%	2.7	2	2	2	3	2,178,191	2,284,998	2,159,600	2,582,527	180,874	146,489	247,024	75,120	18.6	14.3	25.6	6.5	1.0	0.7	-1.0	1	1.2	0.07	-1.1	0.7	1.1	0.1	1.2	0.2
IPI00927883	GUSB	cDNA FLJ53268, highly similar to Beta-glucuronidase	100.0%	3.2	2	2	2	3	2,178,191	2,284,998	2,159,600	2,582,527	180,874	146,489	247,024	75,120	18.6	14.3	25.6	6.5	1.0	0.7	-1.0	1	1.2	0.07	-1.1	0.7	1.1	0.1	1.2	0.2
				GFEEQWYR	2	94.6%	1																									
				WLGANAFR	2	92.3%	1																									
IPI00027782	MMP3	Stromelysin-1	91.9%	3.8	1	1	1	1	2,562,650	2,164,700	2,452,050	2,538,940	561,907	95,116	92,384	179,514	49.0	9.8	8.4	15.8	-1.2	0.5	-1.0	0.9	-1.0	1	1.1	0.06	1.2	0.1	1.0	0.7
				GNQFWAIRGNEVRAGYPR	3	91.9%	1																									
IPI00027798	FAM103A1	Protein FAM103A1	98.2%	12.7	1	1	1	1	15,919,900	16,093,200	15,932,900	18,199,600	828,740	332,210	1,354,922	1,301,638	11.6	4.6	19.0	16.0	1.0	0.9	1.0	1	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.3
				RPPESPPIVEEWNSR	3	97.7%	1																									
IPI00027799	FAM107B	isoform 2 of Protein FAM107B	99.5%	4.3	1	1	1	5	275,325	285,266	217,075	299,238	26,822	13,500	17,710	25,728	21.8	10.6	18.2	19.2	1.0	0.7	-1.3	0.1	1.1	0.5	-1.3	0.02	1.0	0.6	1.4	0.03
IPI00871831	FAM107B	isoform 1 of Protein FAM107B	99.5%	9.9	1	1	1	5	275,325	285,266	217,075	299,238	26,822	13,500	17,710	25,728	21.8	10.6	18.2	19.2	1.0	0.7	-1.3	0.1	1.1	0.5	-1.3	0.02	1.0	0.6	1.4	0.03
IPI00945357	FAM107B	Uncharacterized protein	99.5%	10.3	1	1	1	5	275,325	285,266	217,075	299,238	26,822	13,500	17,710	25,728	21.8	10.6	18.2	19.2	1.0	0.7	-1.3	0.1	1.1	0.5	-1.3	0.02	1.0	0.6	1.4	0.03
IPI00946163	FAM107B	Uncharacterized protein	99.5%	10.4	1	1	1	5	275,325	285,266	217,075	299,238	26,822	13,500	17,710	25,728	21.8	10.6	18.2	19.2	1.0	0.7	-1.3	0.1	1.1	0.5	-1.3	0.02	1.0	0.6	1.4	0.03
IPI00947154	FAM107B	Uncharacterized protein	99.5%	10.2	1	1	1	5	275,325	285,266	217,075	299,238	26,822	13,500	17,710	25,728	21.8	10.6	18.2	19.2	1.0	0.7	-1.3	0.1	1.1	0.5	-1.3	0.02	1.0	0.6	1.4	0.03
				LQEEQENAPEFVK	2	99.5%	1																									
IPI00027834	HNRNPL	Heterogeneous nuclear ribonucleoprotein L	100.0%	27.2	11	13	18	2	80,648,487	84,720,810	72,800,053	98,957,405	9,518,550	5,352,826	4,630,773	2,980,174	26.4	14.1	14.2	6.7	1.1	0.7	-1.1	0.5	1.2	0.1	-1.2	0.1	1.2	0.05	1.4	0.001
IPI00465225	HNRNPL	heterogeneous nuclear ribonucleoprotein L isoform b	100.0%	35.1	11	13	18	2	80,648,487	84,720,810	72,800,053	98,957,405	9,518,550	5,352,826	4,630,773	2,980,174	26.4	14.1	14.2	6.7	1.1	0.7	-1.1	0.5	1.2	0.1	-1.2	0.1	1.2	0.05	1.4	0.001
				AITHLNNNFMFGQK	2	100.0%	1																									
				AITHLNNNFMFGQK	3	99.7%	1																									
				ASLNGADIYSGCCTLK	2	100.0%	2																									
				FSTPEQAAK	2	94.5%	1																									
				LNVCVSK	2	99.4%	1																									
				NDQDTWDYTNPNLSGQGDPGSNPNKR	3	100.0%	2																									
				NGVQAMVEFDSVQSAQR	2	100.0%	1																									
				QPAIMPGQSYGLEDGSCSYK	2	96.3%	1																									
				QPAIMPGQSYGLEDGSCSYKDFSESR	3	94.2%	1																									
				SDALETLGFLNHYQMK	2	100.0%	1																									
				SDALETLGFLNHYQMK	3	100.0%	2																									
				SKPGAAMVEMADGYAVDR	3	100.0%	2																									
				SSSGLLEWESK	2	100.0%	2																									
IPI00027838	RBM4B	RNA-binding protein 4B	100.0%	2.8	1	1	1	7	405,203	398,224	365,918	446,062	56,403	19,294	33,105	20,120	31.1	10.8	20.2	10.1	-1.0	0.9	-1.1	0.6	1.1	0.5	-1.1	0.4	1.1	0.1	1.2	0.07
IPI00977800	RBM4B	Uncharacterized protein	100.0%	6.8	1	1	1	7	405,203	398,224	365,918	446,062	56,403	19,294	33,105	20,120	31.1	10.8	20.2	10.1	-1.0	0.9	-1.1	0.6	1.1	0.5	-1.1	0.4	1.1	0.1	1.2	0.07
IPI00979194	RBM4B	Uncharacterized protein	100.0%	7.0	1	1	1	7	405,203	398,224	365,918	446,062	56,403	19,294	33,105	20,120	31.1	10.8	20.2	10.1	-1.0	0.9	-1.1	0.6	1.1	0.5	-1.1	0.4	1.1	0.1	1.2	0.07
IPI00556034	RBM4	isoform 2 of RNA-binding protein 4	100.0%	5.7	1	1	1	7	405,203	398,224	365,918	446,062	56,403	19,294	33,105	20,120	31.1	10.8	20.2	10.1	-1.0	0.9	-1.1	0.6	1.1	0.5	-1.1	0.4	1.1	0.1	1.2	0.07
IPI00908491	RBM4	RNA-binding protein 4 isoform 3	100.0%	5.8	1	1	1	7	405,203	398,224	365,918	446,062	56,403	19,294	33,105	20,120	31.1	10.8	20.2	10.1	-1.0	0.9	-1.1	0.6	1.1	0.5	-1.1	0.4	1.1	0.1	1.2	0.07
IPI00940890	RBM4	isoform 3 of RNA-binding protein 4	100.0%	7.0	1	1	1	7	405,203	398,224	365,918	446,062	56,403	19,294	33,105	20,120	31.1	10.8	20.2	10.1	-1.0	0.9	-1.1	0.6	1.1	0.5	-1.1	0.4	1.1	0.1	1.2	0.07
IPI00965408	RBM4	Uncharacterized protein	100.0%	6.7	1	1	1	7	405,203	398,224	365,918	446,062	56,403	19,294	33,105	20,120	31.1	10.8	20.2	10.1	-1.0	0.9	-1.1	0.6	1.1	0.5	-1.1	0.4	1.1	0.1	1.2	0.07
				NYGFVHIEDK	2	99.2%	1																									
IPI00027851	HEXA	cDNA FLJ53927, highly similar to Beta-hexosaminidase alpha chain	99.2%	5.7	2	2	2	1	3,750,311	4,352,146	4,366,694	4,457,853	576,627	300,428	378,716	118,956	34.4	15.4	19.4	6.0	1.2	0.4	1.2	0.4	1.2	0.3	1.0	1	1.0	0.8	1.0	0.8
				GYVVWQEVFDNK	2	91.9%	1																									
				HYLPLSSILDTLDVMAYNK	3	99.2%	1																									
IPI00027970	PCBP3	isoform 1 of Poly(rC)-binding protein 3	100.0%	15.4	4	4	7	4	1,579,648	1,645,804	1,395,026	1,754,339	166,046	67,410	92,976	66,812	23.5	9.2	14.9	8.5	1.0	0.7	-1.1	0.4	1.1	0.4	-1.2	0.06	1.1	0.3	1.3	0.01
IPI00167750	PCBP3	isoform 5 of Poly(rC)-binding protein 3	100.0%	16.2	4	4	7	4	1,579,648	1,645,804	1,395,026	1,754,339	166,046	67,410	92,976	66,812	23.5	9.2	14.9	8.5	1.0	0.7	-1.1	0.4	1.1	0.4	-1.2	0.06	1.1	0.3	1.3	0.01
IPI00410587	PCBP3	isoform 4 of Poly(rC)-binding protein 3	100.0%	15.4	4	4	7	4	1,579,648	1,645,804	1,395,026	1,754,339	166,046	67,410	92,976	66,812	23.5	9.2	14.9	8.5	1.0	0.7	-1.1	0.4	1.1	0.4	-1.2	0.06	1.1	0.3	1.3	0.01
IPI00550365	PCBP3	Uncharacterized protein	100.0%	15.8	4	4	7	4	1,579,648	1,645,804	1,395,026	1,754,339	166,046	67,410	92,976	66,812	23.5	9.2	14.9	8.5	1.0	0.7	-1.1	0.4	1.1	0.4	-1.2	0.06	1.1	0.3	1.3	0.01
				ESTGAQVQVAGDMLPNSTER	2	100.0%	2																									
				INISEGNCPER	2	100.0%	2																									
				LVVPASQCGSLIGK	2	100.0%	1																									
				QICVVMLESPPK	2	99.0%	2																									
IPI00027977	TMPRSS3	Transmembrane protease serine 3 isoform 5	91.9%	3.2	1	1	1	1	4,817,100	5,460,400	5,176,980	6,078,250	442,678	249,953	342,552	189,016	20.6	10.2	14.8	7.0	1.1	0.2	1.1	0.5	1.3	0.03	-1.1	0.5	1.1	0.08	1.2	0.05
				MQAVGPKPLPTLLCGGR	3	91.9%	1																									
IPI00027983	CDA	Cytidine deaminase	93.9%	13.7	1	1	1	1	2,146,860	1,890,690	1,951,750	2,145,650	174,743	108,977	148,494	143,767	18.2	12.9	17.0	15.0	-1.1	0.2	-1.1	0.4	-1.0	1	1.0	0.7	1.1	0.2	1.1	0.4
				AIAIASDMQDDFISPCGACR	2	93.9%	1																									
IPI00985452	CORO7-PAM16	CORO7-PAM16 protein	99.4%	3.4	2	2	2	5	2,579,846	2,747,770	2,659,706	2,902,020	293,694	175,818	152,136	79,312	25.5	14.3	12.8	6.1	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
IPI00027996	CORO7	isoform 1 of Coronin-7	99.4%	3.9	2	2	2	5	2,579,846	2,747,770	2,659,706	2,902,020	293,694	175,818	152,136	79,312	25.5	14.3	12.8	6.1	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
IPI00940326	CORO7	isoform 2 of Coronin-7	99.4%	4.3	2	2	2	5	2,579,846	2,747,770	2,659,706	2,902,020	293,694	175,818	152,136	79,312	25.5	14.3	12.8	6.1	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
IPI00981343	CORO7	coronin-7 isoform 2	99.4%	4.0	2	2	2	5	2,579,846	2,747,770	2,659,706	2,902,020	293,694	175,818	152,136	79,312	25.5	14.3	12.8	6.1	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
IPI01013880	CORO7	cDNA FLJ37277 fis, clone BRAMY2012581, highly similar to Coronin-7	99.4%	5.1	2	2	2	5	2,579,846	2,747,770	2,659,706	2,902,020	293,694	175,818	152,136	79,312	25.5	14.3	12.8	6.1	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
				SGPEPLQEGPGPK	2	97.8%	1																									
				VPAEGLEEVLTTPETVLTGHTEK	3	99.4%	1																									
IPI00028004	PSMB3	Proteasome subunit beta type-3	100.0%	8.8	1	2	2	1	1,667,803	1,761,683	2,097,593	2,087,407	124,760	92,926	203,928	82,380	16.7	11.8	21.7	8.8	1.1	0.6	1.3	0.1	1.3	0.02	1.2	0.2	1.2	0.03	-1.0	1
				LYIGLAGLATDVQTVAQR	2	100.0%	1																									
				LYIGLAGLATDVQTVAQR	3	100.0%	1																									
IPI00028005	NUP107	Nuclear pore complex protein Nup107	99.3%	1.1	1	1	1	3	1,668,453	1,819,703	1,781,757	1,935,610	93,530	218,918	55,542	112,310	12.5	26.9	7.0	13.0	1.1	0.5	1.1	0.3	1.2	0.1	-1.0	0.9	1.1	0.7	1.1	0.3
IPI00448974	NUP107	NUP107 protein	99.3%	1.5	1	1	1	3	1,668,453	1,819,703	1,781,757	1,935,610	93,530	218,918	55,542	112,310	12.5	26.9	7.0	13.0	1.1	0.5	1.1	0.3	1.2	0.1	-1.0	0.9	1.1	0.7	1.1	0.3
IPI01011062	NUP107	cDNA FLJ58739, highly similar to Nuclear pore complex protein Nup107	99.3%	1.1	1	1	1	3	1,668,453	1,819,703	1,781,757	1,935,610	93,530	218,918	55,542	112,310	12.5	26.9	7.0	13.0	1.1	0.5	1.1	0.3	1.2	0.1	-1.0	0.9	1.1	0.7	1.1	0.3
				VFEELQATDK	2	82.8%	1																									
IPI00028006	PSMB2	Proteasome subunit beta type-2	100.0%	15.9	2	2	2	2	8,030,162	8,545,757	9,112,038	9,019,437	666,981	616,777	856,518	338,778	18.6	16.1	21.0	8.4	1.1	0.6	1.1	0.3	1.1	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
IPI00978288	PSMB2	proteasome subunit beta type-2 isoform 2	100.0%	18.2	2	2	2	2	8,030,162	8,545,757	9,112,038	9,019,437	666,981	616,777	856,518	338,778	18.6	16.1	21.0	8.4	1.1	0.6	1.1	0.3	1.1	0.2	1.1	0.6	1.1	0.5	-1.0	0.9
				IIDKNGIHDLDNISFPK	3	97.8%	1																									
				NGYELSPTAAANFTR	2	100.0%	1																									
IPI00028031	ACADVL	cDNA FLJ56425, highly similar to Very-long-chain specific acyl-CoAdehydrogenase,	100.0%	23.7	13	13	15	2	20,846,785	22,508,444	22,023,392	26,514,965	2,783,897	1,441,613	1,757,647	820,193	29.9	14.3	17.9	6.9	1.1	0.6	1.1	0.7	1.3	0.1	-1.0	0.8	1.2	0.04	1.2	0.05
IPI00178744	ACADVL	isoform 2 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	100.0%	24.5	13	13	15	2	20,846,785	22,508,444	22,023,392	26,514,965	2,783,897	1,441,613	1,757,647	820,193	29.9	14.3	17.9	6.9	1.1	0.6	1.1	0.7	1.3	0.1	-1.0	0.8	1.2	0.04	1.2	0.05
				AGLGSGLSLSGLVHPELSR	3	100.0%	1																									
				ALEQFATVVEAK	2	100.0%	1																									
				ASNTAEVFFDGVR	2	100.0%	1																									
				EGMAALQSDPWQQELYR	2	99.9%	1																									
				FGMAAALAGTMR	2	100.0%	1																									
				GIVNEQFLLQR	2	99.9%	1																									
				IFEGTNDILR	2	99.4%	1																									
				IHNFGLIQEK	2	99.8%	1																									
				NPFGNAGLLLGEAGK	2	99.9%	2																									
				QLLRLGGGSSR	3	93.7%	1																									
				RDSEMQAAR	2	90.8%	1																									
				TPVTDPATGAVK	2	98.9%	2																									
				VPSENVLGEVGSGFK	2	100.0%	1																									
IPI00028055	TMED10	Transmembrane emp24 domain-containing protein 10	100.0%	27.4	5	6	6	1	15,537,987	15,541,915	16,286,941	17,281,148	1,614,515	638,190	1,220,594	589,286	23.2	9.2	16.8	7.6	1.0	1	1.0	0.7	1.1	0.4	1.0	0.6	1.1	0.08	1.1	0.5
				GKFAFTTEDYDMFEVCFESK	2	87.0%	1																									
				IPDQLVILDMK	2	100.0%	1																									
				ITDSAGHILYSK	2	99.5%	1																									
				LEDLSESIVNDFAYMK	2	94.5%	1																									
				RLEDLSESIVNDFAYMK	2	100.0%	1																									
				RLEDLSESIVNDFAYMK	3	97.8%	1																									
IPI00028076	VEGFC	Vascular endothelial growth factor C	93.5%	2.9	1	1	1	1	4,726,650	4,161,030	4,753,910	4,847,880	455,482	213,044	478,316	366,459	21.6	11.5	22.5	16.9	-1.1	0.3	1.0	1	1.0	0.8	1.1	0.3	1.2	0.1	1.0	0.9
				AGLRPASCGPHK	2	93.5%	1																									
IPI00028083	EIF2B2	Translation initiation factor eIF-2B subunit beta	91.5%	3.4	1	1	1	1	4,736,290	6,342,580	5,196,240	5,444,310	1,034,102	905,963	667,753	568,538	48.8	31.9	28.7	23.4	1.3	0.3	1.1	0.7	1.1	0.6	-1.2	0.3	-1.2	0.4	1.0	0.8
				WSNAGELMELIR	2	91.5%	1																									
IPI00028091	ACTR3	Actin-related protein 3	100.0%	25.6	9	10	12	1	20,840,193	22,730,056	22,449,665	25,839,723	2,659,805	1,036,707	1,663,769	574,963	28.5	10.2	16.6	5.0	1.1	0.5	1.1	0.6	1.2	0.1	-1.0	0.9	1.1	0.03	1.2	0.1
				DITYFIQQLLR	2	100.0%	2																									
				EFNKYDTDGSK	2	98.7%	1																									
				FMEQVIFK	2	86.5%	1																									
				HGIVEDWDLMER	2	100.0%	1																									
				LGYAGNTEPQFIIPSCIAIK	2	100.0%	1																									
				LGYAGNTEPQFIIPSCIAIK	3	94.0%	1																									
				LPACVVDCGTGYTK	2	100.0%	1																									
				LSEELSGGR	2	99.2%	1																									
				NIVLSGGSTMFR	2	100.0%	1																									
				YSYVCPDLVK	2	100.0%	2																									
IPI00028109	DPY30	Protein dpy-30 homolog	97.7%	16.2	1	1	1	1	335,925	336,780	440,307	386,960	110,224	63,817	83,616	29,095	73.4	42.4	42.5	16.8	1.0	1	1.3	0.5	1.2	0.7	1.3	0.4	1.1	0.5	-1.1	0.6
				ERPPNPIEFLASYLLK	3	97.7%	1																									
IPI00028122	PSIP1	isoform 1 of PC4 and SFRS1-interacting protein	100.0%	8.9	4	4	4	1	11,589,108	13,384,003	11,621,866	13,732,809	695,099	852,091	769,005	1,081,425	13.4	14.2	14.8	17.6	1.2	0.1	1.0	1	1.2	0.1	-1.2	0.2	1.0	0.8	1.2	0.2
				DNHEASTK	2	95.6%	1																									
				GFNEGLWEIDNNPK	2	99.9%	1																									
				GYPHWPAR	2	99.0%	1																									
				LPIFFFGTHETAFLGPK	3	99.5%	1																									
IPI00028160	HMBS	isoform 1 of Porphobilinogen deaminase	100.0%	10.8	2	2	2	5	518,720	482,928	589,293	606,451	20,826	50,337	55,502	27,701	9.0	23.3	21.1	10.2	-1.1	0.5	1.1	0.3	1.2	0.04	1.2	0.2	1.3	0.06	1.0	0.8
IPI00219877	HMBS	isoform 2 of Porphobilinogen deaminase	100.0%	11.3	2	2	2	5	518,720	482,928	589,293	606,451	20,826	50,337	55,502	27,701	9.0	23.3	21.1	10.2	-1.1	0.5	1.1	0.3	1.2	0.04	1.2	0.2	1.3	0.06	1.0	0.8
IPI01011378	HMBS	35 kDa protein	100.0%	12.2	2	2	2	5	518,720	482,928	589,293	606,451	20,826	50,337	55,502	27,701	9.0	23.3	21.1	10.2	-1.1	0.5	1.1	0.3	1.2	0.04	1.2	0.2	1.3	0.06	1.0	0.8
IPI01012145	HMBS	Hydroxymethylbilane synthase	100.0%	11.8	2	2	2	5	518,720	482,928	589,293	606,451	20,826	50,337	55,502	27,701	9.0	23.3	21.1	10.2	-1.1	0.5	1.1	0.3	1.2	0.04	1.2	0.2	1.3	0.06	1.0	0.8
IPI01013546	HMBS	33 kDa protein	100.0%	12.8	2	2	2	5	518,720	482,928	589,293	606,451	20,826	50,337	55,502	27,701	9.0	23.3	21.1	10.2	-1.1	0.5	1.1	0.3	1.2	0.04	1.2	0.2	1.3	0.06	1.0	0.8
				ASYPGLQFEIIAMSTTGDK	2	97.4%	1																									
				GPQLAAQNLGISLANLLLSK	2	100.0%	1																									
IPI00028183	PFDN5	MM-1 beta	100.0%	27.3	1	2	2	1	2,151,371	1,961,701	2,469,783	1,957,883	265,899	52,791	172,912	106,388	27.6	6.0	15.7	12.2	-1.1	0.5	1.1	0.3	-1.1	0.5	1.3	0.04	-1.0	1	-1.3	0.04
				NQLDQEVEFLSTSIAQLK	2	100.0%	1																									
				NQLDQEVEFLSTSIAQLK	3	100.0%	1																									
IPI00028275	CKAP5	isoform 1 of Cytoskeleton-associated protein 5	97.2%	1.6	1	1	1	3	892,577	651,490	909,180	904,780	166,734	80,368	129,369	36,442	41.8	27.6	31.8	9.0	-1.4	0.2	1.0	0.9	1.0	0.9	1.4	0.1	1.4	0.02	-1.0	1
IPI00472887	CKAP5	isoform 2 of Cytoskeleton-associated protein 5	97.2%	1.6	1	1	1	3	892,577	651,490	909,180	904,780	166,734	80,368	129,369	36,442	41.8	27.6	31.8	9.0	-1.4	0.2	1.0	0.9	1.0	0.9	1.4	0.1	1.4	0.02	-1.0	1
IPI00921422	CKAP5	isoform 3 of Cytoskeleton-associated protein 5	97.2%	1.6	1	1	1	3	892,577	651,490	909,180	904,780	166,734	80,368	129,369	36,442	41.8	27.6	31.8	9.0	-1.4	0.2	1.0	0.9	1.0	0.9	1.4	0.1	1.4	0.02	-1.0	1
				EQHQHSDLDSNQTHSSGTVTSSSSTANIDDLK	3	87.3%	1																									
IPI00028376	TIMM8A	Mitochondrial import inner membrane translocase subunit Tim8 A	99.6%	22.7	2	2	2	1	19,519,270	20,358,020	19,239,190	22,218,780	1,522,366	743,927	1,486,196	611,785	17.4	8.2	17.3	6.2	1.0	0.6	-1.0	0.9	1.1	0.1	-1.1	0.5	1.1	0.09	1.2	0.1
				FIDTSQFILNR	2	96.4%	1																									
				SKPVFSESLSD	2	89.8%	1																									

IPI00028387	DDRGK1	isoform 1 of DDRGK domain-containing protein 1	100.0%	5.4	1	2	2	1	9,743,099	9,202,156	10,314,197	12,016,871	549,194	507,392	1,928,554	1,584,815	12.6	12.3	41.8	29.5	-1.1	0.5	1.1	0.8	1.2	0.2	1.1	0.6	1.3	0.2	1.2	0.5
				FIYITPEELAAVANFIR	2	99.8%	1																									
				FIYITPEELAAVANFIR	3	90.0%	1																									
IPI00028392	C1orf116	isoform 1 of Specifically androgen-regulated gene protein	99.4%	5.5	2	2	2	2	4,798,235	4,974,299	5,008,545	5,882,590	269,628	408,404	399,437	317,011	12.6	18.4	17.8	12.1	1.0	0.7	1.0	0.7	1.2	0.03	1.0	1	1.2	0.1	1.2	0.1
IPI00845438	C1orf116	isoform 2 of Specifically androgen-regulated gene protein	99.4%	9.3	2	2	2	2	4,798,235	4,974,299	5,008,545	5,882,590	269,628	408,404	399,437	317,011	12.6	18.4	17.8	12.1	1.0	0.7	1.0	0.7	1.2	0.03	1.0	1	1.2	0.1	1.2	0.1
				HTEAAPGDSGLISCSLQEQR	3	99.0%	1																									
				SGVGLSSYLSTEK	2	99.4%	1																									
IPI00029722	KIF5A	Kinesin heavy chain isoform 5A	100.0%	1.3	1	1	2	4	2,116,537	1,979,782	2,360,300	2,041,513	97,081	101,293	148,959	149,394	10.3	11.4	14.1	16.4	-1.1	0.4	1.1	0.2	-1.0	0.7	1.2	0.07	1.0	0.7	-1.2	0.2
IPI01014265	KIF5A	cDNA FLJ53380, highly similar to Kinesin heavy chain isoform 5A	100.0%	1.4	1	1	2	4	2,116,537	1,979,782	2,360,300	2,041,513	97,081	101,293	148,959	149,394	10.3	11.4	14.1	16.4	-1.1	0.4	1.1	0.2	-1.0	0.7	1.2	0.07	1.0	0.7	-1.2	0.2
IPI00028561	KIF5C	isoform 1 of Kinesin heavy chain isoform 5C	100.0%	1.4	1	1	2	4	2,116,537	1,979,782	2,360,300	2,041,513	97,081	101,293	148,959	149,394	10.3	11.4	14.1	16.4	-1.1	0.4	1.1	0.2	-1.0	0.7	1.2	0.07	1.0	0.7	-1.2	0.2
IPI00889664	KIF5C	isoform 2 of Kinesin heavy chain isoform 5C	100.0%	1.8	1	1	2	4	2,116,537	1,979,782	2,360,300	2,041,513	97,081	101,293	148,959	149,394	10.3	11.4	14.1	16.4	-1.1	0.4	1.1	0.2	-1.0	0.7	1.2	0.07	1.0	0.7	-1.2	0.2
				ISFLENNLEQLTK	2	100.0%	2																									
IPI00028565	GBP2	Interferon-induced guanylate-binding protein 2	98.9%	1.9	1	1	1	2	2,370,070	2,391,190	2,194,660	2,475,005	335,542	216,422	204,789	121,529	31.7	20.2	20.9	11.0	1.0	1	-1.1	0.7	1.0	0.8	-1.1	0.5	1.0	0.7	1.1	0.3
IPI00848358	GBP2	Interferon-induced guanylate-binding protein 2	98.9%	1.9	1	1	1	2	2,370,070	2,391,190	2,194,660	2,475,005	335,542	216,422	204,789	121,529	31.7	20.2	20.9	11.0	1.0	1	-1.1	0.7	1.0	0.8	-1.1	0.5	1.0	0.7	1.1	0.3
				GQLVVNPEALK	2	98.9%	1																									
IPI00028618	MGMT	methylated-DNA--protein-cysteine methyltransferase	99.6%	7.6	1	1	1	1	5,609,910	4,366,130	6,372,340	5,742,410	253,761	702,540	466,080	377,608	10.1	36.0	16.4	14.7	-1.3	0.2	1.1	0.2	1.0	0.8	1.5	0.04	1.3	0.1	-1.1	0.3
				FGEVISYQQLAALAGNPK	2	99.6%	1																									
IPI00028635	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	100.0%	12.4	5	5	6	3	3,613,101	4,284,078	3,661,923	4,273,836	373,819	225,375	503,262	112,618	23.1	11.8	30.7	5.9	1.2	0.2	1.0	0.9	1.2	0.2	-1.2	0.3	-1.0	1	1.2	0.3
IPI00383680	RPN2	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 isoform 2 p	100.0%	12.7	5	5	6	3	3,613,101	4,284,078	3,661,923	4,273,836	373,819	225,375	503,262	112,618	23.1	11.8	30.7	5.9	1.2	0.2	1.0	0.9	1.2	0.2	-1.2	0.3	-1.0	1	1.2	0.3
IPI00552972	RPN2	Uncharacterized protein	100.0%	15.4	5	5	6	3	3,613,101	4,284,078	3,661,923	4,273,836	373,819	225,375	503,262	112,618	23.1	11.8	30.7	5.9	1.2	0.2	1.0	0.9	1.2	0.2	-1.2	0.3	-1.0	1	1.2	0.3
				FSSGYYDFLVEVEGDNR	2	99.5%	1																									
				LQVTNVLSQPLTQATVK	2	99.7%	1																									
				SIVEEIEDLVAR	2	100.0%	2																									
				TGQEVVFVAEPDNK	2	99.9%	1																									
				TSFTPVGDVFELNFMNVK	2	100.0%	1																									
IPI00028888	HNRNPD	isoform 1 of Heterogeneous nuclear ribonucleoprotein D0	100.0%	28.2	10	12	18	3	7,352,843	7,760,636	7,219,494	8,331,653	701,365	214,195	463,863	291,700	21.3	6.2	14.4	7.8	1.1	0.6	-1.0	0.9	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.08
IPI00220684	HNRNPD	isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	100.0%	32.7	10	12	18	3	7,352,843	7,760,636	7,219,494	8,331,653	701,365	214,195	463,863	291,700	21.3	6.2	14.4	7.8	1.1	0.6	-1.0	0.9	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.08
IPI00964648	HNRNPD	30 kDa protein	100.0%	38.3	10	12	18	3	7,352,843	7,760,636	7,219,494	8,331,653	701,365	214,195	463,863	291,700	21.3	6.2	14.4	7.8	1.1	0.6	-1.0	0.9	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.08
				ESESVDKVMDQK	2	99.9%	2																									
				EYFGGFGEVESIELPMDNK	2	100.0%	1																									
				FGEVVDCTLK	2	95.0%	2																									
				FGEVVDCTLKLDPITGR	3	99.9%	1																									
				GFCFITFKEEEPVKK	3	83.5%	1																									
				GFGFVLFK	2	100.0%	2																									
				IFVGGLSPDTPEEK	2	100.0%	2																									
				IREYFGGFGEVESIELPMDNK	2	99.9%	1																									
				IREYFGGFGEVESIELPMDNK	3	100.0%	1																									
				MFIGGLSWDTTK	2	100.0%	2																									
				MFIGGLSWDTTKK	2	100.0%	2																									
				MFIGGLSWDTTKK	3	100.0%	1																									
IPI00028931	DSG2	Desmoglein-2	100.0%	10.8	8	8	9	1	41,274,513	42,388,410	42,175,495	46,719,650	3,699,917	579,516	3,270,356	1,485,117	20.0	3.1	17.3	7.1	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	1	1.1	0.04	1.1	0.2
				DMAGAQAAAVALNEEFLR	2	100.0%	2																									
				GQIIGNFQAFDEDTGLPAHAR	3	99.9%	1																									
				ILDVNDNIPVVENK	2	99.5%	1																									
				IVAISEDYPR	2	99.7%	1																									
				LEDRDNWISVDSVTSEIK	3	91.2%	1																									
				QESTSVLLQQSEK	2	100.0%	1																									
				TLAEVCLGQK	2	83.3%	1																									
				VVPSFLPVDQGGSLVGR	2	99.8%	1																									
IPI00028946	RTN3	isoform 3 of Reticulon-3	99.5%	4.7	1	1	1	5	633,420	585,640	550,718	704,016	54,745	49,517	35,658	54,476	19.3	18.9	14.5	17.3	-1.1	0.5	-1.2	0.2	1.1	0.4	-1.1	0.6	1.2	0.1	1.3	0.05
IPI00398795	RTN3	isoform 2 of Reticulon-3	99.5%	1.1	1	1	1	5	633,420	585,640	550,718	704,016	54,745	49,517	35,658	54,476	19.3	18.9	14.5	17.3	-1.1	0.5	-1.2	0.2	1.1	0.4	-1.1	0.6	1.2	0.1	1.3	0.05
IPI00412154	RTN3	isoform 4 of Reticulon-3	99.5%	4.3	1	1	1	5	633,420	585,640	550,718	704,016	54,745	49,517	35,658	54,476	19.3	18.9	14.5	17.3	-1.1	0.5	-1.2	0.2	1.1	0.4	-1.1	0.6	1.2	0.1	1.3	0.05
IPI00743293	RTN3	isoform 1 of Reticulon-3	99.5%	1.1	1	1	1	5	633,420	585,640	550,718	704,016	54,745	49,517	35,658	54,476	19.3	18.9	14.5	17.3	-1.1	0.5	-1.2	0.2	1.1	0.4	-1.1	0.6	1.2	0.1	1.3	0.05
IPI01009279	RTN3	cDNA FLJ60267, highly similar to Homo sapiens reticulon 3 (RTN3), transcript varia	99.5%	1.2	1	1	1	5	633,420	585,640	550,718	704,016	54,745	49,517	35,658	54,476	19.3	18.9	14.5	17.3	-1.1	0.5	-1.2	0.2	1.1	0.4	-1.1	0.6	1.2	0.1	1.3	0.05
				TQIDHYVGIAR	2	99.5%	1																									
IPI00028954	MCM3AP	80 kDa MCM3-associated protein	100.0%	2.3	2	2	2	1	5,339,060	5,218,940	4,904,785	5,410,471	617,339	157,589	446,368	412,318	25.9	6.8	20.4	17.0	-1.0	0.9	-1.1	0.6	1.0	0.9	-1.1	0.5	1.0	0.7	1.1	0.4
				CCEDVCAHLVDLFLVEEIFQTAK	3	92.1%	1																									
				VMMEFVRETCSQELKNAVETDQR	3	99.7%	1																									
IPI00028957	UBE4A	isoform 2 of Ubiquitin conjugation factor E4 A	92.0%	0.8	1	1	1	4	1,171,238	1,258,403	1,192,075	1,496,690	88,367	60,434	111,974	38,405	16.9	10.7	21.0	5.7	1.1	0.4	1.0	0.9	1.3	0.01	-1.1	0.6	1.2	0.01	1.3	0.05
IPI00556075	UBE4A	isoform 1 of Ubiquitin conjugation factor E4 A	92.0%	0.8	1	1	1	4	1,171,238	1,258,403	1,192,075	1,496,690	88,367	60,434	111,974	38,405	16.9	10.7	21.0	5.7	1.1	0.4	1.0	0.9	1.3	0.01	-1.1	0.6	1.2	0.01	1.3	0.05
IPI00807340	UBE4A	UBE4A protein (Fragment)	92.0%	2.3	1	1	1	4	1,171,238	1,258,403	1,192,075	1,496,690	88,367	60,434	111,974	38,405	16.9	10.7	21.0	5.7	1.1	0.4	1.0	0.9	1.3	0.01	-1.1	0.6	1.2	0.01	1.3	0.05
IPI00943223	UBE4A	46 kDa protein	92.0%	2.3	1	1	1	4	1,171,238	1,258,403	1,192,075	1,496,690	88,367	60,434	111,974	38,405	16.9	10.7	21.0	5.7	1.1	0.4	1.0	0.9	1.3	0.01	-1.1	0.6	1.2	0.01	1.3	0.05
				VFVEYIQPK	2	92.0%	1																									
IPI00029011	KIF1B	isoform 1 of Kinesin-like protein KIF1B	93.7%	0.6	1	1	1	4	595,113	645,475	631,468	680,448	34,087	23,998	75,500	72,736	12.8	8.3	26.7	23.9	1.1	0.3	1.1	0.7	1.1	0.3	-1.0	0.9	1.1	0.7	1.1	0.7
IPI00216252	KIF1B	isoform 2 of Kinesin-like protein KIF1B	93.7%	0.6	1	1	1	4	595,113	645,475	631,468	680,448	34,087	23,998	75,500	72,736	12.8	8.3	26.7	23.9	1.1	0.3	1.1	0.7	1.1	0.3	-1.0	0.9	1.1	0.7	1.1	0.7
IPI00397383	KIF1B	isoform 4 of Kinesin-like protein KIF1B	93.7%	0.6	1	1	1	4	595,113	645,475	631,468	680,448	34,087	23,998	75,500	72,736	12.8	8.3	26.7	23.9	1.1	0.3	1.1	0.7	1.1	0.3	-1.0	0.9	1.1	0.7	1.1	0.7
IPI01010528	KIF1B	205 kDa protein	93.7%	0.6	1	1	1	4	595,113	645,475	631,468	680,448	34,087	23,998	75,500	72,736	12.8	8.3	26.7	23.9	1.1	0.3	1.1	0.7	1.1	0.3	-1.0	0.9	1.1	0.7	1.1	0.7
				DLLWGNAVYLK	2	91.1%	1																									
IPI00029012	EIF3A	Eukaryotic translation initiation factor 3 subunit A	100.0%	10.6	12	12	14	1	36,750,813	40,532,193	35,721,902	43,941,876	4,288,808	1,718,905	3,651,482	1,774,975	26.1	9.5	22.9	9.0	1.1	0.4	-1.0	0.9	1.2	0.2	-1.1	0.3	1.1	0.2	1.2	0.08
				ANEFLEVGK	2	98.8%	1																									
				DLYNWLEVEFNPLK	2	100.0%	1																									
				EDAPIGPHLQSMPSEQIR	3	96.9%	1																									
				FNVLQYVVPEVK	2	100.0%	2																									
				ITTMQLER	2	99.2%	1																									
				LESLNIQR	2	93.3%	1																									
				LLDMDGIIVEK	2	99.3%	1																									
				LTSLVPFVDAFQLER	2	97.9%	1																									
				LVQLDSAISMELWQEAFK	2	100.0%	1																									
				NQLTAMSSVLAK	2	99.7%	2																									
				RVPPPALSR	2	98.9%	1																									
				TLSFGSDLNYATR	2	96.9%	1																									
IPI00029019	UBAP2L	isoform 2 of Ubiquitin-associated protein 2-like	100.0%	7.8	5	5	5	5	8,151,325	8,699,354	8,153,764	9,257,556	338,353	204,484	533,871	169,353	9.3	5.3	14.6	4.1	1.1	0.2	1.0	1	1.1	0.02	-1.1	0.4	1.1	0.07	1.1	0.1
IPI00181306	UBAP2L	isoform 3 of Ubiquitin-associated protein 2-like	100.0%	7.2	5	5	5	5	8,151,325	8,699,354	8,153,764	9,257,556	338,353	204,484	533,871	169,353	9.3	5.3	14.6	4.1	1.1	0.2	1.0	1	1.1	0.02	-1.1	0.4	1.1	0.07	1.1	0.1
IPI00514856	UBAP2L	isoform 1 of Ubiquitin-associated protein 2-like	100.0%	7.1	5	5	5	5	8,151,325	8,699,354	8,153,764	9,257,556	338,353	204,484	533,871	169,353	9.3	5.3	14.6	4.1	1.1	0.2	1.0	1	1.1	0.02	-1.1	0.4	1.1	0.07	1.1	0.1
IPI00646016	UBAP2L	cDNA FLJ55671, highly similar to Ubiquitin-associated protein 2-like	100.0%	7.1	5	5	5	5	8,151,325	8,699,354	8,153,764	9,257,556	338,353	204,484	533,871	169,353	9.3	5.3	14.6	4.1	1.1	0.2	1.0	1	1.1	0.02	-1.1	0.4	1.1	0.07	1.1	0.1
IPI00946257	UBAP2L	isoform 4 of Ubiquitin-associated protein 2-like	100.0%	7.9	5	5	5	5	8,151,325	8,699,354	8,153,764	9,257,556	338,353	204,484	533,871	169,353	9.3	5.3	14.6	4.1	1.1	0.2	1.0	1	1.1	0.02	-1.1	0.4	1.1	0.07	1.1	0.1
				AINVLLEGNPDTHSWEMVGK	3	97.3%	1																									
				DGSLASNPYSGDLTK	2	100.0%	1																									
				GGSTTGSQFLEQFK	2	100.0%	1																									
				QAFTPSSTMMEVFLQEK	2	100.0%	1																									
				YPSSISSSPQK	2	80.7%	1																									
IPI00029048	TTLL12	Tubulin--tyrosine ligase-like protein 12	100.0%	12.0	5	5	5	2	17,923,509	18,096,950	17,846,341	19,996,117	1,232,174	663,649	878,182	367,039	15.4	8.2	11.0	4.1	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.04	1.1	0.05
IPI00879002	TTLL12	Tubulin tyrosine ligase-like family, member 12	100.0%	12.1	5	5	5	2	17,923,509	18,096,950	17,846,341	19,996,117	1,232,174	663,649	878,182	367,039	15.4	8.2	11.0	4.1	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.04	1.1	0.05
				AFALNDLDDYEK	2	99.5%	1																									
				FTLTQSEADADILFNFSHFK	3	97.6%	1																									
				MPVWYIMDEFGSR	2	100.0%	1																									
				QYPEFPWTDVQAEIFR	2	99.4%	1																									
				VYTDVQQVASSLTHPR	3	97.4%	1																									
IPI00029056	SEPHS1	Selenide, water dikinase 1	99.9%	10.2	3	3	3	2	6,238,882	6,349,995	6,712,821	6,941,487	401,035	199,943	527,831	549,875	14.4	7.0	17.6	17.7	1.0	0.8	1.1	0.5	1.1	0.3	1.1	0.5	1.1	0.4	1.0	0.8
IPI01013430	SEPHS1	Selenophosphate synthetase 1 +E9a variant	99.9%	12.4	3	3	3	2	6,238,882	6,349,995	6,712,821	6,941,487	401,035	199,943	527,831	549,875	14.4	7.0	17.6	17.7	1.0	0.8	1.1	0.5	1.1	0.3	1.1	0.5	1.1	0.4	1.0	0.8
				ESFNPESYELDK	2	97.0%	1																									
				LGIGMDTCVIPLR	2	82.5%	1																									
				NEVSFVIHNLPVLAK	2	99.7%	1																									
IPI00029079	GMPS	GMP synthase [glutamine-hydrolyzing]	100.0%	14.6	6	6	6	1	16,755,234	18,926,413	16,474,156	20,268,274	1,649,824	862,700	1,445,666	940,101	22.0	10.2	19.6	10.4	1.1	0.3	-1.0	0.9	1.2	0.1	-1.1	0.2	1.1	0.3	1.2	0.06
				ELFVQSEIFPLETPAFAIK	2	99.9%	1																									
				ELGLPEELVSR	2	96.4%	1																									
				GLQKEEVVLLTHGDSVDK	3	100.0%	1																									
				HPFPGPGLAIR	2	86.6%	1																									
				IMYDLTSKPPGTTEWE	2	99.4%	1																									
				TFITSDFMTGIPATPGNEIPVEVVLK	2	99.5%	1																									
IPI00029107	WRN	Werner syndrome ATP-dependent helicase	97.4%	0.6	1	1	1	1	8,587,070	9,785,930	9,212,770	10,564,660	958,414	469,334	475,981	197,001	25.0	10.7	11.6	4.2	1.1	0.3	1.1	0.6	1.2	0.1	-1.1	0.4	1.1	0.2	1.1	0.03
				KLETTAQQR	2	89.1%	1																									
IPI00029143	GNB3	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3	99.5%	6.8	1	1	1	3	596,349	535,477	534,347	671,620	83,675	39,220	53,257	44,376	31.4	16.4	22.3	14.8	-1.1	0.5	-1.1	0.5	1.1	0.4	-1.0	1	1.3	0.05	1.3	0.08
IPI00386304	GNB3	Uncharacterized protein	99.5%	7.7	1	1	1	3	596,349	535,477	534,347	671,620	83,675	39,220	53,257	44,376	31.4	16.4	22.3	14.8	-1.1	0.5	-1.1	0.5	1.1	0.4	-1.0	1	1.3	0.05	1.3	0.08
IPI01011922	GNB3	37 kDa protein	99.5%	6.8	1	1	1	3	596,349	535,477	534,347	671,620	83,675	39,220	53,257	44,376	31.4	16.4	22.3	14.8	-1.1	0.5	-1.1	0.5	1.1	0.4	-1.0	1	1.3	0.05	1.3	0.08
				VSCLGVTADGMAVATGSWDSFLK	2	99.5%	1																									
IPI00029155	SIGIRR	isoform 1 of Single Ig IL-1-related receptor	99.1%	2.9	1	1	1	4	647,783	709,828	699,275	623,463	60,802	33,787	63,957	23,494	21.0	10.6	20.5	8.4	1.1	0.4	1.1	0.6	-1.0	0.7	-1.0	0.9	-1.1	0.07	-1.1	0.3
IPI00432567	SIGIRR	isoform 2 of Single Ig IL-1-related receptor	99.1%	2.4	1	1	1	4	647,783	709,828	699,275	623,463	60,802	33,787	63,957	23,494	21.0	10.6	20.5	8.4	1.1	0.4	1.1	0.6	-1.0	0.7	-1.0	0.9	-1.1	0.07	-1.1	0.3
IPI00952672	SIGIRR	Uncharacterized protein	99.1%	2.4	1	1	1	4	647,783	709,828	699,275	623,463	60,802	33,787	63,957	23,494	21.0	10.6	20.5	8.4	1.1	0.4	1.1	0.6	-1.0	0.7	-1.0	0.9	-1.1	0.07	-1.1	0.3
IPI00982596	SIGIRR	Uncharacterized protein	99.1%	6.4	1	1	1	4	647,783	709,828	699,275	623,463	60,802	33,787	63,957	23,494	21.0	10.6	20.5	8.4	1.1	0.4	1.1	0.6	-1.0	0.7	-1.0	0.9	-1.1	0.07	-1.1	0.3
				LIVVLSDAFLSR	2	99.1%	1																									
IPI00029159	MRE11A	cDNA FLJ38069 fis, clone CTONG2015434, highly similar to DOUBLE-STRAND BR	97.6%	1.4	1	1	1	4	3,810,275	4,213,225	4,012,175	4,564,250	409,955	219,820	281,919	177,150	24.1	11.7	15.7	8.7	1.1	0.4	1.1	0.7	1.2	0.1	-1.1	0.6	1.1	0.2	1.1	0.1
IPI00218853	MRE11A	isoform 2 of Double-strand break repair protein MRE11A	97.6%	1.5	1	1	1	4	3,810,275	4,213,225	4,012,175	4,564,250	409,955	219,820	281,919	177,150	24.1	11.7	15.7	8.7	1.1	0.4	1.1	0.7	1.2	0.1	-1.1	0.6	1.1	0.2	1.1	0.1
IPI00940798	MRE11A	isoform 1 of Double-strand break repair protein MRE11A	97.6%	1.4	1	1	1	4	3,810,275	4,213,225	4,012,175	4,564,250	409,955	219,820	281,919	177,150	24.1	11.7	15.7	8.7	1.1	0.4	1.1	0.7	1.2	0.1	-1.1	0.6	1.1	0.2	1.1	0.1
IPI01011534	MRE11A	81 kDa protein	97.6%	1.4	1	1	1	4	3,810,275	4,213,225	4,012,175	4,564,250	409,955	219,820	281,919	177,150	24.1	11.7	15.7	8.7	1.1	0.4	1.1	0.7	1.2	0.1	-1.1	0.6	1.1	0.2	1.1	0.1
				NVQLSLLTER	2	97.6%	1																									
IPI00029266	SNRPE	Small nuclear ribonucleoprotein E	100.0%	39.1	2	2	3	1	3,979,830	4,478,079	3,863,861	4,840,273	515,811	175,006	425,923	193,063	29.0	8.7	24.7	8.9	1.1	0.4	-1.0	0.9	1.2	0.2	-1.2	0.2	1.1	0.2	1.3	0.07
				IEGCIIGFDEYMNLVLDDAEEIHSK	3	100.0%	1																									
				VMVQPINLIFR	2	99.9%	2																									
IPI00029444	C12orf10	UPF0160 protein MYG1, mitochondrial	98.8%	9.3	2	2	2	2	3,778,405	3,752,560	4,228,845	3,743,145	248,581	126,528	122,029	247,309	14.7	7.5	6.5	14.8	-1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.03	-1.0	1	-1.1	0.1
IPI00304163	C12orf10	cDNA FLJ57902, highly similar to Protein MYG1	98.8%	10.8	2	2	2	2	3,778,405	3,752,560	4,228,845	3,743,145	248,581	126,528	122,029	247,309	14.7	7.5	6.5	14.8	-1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.03	-1.0	1	-1.1	0.1
				FQVDPSGEIVELAK	2	97.5%	1																									
				LLAQLLGTSEEDSMVGTLYDK	2	98.8%	1																									
IPI00029447	GOSR1	Golgi SNAP receptor complex member 1	99.4%	6.0	1	1	1	5	78,396	87,081	82,267	102,050	4,558	14,662	9,200	9,547	13.0	37.7	25.0	20.9	1.1	0.6	1.0	0.7	1.3	0.06	-1.1	0.8	1.2	0.4	1.2	0.2
IPI00044920	GOSR1	GOSR1 protein	99.4%	8.6	1	1	1	5	78,396	87,081	82,267	102,050	4,558	14,662	9,200	9,547	13.0	37.7	25.0	20.9	1.1	0.6	1.0	0.7	1.3	0.06	-1.1	0.8	1.2	0.4	1.2	0.2
IPI00477701	GOSR1	Golgi SNAP receptor complex member 1 isoform 2	99.4%	6.1	1	1	1	5	78,396	87,081	82,267	102,050	4,558	14,662	9,200	9,547	13.0	37.7	25.0	20.9	1.1	0.6	1.0	0.7	1.3	0.06	-1.1	0.8	1.2	0.4	1.2	0.2
IPI00479817	GOSR1	Golgi SNAP receptor complex member 1 isoform 3	99.4%	8.1	1	1	1	5	78,396	87,081	82,267	102,050	4,558	14,662	9,200	9,547	13.0	37.7	25.0	20.9	1.1	0.6	1.0	0.7	1.3	0.06	-1.1	0.8	1.2	0.4	1.2	0.2
IPI00942124	GOSR1	cDNA FLJ58038, highly similar to Golgi SNAP receptor complex member 1	99.4%	8.6	1	1	1	5	78,396	87,081	82,267	102,050	4,558	14,662	9,200	9,547	13.0	37.7	25.0	20.9	1.1	0.6	1.0	0.7	1.3	0.06	-1.1	0.8	1.2	0.4	1.2	0.2
				MFETMAIEIEQLLAR	2	99.4%	1																									
IPI00029468	ACTR1A	Alpha-centractin	100.0%	20.2	5	5	5	1	6,912,849	7,037,495	7,371,980	7,674,487	354,701	217,200	309,620	168,125	11.5	6.9	9.4	4.9	1.0	0.8	1.1	0.4	1.1	0.09	1.0	0.4	1.1	0.05	1.0	0.4
				AGFAGDQIPK	2	90.2%	1																									
				AQYYLPDGSTIEIGPSR	2	100.0%	1																									
				LYSTWIGGSILASLDTFK	2	86.9%	1																									
				LYSTWIGGSILASLDTFKK	3	100.0%	1																									
				TTGVVLDSGDGVTHAVPIYEGFAMPHSIMR	3	100.0%	1																									
IPI00029469	ACTR1B	Beta-centractin	100.0%	17.0	3	3	3	1	4,340,801	4,400,549	4,376,050	5,164,845	334,403	147,105	330,543	377,640	17.2	7.5	16.9	16.4	1.0	0.9	1.0	0.9	1.2	0.1	-1.0	0.9	1.2	0.1	1.2	0.2
				LYSTWIGGSILASLDTFKK	3	100.0%	1																									

				TTGVVLDSGDGVTHAVPIYEGFAMPHSIMR	3	100.0%	1																									
				VMAGALEGDLFIGPK	2	86.4%	1																									
IPI00029473	C17orf75	Protein Njmu-R1	98.7%	2.8	1	1	1	1	608,041	704,821	569,823	676,045	133,671	76,181	77,306	49,680	49.2	24.2	30.3	16.4	1.2	0.5	-1.1	0.8	1.1	0.7	-1.2	0.2	-1.0	0.8	1.2	0.3
				NVIAVLEEFMK	2	98.7%	1																									
IPI00029557	GRPEL1	GrpE protein homolog 1, mitochondrial	97.6%	5.1	1	1	1	2	2,660,980	3,053,290	3,050,495	3,182,145	168,328	167,081	237,457	211,147	14.1	12.2	17.4	14.8	1.1	0.1	1.1	0.2	1.2	0.09	-1.0	1	1.0	0.6	1.0	0.7
IPI00909181	GRPEL1	GrpE protein homolog	97.6%	5.6	1	1	1	2	2,660,980	3,053,290	3,050,495	3,182,145	168,328	167,081	237,457	211,147	14.1	12.2	17.4	14.8	1.1	0.1	1.1	0.2	1.2	0.09	-1.0	1	1.0	0.6	1.0	0.7
				DLLEVADVLEK	2	97.6%	1																									
IPI00029601	CTTN	Src substrate cortactin	100.0%	35.6	14	15	18	1	29,100,658	30,149,738	28,890,091	33,081,306	1,411,050	1,496,026	1,825,438	1,542,910	10.8	11.1	14.1	10.4	1.0	0.6	-1.0	0.9	1.1	0.09	-1.0	0.6	1.1	0.2	1.1	0.1
				ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK	3	100.0%	2																									
				DYSSGFGGK	1	90.9%	1																									
				GPVSGTEPEPVYSMEAADYR	2	100.0%	2																									
				GPVSGTEPEPVYSMEAADYR	3	100.0%	1																									
				LQLHESQKDYK	2	99.4%	1																									
				LRENVFQEHQTLK	3	100.0%	1																									
				NASTFEDVTQVSSAYQK	2	100.0%	1																									
				QDSAAVGFDYK	2	99.9%	1																									
				SAVGFDYQGK	2	100.0%	2																									
				SAVGFEYQGK	2	100.0%	1																									
				TQTPPVSPAPQPTEERLPSSPVYEDAASFK	3	99.0%	1																									
				VDKSAVGFEYQGK	2	100.0%	1																									
				VDQSAVGFEYQGK	2	99.0%	1																									
				YGIDKDKVDK	2	85.2%	1																									
				YGVQADRVDK	2	99.3%	1																									
IPI00029623	PSMA6	Proteasome subunit alpha type-6	100.0%	36.2	7	7	7	1	26,226,235	26,481,440	25,150,630	29,740,350	2,012,080	932,083	1,692,167	1,282,321	17.2	7.9	15.0	9.6	1.0	0.9	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.07	1.2	0.06
				AINQGGLTSVAVR	2	100.0%	1																									
				HITIFSPEGR	2	100.0%	1																									
				ILTEAEIDAHLVALAERD	3	97.0%	1																									
				ITENIGCVMTGMTADSR	2	100.0%	1																									
				LLDSSTVTHLFK	3	100.0%	1																									
				LYQVEYAFK	2	99.9%	1																									
				QTESTSFLEK	2	90.1%	1																									
IPI00029628	RCN2	Reticulocalbin-2	100.0%	27.1	5	5	5	2	38,187,661	42,179,662	37,938,821	47,288,845	4,292,478	2,514,286	3,184,977	2,594,839	25.1	13.3	18.8	12.3	1.1	0.4	-1.0	1	1.2	0.1	-1.1	0.3	1.1	0.2	1.2	0.05
IPI00790214	RCN2	39 kDa protein	100.0%	25.7	5	5	5	2	38,187,661	42,179,662	37,938,821	47,288,845	4,292,478	2,514,286	3,184,977	2,594,839	25.1	13.3	18.8	12.3	1.1	0.4	-1.0	1	1.2	0.1	-1.1	0.3	1.1	0.2	1.2	0.05
				LSEEEILENPDLFLTSEATDYGR	2	100.0%	1																									
				QQFVEYDKNSDDTVTWDEYNIQMYDR	3	98.0%	1																									
				VIDFDENTALDDAEEESFR	2	99.9%	1																									
				WDPTANEDPEWILVEK	2	99.4%	1																									
				WDPTANEDPEWILVEKDR	3	85.1%	1																									
IPI00029629	TRIM25	E3 ubiquitin/ISG15 ligase TRIM25	100.0%	4.6	2	3	3	1	7,822,091	7,542,208	7,711,605	8,187,248	663,900	335,432	435,687	375,981	19.0	9.9	12.6	10.3	-1.0	0.7	-1.0	0.9	1.0	0.6	1.0	0.8	1.1	0.2	1.1	0.4
				NTVLCNVVEQFLQADLAR	2	100.0%	1																									
				NTVLCNVVEQFLQADLAR	3	100.0%	1																									
				VILDYNTAHNK	2	91.9%	1																									
IPI00029631	ERH	Enhancer of rudimentary homolog	100.0%	38.5	4	5	6	1	12,484,916	13,631,211	13,790,898	16,178,052	1,449,105	663,704	1,215,484	655,388	26.0	10.9	19.7	9.1	1.1	0.5	1.1	0.5	1.3	0.05	1.0	0.9	1.2	0.03	1.2	0.1
				ADTQTYQPYNK	2	99.9%	2																									
				ADTQTYQPYNKDWIK	2	99.9%	1																									
				ADTQTYQPYNKDWIK	3	99.0%	1																									
				MYEEHLKR	2	99.8%	1																									
				TYADYESVNECMEGVCK	2	100.0%	1																									
IPI00029693	NRP2	isoform A22 of Neuropilin-2	98.4%	3.7	2	2	2	8	1,652,378	1,625,134	1,339,025	1,737,011	179,085	87,611	110,228	139,896	24.2	12.1	18.4	18.0	-1.0	0.9	-1.2	0.2	1.1	0.7	-1.2	0.08	1.1	0.5	1.3	0.06
IPI00218781	NRP2	isoform A17 of Neuropilin-2	98.4%	3.7	2	2	2	8	1,652,378	1,625,134	1,339,025	1,737,011	179,085	87,611	110,228	139,896	24.2	12.1	18.4	18.0	-1.0	0.9	-1.2	0.2	1.1	0.7	-1.2	0.08	1.1	0.5	1.3	0.06
IPI00300890	NRP2	neuropilin-2 isoform 4 precursor	98.4%	3.8	2	2	2	8	1,652,378	1,625,134	1,339,025	1,737,011	179,085	87,611	110,228	139,896	24.2	12.1	18.4	18.0	-1.0	0.9	-1.2	0.2	1.1	0.7	-1.2	0.08	1.1	0.5	1.3	0.06
IPI00300891	NRP2	neuropilin-2 isoform 5 precursor	98.4%	3.8	2	2	2	8	1,652,378	1,625,134	1,339,025	1,737,011	179,085	87,611	110,228	139,896	24.2	12.1	18.4	18.0	-1.0	0.9	-1.2	0.2	1.1	0.7	-1.2	0.08	1.1	0.5	1.3	0.06
IPI00398766	NRP2	neuropilin-2 isoform 6 precursor	98.4%	6.1	2	2	2	8	1,652,378	1,625,134	1,339,025	1,737,011	179,085	87,611	110,228	139,896	24.2	12.1	18.4	18.0	-1.0	0.9	-1.2	0.2	1.1	0.7	-1.2	0.08	1.1	0.5	1.3	0.06
IPI00914842	NRP2	isoform A0 of Neuropilin-2	98.4%	3.7	2	2	2	8	1,652,378	1,625,134	1,339,025	1,737,011	179,085	87,611	110,228	139,896	24.2	12.1	18.4	18.0	-1.0	0.9	-1.2	0.2	1.1	0.7	-1.2	0.08	1.1	0.5	1.3	0.06
IPI01011597	NRP2	102 kDa protein	98.4%	3.7	2	2	2	8	1,652,378	1,625,134	1,339,025	1,737,011	179,085	87,611	110,228	139,896	24.2	12.1	18.4	18.0	-1.0	0.9	-1.2	0.2	1.1	0.7	-1.2	0.08	1.1	0.5	1.3	0.06
IPI01013755	NRP2	104 kDa protein	98.4%	3.7	2	2	2	8	1,652,378	1,625,134	1,339,025	1,737,011	179,085	87,611	110,228	139,896	24.2	12.1	18.4	18.0	-1.0	0.9	-1.2	0.2	1.1	0.7	-1.2	0.08	1.1	0.5	1.3	0.06
				MDMFPLTWVFLALYFSR	2	81.0%	1																									
				NFTSPNGTIESPGFPEK	3	91.8%	1																									
IPI00029702	PTK2B	isoform 1 of Protein-tyrosine kinase 2-beta	98.0%	1.6	1	1	1	4	1,599,498	1,397,265	1,751,850	1,516,258	95,274	72,399	155,843	30,276	13.3	11.6	19.9	4.5	-1.1	0.1	1.1	0.4	-1.1	0.4	1.3	0.07	1.1	0.2	-1.2	0.2
IPI00216435	PTK2B	isoform 2 of Protein-tyrosine kinase 2-beta	98.0%	1.7	1	1	1	4	1,599,498	1,397,265	1,751,850	1,516,258	95,274	72,399	155,843	30,276	13.3	11.6	19.9	4.5	-1.1	0.1	1.1	0.4	-1.1	0.4	1.3	0.07	1.1	0.2	-1.2	0.2
IPI00443767	PTK2B	Uncharacterized protein	98.0%	2.7	1	1	1	4	1,599,498	1,397,265	1,751,850	1,516,258	95,274	72,399	155,843	30,276	13.3	11.6	19.9	4.5	-1.1	0.1	1.1	0.4	-1.1	0.4	1.3	0.07	1.1	0.2	-1.2	0.2
IPI00985238	PTK2B	Protein	98.0%	8.2	1	1	1	4	1,599,498	1,397,265	1,751,850	1,516,258	95,274	72,399	155,843	30,276	13.3	11.6	19.9	4.5	-1.1	0.1	1.1	0.4	-1.1	0.4	1.3	0.07	1.1	0.2	-1.2	0.2
				RNSLPQIPMLNLEARR	2	98.0%	1																									
IPI00029733	AKR1C1	Aldo-keto reductase family 1 member C1	100.0%	26.3	6	6	7	1	4,973,306	5,091,858	4,887,037	5,726,450	470,948	189,167	306,119	188,496	21.2	8.3	14.0	7.4	1.0	0.8	-1.0	0.9	1.2	0.2	-1.0	0.6	1.1	0.04	1.2	0.05
				HIDSAHLYNNEEQVGLAIR	3	100.0%	1																									
				LAIEAGFR	2	97.8%	1																									
				LNDGHFMPVLGFGTYAPAEVPK	3	100.0%	1																									
				QLEMILNKPGLK	3	81.8%	1																									
				QNVQVFEFQLTSEEMK	2	98.0%	1																									
				TPALIALR	2	99.8%	2																									
IPI00031397	ACSL3	Long-chain-fatty-acid--CoA ligase 3	99.6%	2.5	1	1	2	4	2,244,245	2,554,408	2,183,805	3,003,525	326,213	160,044	288,409	215,446	32.5	14.0	29.5	16.0	1.1	0.4	-1.0	0.9	1.3	0.09	-1.2	0.3	1.2	0.1	1.4	0.05
IPI00029737	ACSL4	isoform Long of Long-chain-fatty-acid--CoA ligase 4	99.6%	2.5	1	1	2	4	2,244,245	2,554,408	2,183,805	3,003,525	326,213	160,044	288,409	215,446	32.5	14.0	29.5	16.0	1.1	0.4	-1.0	0.9	1.3	0.09	-1.2	0.3	1.2	0.1	1.4	0.05
IPI00219897	ACSL4	isoform Short of Long-chain-fatty-acid--CoA ligase 4	99.6%	2.7	1	1	2	4	2,244,245	2,554,408	2,183,805	3,003,525	326,213	160,044	288,409	215,446	32.5	14.0	29.5	16.0	1.1	0.4	-1.0	0.9	1.3	0.09	-1.2	0.3	1.2	0.1	1.4	0.05
IPI00908902	ACSL4	cDNA FLJ57028, highly similar to Long-chain-fatty-acid--CoA ligase 4	99.6%	2.8	1	1	2	4	2,244,245	2,554,408	2,183,805	3,003,525	326,213	160,044	288,409	215,446	32.5	14.0	29.5	16.0	1.1	0.4	-1.0	0.9	1.3	0.09	-1.2	0.3	1.2	0.1	1.4	0.05
				LSPEPWTPETGLVTDAFK	2	99.6%	2																									
IPI00029744	SSBP1	Single-stranded DNA-binding protein, mitochondrial	100.0%	27.7	3	3	4	1	17,285,536	17,395,609	17,212,495	18,721,550	1,830,040	841,123	1,345,343	479,655	23.7	10.8	17.5	5.7	1.0	1	-1.0	1	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.3
				QATTIIADNIIFLSDQTK	3	100.0%	1																									
				SGDSEVYQLGDVSQK	2	100.0%	2																									
				VGQDPVLR	2	99.8%	1																									
IPI00029750	RPS24	isoform 1 of 40S ribosomal protein S24	100.0%	19.6	2	2	2	5	2,519,232	2,757,424	2,913,156	2,842,974	280,971	149,513	248,009	170,073	24.9	12.1	19.0	13.4	1.1	0.5	1.2	0.3	1.1	0.4	1.1	0.6	1.0	0.7	-1.0	0.8
IPI00847986	RPS24	isoform 2 of 40S ribosomal protein S24	100.0%	20.0	2	2	2	5	2,519,232	2,757,424	2,913,156	2,842,974	280,971	149,513	248,009	170,073	24.9	12.1	19.0	13.4	1.1	0.5	1.2	0.3	1.1	0.4	1.1	0.6	1.0	0.7	-1.0	0.8
IPI00903204	RPS24	40S ribosomal protein S24 isoform f	100.0%	19.7	2	2	2	5	2,519,232	2,757,424	2,913,156	2,842,974	280,971	149,513	248,009	170,073	24.9	12.1	19.0	13.4	1.1	0.5	1.2	0.3	1.1	0.4	1.1	0.6	1.0	0.7	-1.0	0.8
IPI00915363	RPS24	40S ribosomal protein S24 isoform d	100.0%	9.0	2	2	2	5	2,519,232	2,757,424	2,913,156	2,842,974	280,971	149,513	248,009	170,073	24.9	12.1	19.0	13.4	1.1	0.5	1.2	0.3	1.1	0.4	1.1	0.6	1.0	0.7	-1.0	0.8
IPI00915463	RPS24	isoform 3 of 40S ribosomal protein S24	100.0%	19.7	2	2	2	5	2,519,232	2,757,424	2,913,156	2,842,974	280,971	149,513	248,009	170,073	24.9	12.1	19.0	13.4	1.1	0.5	1.2	0.3	1.1	0.4	1.1	0.6	1.0	0.7	-1.0	0.8
				QMVIDVLHPGK	3	98.1%	1																									
				TTGFGMIYDSLDYAK	2	100.0%	1																									
IPI00029764	SF3A3	Splicing factor 3A subunit 3	100.0%	10.4	4	4	5	2	9,403,325	10,500,174	9,005,262	11,551,510	1,192,382	574,389	833,321	350,403	28.4	12.2	20.7	6.8	1.1	0.4	-1.0	0.8	1.2	0.1	-1.2	0.2	1.1	0.2	1.3	0.02
IPI00908449	SF3A3	cDNA FLJ58737, highly similar to Splicing factor 3A subunit 3	100.0%	11.6	4	4	5	2	9,403,325	10,500,174	9,005,262	11,551,510	1,192,382	574,389	833,321	350,403	28.4	12.2	20.7	6.8	1.1	0.4	-1.0	0.8	1.2	0.1	-1.2	0.2	1.1	0.2	1.3	0.02
				LFSTKGKSLESLDTSLFAK	3	91.7%	1																									
				SLESLDTSLFAK	2	99.8%	2																									
				VKPLQDQNELFGK	3	95.4%	1																									
				WQPDTEEEYEDSSGNVVNKK	3	99.0%	1																									
IPI00029778	TP53BP1	isoform 1 of Tumor suppressor p53-binding protein 1	96.8%	1.4	2	2	2	3	2,608,840	2,896,233	2,348,183	3,040,867	285,756	182,303	184,473	265,822	24.5	14.1	17.6	19.6	1.1	0.4	-1.1	0.5	1.2	0.3	-1.2	0.07	1.0	0.7	1.3	0.06
IPI00657708	TP53BP1	tumor suppressor p53-binding protein 1 isoform 2	96.8%	1.5	2	2	2	3	2,608,840	2,896,233	2,348,183	3,040,867	285,756	182,303	184,473	265,822	24.5	14.1	17.6	19.6	1.1	0.4	-1.1	0.5	1.2	0.3	-1.2	0.07	1.0	0.7	1.3	0.06
IPI00742743	TP53BP1	isoform 2 of Tumor suppressor p53-binding protein 1	96.8%	1.4	2	2	2	3	2,608,840	2,896,233	2,348,183	3,040,867	285,756	182,303	184,473	265,822	24.5	14.1	17.6	19.6	1.1	0.4	-1.1	0.5	1.2	0.3	-1.2	0.07	1.0	0.7	1.3	0.06
				VITDVYYVDGTEVER	2	95.5%	1																									
				VPETVSAATQTIK	2	96.8%	1																									
IPI00029817	NEU1	Sialidase-1	92.1%	3.9	1	1	1	2	2,248,040	2,222,325	2,313,545	2,777,785	218,345	276,609	216,481	177,454	21.7	27.8	20.9	14.3	-1.0	0.9	1.0	0.8	1.2	0.1	1.0	0.8	1.2	0.1	1.2	0.1
IPI00978251	NEU1	Uncharacterized protein	92.1%	6.0	1	1	1	2	2,248,040	2,222,325	2,313,545	2,777,785	218,345	276,609	216,481	177,454	21.7	27.8	20.9	14.3	-1.0	0.9	1.0	0.8	1.2	0.1	1.0	0.8	1.2	0.1	1.2	0.1
				DGVFCLLSDDHGASWR	3	92.1%	1																									
IPI00029997	PGLS	6-phosphogluconolactonase	100.0%	24.8	5	5	5	1	33,538,350	35,332,395	30,697,240	40,533,210	2,987,893	2,639,545	3,688,011	2,793,721	19.9	16.7	26.9	15.4	1.1	0.7	-1.1	0.6	1.2	0.1	-1.2	0.3	1.1	0.2	1.3	0.07
				AACCLAGAR	2	99.9%	1																									
				ILEDQEENPLPAALVQPHTGK	3	100.0%	1																									
				LCWFLDEAAAR	2	100.0%	1																									
				TVIFVATGEGK	2	99.7%	1																									
				VTLTLPVLNAAR	2	96.6%	1																									
IPI00030009	PAPSS2	isoform A of Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	100.0%	4.7	2	2	2	4	2,119,699	2,419,077	2,513,415	2,383,158	305,555	283,533	370,267	124,364	32.2	26.2	32.9	11.7	1.1	0.5	1.2	0.4	1.1	0.4	1.0	0.8	-1.0	0.9	-1.1	0.8
IPI00220873	PAPSS2	isoform B of Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	100.0%	4.7	2	2	2	4	2,119,699	2,419,077	2,513,415	2,383,158	305,555	283,533	370,267	124,364	32.2	26.2	32.9	11.7	1.1	0.5	1.2	0.4	1.1	0.4	1.0	0.8	-1.0	0.9	-1.1	0.8
IPI00940970	PAPSS2	Uncharacterized protein	100.0%	4.7	2	2	2	4	2,119,699	2,419,077	2,513,415	2,383,158	305,555	283,533	370,267	124,364	32.2	26.2	32.9	11.7	1.1	0.5	1.2	0.4	1.1	0.4	1.0	0.8	-1.0	0.9	-1.1	0.8
IPI01011355	PAPSS2	cDNA FLJ53931, highly similar to Bifunctional 3'-phosphoadenosine5'-phosphosulfat	100.0%	4.7	2	2	2	4	2,119,699	2,419,077	2,513,415	2,383,158	305,555	283,533	370,267	124,364	32.2	26.2	32.9	11.7	1.1	0.5	1.2	0.4	1.1	0.4	1.0	0.8	-1.0	0.9	-1.1	0.8
				HNEFDFISGTR	2	96.7%	1																									
				LDLQWVQVLSEGWATPLK	2	100.0%	1																									
IPI00030023	HNMT	Histamine N-methyltransferase	100.0%	23.3	4	5	6	1	26,499,619	28,948,984	26,145,062	30,545,103	1,831,180	1,472,866	2,352,731	1,341,271	15.5	11.4	20.1	9.8	1.1	0.3	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.4	1.2	0.1
				AELGKDLQEPEFSAK	2	94.6%	1																									
				AELGKDLQEPEFSAK	3	90.4%	1																									
				FFHSLLGTNAK	3	89.1%	1																									
				ILSIGGGAGEIDLQILSK	2	99.8%	2																									
				VQAQYPGVCINNEVVEPSAEQIAK	3	99.8%	1																									
IPI00030033	TACC2	isoform 1 of Transforming acidic coiled-coil-containing protein 2	100.0%	4.9	2	2	2	10	697,648	762,013	699,019	815,422	76,619	51,539	62,159	34,183	24.6	15.1	19.9	9.4	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
IPI00384450	TACC2	isoform 2 of Transforming acidic coiled-coil-containing protein 2	100.0%	8.8	2	2	2	10	697,648	762,013	699,019	815,422	76,619	51,539	62,159	34,183	24.6	15.1	19.9	9.4	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
IPI00410127	TACC2	isoform 5 of Transforming acidic coiled-coil-containing protein 2	100.0%	4.6	2	2	2	10	697,648	762,013	699,019	815,422	76,619	51,539	62,159	34,183	24.6	15.1	19.9	9.4	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
IPI00410301	TACC2	Transforming, acidic coiled-coil containing protein 2	100.0%	4.8	2	2	2	10	697,648	762,013	699,019	815,422	76,619	51,539	62,159	34,183	24.6	15.1	19.9	9.4	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
IPI00642773	TACC2	isoform 6 of Transforming acidic coiled-coil-containing protein 2	100.0%	5.0	2	2	2	10	697,648	762,013	699,019	815,422	76,619	51,539	62,159	34,183	24.6	15.1	19.9	9.4	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
IPI00643465	TACC2	isoform 4 of Transforming acidic coiled-coil-containing protein 2	100.0%	1.7	2	2	2	10	697,648	762,013	699,019	815,422	76,619	51,539	62,159	34,183	24.6	15.1	19.9	9.4	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
IPI00935164	TACC2	isoform 3 of Transforming acidic coiled-coil-containing protein 2	100.0%	1.7	2	2	2	10	697,648	762,013	699,019	815,422	76,619	51,539	62,159	34,183	24.6	15.1	19.9	9.4	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
IPI00943614	TACC2	Transforming, acidic coiled-coil containing protein 2	100.0%	8.7	2	2	2	10	697,648	762,013	699,019	815,422	76,619	51,539	62,159	34,183	24.6	15.1	19.9	9.4	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
IPI00963962	TACC2	Uncharacterized protein	100.0%	1.7	2	2	2	10	697,648	762,013	699,019	815,422	76,619	51,539	62,159	34,183	24.6	15.1	19.9	9.4	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
IPI01012495	TACC2	Uncharacterized protein	100.0%	5.0	2	2	2	10	697,648	762,013	699,019	815,422	76,619	51,539	62,159	34,183	24.6	15.1	19.9	9.4	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
				GTYTFDIDKWDDPNFNPFSSTSK	3	99.4%	1																									
				IGTAEVEKPAGLLFQQPDLDSALQIAR	3	99.5%	1																									
IPI00030104	MYBPC2	Myosin-binding protein C, fast-type	99.9%	1.6	1	1	1	1	6,901,260	6,565,310	5,456,450	6,310,220	1,358,556	822,497	414,026	316,431	44.0	28.0	17.0	11.2	-1.1	0.8	-1.3	0.4	-1.1	0.7	-1.2	0.3	-1.0	0.8	1.2	0.1
				ESHNSASNVYTVELHIGK	3	99.9%	1																									
IPI00830089	-	Thymopoietin zeta isoform	99.9%	14.1	2	2	2	4	1,423,864	1,279,442	1,399,442	1,430,592	65,483	34,165	73,291	69,069	10.3	6.0	11.7	10.8	-1.1	0.09	-1.0	0.8	1.0	0.9	1.1	0.2	1.1	0.09	1.0	0.8
IPI00030131	TMPO	isoform Beta of Lamina-associated polypeptide 2, isoforms beta/gamma	99.9%	7.7	2	2	2	4	1,423,864	1,279,442	1,399,442	1,430,592	65,483	34,165	73,291	69,069	10.3	6.0	11.7	10.8	-1.1	0.09	-1.0	0.8	1.0	0.9	1.1	0.2	1.1	0.09	1.0	0.8
IPI00181409	TMPO	isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma	99.9%	10.1	2	2	2	4	1,423,864	1,279,442	1,399,442	1,430,592	65,483	34,165	73,291	69,069	10.3	6.0	11.7	10.8	-1.1	0.09	-1.0	0.8	1.0	0.9	1.1	0.2	1.1	0.09	1.0	0.8
IPI00873716	TMPO	Lamina-associated polypeptide 2, isoforms beta/gamma variant (Fragment)	99.9%	9.3	2	2	2	4	1,423,864	1,279,442	1,399,442	1,430,592	65,483	34,165	73,291	69,069	10.3	6.0	11.7	10.8	-1.1	0.09	-1.0	0.8	1.0	0.9	1.1	0.2	1.1	0.09	1.0	0.8
				NRPPLPAGTNSK	2	99.0%	1																									
				QEDKDDLDVTELTNEDLLDQLVK	3	98.2%	1																									
IPI00030179	RPL7	60S ribosomal protein L7	100.0%	17.7	4	4	5	3	14,739,616	15,687,937	15,804,881	18,109,991	619,694	812,135	1,194,035	1,163,087	9.4	11.6	16.9	14.4	1.1	0.4	1.1	0.5	1.2	0.03	1.0	0.9	1.2	0.1	1.1	0.2
IPI00472171	RPL7P32;RPL7	30 kDa protein	100.0%	17.0	4	4	5	3	14,739,616	15,687,937	15,804,881	18,109,991	619,694	812,135	1,194,035	1,163,087	9.4	11.6	16.9	14.4	1.1	0.4	1.1	0.5	1.2	0.03	1.0	0.9	1.2	0.1	1.1	0.2
IPI00794746	RPL7P32;RPL7	Uncharacterized protein	100.0%	21.2	4	4	5	3	14,739,616	15,687,937	15,804,881	18,109,991	619,694	812,135	1,194,035	1,163,087	9.4	11.6	16.9	14.4	1.1	0.4	1.1	0.5	1.2	0.03	1.0	0.9	1.2	0.1	1.1	0.2
				EANNFLWPFK	2	99.8%	1																									
				IALTDNALIAR	2	99.9%	1																									
				IVEPYIAWGYPNLK	2	100.0%	2																									
				QIFNGTFVK	2	90.0%	1																									
IPI00030182	GAMT	Guanidinoacetate N-methyltransferase	97.6%	5.9	1	1	1	1	2,426,890	2,624,050	2,624,920	3,040,580	293,533	160,027	119,256	231,811	27.1	13.6	10.2	17.1	1.1	0.6	1.1	0.5	1.3	0.1	1.0	1	1.2	0.2	1.2	0.1
				YYAFPQMITPLVTK	2	97.6%	1																									

IPI00030207	GMDS	GDP-mannose 4,6 dehydratase	99.9%	9.1	2	3	3	1	3,833,779	3,791,785	3,782,521	4,557,045	142,134	224,736	385,597	127,957	8.3	13.3	22.8	6.3	-1.0	0.9	-1.0	0.9	1.2	0.005	-1.0	1	1.2	0.02	1.2	0.1
				ISFDLAEYTADVDGVGTLR	2	99.6%	1																									
				ISFDLAEYTADVDGVGTLR	3	99.5%	1																									
				VQEIPQKETTPFYPR	3	87.2%	1																									
IPI00218830	NMT1	isoform Short of Glycylpeptide N-tetradecanoyltransferase 1	100.0%	3.4	1	1	1	7	199,458	212,231	242,724	220,939	12,430	24,814	19,141	7,640	13.9	26.1	17.6	7.7	1.1	0.7	1.2	0.09	1.1	0.2	1.1	0.4	1.0	0.8	-1.1	0.3
IPI00329692	NMT1	isoform Long of Glycylpeptide N-tetradecanoyltransferase 1	100.0%	2.8	1	1	1	7	199,458	212,231	242,724	220,939	12,430	24,814	19,141	7,640	13.9	26.1	17.6	7.7	1.1	0.7	1.2	0.09	1.1	0.2	1.1	0.4	1.0	0.8	-1.1	0.3
IPI00030223	NMT2	Glycylpeptide N-tetradecanoyltransferase 2	100.0%	2.8	1	1	1	7	199,458	212,231	242,724	220,939	12,430	24,814	19,141	7,640	13.9	26.1	17.6	7.7	1.1	0.7	1.2	0.09	1.1	0.2	1.1	0.4	1.0	0.8	-1.1	0.3
IPI00478260	NMT2	Glycylpeptide N-tetradecanoyltransferase	100.0%	2.7	1	1	1	7	199,458	212,231	242,724	220,939	12,430	24,814	19,141	7,640	13.9	26.1	17.6	7.7	1.1	0.7	1.2	0.09	1.1	0.2	1.1	0.4	1.0	0.8	-1.1	0.3
IPI00815834	NMT2	Uncharacterized protein	100.0%	18.2	1	1	1	7	199,458	212,231	242,724	220,939	12,430	24,814	19,141	7,640	13.9	26.1	17.6	7.7	1.1	0.7	1.2	0.09	1.1	0.2	1.1	0.4	1.0	0.8	-1.1	0.3
IPI01010722	NMT2	Glycylpeptide N-tetradecanoyltransferase	100.0%	2.9	1	1	1	7	199,458	212,231	242,724	220,939	12,430	24,814	19,141	7,640	13.9	26.1	17.6	7.7	1.1	0.7	1.2	0.09	1.1	0.2	1.1	0.4	1.0	0.8	-1.1	0.3
IPI01015827	NMT2	Glycylpeptide N-tetradecanoyltransferase	100.0%	4.5	1	1	1	7	199,458	212,231	242,724	220,939	12,430	24,814	19,141	7,640	13.9	26.1	17.6	7.7	1.1	0.7	1.2	0.09	1.1	0.2	1.1	0.4	1.0	0.8	-1.1	0.3
				GFDVFNALDLMENK	2	100.0%	1																									
IPI00030229	GALE	Uncharacterized protein	100.0%	22.5	6	7	8	1	6,870,419	7,493,092	7,053,961	8,334,200	474,947	302,799	297,611	289,796	15.5	9.0	9.4	7.8	1.1	0.3	1.0	0.8	1.2	0.03	-1.1	0.3	1.1	0.08	1.2	0.02
				DYIHVVDLAK	2	93.1%	1																									
				DYIHVVDLAK	3	99.7%	1																									
				EALNVFGNDYDTEDGTGVR	2	100.0%	1																									
				EALNVFGNDYDTEDGTGVRDYIHVVDLAK	3	99.2%	1																									
				FFIEEMIR	2	99.8%	1																									
				MCEDLWR	2	99.9%	1																									
				VNLTGTIQLLEIMK	2	100.0%	2																									
IPI00030243	PSME3	isoform 1 of Proteasome activator complex subunit 3	100.0%	4.3	1	1	1	4	771,290	934,748	787,295	1,044,078	101,197	74,465	59,301	82,733	29.3	17.8	16.8	17.7	1.2	0.2	1.0	0.9	1.4	0.07	-1.2	0.2	1.1	0.4	1.3	0.04
IPI00219445	PSME3	isoform 2 of Proteasome activator complex subunit 3	100.0%	4.1	1	1	1	4	771,290	934,748	787,295	1,044,078	101,197	74,465	59,301	82,733	29.3	17.8	16.8	17.7	1.2	0.2	1.0	0.9	1.4	0.07	-1.2	0.2	1.1	0.4	1.3	0.04
IPI00795743	PSME3	15 kDa protein	100.0%	8.9	1	1	1	4	771,290	934,748	787,295	1,044,078	101,197	74,465	59,301	82,733	29.3	17.8	16.8	17.7	1.2	0.2	1.0	0.9	1.4	0.07	-1.2	0.2	1.1	0.4	1.3	0.04
IPI01010908	PSME3	cDNA FLJ32659 fis, clone TESTI1000045, highly similar to Proteasome activator co	100.0%	5.7	1	1	1	4	771,290	934,748	787,295	1,044,078	101,197	74,465	59,301	82,733	29.3	17.8	16.8	17.7	1.2	0.2	1.0	0.9	1.4	0.07	-1.2	0.2	1.1	0.4	1.3	0.04
				SNQQLVDIIEK	2	99.5%	1																									
IPI00030255	PLOD3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	100.0%	9.4	5	5	7	1	9,900,982	9,386,288	11,644,142	10,943,275	543,605	452,287	554,628	581,433	12.3	10.8	10.7	11.9	-1.1	0.5	1.2	0.06	1.1	0.2	1.2	0.01	1.2	0.07	-1.1	0.4
				IFQNLNGALDEVVLK	2	96.5%	1																									
				LVGPEEALSPGEAR	2	100.0%	1																									
				LWSNFWGALSPDEYYAR	2	100.0%	2																									
				QVGYEDQWLQLLR	2	100.0%	1																									
				SEDYVELVQR	2	100.0%	2																									
IPI00030275	TRAP1	Heat shock protein 75 kDa, mitochondrial	99.8%	3.8	2	2	2	2	4,742,825	5,006,605	4,835,145	5,203,380	377,235	175,166	328,171	139,373	17.8	7.8	15.2	6.0	1.1	0.5	1.0	0.9	1.1	0.3	-1.0	0.7	1.0	0.4	1.1	0.3
IPI00646055	TRAP1	cDNA FLJ58608, highly similar to Heat shock protein 75 kDa, mitochondrial	99.8%	4.2	2	2	2	2	4,742,825	5,006,605	4,835,145	5,203,380	377,235	175,166	328,171	139,373	17.8	7.8	15.2	6.0	1.1	0.5	1.0	0.9	1.1	0.3	-1.0	0.7	1.0	0.4	1.1	0.3
				AFLDALQNQAEASSK	2	98.7%	1																									
				ELISNASDALEK	2	86.5%	1																									
IPI00030296	EIF4A2	Eukaryotic translation initiation factor 4A, isoform 2	100.0%	4.8	1	1	1	1	4,287,453	5,314,150	4,500,325	5,861,875	966,378	827,310	580,815	593,171	50.4	34.8	28.9	22.6	1.2	0.4	1.0	0.9	1.4	0.2	-1.2	0.4	1.1	0.6	1.3	0.1
				LQAEAPHIVVGTPGR	3	99.9%	1																									
IPI00030303	PFDN5	prefoldin subunit 5 isoform gamma	100.0%	22.9	2	2	2	1	4,264,175	4,028,460	4,151,365	4,694,415	179,875	141,566	445,523	129,356	9.4	7.9	24.0	6.2	-1.1	0.3	-1.0	0.8	1.1	0.09	1.0	0.8	1.2	0.008	1.1	0.3
				IQQLTALGAAQATAK	2	100.0%	1																									
				QAVMEMMSQK	2	89.7%	1																									
IPI00030320	DDX6	Probable ATP-dependent RNA helicase DDX6	100.0%	7.3	2	2	2	2	2,613,320	3,278,875	2,853,330	3,708,915	220,073	320,258	236,692	288,143	18.8	21.8	18.6	17.4	1.3	0.1	1.1	0.5	1.4	0.02	-1.1	0.3	1.1	0.3	1.3	0.05
IPI01015091	DDX6	DDX6 protein	100.0%	18.7	2	2	2	2	2,613,320	3,278,875	2,853,330	3,708,915	220,073	320,258	236,692	288,143	18.8	21.8	18.6	17.4	1.3	0.1	1.1	0.5	1.4	0.02	-1.1	0.3	1.1	0.3	1.3	0.05
				GPVKPTGGPGGGGTQTQQQMNQLK	3	99.6%	1																									
				SGAYLIPLLER	2	97.1%	1																									
IPI00030351	DLG1	isoform 1 of Disks large homolog 1	93.3%	1.3	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00218729	DLG1	isoform 2 of Disks large homolog 1	93.3%	1.3	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00552213	DLG1	isoform 6 of Disks large homolog 1	93.3%	1.4	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00552376	DLG1	isoform 7 of Disks large homolog 1	93.3%	1.3	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00552511	DLG1	isoform 4 of Disks large homolog 1	93.3%	1.3	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00552682	DLG1	isoform 5 of Disks large homolog 1	93.3%	1.4	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00553029	DLG1	isoform 3 of Disks large homolog 1	93.3%	1.4	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00789849	DLG1	disks large homolog 1 isoform 5	93.3%	1.5	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00926279	DLG1	cDNA FLJ58166, highly similar to Disks large homolog 1	93.3%	3.2	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00927003	DLG1	Uncharacterized protein	93.3%	9.8	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00927298	DLG1	30 kDa protein	93.3%	4.2	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
IPI00975721	DLG1	Uncharacterized protein	93.3%	1.4	1	1	1	12	634,649	662,979	582,281	747,578	64,337	53,935	61,299	64,302	22.7	18.2	23.5	19.2	1.0	0.7	-1.1	0.6	1.2	0.2	-1.1	0.4	1.1	0.3	1.3	0.1
				IITGGAAAQDGR	2	93.3%	1																									
IPI00030357	DHFR	Dihydrofolate reductase	99.4%	9.6	1	1	1	2	1,019,155	999,350	1,201,530	1,022,185	154,107	91,159	116,756	87,259	33.8	20.4	21.7	19.1	-1.0	0.9	1.2	0.4	1.0	1	1.2	0.2	1.0	0.9	-1.2	0.3
IPI00968238	DHFRP1;DHFR	cDNA FLJ53008, highly similar to Dihydrofolate reductase	99.4%	13.3	1	1	1	2	1,019,155	999,350	1,201,530	1,022,185	154,107	91,159	116,756	87,259	33.8	20.4	21.7	19.1	-1.0	0.9	1.2	0.4	1.0	1	1.2	0.2	1.0	0.9	-1.2	0.3
				IMQDFESDTFFPEIDLEK	2	99.4%	1																									
IPI00030362	PLP2	Proteolipid protein 2	99.4%	8.6	1	1	1	1	5,362,330	5,031,910	4,991,790	6,329,830	588,596	324,429	620,860	407,292	24.5	14.4	27.8	14.4	-1.1	0.6	-1.1	0.7	1.2	0.2	-1.0	1	1.3	0.04	1.3	0.1
				HTAAPTDPADGPV	2	99.4%	1																									
IPI00030363	ACAT1	Acetyl-CoA acetyltransferase, mitochondrial	100.0%	33.5	9	11	13	1	50,534,788	54,202,212	51,348,094	63,004,948	6,871,831	2,936,979	4,361,048	2,729,096	30.4	12.1	19.0	9.7	1.1	0.6	1.0	0.9	1.2	0.1	-1.1	0.6	1.2	0.06	1.2	0.05
				DGLTDVYNK	2	100.0%	1																									
				EAYMGNVLQGGEGQAPTR	2	100.0%	1																									
				EAYMGNVLQGGEGQAPTR	3	99.7%	1																									
				FGNEVIPVTVTVK	2	100.0%	2																									
				IHMGSCAENTAK	2	96.4%	1																									
				IVAFADAAVEPIDFPIAPVYAASMVLK	2	100.0%	1																									
				IVAFADAAVEPIDFPIAPVYAASMVLK	3	100.0%	1																									
				LGSIAIQGAIEK	2	99.9%	2																									
				NEQDAYAINSYTR	2	100.0%	1																									
				QAVLGAGLPISTPCTTINK	2	100.0%	1																									
				VNINGGAVSLGHPIGMSGAR	3	100.0%	1																									
IPI00030385	SELENBP1	cDNA FLJ13813 fis, clone THYRO1000358, moderately similar to SELENIUM-BIND	100.0%	17.5	3	3	3	2	4,016,984	4,351,127	3,940,470	5,138,384	414,732	171,598	390,183	281,073	23.1	8.8	22.1	12.2	1.1	0.5	-1.0	0.9	1.3	0.06	-1.1	0.4	1.2	0.04	1.3	0.04
IPI00852768	SELENBP1	Selenium binding protein 1	100.0%	13.9	3	3	3	2	4,016,984	4,351,127	3,940,470	5,138,384	414,732	171,598	390,183	281,073	23.1	8.8	22.1	12.2	1.1	0.5	-1.0	0.9	1.3	0.06	-1.1	0.4	1.2	0.04	1.3	0.04
				GGFVLLDGETFEVK	2	99.9%	1																									
				HNVMISTEWAAPNVLR	2	99.8%	1																									
				IYVVDVGSEPR	2	99.7%	1																									
IPI00030702	IDH3A	isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	100.0%	8.7	3	3	3	4	11,490,870	10,499,005	10,252,215	12,419,668	775,678	460,143	793,909	673,931	15.1	9.8	17.3	12.1	-1.1	0.3	-1.1	0.3	1.1	0.4	-1.0	0.8	1.2	0.05	1.2	0.07
IPI00909577	IDH3A	cDNA FLJ52894, highly similar to Isocitrate dehydrogenase	100.0%	9.7	3	3	3	4	11,490,870	10,499,005	10,252,215	12,419,668	775,678	460,143	793,909	673,931	15.1	9.8	17.3	12.1	-1.1	0.3	-1.1	0.3	1.1	0.4	-1.0	0.8	1.2	0.05	1.2	0.07
IPI00792971	IDH3A	isoform 2 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	100.0%	11.1	3	3	3	4	11,490,870	10,499,005	10,252,215	12,419,668	775,678	460,143	793,909	673,931	15.1	9.8	17.3	12.1	-1.1	0.3	-1.1	0.3	1.1	0.4	-1.0	0.8	1.2	0.05	1.2	0.07
IPI00921820	IDH3A	cDNA, FLJ78950, highly similar to Isocitrate dehydrogenase	100.0%	12.5	3	3	3	4	11,490,870	10,499,005	10,252,215	12,419,668	775,678	460,143	793,909	673,931	15.1	9.8	17.3	12.1	-1.1	0.3	-1.1	0.3	1.1	0.4	-1.0	0.8	1.2	0.05	1.2	0.07
				HMGLFDHAAR	3	95.2%	1																									
				IAEFAFEYAR	2	100.0%	1																									
				TPYTDVNIVTIR	2	99.5%	1																									
IPI00030706	AHSA1	Activator of 90 kDa heat shock protein ATPase homolog 1	99.7%	13.0	3	3	4	2	8,794,857	9,775,085	9,298,640	10,436,276	516,509	386,882	467,318	410,606	13.1	8.9	11.2	8.8	1.1	0.2	1.1	0.5	1.2	0.04	-1.1	0.5	1.1	0.3	1.1	0.1
IPI01012490	AHSA1	cDNA FLJ56675, highly similar to Activator of 90 kDa heat shock protein ATPase ho	99.7%	15.3	3	3	4	2	8,794,857	9,775,085	9,298,640	10,436,276	516,509	386,882	467,318	410,606	13.1	8.9	11.2	8.8	1.1	0.2	1.1	0.5	1.2	0.04	-1.1	0.5	1.1	0.3	1.1	0.1
				ETFLTSPEELYR	2	99.5%	2																									
				LDGEASINNR	2	95.5%	1																									
				VFTTQELVQAFTHAPATLEADR	3	97.0%	1																									
IPI00030730	SULT1A4;SULT1A3	Phenol sulfotransferase 1A5*1A possible alternative splicing form	100.0%	14.0	2	2	2	1	5,746,843	5,342,010	5,619,700	6,124,757	418,684	153,875	183,209	219,735	16.3	6.4	7.3	8.0	-1.1	0.4	-1.0	0.8	1.1	0.4	1.1	0.3	1.1	0.02	1.1	0.1
				SHLPLALLPQTLLDQK	3	99.5%	1																									
				YFAEALGPLQSFQARPDDLLINTYPK	3	94.0%	1																									
IPI00030770	PSMG1	isoform 1 of Proteasome assembly chaperone 1	98.3%	5.6	1	1	1	3	827,710	892,123	1,016,650	901,187	62,009	68,324	67,002	41,990	16.8	17.1	14.7	10.4	1.1	0.5	1.2	0.07	1.1	0.4	1.1	0.2	1.0	0.9	-1.1	0.2
IPI00401072	PSMG1	isoform 2 of Proteasome assembly chaperone 1	98.3%	6.0	1	1	1	3	827,710	892,123	1,016,650	901,187	62,009	68,324	67,002	41,990	16.8	17.1	14.7	10.4	1.1	0.5	1.2	0.07	1.1	0.4	1.1	0.2	1.0	0.9	-1.1	0.2
IPI00657997	PSMG1	Protein	98.3%	11.0	1	1	1	3	827,710	892,123	1,016,650	901,187	62,009	68,324	67,002	41,990	16.8	17.1	14.7	10.4	1.1	0.5	1.2	0.07	1.1	0.4	1.1	0.2	1.0	0.9	-1.1	0.2
				LDLITVEAFKPILSTR	3	98.3%	1																									
IPI00030781	STAT1	isoform Alpha of Signal transducer and activator of transcription 1-alpha/beta	91.2%	2.4	1	1	1	7	408,714	430,486	427,239	430,411	26,998	45,679	40,051	45,377	14.8	23.7	21.0	23.6	1.1	0.7	1.0	0.7	1.1	0.7	-1.0	1	-1.0	1	1.0	1
IPI00218188	STAT1	isoform Beta of Signal transducer and activator of transcription 1-alpha/beta	91.2%	2.5	1	1	1	7	408,714	430,486	427,239	430,411	26,998	45,679	40,051	45,377	14.8	23.7	21.0	23.6	1.1	0.7	1.0	0.7	1.1	0.7	-1.0	1	-1.0	1	1.0	1
IPI00795482	STAT1	83 kDa protein	91.2%	2.5	1	1	1	7	408,714	430,486	427,239	430,411	26,998	45,679	40,051	45,377	14.8	23.7	21.0	23.6	1.1	0.7	1.0	0.7	1.1	0.7	-1.0	1	-1.0	1	1.0	1
IPI00797149	STAT1	Uncharacterized protein	91.2%	10.0	1	1	1	7	408,714	430,486	427,239	430,411	26,998	45,679	40,051	45,377	14.8	23.7	21.0	23.6	1.1	0.7	1.0	0.7	1.1	0.7	-1.0	1	-1.0	1	1.0	1
IPI00915841	STAT1	Uncharacterized protein	91.2%	25.7	1	1	1	7	408,714	430,486	427,239	430,411	26,998	45,679	40,051	45,377	14.8	23.7	21.0	23.6	1.1	0.7	1.0	0.7	1.1	0.7	-1.0	1	-1.0	1	1.0	1
IPI00915952	STAT1	Truncated signal transducer and activator of transcription 1	91.2%	9.3	1	1	1	7	408,714	430,486	427,239	430,411	26,998	45,679	40,051	45,377	14.8	23.7	21.0	23.6	1.1	0.7	1.0	0.7	1.1	0.7	-1.0	1	-1.0	1	1.0	1
IPI00916196	STAT1	Uncharacterized protein	91.2%	12.0	1	1	1	7	408,714	430,486	427,239	430,411	26,998	45,679	40,051	45,377	14.8	23.7	21.0	23.6	1.1	0.7	1.0	0.7	1.1	0.7	-1.0	1	-1.0	1	1.0	1
				FLEQVHQLYDDSFPMEIR	3	91.2%	1																									
IPI00030782	STAT6	isoform 1 of Signal transducer and activator of transcription 6	98.9%	1.1	1	1	1	4	1,754,225	1,519,838	1,595,200	1,679,405	273,876	97,601	187,388	89,803	34.9	14.4	26.3	12.0	-1.2	0.5	-1.1	0.6	-1.0	0.8	1.0	0.7	1.1	0.3	1.1	0.7
IPI00792907	STAT6	signal transducer and activator of transcription 6 isoform 2	98.9%	1.2	1	1	1	4	1,754,225	1,519,838	1,595,200	1,679,405	273,876	97,601	187,388	89,803	34.9	14.4	26.3	12.0	-1.2	0.5	-1.1	0.6	-1.0	0.8	1.0	0.7	1.1	0.3	1.1	0.7
IPI01011669	STAT6	cDNA FLJ51958, highly similar to Signal transducer and activator of transcription 6	98.9%	1.2	1	1	1	4	1,754,225	1,519,838	1,595,200	1,679,405	273,876	97,601	187,388	89,803	34.9	14.4	26.3	12.0	-1.2	0.5	-1.1	0.6	-1.0	0.8	1.0	0.7	1.1	0.3	1.1	0.7
IPI01012094	STAT6	Signal transducer and activator of transcription 6, interleukin-4 induced	98.9%	1.3	1	1	1	4	1,754,225	1,519,838	1,595,200	1,679,405	273,876	97,601	187,388	89,803	34.9	14.4	26.3	12.0	-1.2	0.5	-1.1	0.6	-1.0	0.8	1.0	0.7	1.1	0.3	1.1	0.7
				FMAEVGTNR	2	98.9%	1																									
IPI00030847	TM9SF3	Transmembrane 9 superfamily member 3	97.3%	1.9	1	1	1	1	4,807,960	5,472,690	4,762,950	5,714,690	478,254	445,530	354,552	845,078	22.2	18.2	16.7	33.1	1.1	0.3	-1.0	0.9	1.2	0.4	-1.1	0.2	1.0	0.8	1.2	0.3
				NLSGQPNFPCR	2	97.3%	1																									
IPI00030877	15-Sep	15 kDa selenoprotein isoform 1 precursor	100.0%	24.9	4	4	5	1	14,571,470	14,516,180	15,499,640	15,929,030	990,406	440,784	700,439	661,537	15.2	6.8	10.1	9.3	-1.0	1	1.1	0.5	1.1	0.3	1.1	0.3	1.1	0.1	1.0	0.7
				FPQVQAFVR	2	97.3%	1																									
				LLDDNGNIAEELSILK	2	100.0%	2																									
				WNTDSVEEFLSEK	2	99.9%	1																									
				WNTDSVEEFLSEKLER	3	81.8%	1																									
IPI00030911	VAMP8	Vesicle-associated membrane protein 8	99.9%	31.0	3	3	3	1	8,080,475	7,744,980	7,829,690	8,642,515	452,760	299,719	391,433	343,898	12.5	8.7	11.2	8.9	-1.0	0.6	-1.0	0.7	1.1	0.4	1.0	0.9	1.1	0.08	1.1	0.2
				GENLEHLR	2	83.8%	1																									
				NIMTQNVER	2	93.2%	1																									
				NKTEDLEATSEHFK	3	99.2%	1																									
IPI00030915	USP8	Ubiquitin carboxyl-terminal hydrolase 8	98.8%	1.9	1	1	1	2	169,208	180,158	188,999	223,284	18,489	12,799	22,148	11,460	24.4	15.9	26.2	11.5	1.1	0.6	1.1	0.5	1.3	0.04	1.0	0.7	1.2	0.04	1.2	0.2
IPI00941811	USP8	Ubiquitin carboxyl-terminal hydrolase	98.8%	2.1	1	1	1	2	169,208	180,158	188,999	223,284	18,489	12,799	22,148	11,460	24.4	15.9	26.2	11.5	1.1	0.6	1.1	0.5	1.3	0.04	1.0	0.7	1.2	0.04	1.2	0.2
				SDVSPIIQPVPSIKNVPQIDR	3	98.5%	1																									
IPI00030929	MYL9	myosin regulatory light polypeptide 9 isoform b	100.0%	16.1	2	2	4	2	2,921,029	2,857,317	2,781,433	3,081,841	163,566	123,634	115,129	73,689	12.5	9.7	9.3	5.4	-1.0	0.8	-1.1	0.5	1.1	0.4	-1.0	0.7	1.1	0.2	1.1	0.06
IPI00220278	MYL9	Myosin regulatory light polypeptide 9	100.0%	11.1	2	2	4	2	2,921,029	2,857,317	2,781,433	3,081,841	163,566	123,634	115,129	73,689	12.5	9.7	9.3	5.4	-1.0	0.8	-1.1	0.5	1.1	0.4	-1.0	0.7	1.1	0.2	1.1	0.06
				EAFNMIDQNR	2	100.0%	2																									
				ELLTTMGDR	2	100.0%	2																									
IPI00030936	TSPAN1	Tetraspanin-1	99.5%	5.4	1	1	1	1	17,332,000	17,644,900	17,716,000	19,047,800	1,490,404	887,267	1,388,446	1,086,000	19.2	11.2	17.5	12.8	1.0	0.9	1.0	0.9	1.1	0.4	1.0	1	1.1	0.3	1.1	0.5
				VEGCFNQLLYDIR	2	99.5%	1																									
IPI00031030	APLP2	isoform 1 of Amyloid-like protein 2	100.0%	2.6	1	1	1	9	44,236	47,713	95,297	50,460	5,951	4,287	55,111	3,518	30.1	20.1	129.3	15.6	1.1	0.6	2.2	0.4	1.1	0.4	2.0	0.4	1.1	0.6	-1.9	0.5
IPI00220977	APLP2	isoform 2 of Amyloid-like protein 2	100.0%	2.8	1	1	1	9	44,236	47,713	95,297	50,460	5,951	4,287	55,111	3,518	30.1	20.1	129.3	15.6	1.1	0.6	2.2	0.4	1.1	0.4	2.0	0.4	1.1	0.6	-1.9	0.5
IPI00220978	APLP2	isoform 3 of Amyloid-like protein 2	100.0%	2.7	1	1	1	9	44,236	47,713	95,297	50,460	5,951	4,287	55,111	3,518	30.1	20.1	129.3	15.6	1.1	0.6	2.2	0.4	1.1	0.4	2.0	0.4	1.1	0.6	-1.9	0.5
IPI00334946	APLP2	isoform 5 of Amyloid-like protein 2	100.0%	3.8	1	1	1	9	44,236	47,713	95,297	50,460	5,951	4,287	55,111	3,518	30.1	20.1	129.3	15.6	1.1	0.6	2.2	0.4	1.1	0.4	2.0	0.4	1.1	0.6	-1.9	0.5
IPI00884988	APLP2	isoform 4 of Amyloid-like protein 2	100.0%	2.9	1	1	1	9	44,236	47,713	95,297	50,460	5,951	4,287	55,111	3,518	30.1	20.1	129.3	15.6	1.1	0.6	2.2	0.4	1.1	0.4	2.0	0.4	1.1	0.6	-1.9	0.5
IPI00973038	APLP2	cDNA FLJ55088, highly similar to Amyloid-like protein 2	100.0%	5.1	1	1	1	9	44,236	47,713	95,297	50,460	5,951	4,287	55,111	3,518	30.1	20.1	129.3	15.6	1.1	0.6	2.2	0.4	1.1	0.4	2.0	0.4	1.1	0.6	-1.9	0.5
IPI00973819	APLP2	Uncharacterized protein	100.0%	2.6	1	1	1	9	44,236	47,713	95,297	50,460	5,951	4,287	55,111	3,518	30.1	20.1	129.3	15.6	1.1	0.6	2.2	0.4	1.1	0.4	2.0	0.4	1.1	0.6	-1.9	0.5
IPI01013848	APLP2	76 kDa protein	100.0%	3.0	1	1	1	9	44,236	47,713	95,297	50,460	5,951	4,287	55,111	3,518	30.1	20.1	129.3	15.6	1.1	0.6	2.2	0.4	1.1	0.4	2.0	0.4	1.1	0.6	-1.9	0.5
IPI01014180	APLP2	cDNA FLJ55927, highly similar to Amyloid-like protein 2	100.0%	3.6	1	1	1	9	44,236	47,713	95,297	50,460	5,951	4,287	55,111	3,518	30.1	20.1	129.3	15.6	1.1	0.6	2.2	0.4	1.1	0.4	2.0	0.4	1.1	0.6	-1.9	0.5
				VPYVAQEIQEEIDELLQEQR	3	100.0%	1																									
IPI00031091	EFHD1	EF-hand domain-containing protein D1	100.0%	8.8	2	2	3	2	3,245,028	3,563,918	3,347,845	3,260,778	173,671	66,632	71,702	60,588	12.0	4.2	4.8	4.2	1.1	0.1	1.0	0.6	1.0	0.9	-1.1	0.06	-1.1	0.01	-1.0	0.4
IPI00916914	EFHD1	Uncharacterized protein	100.0%	14.7	2	2	3	2	3,245,028	3,563,918	3,347,845	3,260,778	173,671	66,632	71,702	60,588	12.0	4.2	4.8	4.2	1.1	0.1	1.0	0.6	1.0	0.9	-1.1	0.06	-1.1	0.01	-1.0	0.4
				DGFIDLMELK	2	100.0%	2																									
				LGAPQTHLGLK	3	100.0%	1																									
IPI00031106	PSMG3	Proteasome assembly chaperone 3	98.2%	10.7	1	1	1	1	3,326,860	3,768,170	3,685,610	4,242,990	489,369	220,035	202,131	219,081	32.9	13.1	12.3	11.6	1.1	0.4	1.1	0.5	1.3	0.1	-1.0	0.8	1.1	0.2	1.2	0.1
				NLVAFVSQEAGNR	2	98.2%	1																									

IPI00031107	HSDL2	isoform 2 of Hydroxysteroid dehydrogenase-like protein 2	99.6%	5.2	1	1	1	1	2,963,645	2,747,620	3,284,945	3,192,515	112,179	133,993	253,400	200,893	8.5	10.9	17.3	14.1	-1.1	0.3	1.1	0.3	1.1	0.3	1.2	0.1	1.2	0.1	-1.0	0.8
				LLGTIYTAAEEIEAVGGK	2	99.6%	1																									
IPI00031131	C20orf3	isoform 1 of Adipocyte plasma membrane-associated protein	99.3%	2.9	1	1	1	3	1,335,740	1,125,653	1,157,300	1,171,897	144,469	55,239	100,664	46,819	24.2	11.0	19.5	8.9	-1.2	0.2	-1.2	0.3	-1.1	0.3	1.0	0.8	1.0	0.5	1.0	0.9
IPI00791304	C20orf3	Chromosome 20 open reading frame 3	99.3%	2.9	1	1	1	3	1,335,740	1,125,653	1,157,300	1,171,897	144,469	55,239	100,664	46,819	24.2	11.0	19.5	8.9	-1.2	0.2	-1.2	0.3	-1.1	0.3	1.0	0.8	1.0	0.5	1.0	0.9
IPI00929530	C20orf3	isoform 2 of Adipocyte plasma membrane-associated protein	99.3%	4.2	1	1	1	3	1,335,740	1,125,653	1,157,300	1,171,897	144,469	55,239	100,664	46,819	24.2	11.0	19.5	8.9	-1.2	0.2	-1.2	0.3	-1.1	0.3	1.0	0.8	1.0	0.5	1.0	0.9
				LLLSSETPIEGK	2	98.8%	1																									
IPI00031169	RAB2A	Ras-related protein Rab-2A	100.0%	32.1	5	5	5	1	6,501,585	6,379,691	6,672,372	7,039,605	435,851	239,152	489,159	389,820	15.0	8.4	16.4	12.4	-1.0	0.8	1.0	0.8	1.1	0.4	1.0	0.6	1.1	0.2	1.1	0.6
				DTFNHLTTWLEDAR	2	99.9%	1																									
				IQEGVFDINNEANGIK	2	99.2%	1																									
				LQIWDTAGQESFR	2	100.0%	1																									
				TASNVEEAFINTAK	2	99.7%	1																									
				YIIIGDTGVGK	2	99.8%	1																									
IPI00031242	SEC16A	isoform 5 of Protein transport protein Sec16A	100.0%	1.0	2	2	2	5	2,993,740	3,519,962	2,907,086	3,907,834	419,060	327,309	148,323	175,776	31.3	20.8	11.4	10.1	1.2	0.4	-1.0	0.9	1.3	0.08	-1.2	0.1	1.1	0.3	1.3	0.002
IPI00166487	SEC16A	isoform 3 of Protein transport protein Sec16A	100.0%	1.1	2	2	2	5	2,993,740	3,519,962	2,907,086	3,907,834	419,060	327,309	148,323	175,776	31.3	20.8	11.4	10.1	1.2	0.4	-1.0	0.9	1.3	0.08	-1.2	0.1	1.1	0.3	1.3	0.002
IPI00219314	SEC16A	isoform 2 of Protein transport protein Sec16A	100.0%	1.1	2	2	2	5	2,993,740	3,519,962	2,907,086	3,907,834	419,060	327,309	148,323	175,776	31.3	20.8	11.4	10.1	1.2	0.4	-1.0	0.9	1.3	0.08	-1.2	0.1	1.1	0.3	1.3	0.002
IPI00641384	SEC16A	protein transport protein Sec16A	100.0%	1.0	2	2	2	5	2,993,740	3,519,962	2,907,086	3,907,834	419,060	327,309	148,323	175,776	31.3	20.8	11.4	10.1	1.2	0.4	-1.0	0.9	1.3	0.08	-1.2	0.1	1.1	0.3	1.3	0.002
IPI00896436	SEC16A	isoform 4 of Protein transport protein Sec16A	100.0%	1.1	2	2	2	5	2,993,740	3,519,962	2,907,086	3,907,834	419,060	327,309	148,323	175,776	31.3	20.8	11.4	10.1	1.2	0.4	-1.0	0.9	1.3	0.08	-1.2	0.1	1.1	0.3	1.3	0.002
				QSGPGAPNLDR	2	97.0%	1																									
				TMATMGDTLASR	2	99.5%	1																									
IPI00031370	TUBB2B	Tubulin beta-2B chain	100.0%	41.8	9	11	16	1	35,615,661	34,158,852	36,245,437	41,018,723	3,826,870	1,576,262	3,147,255	1,608,418	24.0	10.3	19.4	8.8	-1.0	0.7	1.0	0.9	1.2	0.2	1.1	0.6	1.2	0.02	1.1	0.2
				AILVDLEPGTMDSVR	2	100.0%	2																									
				ALTVPELTQQMFDSK	2	100.0%	1																									
				EIVHIQAGQCGNQIGAK	2	99.5%	2																									
				ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	3	99.9%	1																									
				FWEVISDEHGIDPTGSYHGDSDLQLER	3	98.2%	1																									
				INVYYNEATGNK	2	100.0%	1																									
				LTTPTYGDLNHLVSATMSGVTTCLR	2	100.0%	2																									
				MSATFIGNSTAIQELFK	2	99.2%	1																									
				MSATFIGNSTAIQELFK	3	90.7%	1																									
				SGPFGQIFRPDNFVFGQSGAGNNWAK	2	100.0%	2																									
				SGPFGQIFRPDNFVFGQSGAGNNWAK	3	100.0%	2																									
IPI00031420	UGDH	UDP-glucose 6-dehydrogenase	100.0%	48.0	16	18	21	1	44,072,260	45,043,466	45,007,427	50,097,221	2,639,204	1,344,633	2,789,245	1,291,057	13.4	6.7	13.9	5.8	1.0	0.8	1.0	0.8	1.1	0.07	-1.0	1	1.1	0.03	1.1	0.1
				AVQALCAVYEHWVPR	3	99.7%	1																									
				DVLNLVYLCEALNLPEVAR	2	100.0%	1																									
				DVLNLVYLCEALNLPEVAR	3	100.0%	1																									
				EQIVVDLSHPGVSEDDQVSR	3	99.9%	2																									
				IAILGFAFK	2	100.0%	1																									
				IFDANTKPNLNLQVLSNPEFLAEGTAIK	3	96.2%	1																									
				IIDSLFNTVTDKK	2	98.9%	1																									
				ILTTNTWSSELSK	2	100.0%	1																									
				INAWNSPTLPIYEPGLK	2	100.0%	2																									
				ISSINSISALCEATGADVEEVATAIGMDQR	3	100.0%	1																									
				LAANAFLAQR	2	100.0%	1																									
				MLKPAFIFDGR	3	100.0%	1																									
				VLDGLHNELQTIGFQIETIGK	2	100.0%	1																									
				VLDGLHNELQTIGFQIETIGK	3	100.0%	1																									
				VLDGLHNELQTIGFQIETIGKK	3	99.9%	1																									
				VTVVDVNESR	2	100.0%	1																									
				YIEACAR	2	84.6%	1																									
				YWQQVIDMNDYQR	2	100.0%	2																									
IPI00031461	GDI2	cDNA FLJ60299, highly similar to Rab GDP dissociation inhibitor beta	100.0%	55.2	22	27	37	2	50,628,630	54,206,300	50,761,648	61,506,155	6,676,444	3,095,863	4,606,549	1,602,792	29.5	12.8	20.3	5.8	1.1	0.6	1.0	1	1.2	0.2	-1.1	0.6	1.1	0.07	1.2	0.08
IPI00940148	GDI2	Rab GDP dissociation inhibitor beta	100.0%	55.7	22	27	37	2	50,628,630	54,206,300	50,761,648	61,506,155	6,676,444	3,095,863	4,606,549	1,602,792	29.5	12.8	20.3	5.8	1.1	0.6	1.0	1	1.2	0.2	-1.1	0.6	1.1	0.07	1.2	0.08
				DLGTESQIFISR	2	100.0%	2																									
				FDLGQDVIDFTGHALALYR	2	100.0%	1																									
				FDLGQDVIDFTGHALALYR	3	100.0%	1																									
				FLMANGQLVK	2	99.5%	2																									
				FVSISDLLVPK	2	100.0%	2																									
				IYKVPSTEAEALASSLMGLFEK	3	99.9%	1																									
				KFDLGQDVIDFTGHALALYR	3	100.0%	2																									
				LYSESLAR	2	99.0%	1																									
				MLLYTEVTR	2	100.0%	2																									
				MTGSEFDFEEMK	2	100.0%	1																									
				MTGSEFDFEEMKR	2	99.7%	1																									
				MTGSEFDFEEMKR	3	100.0%	1																									
				NPYYGGESASITPLEDLYK	2	100.0%	1																									
				NPYYGGESASITPLEDLYK	3	99.3%	1																									
				NPYYGGESASITPLEDLYKR	3	100.0%	2																									
				NTNDANSCQIIIPQNQVNR	2	99.9%	1																									
				PALELLEPIEQK	2	98.8%	1																									
				SDIYVCMISFAHNVAAQGK	3	86.5%	1																									
				SPYLYPLYGLGELPQGFAR	2	100.0%	2																									
				SPYLYPLYGLGELPQGFAR	3	100.0%	2																									
				TDDYLDQPCYETINR	2	100.0%	2																									
				TFEGIDPK	2	99.9%	1																									
				VICILSHPIK	3	99.2%	1																									
				VPSTEAEALASSLMGLFEK	2	100.0%	2																									
				VPSTEAEALASSLMGLFEK	3	100.0%	1																									
				VTEGSFVYK	2	99.4%	1																									
				YIAIVSTTVETK	2	98.3%	1																									
IPI00031517	MCM6	DNA replication licensing factor MCM6	99.1%	5.1	3	3	3	1	14,709,485	14,780,235	15,053,890	16,362,920	856,420	930,223	1,042,089	693,790	13.0	14.1	15.5	9.5	1.0	1	1.0	0.8	1.1	0.2	1.0	0.8	1.1	0.2	1.1	0.3
				LFLDFLEEFQSSDGEIK	2	99.1%	1																									
				QNINLSAPIMSR	2	94.8%	1																									
				VSGVDGYETEGIR	2	96.3%	1																									
IPI00031522	HADHA	Trifunctional enzyme subunit alpha, mitochondrial	100.0%	28.4	16	17	18	1	68,808,814	70,065,672	66,756,663	75,463,362	6,846,897	2,910,025	4,310,057	2,526,041	22.3	9.3	14.4	7.5	1.0	0.9	-1.0	0.8	1.1	0.4	-1.0	0.5	1.1	0.2	1.1	0.1
				ADMVIEAVFEDLSLK	2	100.0%	1																									
				ADMVIEAVFEDLSLK	3	99.5%	1																									
				CLAPMMSEVIR	2	99.9%	1																									
				DLNSDMDSILASLK	2	100.0%	1																									
				DSIFSNLTGQLDYQGFEK	2	100.0%	1																									
				DTSASAVAVGLK	2	99.9%	1																									
				ELHSEFSEVMNEIWASDQIR	3	100.0%	1																									
				FGELVMTK	2	95.0%	1																									
				FGGGNPELLTQMVSK	2	100.0%	1																									
				GFYIYQEGVK	2	100.0%	1																									
				ILQEGVDPK	2	97.7%	1																									
				MGLVDQLVEPLGPGLKPPEER	3	99.9%	1																									
				MQLLEIITTEK	2	100.0%	2																									
				TIEYLEEVAITFAK	2	100.0%	1																									
				TLQEVTQLSQEAQR	2	100.0%	1																									
				TLQEVTQLSQEAQRIVEK	3	85.1%	1																									
				TVLGTPEVLLGALPGAGGTQR	3	98.5%	1																									
IPI00031526	C19orf43	Uncharacterized protein C19orf43	92.9%	6.8	1	1	1	1	15,678,500	15,423,300	14,306,300	18,000,800	1,599,086	1,047,162	1,038,237	677,895	22.8	15.2	16.2	8.4	-1.0	0.9	-1.1	0.5	1.1	0.2	-1.1	0.5	1.2	0.07	1.3	0.02
				GGPGSTLSFVGK	2	92.9%	1																									
IPI00031545	ITPR2	isoform Long of Inositol 1,4,5-trisphosphate receptor type 2	94.7%	0.8	1	1	1	1	6,962,660	7,194,270	6,672,960	7,907,580	772,392	262,528	460,939	400,252	24.8	8.2	15.5	11.3	1.0	0.8	-1.0	0.8	1.1	0.3	-1.1	0.4	1.1	0.2	1.2	0.08
				HLAQEAKEGTKADLEVLTYYR	3	94.7%	1																									
IPI00031556	U2AF2	isoform 1 of Splicing factor U2AF 65 kDa subunit	100.0%	24.4	8	9	11	2	25,422,809	26,336,969	29,641,831	28,716,650	1,800,651	1,203,360	1,386,962	1,735,686	15.8	10.2	10.5	13.5	1.0	0.7	1.2	0.1	1.1	0.2	1.1	0.1	1.1	0.3	-1.0	0.7
IPI00830039	U2AF2	isoform 2 of Splicing factor U2AF 65 kDa subunit	100.0%	24.6	8	9	11	2	25,422,809	26,336,969	29,641,831	28,716,650	1,800,651	1,203,360	1,386,962	1,735,686	15.8	10.2	10.5	13.5	1.0	0.7	1.2	0.1	1.1	0.2	1.1	0.1	1.1	0.3	-1.0	0.7
				AMQGLTGR	2	96.5%	2																									
				IFVEFTSVFDCQK	2	100.0%	1																									
				LFIGGLPNYLNDDQVK	2	100.0%	2																									
				LFIGGLPNYLNDDQVKELLTSFGPLK	3	100.0%	1																									
				LGGLTQAPGNPVLAVQINQDK	3	100.0%	1																									
				LGGLTQAPGNPVLAVQINQDKNFAFLEFR	3	100.0%	1																									
				SIEIPRPVDGVEVPGCGK	3	100.0%	1																									
				SVDETTQAMAFDGIIFQGQSLK	2	100.0%	1																									
				SVDETTQAMAFDGIIFQGQSLK	3	100.0%	1																									
IPI00031557	CTH	isoform 1 of Cystathionine gamma-lyase	99.8%	4.9	1	1	1	3	210,299	255,586	250,325	256,374	27,986	35,663	45,936	31,899	29.8	31.2	41.0	27.8	1.2	0.3	1.2	0.5	1.2	0.3	-1.0	0.9	1.0	1	1.0	0.9
IPI00221301	CTH	isoform 2 of Cystathionine gamma-lyase	99.8%	5.5	1	1	1	3	210,299	255,586	250,325	256,374	27,986	35,663	45,936	31,899	29.8	31.2	41.0	27.8	1.2	0.3	1.2	0.5	1.2	0.3	-1.0	0.9	1.0	1	1.0	0.9
IPI00908512	CTH	cystathionine gamma-lyase isoform 3	99.8%	5.4	1	1	1	3	210,299	255,586	250,325	256,374	27,986	35,663	45,936	31,899	29.8	31.2	41.0	27.8	1.2	0.3	1.2	0.5	1.2	0.3	-1.0	0.9	1.0	1	1.0	0.9
				LSVGLEDEEDLLEDLDQALK	2	99.1%	1																									
IPI00031564	GGCT	isoform 1 of Gamma-glutamylcyclotransferase	100.0%	27.1	4	4	4	1	6,803,953	7,333,495	6,718,153	8,311,240	938,449	377,963	528,455	250,664	30.8	11.5	17.6	6.7	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.06	1.2	0.03
				AIEPNDYTGK	2	97.2%	1																									
				SNLNSLDEQEGVK	2	100.0%	1																									
				SYLMTNYESAPPSPQYKK	2	86.6%	1																									
				VSEEIEDIIK	2	99.9%	1																									
IPI00031570	NTPCR	Cancer-related nucleoside-triphosphatase	98.5%	6.3	1	1	1	2	1,974,895	2,145,420	2,138,690	2,006,030	187,688	107,804	116,446	161,593	21.3	11.2	12.2	18.0	1.1	0.5	1.1	0.5	1.0	0.9	-1.0	1	-1.1	0.5	-1.1	0.5
IPI00514501	NTPCR	Chromosome 1 open reading frame 57, isoform CRA_a	98.5%	5.3	1	1	1	2	1,974,895	2,145,420	2,138,690	2,006,030	187,688	107,804	116,446	161,593	21.3	11.2	12.2	18.0	1.1	0.5	1.1	0.5	1.0	0.9	-1.0	1	-1.1	0.5	-1.1	0.5
				HVFLTGPPGVGK	2	98.5%	1																									
IPI00031583	USO1	isoform 2 of General vesicular transport factor p115	100.0%	20.3	14	14	14	2	23,189,172	25,016,810	22,627,595	27,561,979	2,210,588	1,083,115	1,425,343	854,929	21.3	9.7	14.1	6.9	1.1	0.5	-1.0	0.8	1.2	0.1	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00941161	USO1	isoform 1 of General vesicular transport factor p115	100.0%	20.5	14	14	14	2	23,189,172	25,016,810	22,627,595	27,561,979	2,210,588	1,083,115	1,425,343	854,929	21.3	9.7	14.1	6.9	1.1	0.5	-1.0	0.8	1.2	0.1	-1.1	0.2	1.1	0.1	1.2	0.02
				DNQHQGSYSEGAQMNGIQPEEIGR	3	99.9%	1																									
				DSEQVAELKQELATLK	3	100.0%	1																									
				EQDDLLVLLADQDQK	2	100.0%	1																									
				EQDLQLEELR	2	99.8%	1																									
				GVMGGQSAGPQHTEAETIQK	3	99.0%	1																									
				IVAFENAFER	2	100.0%	1																									
				LMDLLADSR	2	95.8%	1																									
				LSALLQETK	2	83.1%	1																									
				NDGVLLLQALTR	2	100.0%	1																									
				NQELLQSQLTEK	2	83.8%	1																									
				NQELLQSQLTEKDSMIENMK	3	99.8%	1																									
				QLGPQVQQIILVSPMGVSR	2	99.9%	1																									
				QSEDLGSQFTEIFIK	2	100.0%	1																									
				SSQTSGTNEQSSAIVSAR	2	100.0%	1																									
IPI00031608	SPATA5L1	isoform 1 of Spermatogenesis-associated protein 5-like protein 1	93.7%	3.5	1	1	1	2	1,762,025	1,826,815	1,631,320	2,223,605	142,602	139,687	122,752	93,963	18.1	17.1	16.8	9.5	1.0	0.8	-1.1	0.5	1.3	0.03	-1.1	0.3	1.2	0.05	1.4	0.005
IPI01012737	SPATA5L1	Protein	93.7%	10.1	1	1	1	2	1,762,025	1,826,815	1,631,320	2,223,605	142,602	139,687	122,752	93,963	18.1	17.1	16.8	9.5	1.0	0.8	-1.1	0.5	1.3	0.03	-1.1	0.3	1.2	0.05	1.4	0.005
				TMPIGPDVSLENLAAETCFFSGADLR	3	93.7%	1																									

IPI00031670	FAM114A1	Protein NOXP20	100.0%	6.2	2	2	2	1	4,134,390	4,179,380	3,852,025	4,296,480	264,781	229,136	235,664	139,320	14.3	12.3	13.7	7.3	1.0	0.9	-1.1	0.4	1.0	0.6	-1.1	0.3	1.0	0.7	1.1	0.1
				SVLTGGLDALEFIGK	2	99.8%	1																									
				VAELILHGQEEEKPAQDQAK	3	98.5%	1																									
IPI00795717	-	19 kDa protein	100.0%	32.7	4	4	4	3	5,331,268	5,090,962	4,617,030	5,985,111	547,445	281,845	451,609	192,434	23.0	12.4	21.9	7.2	-1.0	0.7	-1.2	0.3	1.1	0.3	-1.1	0.4	1.2	0.03	1.3	0.02
IPI00031691	RPL9	60S ribosomal protein L9	100.0%	28.1	4	4	4	3	5,331,268	5,090,962	4,617,030	5,985,111	547,445	281,845	451,609	192,434	23.0	12.4	21.9	7.2	-1.0	0.7	-1.2	0.3	1.1	0.3	-1.1	0.4	1.2	0.03	1.3	0.02
IPI00965303	RPL9	Uncharacterized protein	100.0%	29.7	4	4	4	3	5,331,268	5,090,962	4,617,030	5,985,111	547,445	281,845	451,609	192,434	23.0	12.4	21.9	7.2	-1.0	0.7	-1.2	0.3	1.1	0.3	-1.1	0.4	1.2	0.03	1.3	0.02
				DFNHINVELSLLGK	2	99.9%	1																									
				FLDGIYVSEK	2	100.0%	1																									
				TICSHVQNMIK	2	89.6%	1																									
				TILSNQTVDIPENVDITLK	2	100.0%	1																									
IPI00031697	TMEM109	Transmembrane protein 109	99.1%	4.9	1	1	1	2	3,108,065	3,426,905	2,608,700	3,490,735	339,026	209,612	231,445	107,533	24.4	13.7	19.8	6.9	1.1	0.4	-1.2	0.3	1.1	0.3	-1.3	0.03	1.0	0.8	1.3	0.009
IPI00908304	TMEM109	cDNA FLJ57860, highly similar to Transmembrane protein 109	99.1%	5.1	1	1	1	2	3,108,065	3,426,905	2,608,700	3,490,735	339,026	209,612	231,445	107,533	24.4	13.7	19.8	6.9	1.1	0.4	-1.2	0.3	1.1	0.3	-1.3	0.03	1.0	0.8	1.3	0.009
				EAPVDVLTQIGR	2	99.1%	1																									
IPI00031801	CSDA	isoform 1 of DNA-binding protein A	100.0%	17.7	5	5	6	4	4,778,125	4,607,779	4,529,718	5,389,783	230,569	251,931	191,929	185,401	10.8	12.2	9.5	7.7	-1.0	0.6	-1.1	0.4	1.1	0.07	-1.0	0.8	1.2	0.04	1.2	0.01
IPI00219147	CSDA	isoform 2 of DNA-binding protein A	100.0%	21.8	5	5	6	4	4,778,125	4,607,779	4,529,718	5,389,783	230,569	251,931	191,929	185,401	10.8	12.2	9.5	7.7	-1.0	0.6	-1.1	0.4	1.1	0.07	-1.0	0.8	1.2	0.04	1.2	0.01
IPI00219148	CSDA	isoform 3 of DNA-binding protein A	100.0%	19.3	5	5	6	4	4,778,125	4,607,779	4,529,718	5,389,783	230,569	251,931	191,929	185,401	10.8	12.2	9.5	7.7	-1.0	0.6	-1.1	0.4	1.1	0.07	-1.0	0.8	1.2	0.04	1.2	0.01
IPI00555698	CSDA	CSDA protein variant (Fragment)	100.0%	49.3	5	5	6	4	4,778,125	4,607,779	4,529,718	5,389,783	230,569	251,931	191,929	185,401	10.8	12.2	9.5	7.7	-1.0	0.6	-1.1	0.4	1.1	0.07	-1.0	0.8	1.2	0.04	1.2	0.01
				GAEAANVTGPDGVPVEGSR	2	100.0%	1																									
				NDTKEDVFVHQTAIKK	3	100.0%	1																									
				NGYGFINR	2	100.0%	1																									
				SVGDGETVEFDVVEGEK	2	100.0%	2																									
				VLGTVK	1	86.2%	1																									
IPI00031812	YBX1	Nuclease-sensitive element-binding protein 1	100.0%	38.3	9	10	12	1	40,976,945	38,163,672	40,637,579	45,060,525	2,805,424	1,838,110	2,154,210	2,524,954	15.3	10.8	11.9	12.5	-1.1	0.4	-1.0	0.9	1.1	0.3	1.1	0.4	1.2	0.06	1.1	0.2
				GAEAANVTGPGGVPVQGSK	2	100.0%	2																									
				NDTKEDVFVHQTAIK	2	100.0%	1																									
				NDTKEDVFVHQTAIK	3	99.8%	1																									
				NDTKEDVFVHQTAIKK	3	100.0%	1																									
				NGYGFINR	2	100.0%	1																									
				NYQQNYQNSESGEKNEGSESAPEGQAQQR	3	100.0%	1																									
				RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	3	100.0%	1																									
				SVGDGETVEFDVVEGEK	2	100.0%	2																									
				SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK	3	100.0%	1																									
				WFNVRNGYGFINRNDTK	2	84.0%	1																									
IPI00031820	FARSA	Phenylalanyl-tRNA synthetase alpha chain	100.0%	3.2	1	1	1	1	4,666,530	4,657,420	4,291,140	5,331,110	428,153	211,474	401,734	220,550	20.5	10.2	20.9	9.3	-1.0	1	-1.1	0.5	1.1	0.2	-1.1	0.4	1.1	0.06	1.2	0.05
				QETELSPEMISSGSWR	2	99.4%	1																									
IPI00031982	NCKAP1	isoform 1 of Nck-associated protein 1	94.5%	0.9	1	1	1	2	1,820,090	1,589,170	1,600,585	1,715,595	216,495	126,409	92,457	90,407	26.6	17.8	12.9	11.8	-1.1	0.4	-1.1	0.4	-1.1	0.7	1.0	0.9	1.1	0.4	1.1	0.4
IPI00409684	NCKAP1	isoform 2 of Nck-associated protein 1	94.5%	0.9	1	1	1	2	1,820,090	1,589,170	1,600,585	1,715,595	216,495	126,409	92,457	90,407	26.6	17.8	12.9	11.8	-1.1	0.4	-1.1	0.4	-1.1	0.7	1.0	0.9	1.1	0.4	1.1	0.4
				MMEEFVPHSK	3	94.5%	1																									
IPI00032134	SERPINB8	Serpin B8	100.0%	2.7	1	1	2	6	6,445,280	6,593,470	7,005,000	8,325,430	1,002,982	449,049	784,495	300,490	34.8	15.2	25.0	8.1	1.0	0.9	1.1	0.7	1.3	0.1	1.1	0.7	1.3	0.01	1.2	0.2
IPI00375668	SERPINB8	serpin B8 isoform b	100.0%	4.1	1	1	2	6	6,445,280	6,593,470	7,005,000	8,325,430	1,002,982	449,049	784,495	300,490	34.8	15.2	25.0	8.1	1.0	0.9	1.1	0.7	1.3	0.1	1.1	0.7	1.3	0.01	1.2	0.2
IPI00657847	SERPINB8	Protein	100.0%	5.3	1	1	2	6	6,445,280	6,593,470	7,005,000	8,325,430	1,002,982	449,049	784,495	300,490	34.8	15.2	25.0	8.1	1.0	0.9	1.1	0.7	1.3	0.1	1.1	0.7	1.3	0.01	1.2	0.2
IPI00790112	SERPINB8	27 kDa protein	100.0%	4.2	1	1	2	6	6,445,280	6,593,470	7,005,000	8,325,430	1,002,982	449,049	784,495	300,490	34.8	15.2	25.0	8.1	1.0	0.9	1.1	0.7	1.3	0.1	1.1	0.7	1.3	0.01	1.2	0.2
IPI00795490	SERPINI2	cDNA FLJ56490, highly similar to Serpin I2	100.0%	2.4	1	1	2	6	6,445,280	6,593,470	7,005,000	8,325,430	1,002,982	449,049	784,495	300,490	34.8	15.2	25.0	8.1	1.0	0.9	1.1	0.7	1.3	0.1	1.1	0.7	1.3	0.01	1.2	0.2
IPI00944915	SERPINI2	Uncharacterized protein	100.0%	4.9	1	1	2	6	6,445,280	6,593,470	7,005,000	8,325,430	1,002,982	449,049	784,495	300,490	34.8	15.2	25.0	8.1	1.0	0.9	1.1	0.7	1.3	0.1	1.1	0.7	1.3	0.01	1.2	0.2
				LVLVNAIYFK	2	100.0%	2																									
IPI00032139	SERPINB9	Serpin B9	100.0%	5.6	2	2	3	1	10,842,620	11,576,010	11,243,860	13,713,990	1,315,819	1,031,747	1,153,249	279,437	27.1	19.9	22.9	4.6	1.1	0.7	1.0	0.8	1.3	0.09	-1.0	0.8	1.2	0.1	1.2	0.1
				AFQSLLTEVNK	2	99.9%	1																									
				LVLVNAIYFK	2	100.0%	2																									
IPI00032140	SERPINH1	Serpin H1	100.0%	38.3	10	12	16	1	41,107,425	38,265,089	47,827,257	45,776,264	1,426,290	2,157,031	2,572,907	2,254,344	7.8	12.6	12.0	11.0	-1.1	0.3	1.2	0.05	1.1	0.1	1.2	0.02	1.2	0.04	-1.0	0.6
				AVLSAEQLRDEEVHAGLGELLR	3	100.0%	1																									
				DQAVENILVSPVVVASSLGLVSLGGK	2	100.0%	2																									
				DQAVENILVSPVVVASSLGLVSLGGK	3	100.0%	2																									
				GVVEVTHDLQK	2	100.0%	2																									
				HLAGLGLTEAIDKNK	3	100.0%	1																									
				LFYADHPFIFLVR	2	99.9%	1																									
				LQIVEMPLAHK	2	99.9%	1																									
				LQIVEMPLAHK	3	99.1%	1																									
				LYGPSSVSFADDFVR	2	100.0%	2																									
				SALQSINEWAAQTTDGKLPEVTK	3	100.0%	1																									
				SYTVGVMMMHR	2	89.6%	1																									
				TGLYNYYDDEKEK	3	83.2%	1																									
IPI00032220	AGT	Angiotensinogen	99.6%	6.8	2	2	2	1	6,433,658	6,414,002	6,678,293	7,256,064	842,685	371,036	547,543	223,064	29.3	12.9	18.3	6.9	-1.0	1	1.0	0.8	1.1	0.4	1.0	0.7	1.1	0.09	1.1	0.4
				ADSQAQLLLSTVVGVFTAPGLHLK	3	99.6%	1																									
				FMQAVTGWK	2	91.8%	1																									
IPI00032293	CST3	Cystatin-C	98.6%	7.5	1	1	1	1	5,977,030	6,418,980	5,636,560	6,906,640	455,380	262,470	305,463	259,993	17.0	9.1	12.1	8.4	1.1	0.4	-1.1	0.6	1.2	0.1	-1.1	0.09	1.1	0.2	1.2	0.01
				ALDFAVGEYNK	2	98.6%	1																									
IPI00032304	PLS1	Plastin-1	100.0%	20.5	8	10	13	1	24,455,330	23,376,872	23,432,118	26,626,668	1,544,329	681,701	1,238,044	1,545,826	14.1	6.5	11.8	13.0	-1.0	0.5	-1.0	0.6	1.1	0.3	1.0	1	1.1	0.09	1.1	0.1
				HLIPMNPNDDSLFK	2	83.7%	1																									
				ILSVADSNKDGK	2	99.9%	1																									
				ISFEEFVSLMQELK	2	100.0%	2																									
				ISFEEFVSLMQELK	3	100.0%	1																									
				MINLSEPDTIDER	2	100.0%	2																									
				NEALIALLNEGEELEELMK	2	100.0%	1																									
				QFVTPADVVSGNPK	2	100.0%	2																									
				SISTSLPVLDLIDAIAPNAVR	2	100.0%	1																									
				SISTSLPVLDLIDAIAPNAVR	3	100.0%	1																									
				YTLNVLSDLGEGEKVNDEIIIK	3	100.0%	1																									
IPI00032313	S100A4	Protein S100-A4	100.0%	45.5	5	6	9	1	41,837,200	42,235,230	42,835,975	49,506,635	3,766,793	1,643,816	2,909,860	2,098,418	20.1	8.7	15.2	9.5	1.0	0.9	1.0	0.8	1.2	0.1	1.0	0.9	1.2	0.03	1.2	0.1
				ALDVMVSTFHK	2	100.0%	2																									
				ALDVMVSTFHK	3	100.0%	2																									
				ELPSFLGK	2	98.6%	1																									
				LMSNLDSNR	2	99.9%	1																									
				RTDEAAFQK	2	100.0%	2																									
				SELKELLTR	2	99.3%	1																									
IPI00032374	RRP1B	isoform 2 of Ribosomal RNA processing protein 1 homolog B	100.0%	3.7	2	2	2	2	2,968,910	2,840,760	2,956,185	3,390,400	156,760	69,805	295,868	296,576	11.8	5.5	22.4	19.6	-1.0	0.5	-1.0	1	1.1	0.2	1.0	0.7	1.2	0.1	1.1	0.3
IPI00290952	RRP1B	isoform 1 of Ribosomal RNA processing protein 1 homolog B	100.0%	3.6	2	2	2	2	2,968,910	2,840,760	2,956,185	3,390,400	156,760	69,805	295,868	296,576	11.8	5.5	22.4	19.6	-1.0	0.5	-1.0	1	1.1	0.2	1.0	0.7	1.2	0.1	1.1	0.3
				FHFIDIYLDELSK	2	81.1%	1																									
				TPTSSPASSPLVAK	2	99.7%	1																									
IPI00032406	DNAJA2	DnaJ homolog subfamily A member 2	99.4%	2.4	1	1	1	1	3,696,900	3,933,050	3,889,570	4,703,220	378,275	284,464	414,318	261,891	22.9	16.2	23.8	12.5	1.1	0.6	1.1	0.7	1.3	0.06	-1.0	0.9	1.2	0.08	1.2	0.1
				VSLEDLYNGK	2	99.0%	1																									
IPI00032409	LAMTOR2	isoform 1 of Ragulator complex protein LAMTOR2	99.2%	9.6	1	1	1	3	975,337	1,093,357	1,255,633	996,607	93,677	72,780	79,561	92,362	21.5	14.9	14.2	20.7	1.1	0.3	1.3	0.05	1.0	0.9	1.1	0.2	-1.1	0.4	-1.3	0.07
IPI00477441	LAMTOR2	isoform 2 of Ragulator complex protein LAMTOR2	99.2%	8.0	1	1	1	3	975,337	1,093,357	1,255,633	996,607	93,677	72,780	79,561	92,362	21.5	14.9	14.2	20.7	1.1	0.3	1.3	0.05	1.0	0.9	1.1	0.2	-1.1	0.4	-1.3	0.07
IPI00477454	LAMTOR2	isoform 3 of Ragulator complex protein LAMTOR2	99.2%	12.6	1	1	1	3	975,337	1,093,357	1,255,633	996,607	93,677	72,780	79,561	92,362	21.5	14.9	14.2	20.7	1.1	0.3	1.3	0.05	1.0	0.9	1.1	0.2	-1.1	0.4	-1.3	0.07
				NGNQAFNEDNLK	2	99.2%	1																									
IPI00909671	-	cDNA FLJ51284, highly similar to Adapter-relatedprotein complex 3 mu-1 subunit	100.0%	9.6	2	2	2	2	8,724,049	6,164,067	9,500,926	6,704,213	1,075,162	726,269	939,529	441,349	27.6	26.4	22.1	14.7	-1.4	0.08	1.1	0.6	-1.3	0.1	1.5	0.02	1.1	0.5	-1.4	0.03
IPI00032459	AP3M1	AP-3 complex subunit mu-1	100.0%	8.4	2	2	2	2	8,724,049	6,164,067	9,500,926	6,704,213	1,075,162	726,269	939,529	441,349	27.6	26.4	22.1	14.7	-1.4	0.08	1.1	0.6	-1.3	0.1	1.5	0.02	1.1	0.5	-1.4	0.03
				LSGMPDLSLSFMNPR	2	84.8%	1																									
				YTNNEAYFDVVEEIDAIIDK	2	99.9%	1																									
IPI00032460	LSM2	U6 snRNA-associated Sm-like protein LSm2	100.0%	20.0	1	2	2	1	10,370,950	10,218,030	10,581,720	12,004,460	547,983	740,761	673,665	631,745	11.8	16.2	14.2	11.8	-1.0	0.9	1.0	0.8	1.2	0.09	1.0	0.7	1.2	0.1	1.1	0.2
				YVQLPADEVDTQLLQDAAR	2	100.0%	1																									
				YVQLPADEVDTQLLQDAAR	3	100.0%	1																									
IPI00032506	C14orf142	Uncharacterized protein C14orf142	99.5%	18.0	1	1	1	1	7,493,580	7,158,180	7,602,060	8,017,710	925,454	381,335	495,941	318,089	27.6	11.9	14.6	8.9	-1.0	0.7	1.0	0.9	1.1	0.6	1.1	0.5	1.1	0.1	1.1	0.5
				DMVTELFDPLVQGEVQHR	3	99.5%	1																									
IPI00032516	AP1M1	AP-1 complex subunit mu-1	100.0%	5.7	2	2	2	4	1,744,473	1,838,485	1,760,579	2,252,620	447,643	142,574	165,360	73,344	57.4	17.3	21.0	7.3	1.1	0.8	1.0	1	1.3	0.3	-1.0	0.7	1.2	0.03	1.3	0.03
IPI00910088	AP1M1	AP-1 complex subunit mu-1 isoform 1	100.0%	5.5	2	2	2	4	1,744,473	1,838,485	1,760,579	2,252,620	447,643	142,574	165,360	73,344	57.4	17.3	21.0	7.3	1.1	0.8	1.0	1	1.3	0.3	-1.0	0.7	1.2	0.03	1.3	0.03
IPI00910344	AP1M1	cDNA FLJ58317, highly similar to Adaptor-relatedprotein complex 1 mu-1 subunit	100.0%	6.5	2	2	2	4	1,744,473	1,838,485	1,760,579	2,252,620	447,643	142,574	165,360	73,344	57.4	17.3	21.0	7.3	1.1	0.8	1.0	1	1.3	0.3	-1.0	0.7	1.2	0.03	1.3	0.03
IPI01012853	AP1M1	cDNA FLJ57898, highly similar to Adaptor-relatedprotein complex 1 mu-1 subunit	100.0%	6.8	2	2	2	4	1,744,473	1,838,485	1,760,579	2,252,620	447,643	142,574	165,360	73,344	57.4	17.3	21.0	7.3	1.1	0.8	1.0	1	1.3	0.3	-1.0	0.7	1.2	0.03	1.3	0.03
				FEIPYFTTSGIQVR	2	99.6%	1																									
				SGYQALPWVR	2	99.6%	1																									
IPI00032533	WDR18	WD repeat-containing protein 18	97.5%	3.9	1	1	1	1	2,534,680	2,263,140	2,598,410	2,484,930	237,142	262,918	443,758	298,539	20.9	26.0	38.2	26.9	-1.1	0.5	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.6	-1.0	0.8
				GLALLNGEYLLAAQLGK	2	97.5%	1																									
IPI00032561	CAB39	Calcium-binding protein 39	94.7%	3.2	1	1	1	1	4,924,130	5,637,190	5,187,570	6,397,350	76,828	367,409	268,229	427,165	3.5	14.6	11.6	14.9	1.1	0.1	1.1	0.4	1.3	0.02	-1.1	0.4	1.1	0.2	1.2	0.04
				DVAQIFNNILR	2	94.7%	1																									
IPI00032808	RAB3D	Ras-related protein Rab-3D	100.0%	15.5	2	2	2	1	8,034,203	7,151,930	8,985,780	8,046,687	308,896	312,592	496,079	157,035	8.6	9.8	12.3	4.4	-1.1	0.08	1.1	0.1	1.0	1	1.3	0.01	1.1	0.03	-1.1	0.1
				LADDLGFEFFEASAK	2	100.0%	1																									
				YADDSFTPAFVSTVGIDFK	2	100.0%	1																									
IPI00032826	ST13	Hsc70-interacting protein	100.0%	17.1	5	5	7	1	17,252,021	18,782,562	16,664,390	19,258,628	1,266,890	790,681	759,116	582,944	16.4	9.4	10.2	6.8	1.1	0.3	-1.0	0.7	1.1	0.2	-1.1	0.09	1.0	0.6	1.2	0.03
				AIEINPDSAQPYK	2	100.0%	2																									
				EWVESMGGK	2	99.7%	1																									
				LDYDEDASAMLK	2	100.0%	2																									
				LLGHWEEAAHDLALACK	3	100.0%	1																									
				QDPSVLHTEEMR	2	97.2%	1																									
IPI00032827	SF3B14	Pre-mRNA branch site protein p14	99.5%	9.6	1	1	1	1	4,269,210	4,696,080	4,709,800	4,717,610	270,486	111,873	328,657	223,315	14.2	5.3	15.6	10.6	1.1	0.2	1.1	0.3	1.1	0.2	1.0	1	1.0	0.9	1.0	1
				ITAEEMYDIFGK	2	99.5%	1																									
IPI00032831	SNAP29	Synaptosomal-associated protein 29	99.5%	9.3	2	2	2	1	22,071,695	22,971,690	19,429,945	25,764,545	2,276,953	1,188,558	1,629,512	1,915,610	23.1	11.6	18.8	16.6	1.0	0.7	-1.1	0.4	1.2	0.2	-1.2	0.1	1.1	0.3	1.3	0.04
				GAGSAMSTDAYPK	2	99.5%	1																									
				VGVASSEELAR	2	92.9%	1																									
IPI00032851	COPZ1	Coatomer subunit zeta-1	98.6%	5.7	1	1	2	1	4,726,060	5,123,830	4,410,130	5,630,170	459,877	421,530	341,725	287,842	21.8	18.4	17.3	11.4	1.1	0.5	-1.1	0.6	1.2	0.1	-1.2	0.2	1.1	0.4	1.3	0.03
				YYDDTYPSVK	2	99.6%	2																									
IPI00032853	NOP10	H/ACA ribonucleoprotein complex subunit 3	92.9%	20.3	1	1	1	2	16,457,350	18,540,050	19,129,850	21,788,100	2,176,333	1,115,830	1,760,497	706,453	29.6	13.5	20.6	7.3	1.1	0.4	1.2	0.4	1.3	0.07	1.0	0.8	1.2	0.04	1.1	0.2
IPI00798039	NOP10	4 kDa protein	92.9%	36.1	1	1	1	2	16,457,350	18,540,050	19,129,850	21,788,100	2,176,333	1,115,830	1,760,497	706,453	29.6	13.5	20.6	7.3	1.1	0.4	1.2	0.4	1.3	0.07	1.0	0.8	1.2	0.04	1.1	0.2
				MFLQYYLNEQGDR	2	92.9%	1																									
IPI00032955	RNF114	isoform 1 of RING finger protein 114	96.9%	4.4	1	1	1	3	838,083	1,052,923	1,086,923	1,113,723	75,447	74,503	183,287	144,657	20.1	15.8	37.7	29.0	1.3	0.08	1.3	0.2	1.3	0.1	1.0	0.9	1.1	0.7	1.0	0.9
IPI00908327	RNF114	isoform 2 of RING finger protein 114	96.9%	5.2	1	1	1	3	838,083	1,052,923	1,086,923	1,113,723	75,447	74,503	183,287	144,657	20.1	15.8	37.7	29.0	1.3	0.08	1.3	0.2	1.3	0.1	1.0	0.9	1.1	0.7	1.0	0.9
IPI00952952	RNF114	21 kDa protein	96.9%	5.2	1	1	1	3	838,083	1,052,923	1,086,923	1,113,723	75,447	74,503	183,287	144,657	20.1	15.8	37.7	29.0	1.3	0.08	1.3	0.2	1.3	0.1	1.0	0.9	1.1	0.7	1.0	0.9
				YQNYIMEGVK	2	96.9%	1																									
IPI00032957	UBE2I	SUMO-conjugating enzyme UBC9	90.6%	12.0	1	1	1	2	2,889,335	3,151,535	2,971,770	3,362,865	315,563	303,493	418,085	181,612	24.4	21.5	31.5	12.1	1.1	0.6	1.0	0.9	1.2	0.2	-1.1	0.7	1.1	0.6	1.1	0.4
IPI00450472	UBE2I	Ubiquitin carrier protein	90.6%	10.3	1	1	1	2	2,889,335	3,151,535	2,971,770	3,362,865	315,563	303,493	418,085	181,612	24.4	21.5	31.5	12.1	1.1	0.6	1.0	0.9	1.2	0.2	-1.1	0.7	1.1	0.6	1.1	0.4
				NPDGTMNLMNWECAIPGKK	3	90.6%	1																									
IPI00032958	ANLN	isoform 2 of Actin-binding protein anillin	94.6%	3.0	1	1	1	3	975,350	800,203	922,130	904,473	46,714	37,624	32,785	41,033	10.7	10.5	8.0	10.1	-1.2	0.02	-1.1	0.4	-1.1	0.3	1.2	0.04	1.1	0.1	-1.0	0.7
IPI00743594	ANLN	Actin-binding protein anillin	94.6%	2.9	1	1	1	3	975,350	800,203	922,130	904,473	46,714	37,624	32,785	41,033	10.7	10.5	8.0	10.1	-1.2	0.02	-1.1	0.4	-1.1	0.3	1.2	0.04	1.1	0.1	-1.0	0.7
IPI00926483	ANLN	Uncharacterized protein	94.6%	19.5	1	1	1	3	975,350	800,203	922,130	904,473	46,714	37,624	32,785	41,033	10.7	10.5	8.0	10.1	-1.2	0.02	-1.1	0.4	-1.1	0.3	1.2	0.04	1.1	0.1	-1.0	0.7
				SCSPSPVSPQVQPQAADTISDSVAVPASLLGMR	3	94.6%	1																									
IPI00033022	DNM2	isoform 1 of Dynamin-2	100.0%	27.2	16	17	17	3	25,796,047	26,214,315	27,048,853	30,429,355	2,596,729	1,115,439	2,164,922	694,468	22.5	9.5	17.9	5.1	1.0	0.9	1.0	0.7	1.2	0.2	1.0	0.7	1.2	0.01	1.1	0.2
IPI00218889	DNM2	isoform 2 of Dynamin-2	100.0%	27.4	16	17	17	3	25,796,047	26,214,315	27,048,853	30,429,355	2,596,729	1,115,439	2,164,922	694,468	22.5	9.5	17.9	5.1	1.0	0.9	1.0	0.7	1.2	0.2	1.0	0.7	1.2	0.01	1.1	0.2
IPI00980612	DNM2	dynamin-2 isoform 5	100.0%	27.3	16	17	17	3	25,796,047	26,214,315	27,048,853	30,429,355	2,596,729	1,115,439	2,164,922	694,468	22.5	9.5	17.9	5.1	1.0	0.9	1.0	0.7	1.2	0.2	1.0	0.7	1.2	0.01	1.1	0.2
				AGVYPEKDQAENEDGAQENTFSMDPQLER	3	99.9%	1																									

				ALLQMVQQFGVDFEK	2	100.0%	1																									
				ALLQMVQQFGVDFEKR	3	100.0%	1																									
				CVDLVIQELINTVR	2	99.9%	1																									
				CVDLVIQELINTVR	3	81.6%	1																									
				ESSLILAVTPANMDLANSDALK	2	100.0%	1																									
				FTDFDEVRQEIEAETDR	3	97.9%	1																									
				GISPVPINLR	2	84.2%	1																									
				GMEELIPLVNK	2	99.7%	1																									
				GWLTINNISLMK	2	99.4%	1																									
				IEGSGDQVDTLELSGGAR	2	100.0%	1																									
				LDLMDEGTDARDVLENK	3	84.1%	1																									
				NLVDSYVAIINK	2	100.0%	1																									
				SSVLENFVGR	2	99.9%	1																									
				TGLFTPDLAFEAIVK	2	100.0%	1																									
				VPVGDQPPDIEYQIK	2	100.0%	1																									
				VYSPHVLNLTLIDLPGITK	3	100.0%	1																									
IPI00033025	SEP7	Uncharacterized protein	100.0%	5.3	1	1	1	7	342,761	344,304	318,344	384,710	28,646	27,464	22,352	20,513	18.7	17.8	15.7	11.9	1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.06
IPI00816201	SEP7	isoform 2 of Septin-7	100.0%	5.3	1	1	1	7	342,761	344,304	318,344	384,710	28,646	27,464	22,352	20,513	18.7	17.8	15.7	11.9	1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.06
IPI00941534	SEP7	isoform 1 of Septin-7	100.0%	5.3	1	1	1	7	342,761	344,304	318,344	384,710	28,646	27,464	22,352	20,513	18.7	17.8	15.7	11.9	1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.06
IPI01009775	SEP7	cDNA FLJ52574, highly similar to Septin-7	100.0%	6.0	1	1	1	7	342,761	344,304	318,344	384,710	28,646	27,464	22,352	20,513	18.7	17.8	15.7	11.9	1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.06
IPI01011635	SEP7	CDC10 protein variant (Fragment)	100.0%	6.0	1	1	1	7	342,761	344,304	318,344	384,710	28,646	27,464	22,352	20,513	18.7	17.8	15.7	11.9	1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.06
IPI01011947	SEP7	27 kDa protein	100.0%	9.8	1	1	1	7	342,761	344,304	318,344	384,710	28,646	27,464	22,352	20,513	18.7	17.8	15.7	11.9	1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.06
IPI01015990	SEP7	51 kDa protein	100.0%	5.3	1	1	1	7	342,761	344,304	318,344	384,710	28,646	27,464	22,352	20,513	18.7	17.8	15.7	11.9	1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.06
				STLINSLFLTDLYSPEYPGPSHR	3	100.0%	1																									
IPI00911048	-	cDNA FLJ56666, highly similar to Adhesion-regulating molecule 1	99.1%	4.8	1	1	2	3	999,647	1,141,627	1,111,500	1,075,153	71,184	98,686	76,398	77,183	15.9	19.3	15.4	16.1	1.1	0.3	1.1	0.3	1.1	0.5	-1.0	0.8	-1.1	0.6	-1.0	0.7
IPI00033030	ADRM1	Proteasomal ubiquitin receptor ADRM1	99.1%	2.2	1	1	2	3	999,647	1,141,627	1,111,500	1,075,153	71,184	98,686	76,398	77,183	15.9	19.3	15.4	16.1	1.1	0.3	1.1	0.3	1.1	0.5	-1.0	0.8	-1.1	0.6	-1.0	0.7
IPI00470921	ADRM1	Uncharacterized protein	99.1%	2.3	1	1	2	3	999,647	1,141,627	1,111,500	1,075,153	71,184	98,686	76,398	77,183	15.9	19.3	15.4	16.1	1.1	0.3	1.1	0.3	1.1	0.5	-1.0	0.8	-1.1	0.6	-1.0	0.7
				LFFWMQEPK	2	99.1%	2																									
IPI00033036	METAP2	Methionine aminopeptidase 2	98.6%	7.5	2	2	2	3	2,426,297	2,239,628	2,301,834	2,450,844	233,823	164,141	204,093	223,002	21.6	16.4	19.8	20.4	-1.1	0.5	-1.1	0.7	1.0	0.9	1.0	0.8	1.1	0.5	1.1	0.6
IPI00789396	METAP2	Methionine aminopeptidase	98.6%	7.9	2	2	2	3	2,426,297	2,239,628	2,301,834	2,450,844	233,823	164,141	204,093	223,002	21.6	16.4	19.8	20.4	-1.1	0.5	-1.1	0.7	1.0	0.9	1.0	0.8	1.1	0.5	1.1	0.6
IPI01010256	METAP2	Methionine aminopeptidase	98.6%	11.0	2	2	2	3	2,426,297	2,239,628	2,301,834	2,450,844	233,823	164,141	204,093	223,002	21.6	16.4	19.8	20.4	-1.1	0.5	-1.1	0.7	1.0	0.9	1.0	0.8	1.1	0.5	1.1	0.6
				ALDQASEEIWNDFR	2	98.1%	1																									
				LCDVGEAIQEVMESYEVEIDGK	2	98.6%	1																									
IPI00033130	SAE1	SUMO-activating enzyme subunit 1	100.0%	15.3	4	5	5	1	6,833,981	7,054,263	7,385,638	8,530,429	661,292	409,778	400,151	161,825	21.6	13.0	12.1	4.2	1.0	0.8	1.1	0.5	1.2	0.06	1.0	0.6	1.2	0.02	1.2	0.03
				AKLDSSETTMVK	2	99.8%	1																									
				EALEVDWSSEK	2	97.0%	1																									
				VLLVGLK	2	82.2%	1																									
				YCFSEMAPVCAVVGGILAQEIVK	2	100.0%	1																									
				YCFSEMAPVCAVVGGILAQEIVK	3	100.0%	1																									
IPI00033143	EIF3K	Eukaryotic translation initiation factor 3 subunit K	100.0%	22.9	3	3	4	2	4,466,688	4,272,123	4,924,453	4,469,957	187,125	214,467	312,184	141,200	9.4	11.2	14.2	7.1	-1.0	0.5	1.1	0.2	1.0	1	1.2	0.1	1.0	0.5	-1.1	0.2
IPI01013095	EIF3K	cDNA, FLJ79243, highly similar to Eukaryotic translation initiation factor 3 subunit 12	100.0%	23.7	3	3	4	2	4,466,688	4,272,123	4,924,453	4,469,957	187,125	214,467	312,184	141,200	9.4	11.2	14.2	7.1	-1.0	0.5	1.1	0.2	1.0	1	1.2	0.1	1.0	0.5	-1.1	0.2
				ENAYDLEANLAVLK	2	100.0%	1																									
				LYQFNPAFFQTTVTAQILLK	2	99.4%	1																									
				WLLAEMLGDLSDSQLK	2	100.0%	2																									
IPI00033153	NXF1	Nuclear RNA export factor 1	97.5%	1.9	1	1	1	2	918,702	790,490	930,915	1,077,455	151,885	59,423	111,454	65,052	37.0	16.8	26.8	13.5	-1.2	0.5	1.0	0.9	1.2	0.4	1.2	0.3	1.4	0.01	1.2	0.3
IPI00978175	NXF1	Uncharacterized protein	97.5%	2.0	1	1	1	2	918,702	790,490	930,915	1,077,455	151,885	59,423	111,454	65,052	37.0	16.8	26.8	13.5	-1.2	0.5	1.0	0.9	1.2	0.4	1.2	0.3	1.4	0.01	1.2	0.3
				LNVVAFLNELPK	2	97.5%	1																									
IPI00033419	FEM1B	Protein fem-1 homolog B	93.5%	2.6	1	1	1	1	2,447,610	2,389,050	2,361,500	2,239,360	229,424	185,363	156,570	158,442	21.0	17.4	14.8	15.8	-1.0	0.8	-1.0	0.8	-1.1	0.5	-1.0	0.9	-1.1	0.6	-1.1	0.6
				FAQVFSQMIHLNETVK	3	93.5%	1																									
IPI00220573	MYL12A	Myosin regulatory light chain 12A	100.0%	62.6	9	11	17	3	16,235,041	16,529,531	16,206,030	18,696,918	1,344,851	613,408	980,969	423,553	18.5	8.3	13.5	5.1	1.0	0.8	-1.0	1	1.2	0.1	-1.0	0.8	1.1	0.02	1.2	0.05
IPI00604523	MYL12A	Myosin regulatory light chain MRCL3 variant	100.0%	60.5	9	11	17	3	16,235,041	16,529,531	16,206,030	18,696,918	1,344,851	613,408	980,969	423,553	18.5	8.3	13.5	5.1	1.0	0.8	-1.0	1	1.2	0.1	-1.0	0.8	1.1	0.02	1.2	0.05
IPI00033494	MYL12B	Myosin regulatory light chain 12B	100.0%	62.2	9	11	17	3	16,235,041	16,529,531	16,206,030	18,696,918	1,344,851	613,408	980,969	423,553	18.5	8.3	13.5	5.1	1.0	0.8	-1.0	1	1.2	0.1	-1.0	0.8	1.1	0.02	1.2	0.05
				ATSNVFAMFDQSQIQEFK	2	100.0%	1																									
				ATSNVFAMFDQSQIQEFK	3	99.3%	1																									
				DGFIDKEDLHDMLASLGK	3	100.0%	2																									
				EAFNMIDQNR	2	100.0%	2																									
				ELLTTMGDR	2	100.0%	2																									
				ELLTTMGDRFTDEEVDELYR	3	99.9%	1																									
				FTDEEVDELYR	2	100.0%	2																									
				GNFNYIEFTR	2	100.0%	2																									
				LNGTDPEDVIR	2	100.0%	2																									
				NAFACFDEEATGTIQEDYLR	2	100.0%	1																									
				NAFACFDEEATGTIQEDYLR	3	100.0%	1																									
IPI00033561	RNPS1	isoform 1 of RNA-binding protein with serine-rich domain 1	100.0%	4.9	1	1	1	3	1,338,453	1,779,453	1,043,963	1,537,267	250,219	214,598	116,388	175,972	41.8	27.0	24.9	25.6	1.3	0.2	-1.3	0.3	1.1	0.5	-1.7	0.02	-1.2	0.4	1.5	0.05
IPI00479871	RNPS1	isoform 2 of RNA-binding protein with serine-rich domain 1	100.0%	5.3	1	1	1	3	1,338,453	1,779,453	1,043,963	1,537,267	250,219	214,598	116,388	175,972	41.8	27.0	24.9	25.6	1.3	0.2	-1.3	0.3	1.1	0.5	-1.7	0.02	-1.2	0.4	1.5	0.05
IPI00783594	RNPS1	isoform 3 of RNA-binding protein with serine-rich domain 1	100.0%	5.6	1	1	1	3	1,338,453	1,779,453	1,043,963	1,537,267	250,219	214,598	116,388	175,972	41.8	27.0	24.9	25.6	1.3	0.2	-1.3	0.3	1.1	0.5	-1.7	0.02	-1.2	0.4	1.5	0.05
				GYAYVEFENPDEAEK	2	100.0%	1																									
IPI00033600	PPP1R7	isoform 1 of Protein phosphatase 1 regulatory subunit 7	100.0%	20.8	5	5	5	1	8,083,218	7,888,820	8,954,300	10,540,177	1,006,197	867,941	1,177,106	796,319	27.8	24.6	29.4	16.9	-1.0	0.9	1.1	0.6	1.3	0.09	1.1	0.5	1.3	0.05	1.2	0.3
				ELYLSHNGIEVIEGLENNNK	3	99.9%	1																									
				GAGQQQSQEMMEVDR	2	100.0%	1																									
				IEGLQNLVNLR	2	99.8%	1																									
				LQNLDALTNLTVLSMQSNR	2	81.1%	1																									
				LTMLDIASNR	2	99.4%	1																									
IPI00034015	CELF1	isoform 1 of CUGBP Elav-like family member 1	96.1%	2.7	1	1	1	6	592,327	557,423	550,470	604,365	70,150	38,486	48,491	62,913	26.5	15.4	19.7	23.3	-1.1	0.7	-1.1	0.6	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.5
IPI00218388	CELF1	isoform 2 of CUGBP Elav-like family member 1	96.1%	2.7	1	1	1	6	592,327	557,423	550,470	604,365	70,150	38,486	48,491	62,913	26.5	15.4	19.7	23.3	-1.1	0.7	-1.1	0.6	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.5
IPI00218389	CELF1	isoform 3 of CUGBP Elav-like family member 1	96.1%	2.7	1	1	1	6	592,327	557,423	550,470	604,365	70,150	38,486	48,491	62,913	26.5	15.4	19.7	23.3	-1.1	0.7	-1.1	0.6	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.5
IPI00853009	CELF1	isoform 4 of CUGBP Elav-like family member 1	96.1%	2.5	1	1	1	6	592,327	557,423	550,470	604,365	70,150	38,486	48,491	62,913	26.5	15.4	19.7	23.3	-1.1	0.7	-1.1	0.6	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.5
IPI00956101	CELF1	CUGBP Elav-like family member 1 isoform 5	96.1%	2.7	1	1	1	6	592,327	557,423	550,470	604,365	70,150	38,486	48,491	62,913	26.5	15.4	19.7	23.3	-1.1	0.7	-1.1	0.6	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.5
IPI00984962	CELF1	55 kDa protein	96.1%	2.5	1	1	1	6	592,327	557,423	550,470	604,365	70,150	38,486	48,491	62,913	26.5	15.4	19.7	23.3	-1.1	0.7	-1.1	0.6	1.0	0.9	-1.0	0.9	1.1	0.5	1.1	0.5
				VMFSSFGQIEECR	2	96.1%	1																									
IPI00034049	UPF1	isoform 1 of Regulator of nonsense transcripts 1	100.0%	7.8	7	7	8	2	22,029,086	22,648,645	20,965,326	24,599,238	1,170,202	969,697	913,685	697,710	11.9	9.6	9.7	6.3	1.0	0.7	-1.1	0.5	1.1	0.1	-1.1	0.2	1.1	0.1	1.2	0.01
IPI00399170	UPF1	isoform 2 of Regulator of nonsense transcripts 1	100.0%	7.9	7	7	8	2	22,029,086	22,648,645	20,965,326	24,599,238	1,170,202	969,697	913,685	697,710	11.9	9.6	9.7	6.3	1.0	0.7	-1.1	0.5	1.1	0.1	-1.1	0.2	1.1	0.1	1.2	0.01
				AGLSQSLFER	2	99.2%	1																									
				ANEHQGIGFLNDPR	3	81.2%	1																									
				EAIIPGSVYDR	2	97.8%	1																									
				LLGHEVEDVIIK	2	100.0%	1																									
				NVFLLGFIPAK	2	100.0%	1																									
				VPDNYGDEIAIELR	2	99.9%	2																									
				YEDAYQYQNIFGPLVK	2	99.9%	1																									
IPI00034280	DHRS11	isoform 1 of Dehydrogenase/reductase SDR family member 11	100.0%	14.2	3	3	4	1	5,567,748	5,305,011	5,400,398	6,432,902	456,369	212,238	353,995	259,229	18.3	9.0	14.7	9.0	-1.0	0.6	-1.0	0.8	1.2	0.1	1.0	0.8	1.2	0.01	1.2	0.05
				AAATYEQMK	2	93.0%	1																									
				LALVTGASGGIGAAVAR	2	99.8%	1																									
				YAVTALTEGLR	2	99.9%	2																									
IPI00034319	CUTA	isoform A of Protein CutA	100.0%	22.7	2	2	2	3	1,738,195	1,724,896	1,938,579	2,250,274	228,849	137,949	192,205	102,868	29.4	17.9	22.2	10.2	-1.0	1	1.1	0.5	1.3	0.08	1.1	0.4	1.3	0.02	1.2	0.2
IPI00554556	CUTA	isoform C of Protein CutA	100.0%	28.9	2	2	2	3	1,738,195	1,724,896	1,938,579	2,250,274	228,849	137,949	192,205	102,868	29.4	17.9	22.2	10.2	-1.0	1	1.1	0.5	1.3	0.08	1.1	0.4	1.3	0.02	1.2	0.2
IPI00554634	CUTA	isoform B of Protein CutA	100.0%	25.1	2	2	2	3	1,738,195	1,724,896	1,938,579	2,250,274	228,849	137,949	192,205	102,868	29.4	17.9	22.2	10.2	-1.0	1	1.1	0.5	1.3	0.08	1.1	0.4	1.3	0.02	1.2	0.2
				LAACVNLIPQITSIYEWK	2	100.0%	1																									
				SVHPYEVAEVIALPVEQGNFPYLQWVR	3	100.0%	1																									
IPI00037283	DNM1L	isoform 5 of Dynamin-1-like protein	100.0%	11.1	5	5	5	7	3,050,864	3,068,464	3,284,291	3,717,102	364,337	152,592	279,059	59,136	26.7	11.1	19.0	3.6	1.0	1	1.1	0.6	1.2	0.1	1.1	0.5	1.2	0.01	1.1	0.2
IPI00146935	DNM1L	isoform 1 of Dynamin-1-like protein	100.0%	10.7	5	5	5	7	3,050,864	3,068,464	3,284,291	3,717,102	364,337	152,592	279,059	59,136	26.7	11.1	19.0	3.6	1.0	1	1.1	0.6	1.2	0.1	1.1	0.5	1.2	0.01	1.1	0.2
IPI00473085	DNM1L	isoform 3 of Dynamin-1-like protein	100.0%	11.3	5	5	5	7	3,050,864	3,068,464	3,284,291	3,717,102	364,337	152,592	279,059	59,136	26.7	11.1	19.0	3.6	1.0	1	1.1	0.6	1.2	0.1	1.1	0.5	1.2	0.01	1.1	0.2
IPI00555883	DNM1L	isoform 4 of Dynamin-1-like protein	100.0%	10.9	5	5	5	7	3,050,864	3,068,464	3,284,291	3,717,102	364,337	152,592	279,059	59,136	26.7	11.1	19.0	3.6	1.0	1	1.1	0.6	1.2	0.1	1.1	0.5	1.2	0.01	1.1	0.2
IPI00871742	DNM1L	isoform 6 of Dynamin-1-like protein	100.0%	10.6	5	5	5	7	3,050,864	3,068,464	3,284,291	3,717,102	364,337	152,592	279,059	59,136	26.7	11.1	19.0	3.6	1.0	1	1.1	0.6	1.2	0.1	1.1	0.5	1.2	0.01	1.1	0.2
IPI00942042	DNM1L	isoform 2 of Dynamin-1-like protein	100.0%	11.1	5	5	5	7	3,050,864	3,068,464	3,284,291	3,717,102	364,337	152,592	279,059	59,136	26.7	11.1	19.0	3.6	1.0	1	1.1	0.6	1.2	0.1	1.1	0.5	1.2	0.01	1.1	0.2
IPI01010281	DNM1L	Dynamin 1-like, isoform CRA_c	100.0%	10.0	5	5	5	7	3,050,864	3,068,464	3,284,291	3,717,102	364,337	152,592	279,059	59,136	26.7	11.1	19.0	3.6	1.0	1	1.1	0.6	1.2	0.1	1.1	0.5	1.2	0.01	1.1	0.2
				ALQGASQIIAEIR	2	94.7%	1																									
				IFSPNVVNLTLVDLPGMTK	2	99.4%	1																									
				LDLMDAGTDAMDVLMGR	2	99.4%	1																									
				LGIIGVVNR	2	92.5%	1																									
				TLESVDPLGGLNTIDILTAIR	2	100.0%	1																									
IPI00037448	GRHPR	Glyoxylate reductase/hydroxypyruvate reductase	99.6%	7.3	1	1	1	2	2,055,455	2,491,190	2,400,445	1,945,215	356,205	157,603	271,593	158,808	38.8	14.2	25.3	18.3	1.2	0.3	1.2	0.5	-1.1	0.8	-1.0	0.8	-1.3	0.04	-1.2	0.2
IPI00550682	GRHPR	GRHPR protein (Fragment)	99.6%	7.0	1	1	1	2	2,055,455	2,491,190	2,400,445	1,945,215	356,205	157,603	271,593	158,808	38.8	14.2	25.3	18.3	1.2	0.3	1.2	0.5	-1.1	0.8	-1.0	0.8	-1.3	0.04	-1.2	0.2
				IAAAGLDVTSPEPLPTNHPLLTLK	3	99.6%	1																									
IPI00038378	ENOPH1	isoform 1 of Enolase-phosphatase E1	100.0%	16.1	2	2	2	2	1,159,793	1,246,913	1,497,390	1,328,037	45,078	150,280	92,193	44,961	8.7	27.0	13.8	7.6	1.1	0.6	1.3	0.01	1.1	0.03	1.2	0.2	1.1	0.6	-1.1	0.1
IPI00966573	ENOPH1	Uncharacterized protein	100.0%	24.3	2	2	2	2	1,159,793	1,246,913	1,497,390	1,328,037	45,078	150,280	92,193	44,961	8.7	27.0	13.8	7.6	1.1	0.6	1.3	0.01	1.1	0.03	1.2	0.2	1.1	0.6	-1.1	0.1
				IADSIGCSTNNILFLTDVTR	2	99.6%	1																									
				LLFGHSTEGDILELVDGHFDTK	3	100.0%	1																									
IPI00233885	UGT1A10	UDP-glucuronosyltransferase 1-10	99.8%	4.0	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00657799	UGT1A10	UGT1A10 protein	99.8%	4.8	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00434346	UGT1A1	UDP-glucuronosyltransferase 1-1	99.8%	3.9	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI01012357	UGT1A1	UDP-glucuronosyltransferase 1 family polypeptide A1s	99.8%	4.7	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00473079	UGT1A3	UDP-glucuronosyltransferase 1-3	99.8%	3.9	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00439935	UGT1A4	UDP-glucuronosyltransferase 1-4	99.8%	3.9	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00893254	UGT1A4	UDP-glucuronosyltransferase 1 family polypeptide A4s	99.8%	4.7	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI01012892	UGT1A4	UDP-glucuronosyltransferase 1 family polypeptide A3s (Fragment)	99.8%	10.6	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00472824	UGT1A5	UDP-glucuronosyltransferase 1-5	99.8%	3.9	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00410366	UGT1A6	UDP-glucuronosyltransferase 1-6 isoform 2	99.8%	7.9	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00451965	UGT1A6	UDP-glucuronosyltransferase 1-6	99.8%	4.0	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00892843	UGT1A6	Uncharacterized protein	99.8%	11.9	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00384872	UGT1A7	UDP-glucuronosyltransferase 1-7	99.8%	4.0	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00039666	UGT1A8	UDP-glucuronosyltransferase 1-8	99.8%	4.0	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
IPI00872012	UGT1A9	Uncharacterized protein	99.8%	4.0	1	1	1	15	68,642	86,517	94,255	100,702	11,769	8,723	10,727	12,255	38.3	22.5	25.5	27.2	1.3	0.3	1.4	0.1	1.5	0.1	1.1	0.6	1.2	0.4	1.1	0.7
				GAGVTLNVLEMTSEDLENALK	2	99.8%	1																									
IPI00042932	ABCB4	isoform 1 of Multidrug resistance protein 3	92.8%	0.6	1	1	1	3	2,536,677	2,904,337	2,637,997	3,394,310	284,418	252,613	252,405	173,796	25.1	19.5	21.4	11.5	1.1	0.4	1.0	0.8	1.3	0.03	-1.1	0.5	1.2	0.1	1.3	0.04
IPI00218731	ABCB4	isoform 2 of Multidrug resistance protein 3	92.8%	0.6	1	1	1	3	2,536,677	2,904,337	2,637,997	3,394,310	284,418	252,613	252,405	173,796	25.1	19.5	21.4	11.5	1.1	0.4	1.0	0.8	1.3	0.03	-1.1	0.5	1.2	0.1	1.3	0.04
IPI00927655	ABCB4	multidrug resistance protein 3 isoform C	92.8%	0.7	1	1	1	3	2,536,677	2,904,337	2,637,997	3,394,310	284,418	252,613	252,405	173,796	25.1	19.5	21.4	11.5	1.1	0.4	1.0	0.8	1.3	0.03	-1.1	0.5	1.2	0.1	1.3	0.04
				NFNVNYLR	2	92.8%	1																									
IPI00043863	MAP4	isoform 3 of Microtubule-associated protein 4	100.0%	4.1	2	2	2	3	851,823	936,450	788,349	917,624	65,660	81,850	72,790	60,422	17.2	19.5	20.7	14.7	1.1	0.4	-1.1	0.5	1.1	0.5	-1.2	0.2	-1.0	0.9	1.2	0.2
IPI00910596	MAP4	Microtubule-associated protein	100.0%	13.7	2	2	2	3	851,823	936,450	788,349	917,624	65,660	81,850	72,790	60,422	17.2	19.5	20.7	14.7	1.1	0.4	-1.1	0.5	1.1	0.5	-1.2	0.2	-1.0	0.9	1.2	0.2
IPI00924603	MAP4	Microtubule-associated protein	100.0%	4.2	2	2	2	3	851,823	936,450	788,349	917,624	65,660	81,850	72,790	60,422	17.2	19.5	20.7	14.7	1.1	0.4	-1.1	0.5	1.1	0.5	-1.2	0.2	-1.0	0.9	1.2	0.2
				TTTLSGTAPAAGVVPSR	2	100.0%	1																									
				VGSLDNVGHLPAGGAVK	3	100.0%	1																									
IPI00044748	FMNL2	Similar to FMNL2	91.4%	0.6	1	1	1	1	31,202,100	31,831,600	29,347,600	36,883,500	2,802,657	1,716,325	2,471,384	1,652,213	20.1	12.1	18.8	10.0	1.0	0.9	-1.1	0.6	1.2	0.1	-1.1	0.4	1.2	0.07	1.3	0.03
				FDDQNLR	2	91.4%	1																									
IPI00044761	PUS7	Pseudouridylate synthase 7 homolog	99.6%	4.4	1	1	1	2	582,391	569,023	582,490	589,460	51,649	30,170	74,270	34,414	19.8	11.9	28.5	13.1	-1.0	0.8	1.0	1	1.0	0.9	1.0	0.9	1.0	0.7	1.0	0.9
IPI00945342	PUS7	Uncharacterized protein	99.6%	6.5	1	1	1	2	582,391	569,023	582,490	589,460	51,649	30,170	74,270	34,414	19.8	11.9	28.5	13.1	-1.0	0.8	1.0	1	1.0	0.9	1.0	0.9	1.0	0.7	1.0	0.9
				ISHLNDLSIPVDEEDPSEDIFTVLTAEEK	3	99.6%	1																									

IPI00219037	H2AFX	Histone H2A.x	100.0%	32.2	5	7	12	2	17,339,182	18,190,289	18,135,744	21,521,502	1,556,739	694,505	1,425,255	871,651	20.1	8.5	17.6	9.1	1.0	0.6	1.0	0.7	1.2	0.05	-1.0	1	1.2	0.02	1.2	0.08
IPI00045109	HIST1H2AA	Histone H2A type 1-A	100.0%	35.1	5	7	12	2	17,339,182	18,190,289	18,135,744	21,521,502	1,556,739	694,505	1,425,255	871,651	20.1	8.5	17.6	9.1	1.0	0.6	1.0	0.7	1.2	0.05	-1.0	1	1.2	0.02	1.2	0.08
				AGLQFPVGR	2	100.0%	2																									
				HLQLAIR	2	99.9%	2																									
				LLGGVTIAQGGVLPNIQAVLLPK	2	100.0%	2																									
				LLGGVTIAQGGVLPNIQAVLLPK	3	100.0%	1																									
				NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	3	100.0%	1																									
				VTIAQGGVLPNIQAVLLPK	2	100.0%	2																									
				VTIAQGGVLPNIQAVLLPK	3	100.0%	2																									
IPI00045360	CIC	Protein capicua homolog	99.7%	2.1	1	1	1	1	9,040,300	9,522,430	9,144,260	11,880,290	2,162,821	903,341	1,469,056	762,966	53.5	21.2	35.9	14.4	1.1	0.8	1.0	1	1.3	0.3	-1.0	0.8	1.2	0.08	1.3	0.1
				AAIASIPVGSFEAGASGRPGPAPRQPLEPGPVR	3	99.7%	1																									
IPI00045396	CALU	isoform 2 of Calumenin	100.0%	26.7	5	5	5	2	8,019,624	7,908,332	7,768,817	8,902,779	566,718	302,284	403,663	225,118	15.8	8.6	11.6	5.7	-1.0	0.9	-1.0	0.7	1.1	0.2	-1.0	0.8	1.1	0.03	1.1	0.04
IPI00982476	CALU	calumenin isoform d precursor	100.0%	26.0	5	5	5	2	8,019,624	7,908,332	7,768,817	8,902,779	566,718	302,284	403,663	225,118	15.8	8.6	11.6	5.7	-1.0	0.9	-1.0	0.7	1.1	0.2	-1.0	0.8	1.1	0.03	1.1	0.04
				EEIVDKYDLFVGSQATDFGEALVR	3	100.0%	1																									
				HLVYESDQNKDGK	3	100.0%	1																									
				LGMIVDKIDADKDGFVTEGELK	3	99.9%	1																									
				MADKDGDLIATK	2	99.1%	1																									
				TFDQLTPEESKER	3	99.6%	1																									
IPI00045660	C1orf31	isoform 1 of Uncharacterized protein C1orf31	91.7%	10.4	1	1	1	4	1,624,273	1,760,980	1,662,475	1,907,938	234,016	119,528	146,175	141,964	32.2	15.2	19.7	16.6	1.1	0.6	1.0	0.9	1.2	0.3	-1.1	0.6	1.1	0.5	1.1	0.3
IPI00552131	C1orf31	cDNA FLJ60021, moderately similar to Protein transport protein Sec61 subunit alpha	91.7%	8.4	1	1	1	4	1,624,273	1,760,980	1,662,475	1,907,938	234,016	119,528	146,175	141,964	32.2	15.2	19.7	16.6	1.1	0.6	1.0	0.9	1.2	0.3	-1.1	0.6	1.1	0.5	1.1	0.3
IPI00646750	C1orf31	isoform 3 of Uncharacterized protein C1orf31	91.7%	16.5	1	1	1	4	1,624,273	1,760,980	1,662,475	1,907,938	234,016	119,528	146,175	141,964	32.2	15.2	19.7	16.6	1.1	0.6	1.0	0.9	1.2	0.3	-1.1	0.6	1.1	0.5	1.1	0.3
IPI00830136	C1orf31	isoform 2 of Uncharacterized protein C1orf31	91.7%	8.3	1	1	1	4	1,624,273	1,760,980	1,662,475	1,907,938	234,016	119,528	146,175	141,964	32.2	15.2	19.7	16.6	1.1	0.6	1.0	0.9	1.2	0.3	-1.1	0.6	1.1	0.5	1.1	0.3
				SSFESSCPQQWIK	2	91.7%	1																									
IPI00045954	-	Envelope protein (Fragment)	99.7%	18.3	2	2	2	1	4,206,670	4,374,960	4,491,940	4,904,720	385,170	234,535	254,328	238,711	20.5	12.0	12.7	10.9	1.0	0.7	1.1	0.6	1.2	0.2	1.0	0.7	1.1	0.2	1.1	0.3
				RVPILSFVIGAGVLDGLGAGIGGIKTSTQFYYK	3	95.9%	1																									
				VPILSFVIGAGVLDGLGAGIGGIK	2	92.6%	1																									
IPI00046828	CCDC58	Coiled-coil domain-containing protein 58	99.6%	19.4	2	2	2	3	3,060,738	3,268,590	3,018,904	3,665,589	240,834	86,016	198,262	238,099	17.6	5.9	14.7	14.5	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.2	1.2	0.07
IPI00945719	CCDC58	Uncharacterized protein	99.6%	21.5	2	2	2	3	3,060,738	3,268,590	3,018,904	3,665,589	240,834	86,016	198,262	238,099	17.6	5.9	14.7	14.5	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.2	1.2	0.07
IPI00945888	CCDC58	Protein	99.6%	19.9	2	2	2	3	3,060,738	3,268,590	3,018,904	3,665,589	240,834	86,016	198,262	238,099	17.6	5.9	14.7	14.5	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.2	1.2	0.07
				QLYESLMAAHASR	3	82.3%	1																									
				WMQSELNVEEVVNDR	2	99.6%	1																									
IPI00046955	MAGEB17	Melanoma-associated antigen B17	90.8%	5.9	1	1	1	3	444,364	372,637	509,904	443,724	20,101	25,689	36,711	35,262	10.1	15.4	16.1	17.8	-1.2	0.06	1.1	0.2	-1.0	1	1.4	0.02	1.2	0.1	-1.1	0.2
IPI00887931	MAGEB17	melanoma-associated antigen B17	90.8%	5.9	1	1	1	3	444,364	372,637	509,904	443,724	20,101	25,689	36,711	35,262	10.1	15.4	16.1	17.8	-1.2	0.06	1.1	0.2	-1.0	1	1.4	0.02	1.2	0.1	-1.1	0.2
IPI00982820	MAGEB17	melanoma-associated antigen B17 isoform 2, partial	90.8%	8.0	1	1	1	3	444,364	372,637	509,904	443,724	20,101	25,689	36,711	35,262	10.1	15.4	16.1	17.8	-1.2	0.06	1.1	0.2	-1.0	1	1.4	0.02	1.2	0.1	-1.1	0.2
				LPSSSSPACQSPPQSFPNAGIPQESQR	3	90.8%	1																									
IPI00052885	-	23 kDa protein	90.2%	7.2	1	1	1	5	353,174	417,958	394,060	478,124	72,524	50,504	28,140	54,340	45.9	27.0	16.0	25.4	1.2	0.5	1.1	0.6	1.4	0.2	-1.1	0.7	1.1	0.4	1.2	0.2
IPI00173589	-	17 kDa protein	90.2%	9.7	1	1	1	5	353,174	417,958	394,060	478,124	72,524	50,504	28,140	54,340	45.9	27.0	16.0	25.4	1.2	0.5	1.1	0.6	1.4	0.2	-1.1	0.7	1.1	0.4	1.2	0.2
IPI00792336	-	26 kDa protein	90.2%	6.5	1	1	1	5	353,174	417,958	394,060	478,124	72,524	50,504	28,140	54,340	45.9	27.0	16.0	25.4	1.2	0.5	1.1	0.6	1.4	0.2	-1.1	0.7	1.1	0.4	1.2	0.2
IPI00792866	-	27 kDa protein	90.2%	6.1	1	1	1	5	353,174	417,958	394,060	478,124	72,524	50,504	28,140	54,340	45.9	27.0	16.0	25.4	1.2	0.5	1.1	0.6	1.4	0.2	-1.1	0.7	1.1	0.4	1.2	0.2
IPI00419919	RPL29	Ribosomal protein L29	90.2%	9.3	1	1	1	5	353,174	417,958	394,060	478,124	72,524	50,504	28,140	54,340	45.9	27.0	16.0	25.4	1.2	0.5	1.1	0.6	1.4	0.2	-1.1	0.7	1.1	0.4	1.2	0.2
				AQAAAPASVPAQAPK	2	90.2%	1																									
IPI00054042	GTF2I	isoform 1 of General transcription factor II-I	100.0%	12.4	9	9	10	6	8,173,103	8,824,458	8,693,043	9,671,395	471,673	456,875	530,252	250,822	12.9	11.6	13.6	5.8	1.1	0.4	1.1	0.5	1.2	0.02	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00217449	GTF2I	isoform 3 of General transcription factor II-I	100.0%	12.7	9	9	10	6	8,173,103	8,824,458	8,693,043	9,671,395	471,673	456,875	530,252	250,822	12.9	11.6	13.6	5.8	1.1	0.4	1.1	0.5	1.2	0.02	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00217450	GTF2I	isoform 4 of General transcription factor II-I	100.0%	12.7	9	9	10	6	8,173,103	8,824,458	8,693,043	9,671,395	471,673	456,875	530,252	250,822	12.9	11.6	13.6	5.8	1.1	0.4	1.1	0.5	1.2	0.02	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00293242	GTF2I	isoform 2 of General transcription factor II-I	100.0%	13.0	9	9	10	6	8,173,103	8,824,458	8,693,043	9,671,395	471,673	456,875	530,252	250,822	12.9	11.6	13.6	5.8	1.1	0.4	1.1	0.5	1.2	0.02	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00943949	GTF2I	general transcription factor II-I isoform 5	100.0%	12.7	9	9	10	6	8,173,103	8,824,458	8,693,043	9,671,395	471,673	456,875	530,252	250,822	12.9	11.6	13.6	5.8	1.1	0.4	1.1	0.5	1.2	0.02	-1.0	0.9	1.1	0.1	1.1	0.1
IPI01013471	GTF2I	cDNA FLJ55916, highly similar to General transcription factor II-I	100.0%	12.5	9	9	10	6	8,173,103	8,824,458	8,693,043	9,671,395	471,673	456,875	530,252	250,822	12.9	11.6	13.6	5.8	1.1	0.4	1.1	0.5	1.2	0.02	-1.0	0.9	1.1	0.1	1.1	0.1
				APSYLEISSMR	2	100.0%	1																									
				DQSAVVVQGLPEGVAFK	2	99.5%	1																									
				FAQALGLTEAVK	2	100.0%	2																									
				HPENYDLATLK	2	99.5%	1																									
				ILDSAEFIK	2	92.1%	1																									
				KPEMFETAIK	2	99.2%	1																									
				RPELLTHSTTEVTQPR	3	100.0%	1																									
				SILSPGGSCGPIK	2	92.0%	1																									
				VPYPVFESNPEFLYVEGLPEGIPFR	2	99.9%	1																									
IPI00056314	TSR2	Pre-rRNA-processing protein TSR2 homolog	98.8%	6.3	1	1	1	1	3,069,450	3,740,550	3,193,200	2,911,850	87,958	280,346	497,350	157,594	6.4	16.8	34.8	12.1	1.2	0.07	1.0	0.8	-1.1	0.4	-1.2	0.4	-1.3	0.03	-1.1	0.6
				WLGGAVEDYFMR	2	98.8%	1																									
IPI00056357	C19orf10	UPF0556 protein C19orf10	99.5%	6.9	1	1	1	1	5,865,560	6,004,670	6,722,160	6,288,420	427,281	270,537	367,952	327,454	16.3	10.1	12.2	11.6	1.0	0.8	1.1	0.2	1.1	0.5	1.1	0.2	1.0	0.5	-1.1	0.4
				GAEIEYAMAYSK	2	99.5%	1																									
IPI00056414	MAL2	Protein MAL2	99.1%	6.3	1	1	1	1	6,192,550	7,908,060	7,260,110	8,238,460	749,422	543,112	680,390	465,835	27.1	15.4	21.0	12.6	1.3	0.1	1.2	0.3	1.3	0.05	-1.1	0.5	1.0	0.7	1.1	0.3
				VTLPAGPDILR	2	99.1%	1																									
IPI00058192	POFUT1	isoform 1 of GDP-fucose protein O-fucosyltransferase 1	95.0%	2.6	1	1	1	2	3,419,165	4,049,335	3,337,070	3,919,430	94,824	231,191	278,057	307,009	6.2	12.8	18.6	17.5	1.2	0.04	-1.0	0.8	1.1	0.2	-1.2	0.08	-1.0	0.7	1.2	0.2
IPI00218176	POFUT1	isoform 2 of GDP-fucose protein O-fucosyltransferase 1	95.0%	5.2	1	1	1	2	3,419,165	4,049,335	3,337,070	3,919,430	94,824	231,191	278,057	307,009	6.2	12.8	18.6	17.5	1.2	0.04	-1.0	0.8	1.1	0.2	-1.2	0.08	-1.0	0.7	1.2	0.2
				VISLEDFMEK	2	95.0%	1																									
IPI00059242	SYAP1	Synapse-associated protein 1	95.7%	2.6	1	1	1	1	1,740,144	2,003,400	1,835,290	2,266,570	351,363	207,811	201,915	147,098	45.2	23.2	24.6	14.5	1.2	0.5	1.1	0.8	1.3	0.2	-1.1	0.6	1.1	0.3	1.2	0.1
				LVKEEVFWR	3	95.7%	1																									
IPI00059366	H2AFY	isoform 3 of Core histone macro-H2A.1	100.0%	18.1	4	4	4	3	5,160,673	5,086,070	5,610,069	5,857,982	280,200	238,327	344,078	93,676	12.1	10.5	13.7	3.6	-1.0	0.8	1.1	0.3	1.1	0.07	1.1	0.2	1.2	0.03	1.0	0.5
IPI00304171	H2AFY	isoform 2 of Core histone macro-H2A.1	100.0%	18.0	4	4	4	3	5,160,673	5,086,070	5,610,069	5,857,982	280,200	238,327	344,078	93,676	12.1	10.5	13.7	3.6	-1.0	0.8	1.1	0.3	1.1	0.07	1.1	0.2	1.2	0.03	1.0	0.5
IPI00744148	H2AFY	isoform 1 of Core histone macro-H2A.1	100.0%	18.2	4	4	4	3	5,160,673	5,086,070	5,610,069	5,857,982	280,200	238,327	344,078	93,676	12.1	10.5	13.7	3.6	-1.0	0.8	1.1	0.3	1.1	0.07	1.1	0.2	1.2	0.03	1.0	0.5
				EFVEAVLELR	2	99.5%	1																									
				GVTIASGGVLPNIHPELLAK	3	98.2%	1																									
				HILLAVANDEELNQLLK	3	99.9%	1																									
				NGPLEVAGAAVSAGHGLPAK	3	98.5%	1																									
IPI00059685	ASAH1	acid ceramidase isoform c	100.0%	2.8	1	1	1	1	768,395	728,818	723,953	792,678	58,352	39,045	78,530	72,948	17.0	12.0	24.3	20.6	-1.1	0.6	-1.1	0.7	1.0	0.8	-1.0	1	1.1	0.5	1.1	0.5
				ESLDVYELDAK	2	99.8%	1																									
IPI00059944	RNF25	E3 ubiquitin-protein ligase RNF25	97.9%	2.6	1	1	1	1	5,988,340	5,199,960	5,932,500	5,315,750	744,140	309,523	247,470	262,276	27.8	13.3	9.3	11.0	-1.2	0.4	-1.0	0.9	-1.1	0.4	1.1	0.1	1.0	0.8	-1.1	0.1
				GGIIDLEAERNR	2	97.9%	1																									
IPI00060181	EFHD2	EF-hand domain-containing protein D2	100.0%	35.8	7	7	9	1	38,373,083	39,866,520	34,786,423	45,536,605	3,165,503	2,503,933	3,407,743	2,602,966	18.5	14.0	21.9	12.8	1.0	0.7	-1.1	0.5	1.2	0.1	-1.1	0.3	1.1	0.2	1.3	0.04
				AAAGELQEDSGLCVLAR	2	100.0%	1																									
				ADLNQGIGEPQSPSR	2	100.0%	1																									
				DGFIDLMELK	2	100.0%	2																									
				FEEEIKAEQEER	3	87.2%	1																									
				LGAPQTHLGLK	2	98.9%	1																									
				LSEIDVSSEGVK	2	100.0%	2																									
				VQAINVSSR	2	99.9%	1																									
IPI00060200	GALM	Aldose 1-epimerase	100.0%	7.9	2	2	2	1	4,917,580	5,379,528	4,635,290	5,206,855	292,959	405,297	321,059	245,169	13.3	16.9	15.5	10.5	1.1	0.4	-1.1	0.5	1.1	0.5	-1.2	0.2	-1.0	0.7	1.1	0.2
				ASDVVLGFAELEGYLQK	2	100.0%	1																									
				VLSNGVQFSR	2	98.1%	1																									
IPI00060650	PCNP	isoform 2 of PEST proteolytic signal-containing nuclear protein	99.5%	32.3	3	3	3	2	3,829,242	4,019,299	3,768,897	4,212,411	390,164	181,336	273,664	121,060	22.8	10.1	16.2	6.4	1.0	0.7	-1.0	0.9	1.1	0.4	-1.1	0.5	1.0	0.4	1.1	0.2
IPI00790305	PCNP	PEST proteolytic signal containing nuclear protein, isoform CRA_a	99.5%	21.1	3	3	3	2	3,829,242	4,019,299	3,768,897	4,212,411	390,164	181,336	273,664	121,060	22.8	10.1	16.2	6.4	1.0	0.7	-1.0	0.9	1.1	0.4	-1.1	0.5	1.0	0.4	1.1	0.2
				AGAAGGPEEEAEKPVK	2	99.4%	1																									
				FGFAIGSQTTK	2	95.5%	1																									
				SAEEEAADLPTKPTK	2	99.5%	1																									
IPI00060715	KCTD12	BTB/POZ domain-containing protein KCTD12	97.1%	4.0	1	1	1	1	3,034,210	3,088,550	3,439,320	3,618,600	192,324	289,792	97,151	342,422	14.2	21.0	6.3	21.2	1.0	0.9	1.1	0.1	1.2	0.2	1.1	0.3	1.2	0.3	1.1	0.6
				DLQLVLPDYFPER	2	97.1%	1																									
IPI00061033	NOBOX	isoform 1 of Homeobox protein NOBOX	93.0%	3.6	1	1	1	1	3,917,720	3,522,030	4,137,520	3,457,670	204,449	273,600	199,965	290,379	11.7	17.4	10.8	18.8	-1.1	0.3	1.1	0.5	-1.1	0.2	1.2	0.1	-1.0	0.9	-1.2	0.09
				GAGSLVAGWSGGGPTIETLELQSER	3	93.0%	1																									
IPI00061178	RBMXL1	Heterogeneous nuclear ribonucleoprotein G-like 1	100.0%	13.3	4	4	6	1	5,269,873	5,306,890	5,774,733	6,599,755	461,804	344,406	599,979	440,671	19.6	14.5	23.2	14.9	1.0	1	1.1	0.5	1.3	0.07	1.1	0.5	1.2	0.05	1.1	0.3
				DRDYSDHPSGGSYR	3	97.3%	1																									
				GFAFVTFESPADAK	2	100.0%	2																									
				GPPPSYGGSSR	2	100.0%	1																									
				LFIGGLNTETNEK	2	100.0%	2																									
IPI00061200	KRT71	Keratin, type II cytoskeletal 71	98.5%	5.0	2	2	2	4	2,019,197	1,971,589	1,802,851	2,311,473	216,901	52,768	105,885	129,946	24.0	6.0	13.1	12.6	-1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.2	1.2	0.04	1.3	0.02
IPI00103481	KRT72	isoform 1 of Keratin, type II cytoskeletal 72	98.5%	5.1	2	2	2	4	2,019,197	1,971,589	1,802,851	2,311,473	216,901	52,768	105,885	129,946	24.0	6.0	13.1	12.6	-1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.2	1.2	0.04	1.3	0.02
IPI00794272	KRT72	isoform 2 of Keratin, type II cytoskeletal 72	98.5%	5.1	2	2	2	4	2,019,197	1,971,589	1,802,851	2,311,473	216,901	52,768	105,885	129,946	24.0	6.0	13.1	12.6	-1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.2	1.2	0.04	1.3	0.02
IPI00910219	KRT72	keratin, type II cytoskeletal 72 isoform 2	98.5%	5.5	2	2	2	4	2,019,197	1,971,589	1,802,851	2,311,473	216,901	52,768	105,885	129,946	24.0	6.0	13.1	12.6	-1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.2	1.2	0.04	1.3	0.02
				ALNNKFASFIDKVR	3	98.5%	1																									
				FLEQQNQVLETK	2	94.2%	1																									
IPI00061282	PRKAA1	Protein kinase, AMP-activated, alpha 1 catalytic subunit, isoform CRA_b	94.9%	8.2	1	1	1	4	522,008	541,908	476,525	567,460	40,835	25,720	21,919	56,086	17.5	10.6	10.3	22.1	1.0	0.7	-1.1	0.4	1.1	0.5	-1.1	0.09	1.0	0.7	1.2	0.2
IPI00410287	PRKAA1	isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1	94.9%	3.0	1	1	1	4	522,008	541,908	476,525	567,460	40,835	25,720	21,919	56,086	17.5	10.6	10.3	22.1	1.0	0.7	-1.1	0.4	1.1	0.5	-1.1	0.09	1.0	0.7	1.2	0.2
IPI00792482	PRKAA1	isoform 1 of 5'-AMP-activated protein kinase catalytic subunit alpha-1	94.9%	3.0	1	1	1	4	522,008	541,908	476,525	567,460	40,835	25,720	21,919	56,086	17.5	10.6	10.3	22.1	1.0	0.7	-1.1	0.4	1.1	0.5	-1.1	0.09	1.0	0.7	1.2	0.2
IPI00307755	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2	94.9%	3.1	1	1	1	4	522,008	541,908	476,525	567,460	40,835	25,720	21,919	56,086	17.5	10.6	10.3	22.1	1.0	0.7	-1.1	0.4	1.1	0.5	-1.1	0.09	1.0	0.7	1.2	0.2
				IADFGLSNMMSDGEFLR	2	94.9%	1																									
IPI00061476	KLC4	kinesin light chain 4 isoform c	100.0%	18.7	4	4	4	3	1,830,789	1,782,148	1,845,738	2,130,613	171,939	83,931	134,908	108,608	21.0	10.5	16.3	11.4	-1.0	0.8	1.0	0.9	1.2	0.2	1.0	0.7	1.2	0.03	1.2	0.1
IPI00398812	KLC4	isoform 1 of Kinesin light chain 4	100.0%	9.5	4	4	4	3	1,830,789	1,782,148	1,845,738	2,130,613	171,939	83,931	134,908	108,608	21.0	10.5	16.3	11.4	-1.0	0.8	1.0	0.9	1.2	0.2	1.0	0.7	1.2	0.03	1.2	0.1
IPI00743879	KLC4	isoform 3 of Kinesin light chain 4	100.0%	9.3	4	4	4	3	1,830,789	1,782,148	1,845,738	2,130,613	171,939	83,931	134,908	108,608	21.0	10.5	16.3	11.4	-1.0	0.8	1.0	0.9	1.2	0.2	1.0	0.7	1.2	0.03	1.2	0.1
				HLEFLGQLR	2	99.6%	1																									
				LSQEEILGSTR	2	100.0%	1																									
				LVSQGLEALR	2	99.7%	1																									
				SMENIELGLSEAQVMLALASHLSTVESEK	3	99.7%	1																									
IPI00061525	GNPNAT1	Glucosamine 6-phosphate N-acetyltransferase	99.8%	6.0	1	1	1	2	896,788	894,700	809,783	1,288,930	110,469	109,939	187,377	77,088	27.5	27.5	51.7	13.4	-1.0	1	-1.1	0.7	1.4	0.02	-1.1	0.7	1.4	0.02	1.6	0.05
IPI00924703	GNPNAT1	18 kDa protein	99.8%	6.9	1	1	1	2	896,788	894,700	809,783	1,288,930	110,469	109,939	187,377	77,088	27.5	27.5	51.7	13.4	-1.0	1	-1.1	0.7	1.4	0.02	-1.1	0.7	1.4	0.02	1.6	0.05
				LLLSTLTLLSK	2	99.5%	1																									
IPI00061926	DDX11	isoform 1 of Probable ATP-dependent RNA helicase DDX11	91.4%	2.7	1	1	1	1	1,994,867	2,131,300	1,985,898	2,334,330	215,815	211,016	267,492	182,638	24.2	22.1	30.1	17.5	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.7	1.1	0.5	1.2	0.3
				HCCCAEVSPGEVGLFLMGNHTTAWRR	3	91.4%	1																									
IPI00062003	ACAT1	ACAT1 protein	100.0%	10.5	1	1	2	2	809,270	632,613	756,907	713,007	119,722	39,684	49,440	100,683	33.1	14.0	14.6	31.6	-1.3	0.2	-1.1	0.7	-1.1	0.6	1.2	0.09	1.1	0.5	-1.1	0.7
IPI00983400	ACAT1	Uncharacterized protein	100.0%	12.1	1	1	2	2	809,270	632,613	756,907	713,007	119,722	39,684	49,440	100,683	33.1	14.0	14.6	31.6	-1.3	0.2	-1.1	0.7	-1.1	0.6	1.2	0.09	1.1	0.5	-1.1	0.7
				TPIGSFLGSLSLLPATK	2	100.0%	2																									
IPI00062037	DYNLL2	Dynein light chain 2, cytoplasmic	99.6%	24.7	1	1	1	1	1,776,318	2,116,726	2,106,930	2,370,560	186,744	230,138	320,509	85,675	23.5	24.3	34.0	8.1	1.2	0.3	1.2	0.4	1.3	0.02	-1.0	1	1.1	0.3	1.1	0.5
				NADMSEDMQQDAVDCATQAMEK	2	99.6%	1																									
IPI00062120	S100A16	Protein S100-A16	100.0%	57.3	5	5	8	1	20,359,810	20,031,530	21,931,000	24,676,300	971,501	942,803	803,360	714,251	10.7	10.5	8.2	6.5	-1.0	0.8	1.1	0.2	1.2	0.007	1.1	0.2	1.2	0.004	1.1	0.03
				AADKLIQNLDANHDGR	3	93.6%	1																									
				AVIVLVENFYK	2	100.0%	2																									
				ELNHMLSDTGNRK	3	99.9%	1																									
				ISFDEYWTLIGGITGPIAK	2	100.0%	2																									
				LIQNLDANHDGR	2	100.0%	2																									
IPI00062206	DDX39A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 transcript variant	100.0%	9.5	3	4	4	2	1,655,156	1,693,835	1,615,702	1,824,420	128,416	70,439	96,129	54,743	17.4	9.3	13.3	6.7	1.0	0.8	-1.0	0.8	1.1	0.3	-1.0	0.5	1.1	0.2	1.1	0.1
IPI00166874	DDX39A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39, isoform CRA_c	100.0%	9.3	3	4	4	2	1,655,156	1,693,835	1,615,702	1,824,420	128,416	70,439	96,129	54,743	17.4	9.3	13.3	6.7	1.0	0.8	-1.0	0.8	1.1	0.3	-1.0	0.5	1.1	0.2	1.1	0.1
				DFLLKPELLR	2	99.3%	1																									
				DFLLKPELLR	3	90.9%	1																									
				GSYVSIHSSGFR	2	99.7%	1																									
				MLEQLDMR	2	100.0%	1																									
IPI00062264	SCYL1	isoform 4 of N-terminal kinase-like protein	97.0%	1.5	1	1	1	9	350,454	326,386	278,834	332,869	51,154	26,388	40,383	41,014	32.6	18.1	32.4	27.6	-1.1	0.7	-1.3	0.3	-1.1	0.8	-1.2	0.4	1.0	0.9	1.2	0.4
IPI00102059	SCYL1	isoform 1 of N-terminal kinase-like protein	97.0%	1.5	1	1	1	9	350,454	326,386	278,834	332,869	51,154	26,388	40,383	41,014	32.6	18.1	32.4	27.6	-1.1	0.7	-1.3	0.3	-1.1	0.8	-1.2	0.4	1.0	0.9	1.2	0.4
IPI00186969	SCYL1	isoform 6 of N-terminal kinase-like protein	97.0%	1.5	1	1	1	9	350,454	326,386	278,834	332,869	51,154	26,388	40,383	41,014	32.6	18.1	32.4	27.6	-1.1	0.7	-1.3	0.3	-1.1	0.8	-1.2	0.4	1.0	0.9	1.2	0.4
IPI00787009	SCYL1	isoform 2 of N-terminal kinase-like protein	97.0%	1.5	1	1	1	9	350,454	326,386	278,834	332,869	51,154	26,388	40,383	41,014	32.6	18.1	32.4	27.6	-1.1	0.7	-1.3	0.3	-1.1	0.8	-1.2	0.4	1.0	0.9	1.2	0.4

IPI00788043	SCYL1	isoform 3 of N-terminal kinase-like protein	97.0%	1.7	1	1	1	9	350,454	326,386	278,834	332,869	51,154	26,388	40,383	41,014	32.6	18.1	32.4	27.6	-1.1	0.7	-1.3	0.3	-1.1	0.8	-1.2	0.4	1.0	0.9	1.2	0.4
IPI00788089	SCYL1	isoform 5 of N-terminal kinase-like protein	97.0%	1.9	1	1	1	9	350,454	326,386	278,834	332,869	51,154	26,388	40,383	41,014	32.6	18.1	32.4	27.6	-1.1	0.7	-1.3	0.3	-1.1	0.8	-1.2	0.4	1.0	0.9	1.2	0.4
IPI00978883	SCYL1	Uncharacterized protein	97.0%	1.8	1	1	1	9	350,454	326,386	278,834	332,869	51,154	26,388	40,383	41,014	32.6	18.1	32.4	27.6	-1.1	0.7	-1.3	0.3	-1.1	0.8	-1.2	0.4	1.0	0.9	1.2	0.4
IPI00979496	SCYL1	Protein	97.0%	6.9	1	1	1	9	350,454	326,386	278,834	332,869	51,154	26,388	40,383	41,014	32.6	18.1	32.4	27.6	-1.1	0.7	-1.3	0.3	-1.1	0.8	-1.2	0.4	1.0	0.9	1.2	0.4
IPI00979583	SCYL1	Uncharacterized protein	97.0%	1.6	1	1	1	9	350,454	326,386	278,834	332,869	51,154	26,388	40,383	41,014	32.6	18.1	32.4	27.6	-1.1	0.7	-1.3	0.3	-1.1	0.8	-1.2	0.4	1.0	0.9	1.2	0.4
				LNEANLNVELMK	2	97.0%	1																									
IPI00062266	SCRN2	Secernin-2	100.0%	14.8	4	4	4	2	4,673,413	4,789,369	4,723,413	5,592,016	443,586	141,399	402,886	322,708	21.2	6.6	19.1	12.9	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.9	1.2	0.05	1.2	0.1
IPI00402502	SCRN2	secernin-2 isoform 2	100.0%	16.7	4	4	4	2	4,673,413	4,789,369	4,723,413	5,592,016	443,586	141,399	402,886	322,708	21.2	6.6	19.1	12.9	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.9	1.2	0.05	1.2	0.1
				EPVGEGEALLGMDLLR	2	99.7%	1																									
				LQCTYIEVEQVSK	2	94.7%	1																									
				NISNQLSIGTDISAQHPELR	3	100.0%	1																									
				QGGITAEVMMGILR	2	100.0%	1																									
IPI00062884	CTTN	src substrate cortactin isoform b	100.0%	24.2	9	10	13	1	14,230,280	14,190,325	14,071,366	16,140,330	904,041	683,577	915,003	656,937	14.2	10.8	14.5	9.1	-1.0	1	-1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.07	1.1	0.1
				ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK	3	100.0%	2																									
				DYSSGFGGK	1	90.9%	1																									
				GPVSGTEPEPVYSMEAADYR	2	100.0%	2																									
				GPVSGTEPEPVYSMEAADYR	3	100.0%	1																									
				LRENVFQEHQTLK	3	100.0%	1																									
				NASTFEDVTQVSSAYQK	2	100.0%	1																									
				SAVGFDYQGK	2	100.0%	2																									
				SAVGFEYQGK	2	100.0%	1																									
				VDQSAVGFEYQGK	2	99.0%	1																									
				YGVQADRVDK	2	99.3%	1																									
IPI00063234	PRKAR2A	Protein kinase, cAMP-dependent, regulatory, type II, alpha, isoform CRA_b	100.0%	13.4	4	4	5	2	5,736,364	6,291,711	6,114,913	7,363,367	506,936	315,014	498,462	205,663	19.8	11.2	18.2	6.3	1.1	0.4	1.1	0.6	1.3	0.02	-1.0	0.8	1.2	0.02	1.2	0.05
IPI00219774	PRKAR2A	cAMP-dependent protein kinase type II-alpha regulatory subunit	100.0%	12.6	4	4	5	2	5,736,364	6,291,711	6,114,913	7,363,367	506,936	315,014	498,462	205,663	19.8	11.2	18.2	6.3	1.1	0.4	1.1	0.6	1.3	0.02	-1.0	0.8	1.2	0.02	1.2	0.05
				APASVLPAATPR	2	99.9%	1																									
				GTYDILVTK	2	91.2%	1																									
				MFESFIESVPLLK	2	98.6%	1																									
				NLDQEQLSQVLDAMFER	2	100.0%	2																									
IPI00063242	PGAM5	isoform 2 of Serine/threonine-protein phosphatase PGAM5, mitochondrial	95.8%	3.9	1	1	1	3	3,912,673	3,885,293	3,849,250	4,265,433	96,498	241,348	191,780	183,695	5.5	13.9	11.1	9.6	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.9	1.1	0.2	1.1	0.2
IPI00788907	PGAM5	isoform 1 of Serine/threonine-protein phosphatase PGAM5, mitochondrial	95.8%	3.5	1	1	1	3	3,912,673	3,885,293	3,849,250	4,265,433	96,498	241,348	191,780	183,695	5.5	13.9	11.1	9.6	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.9	1.1	0.2	1.1	0.2
IPI00954934	PGAM5	serine/threonine-protein phosphatase PGAM5, mitochondrial isoform 2	95.8%	3.5	1	1	1	3	3,912,673	3,885,293	3,849,250	4,265,433	96,498	241,348	191,780	183,695	5.5	13.9	11.1	9.6	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.9	1.1	0.2	1.1	0.2
				AIETTDIISR	2	95.8%	1																									
IPI00063245	FUBP3	Uncharacterized protein	100.0%	15.0	3	3	3	2	10,586,550	10,824,950	10,467,175	12,107,620	837,506	352,209	603,093	416,790	17.7	7.3	12.9	7.7	1.0	0.8	-1.0	0.9	1.1	0.1	-1.0	0.6	1.1	0.05	1.2	0.06
IPI00377261	FUBP3	isoform 1 of Far upstream element-binding protein 3	100.0%	8.4	3	3	3	2	10,586,550	10,824,950	10,467,175	12,107,620	837,506	352,209	603,093	416,790	17.7	7.3	12.9	7.7	1.0	0.8	-1.0	0.9	1.1	0.1	-1.0	0.6	1.1	0.05	1.2	0.06
				MGGGSIEVSVPR	2	95.6%	1																									
				MVMIQDGPLPTGADKPLR	3	100.0%	1																									
				RPLDDGVGNQLGALVHQR	3	82.0%	1																									
IPI00063827	ABHD14B	isoform 1 of Abhydrolase domain-containing protein 14B	100.0%	28.1	4	5	5	2	6,301,444	6,708,631	6,383,408	7,260,119	657,136	305,255	569,561	246,112	23.3	10.2	20.0	7.6	1.1	0.6	1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.2	1.1	0.2
IPI00910706	ABHD14B	cDNA FLJ52710, highly similar to Abhydrolase domain-containing protein 14B	100.0%	31.9	4	5	5	2	6,301,444	6,708,631	6,383,408	7,260,119	657,136	305,255	569,561	246,112	23.3	10.2	20.0	7.6	1.1	0.6	1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.2	1.1	0.2
				AVAIDLPGLGHSK	2	99.2%	1																									
				EGTIQVQGQALFFR	2	98.0%	1																									
				FSVLLLHGIR	2	99.1%	1																									
				FSVLLLHGIR	3	93.5%	1																									
				TPALIVYGDQDPMGQTSFEHLK	3	100.0%	1																									
IPI00064086	EEF1D	elongation factor 1-delta isoform 4	100.0%	24.9	5	5	9	2	2,432,072	2,403,041	2,193,131	2,637,234	132,615	80,000	134,036	101,045	12.2	7.4	13.7	8.6	-1.0	0.9	-1.1	0.2	1.1	0.3	-1.1	0.2	1.1	0.1	1.2	0.03
IPI01009986	EEF1D	EEF1D protein	100.0%	11.1	5	5	9	2	2,432,072	2,403,041	2,193,131	2,637,234	132,615	80,000	134,036	101,045	12.2	7.4	13.7	8.6	-1.0	0.9	-1.1	0.2	1.1	0.3	-1.1	0.2	1.1	0.1	1.2	0.03
				ATAPQTQHVSPMR	3	92.1%	1																									
				FYEQMNGPVAGASR	2	100.0%	2																									
				GVVQELQQAISK	2	100.0%	2																									
				IASLEVENQSLR	2	100.0%	2																									
				SIQLDGLVWGASK	2	100.0%	2																									
IPI00064666	FAM84B	Protein FAM84B	99.7%	10.0	2	2	2	1	6,674,500	7,125,450	7,911,130	7,461,700	875,854	648,096	599,157	624,070	29.3	20.3	16.9	18.7	1.1	0.7	1.2	0.3	1.1	0.5	1.1	0.4	1.0	0.7	-1.1	0.6
				LEVINSFLTDASQGR	2	85.2%	1																									
				SHTLEFQSLEDLIMEK	2	98.0%	1																									
IPI00065055	C3orf48	isoform 2 of PP2C-like domain-containing protein C3orf48	92.6%	1.9	1	1	1	3	872,630	883,230	837,960	1,067,240	108,080	88,472	90,313	52,392	27.7	22.4	24.1	11.0	1.0	0.9	-1.0	0.8	1.2	0.1	-1.1	0.7	1.2	0.1	1.3	0.06
IPI00784436	C3orf48	isoform 3 of PP2C-like domain-containing protein C3orf48	92.6%	1.9	1	1	1	3	872,630	883,230	837,960	1,067,240	108,080	88,472	90,313	52,392	27.7	22.4	24.1	11.0	1.0	0.9	-1.0	0.8	1.2	0.1	-1.1	0.7	1.2	0.1	1.3	0.06
IPI00871533	C3orf48	isoform 1 of PP2C-like domain-containing protein C3orf48	92.6%	1.1	1	1	1	3	872,630	883,230	837,960	1,067,240	108,080	88,472	90,313	52,392	27.7	22.4	24.1	11.0	1.0	0.9	-1.0	0.8	1.2	0.1	-1.1	0.7	1.2	0.1	1.3	0.06
				IFDNIDR	1	89.2%	1																									
IPI00065121	CCDC36	isoform 2 of Coiled-coil domain-containing protein 36	97.8%	5.6	2	2	2	1	5,973,250	5,845,450	5,736,830	6,154,510	343,659	237,873	366,234	225,318	12.9	9.1	14.3	8.2	-1.0	0.8	-1.0	0.7	1.0	0.7	-1.0	0.8	1.1	0.4	1.1	0.4
				PVCPILGGTVMPNKTVRAVQGR	2	84.1%	1																									
				YQTKPQFEEK	2	86.7%	1																									
IPI00065435	FGD4	isoform 1 of FYVE, RhoGEF and PH domain-containing protein 4	90.8%	3.7	1	1	1	3	923,903	962,720	1,045,663	1,055,020	70,704	99,859	115,994	107,580	17.1	23.2	24.8	22.8	1.0	0.8	1.1	0.4	1.1	0.3	1.1	0.6	1.1	0.5	1.0	1
IPI00980605	FGD4	cDNA FLJ55905, highly similar to FYVE, RhoGEF and PH domain-containing protei	90.8%	3.3	1	1	1	3	923,903	962,720	1,045,663	1,055,020	70,704	99,859	115,994	107,580	17.1	23.2	24.8	22.8	1.0	0.8	1.1	0.4	1.1	0.3	1.1	0.6	1.1	0.5	1.0	1
IPI00982642	FGD4	cDNA FLJ56188, highly similar to FYVE, RhoGEF and PH domain-containing protei	90.8%	3.2	1	1	1	3	923,903	962,720	1,045,663	1,055,020	70,704	99,859	115,994	107,580	17.1	23.2	24.8	22.8	1.0	0.8	1.1	0.4	1.1	0.3	1.1	0.6	1.1	0.5	1.0	1
				VILLAVTGETPGGPNEHPATLDDHPEPK	3	88.3%	1																									
IPI00065486	ABCB6	isoform 2 of ATP-binding cassette sub-family B member 6, mitochondrial	96.1%	1.9	1	1	1	2	1,218,550	1,644,505	1,447,857	1,574,805	172,516	96,709	217,463	114,909	31.7	13.2	33.6	16.3	1.3	0.06	1.2	0.4	1.3	0.1	-1.1	0.4	-1.0	0.7	1.1	0.6
IPI00742677	ABCB6	isoform 1 of ATP-binding cassette sub-family B member 6, mitochondrial	96.1%	1.8	1	1	1	2	1,218,550	1,644,505	1,447,857	1,574,805	172,516	96,709	217,463	114,909	31.7	13.2	33.6	16.3	1.3	0.06	1.2	0.4	1.3	0.1	-1.1	0.4	-1.0	0.7	1.1	0.6
				IDGQDISQVTQASLR	2	96.1%	1																									
IPI00065500	BROX	BRO1 domain-containing protein BROX	98.8%	2.7	1	1	2	2	2,501,965	2,339,735	2,556,710	2,678,080	256,816	108,056	215,212	167,213	23.0	10.3	18.8	14.0	-1.1	0.6	1.0	0.9	1.1	0.6	1.1	0.4	1.1	0.1	1.0	0.7
IPI00922787	BROX	cDNA FLJ50123	98.8%	2.9	1	1	2	2	2,501,965	2,339,735	2,556,710	2,678,080	256,816	108,056	215,212	167,213	23.0	10.3	18.8	14.0	-1.1	0.6	1.0	0.9	1.1	0.6	1.1	0.4	1.1	0.1	1.0	0.7
				IPTEAPQLELK	2	98.8%	2																									
IPI00066817	IFT122	isoform 1 of Intraflagellar transport protein 122 homolog	95.7%	1.1	1	1	1	10	600,946	691,182	681,150	822,337	193,900	102,157	172,434	133,880	72.2	33.1	56.6	36.4	1.2	0.7	1.1	0.8	1.4	0.4	-1.0	1	1.2	0.5	1.2	0.5
IPI00165352	IFT122	cDNA FLJ59375, highly similar to Intraflagellar transport 122 homolog	95.7%	1.2	1	1	1	10	600,946	691,182	681,150	822,337	193,900	102,157	172,434	133,880	72.2	33.1	56.6	36.4	1.2	0.7	1.1	0.8	1.4	0.4	-1.0	1	1.2	0.5	1.2	0.5
IPI00296605	IFT122	intraflagellar transport protein 122 homolog isoform 3	95.7%	1.1	1	1	1	10	600,946	691,182	681,150	822,337	193,900	102,157	172,434	133,880	72.2	33.1	56.6	36.4	1.2	0.7	1.1	0.8	1.4	0.4	-1.0	1	1.2	0.5	1.2	0.5
IPI00307430	IFT122	intraflagellar transport protein 122 homolog isoform 1	95.7%	1.0	1	1	1	10	600,946	691,182	681,150	822,337	193,900	102,157	172,434	133,880	72.2	33.1	56.6	36.4	1.2	0.7	1.1	0.8	1.4	0.4	-1.0	1	1.2	0.5	1.2	0.5
IPI00795933	IFT122	cDNA FLJ12938 fis, clone NT2RP2005022, highly similar to Intraflagellar transport 1	95.7%	1.3	1	1	1	10	600,946	691,182	681,150	822,337	193,900	102,157	172,434	133,880	72.2	33.1	56.6	36.4	1.2	0.7	1.1	0.8	1.4	0.4	-1.0	1	1.2	0.5	1.2	0.5
IPI00908370	IFT122	cDNA FLJ12463 fis, clone NT2RM1000772, weakly similar to VEGETATIBLE INCO	95.7%	1.4	1	1	1	10	600,946	691,182	681,150	822,337	193,900	102,157	172,434	133,880	72.2	33.1	56.6	36.4	1.2	0.7	1.1	0.8	1.4	0.4	-1.0	1	1.2	0.5	1.2	0.5
IPI00943167	IFT122	125 kDa protein	95.7%	1.2	1	1	1	10	600,946	691,182	681,150	822,337	193,900	102,157	172,434	133,880	72.2	33.1	56.6	36.4	1.2	0.7	1.1	0.8	1.4	0.4	-1.0	1	1.2	0.5	1.2	0.5
IPI00964473	IFT122	Uncharacterized protein	95.7%	1.1	1	1	1	10	600,946	691,182	681,150	822,337	193,900	102,157	172,434	133,880	72.2	33.1	56.6	36.4	1.2	0.7	1.1	0.8	1.4	0.4	-1.0	1	1.2	0.5	1.2	0.5
IPI00965471	IFT122	cDNA FLJ56621, highly similar to Intraflagellar transport 122 homolog	95.7%	1.2	1	1	1	10	600,946	691,182	681,150	822,337	193,900	102,157	172,434	133,880	72.2	33.1	56.6	36.4	1.2	0.7	1.1	0.8	1.4	0.4	-1.0	1	1.2	0.5	1.2	0.5
IPI01010681	IFT122	intraflagellar transport protein 122 homolog isoform 4	95.7%	1.2	1	1	1	10	600,946	691,182	681,150	822,337	193,900	102,157	172,434	133,880	72.2	33.1	56.6	36.4	1.2	0.7	1.1	0.8	1.4	0.4	-1.0	1	1.2	0.5	1.2	0.5
				IFVDNLFAIVLLK	2	95.7%	1																									
IPI00068254	BCCIP	BRCA2 and CDKN1A-interacting protein isoform C	100.0%	13.0	2	2	2	3	2,055,395	2,065,528	2,107,534	2,300,055	174,514	121,296	174,165	81,756	19.0	13.1	18.5	8.0	1.0	1	1.0	0.8	1.1	0.2	1.0	0.8	1.1	0.1	1.1	0.3
IPI00220152	BCCIP	isoform 2 of BRCA2 and CDKN1A-interacting protein	100.0%	11.8	2	2	2	3	2,055,395	2,065,528	2,107,534	2,300,055	174,514	121,296	174,165	81,756	19.0	13.1	18.5	8.0	1.0	1	1.0	0.8	1.1	0.2	1.0	0.8	1.1	0.1	1.1	0.3
IPI00786906	BCCIP	isoform 3 of BRCA2 and CDKN1A-interacting protein	100.0%	13.0	2	2	2	3	2,055,395	2,065,528	2,107,534	2,300,055	174,514	121,296	174,165	81,756	19.0	13.1	18.5	8.0	1.0	1	1.0	0.8	1.1	0.2	1.0	0.8	1.1	0.1	1.1	0.3
				APVNTAELTDLLIQQNHIGSVIK	3	100.0%	1																									
				KGTQCVEQIQELVLR	3	81.5%	1																									
IPI00068430	SNRPEL1	Putative small nuclear ribonucleoprotein polypeptide E-like protein 1	100.0%	12.0	1	1	2	1	3,133,320	3,437,930	2,969,220	3,607,875	343,384	242,551	351,632	167,085	24.5	15.8	26.5	10.4	1.1	0.5	-1.1	0.7	1.2	0.2	-1.2	0.3	1.0	0.6	1.2	0.1
				VMVQPINLIFR	2	99.9%	2																									
IPI00069750	PUF60	isoform 1 of Poly(U)-binding-splicing factor PUF60	100.0%	16.6	6	6	7	3	3,141,445	3,141,336	3,077,414	3,528,893	195,156	174,971	215,725	157,342	13.9	12.5	15.7	10.0	-1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00797595	PUF60	isoform 3 of Poly(U)-binding-splicing factor PUF60	100.0%	18.0	6	6	7	3	3,141,445	3,141,336	3,077,414	3,528,893	195,156	174,971	215,725	157,342	13.9	12.5	15.7	10.0	-1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00856076	PUF60	isoform 5 of Poly(U)-binding-splicing factor PUF60	100.0%	17.6	6	6	7	3	3,141,445	3,141,336	3,077,414	3,528,893	195,156	174,971	215,725	157,342	13.9	12.5	15.7	10.0	-1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
				AQSSQDAVSSMNLFDLGGQYLR	2	100.0%	1																									
				GYGFIEYEK	2	99.7%	1																									
				IYVASVHQDLSDDDIKSVFEAFGK	3	84.0%	1																									
				LGLPPLTPEQQEALQK	2	100.0%	2																									
				QGEEEDAEIIVK	2	99.9%	1																									
				VVAEVYDQER	2	99.9%	1																									
IPI00070943	PI4KA	isoform 1 of Phosphatidylinositol 4-kinase alpha	92.8%	0.6	1	1	1	1	5,857,700	6,691,600	4,919,360	4,964,960	634,232	591,044	137,917	259,512	24.2	19.8	6.3	11.7	1.1	0.4	-1.2	0.2	-1.2	0.2	-1.4	0.04	-1.3	0.03	1.0	0.9
				VFDAFLNMMADK	2	92.8%	1																									
IPI00071059	BAX	isoform Epsilon of Apoptosis regulator BAX	100.0%	22.0	3	3	4	4	2,566,010	2,643,376	2,723,368	3,329,630	274,521	169,152	221,630	194,234	23.9	14.3	18.2	13.0	1.0	0.8	1.1	0.7	1.3	0.05	1.0	0.8	1.3	0.03	1.2	0.07
IPI00443773	BAX	isoform Alpha of Apoptosis regulator BAX	100.0%	18.8	3	3	4	4	2,566,010	2,643,376	2,723,368	3,329,630	274,521	169,152	221,630	194,234	23.9	14.3	18.2	13.0	1.0	0.8	1.1	0.7	1.3	0.05	1.0	0.8	1.3	0.03	1.2	0.07
IPI00444945	BAX	isoform Beta of Apoptosis regulator BAX	100.0%	16.5	3	3	4	4	2,566,010	2,643,376	2,723,368	3,329,630	274,521	169,152	221,630	194,234	23.9	14.3	18.2	13.0	1.0	0.8	1.1	0.7	1.3	0.05	1.0	0.8	1.3	0.03	1.2	0.07
IPI00845474	BAX	isoform Sigma of Apoptosis regulator BAX	100.0%	20.1	3	3	4	4	2,566,010	2,643,376	2,723,368	3,329,630	274,521	169,152	221,630	194,234	23.9	14.3	18.2	13.0	1.0	0.8	1.1	0.7	1.3	0.05	1.0	0.8	1.3	0.03	1.2	0.07
				GGGPTSSEQIMK	2	99.9%	1																									
				IGDELDSNMELQR	2	100.0%	2																									
				MIAAVDTDSPR	2	99.0%	1																									
IPI00071180	UBQLN1	isoform 2 of Ubiquilin-1	100.0%	7.1	3	4	4	2	12,012,144	11,696,562	11,261,678	12,420,244	790,473	620,290	978,177	762,808	14.7	11.9	19.4	13.7	-1.0	0.8	-1.1	0.6	1.0	0.7	-1.0	0.7	1.1	0.5	1.1	0.4
IPI00099550	UBQLN1	isoform 1 of Ubiquilin-1	100.0%	6.8	3	4	4	2	12,012,144	11,696,562	11,261,678	12,420,244	790,473	620,290	978,177	762,808	14.7	11.9	19.4	13.7	-1.0	0.8	-1.1	0.6	1.0	0.7	-1.0	0.7	1.1	0.5	1.1	0.4
				NPAMMQEMMR	2	100.0%	1																									
				NPEISHMLNNPDIMR	3	99.7%	1																									
				QLIMANPQMQQLIQR	2	100.0%	1																									
				QLIMANPQMQQLIQR	3	100.0%	1																									
IPI00071318	LUC7L	isoform 1 of Putative RNA-binding protein Luc7-like 1	100.0%	5.9	2	2	2	7	558,530	587,837	534,789	613,346	36,978	41,126	75,317	42,856	14.8	15.6	31.5	15.6	1.1	0.6	-1.0	0.8	1.1	0.4	-1.1	0.6	1.0	0.7	1.1	0.4
IPI00410026	LUC7L	isoform 2 of Putative RNA-binding protein Luc7-like 1	100.0%	6.8	2	2	2	7	558,530	587,837	534,789	613,346	36,978	41,126	75,317	42,856	14.8	15.6	31.5	15.6	1.1	0.6	-1.0	0.8	1.1	0.4	-1.1	0.6	1.0	0.7	1.1	0.4
IPI00410027	LUC7L	isoform 3 of Putative RNA-binding protein Luc7-like 1	100.0%	6.2	2	2	2	7	558,530	587,837	534,789	613,346	36,978	41,126	75,317	42,856	14.8	15.6	31.5	15.6	1.1	0.6	-1.0	0.8	1.1	0.4	-1.1	0.6	1.0	0.7	1.1	0.4
IPI00793246	LUC7L	24 kDa protein	100.0%	10.7	2	2	2	7	558,530	587,837	534,789	613,346	36,978	41,126	75,317	42,856	14.8	15.6	31.5	15.6	1.1	0.6	-1.0	0.8	1.1	0.4	-1.1	0.6	1.0	0.7	1.1	0.4
IPI00798019	LUC7L	LUC7-like (S. cerevisiae), isoform CRA_a	100.0%	7.7	2	2	2	7	558,530	587,837	534,789	613,346	36,978	41,126	75,317	42,856	14.8	15.6	31.5	15.6	1.1	0.6	-1.0	0.8	1.1	0.4	-1.1	0.6	1.0	0.7	1.1	0.4
IPI00853373	LUC7L	Uncharacterized protein	100.0%	8.1	2	2	2	7	558,530	587,837	534,789	613,346	36,978	41,126	75,317	42,856	14.8	15.6	31.5	15.6	1.1	0.6	-1.0	0.8	1.1	0.4	-1.1	0.6	1.0	0.7	1.1	0.4
IPI00893219	LUC7L	LUC7-like	100.0%	12.1	2	2	2	7	558,530	587,837	534,789	613,346	36,978	41,126	75,317	42,856	14.8	15.6	31.5	15.6	1.1	0.6	-1.0	0.8	1.1	0.4	-1.1	0.6	1.0	0.7	1.1	0.4
				NSMPASSFQQQK	2	99.9%	1																									
				VHELNEEIGK	2	99.4%	1																									
IPI00071697	NFYC	isoform 3 of Nuclear transcription factor Y subunit gamma	93.7%	2.6	1	1	1	10	1,896,980	1,853,770	1,829,530	2,146,970	120,775	150,486	147,333	94,720	14.2	18.2	18.0	9.9	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.9	1.2	0.1	1.2	0.1
IPI00216407	NFYC	isoform 2 of Nuclear transcription factor Y subunit gamma	93.7%	2.7	1	1	1	10	1,896,980	1,853,770	1,829,530	2,146,970	120,775	150,486	147,333	94,720	14.2	18.2	18.0	9.9	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.9	1.2	0.1	1.2	0.1
IPI00513906	NFYC	Uncharacterized protein	93.7%	3.2	1	1	1	10	1,896,980	1,853,770	1,829,530	2,146,970	120,775	150,486	147,333	94,720	14.2	18.2	18.0	9.9	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.9	1.2	0.1	1.2	0.1
IPI00514289	NFYC	nuclear transcription factor Y subunit gamma isoform 1	93.7%	3.4	1	1	1	10	1,896,980	1,853,770	1,829,530	2,146,970	120,775	150,486	147,333	94,720	14.2	18.2	18.0	9.9	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.9	1.2	0.1	1.2	0.1
IPI00644539	NFYC	Uncharacterized protein	93.7%	6.7	1	1	1	10	1,896,980	1,853,770	1,829,530	2,146,970	120,775	150,486	147,333	94,720	14.2	18.2	18.0	9.9	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.9	1.2	0.1	1.2	0.1
IPI00645066	NFYC	nuclear transcription factor Y subunit gamma isoform 3	93.7%	3.6	1	1	1	10	1,896,980	1,853,770	1,829,530	2,146,970	120,775	150,486	147,333	94,720	14.2	18.2	18.0	9.9	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.9	1.2	0.1	1.2	0.1
IPI00646320	NFYC	nuclear transcription factor Y subunit gamma isoform 5	93.7%	4.0	1	1	1	10	1,896,980	1,853,770	1,829,530	2,146,970	120,775	150,486	147,333	94,720	14.2	18.2	18.0	9.9	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.9	1.2	0.1	1.2	0.1
IPI00911001	NFYC	isoform 1 of Nuclear transcription factor Y subunit gamma	93.7%	3.6	1	1	1	10	1,896,980	1,853,770	1,829,530	2,146,970	120,775	150,486	147,333	94,720	14.2	18.2	18.0	9.9	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.9	1.2	0.1	1.2	0.1
IPI00979585	NFYC	Nuclear transcription factor Y, gamma	93.7%	9.3	1	1	1	10	1,896,980	1,853,770	1,829,530	2,146,970	120,775	150,486	147,333	94,720	14.2	18.2	18.0	9.9	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.9	1.2	0.1	1.2	0.1
IPI01015480	NFYC	Uncharacterized protein	93.7%	8.5	1	1	1	10	1,896,980	1,853,770	1,829,530	2,146,970	120,775	150,486	147,333	94,720	14.2	18.2	18.0	9.9	-1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.9	1.2	0.1	1.2	0.1
				MISAEAPVLFAK	2	94.4%	1																									
IPI00072044	C11orf54	isoform 1 of Ester hydrolase C11orf54	100.0%	6.0	2	2	2	3	3,793,725	3,694,615	3,768,155	4,234,788	357,626	177,826	273,725	157,630	21.1	10.8	16.2	8.3	-1.0	0.8	-1.0	1	1.1	0.3	1.0	0.8	1.1	0.05	1.1	0.2
IPI00760666	C11orf54	isoform 4 of Ester hydrolase C11orf54	100.0%	9.3	2	2	2	3	3,793,725	3,694,615	3,768,155	4,234,788	357,626	177,826	273,725	157,630	21.1	10.8	16.2	8.3	-1.0	0.8	-1.0	1	1.1	0.3	1.0	0.8	1.1	0.05	1.1	0.2
IPI00761072	C11orf54	isoform 2 of Ester hydrolase C11orf54	100.0%	6.4	2	2	2	3	3,793,725	3,694,615	3,768,155	4,234,788	357,626	177,826	273,725	157,630	21.1	10.8	16.2	8.3	-1.0	0.8	-1.0	1	1.1	0.3	1.0	0.8	1.1	0.05	1.1	0.2
				APLVCLPVFVSR	2	100.0%	1																									
				DPGFDLR	2	95.3%	1																									
IPI00072257	DNPEP	cDNA FLJ10915 fis, clone OVARC1000288, weakly similar to VACUOLAR AMINOP	100.0%	9.1	2	2	2	1	1,235,156	1,268,754	1,222,496	1,403,073	71,920	54,285	116,602	79,920	13.0	9.6	21.3	12.7	1.0	0.7	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.1	0.2
				NINENFGPNTEMHLVPILATAIQEELEK	3	99.3%	1																									
				YASNAVSEALIR	2	99.9%	1																									
IPI00072377	SET	isoform 1 of Protein SET	100.0%	20.7	5	7	9	4	19,203,458	19,588,141	18,518,048	21,413,908	1,408,741	727,927	1,317,292	744,678	16.4	8.3	15.9	7.8	1.0	0.8	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.1	1.2	0.09
IPI00301311	SET	isoform 2 of Protein SET	100.0%	21.7	5	7	9	4	19,203,458	19,588,141	18,518,048	21,413,908	1,408,741	727,927	1,317,292	744,678	16.4	8.3	15.9	7.8	1.0	0.8	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.1	1.2	0.09
IPI00844040	SET	cDNA FLJ59759, highly similar to Protein SET	100.0%	22.6	5	7	9	4	19,203,458	19,588,141	18,518,048	21,413,908	1,408,741	727,927	1,317,292	744,678	16.4	8.3	15.9	7.8	1.0	0.8	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.1	1.2	0.09
IPI00896523	SET	SET nuclear oncogene	100.0%	22.4	5	7	9	4	19,203,458	19,588,141	18,518,048	21,413,908	1,408,741	727,927	1,317,292	744,678	16.4	8.3	15.9	7.8	1.0	0.8	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.1	1.2	0.09
				EFHLNESGDPSSK	2	100.0%	1																									

				EFHLNESGDPSSK	3	99.9%	1																									
				IDFYFDENPYFENK	2	100.0%	2																									
				IDFYFDENPYFENK	3	100.0%	1																									
				LNEQASEEILKVEQK	3	99.7%	1																									
				LRQPFFQK	2	95.9%	1																									
				VEVTEFEDIK	2	100.0%	2																									
IPI00072534	UNC45A	isoform 1 of Protein unc-45 homolog A	100.0%	2.1	1	2	2	2	315,823	293,535	349,675	403,319	37,156	21,109	37,410	29,387	26.3	16.1	23.9	16.3	-1.1	0.6	1.1	0.5	1.3	0.1	1.2	0.2	1.4	0.02	1.2	0.3
IPI00735181	UNC45A	isoform 2 of Protein unc-45 homolog A	100.0%	2.2	1	2	2	2	315,823	293,535	349,675	403,319	37,156	21,109	37,410	29,387	26.3	16.1	23.9	16.3	-1.1	0.6	1.1	0.5	1.3	0.1	1.2	0.2	1.4	0.02	1.2	0.3
				VLISNLLDLLTEVGVSGQGR	2	100.0%	1																									
				VLISNLLDLLTEVGVSGQGR	3	100.0%	1																									
IPI00073713	MSI2	isoform 1 of RNA-binding protein Musashi homolog 2	100.0%	14.0	3	3	3	4	4,106,253	3,965,663	4,095,785	4,559,425	430,458	134,927	297,971	128,027	23.4	7.6	16.3	6.3	-1.0	0.8	-1.0	1	1.1	0.4	1.0	0.7	1.1	0.01	1.1	0.2
IPI00167806	MSI2	isoform 2 of RNA-binding protein Musashi homolog 2	100.0%	18.3	3	3	3	4	4,106,253	3,965,663	4,095,785	4,559,425	430,458	134,927	297,971	128,027	23.4	7.6	16.3	6.3	-1.0	0.8	-1.0	1	1.1	0.4	1.0	0.7	1.1	0.01	1.1	0.2
IPI00792475	MSI2	29 kDa protein	100.0%	18.0	3	3	3	4	4,106,253	3,965,663	4,095,785	4,559,425	430,458	134,927	297,971	128,027	23.4	7.6	16.3	6.3	-1.0	0.8	-1.0	1	1.1	0.4	1.0	0.7	1.1	0.01	1.1	0.2
IPI00910884	MSI2	cDNA FLJ56904, highly similar to RNA-binding protein Musashi homolog 2	100.0%	14.2	3	3	3	4	4,106,253	3,965,663	4,095,785	4,559,425	430,458	134,927	297,971	128,027	23.4	7.6	16.3	6.3	-1.0	0.8	-1.0	1	1.1	0.4	1.0	0.7	1.1	0.01	1.1	0.2
				GFGFVTFADPASVDK	2	99.1%	1																									
				GFGFVTFENEDVVEK	2	100.0%	1																									
				IFVGGLSANTVVEDVK	2	99.9%	1																									
IPI00073772	FBP1	Fructose-1,6-bisphosphatase 1	100.0%	20.4	5	5	6	1	13,627,240	14,278,075	14,928,489	17,004,390	1,465,419	675,797	1,271,498	581,298	24.1	10.6	19.1	7.6	1.0	0.7	1.1	0.5	1.2	0.06	1.0	0.7	1.2	0.02	1.1	0.2
				APVILGSPDDVLEFLK	2	100.0%	2																									
				DFDPAVTEYIQR	2	100.0%	1																									
				EAVLDVIPTDIHQR	2	94.1%	1																									
				GTGELTQLLNSLCTAVK	2	100.0%	1																									
				HAIIVEPEKR	2	81.8%	1																									
IPI00074224	EIF1AXP1	S1, IF1 type family protein	100.0%	46.5	4	4	5	1	2,840,724	3,128,953	2,808,238	3,423,293	381,980	213,005	209,634	190,167	30.1	15.2	16.7	12.4	1.1	0.5	-1.0	0.9	1.2	0.2	-1.1	0.3	1.1	0.3	1.2	0.06
				DYQDNKADVILK	2	99.8%	1																									
				EDGQEYAQVIK	2	97.6%	1																									
				INETDTFGPGDDDEIQFDDIGDDDEDIDDI	3	97.6%	1																									
				VWINTSDIILVGLR	2	100.0%	2																									
IPI00074489	NDUFB10	NDUFB10 protein	100.0%	6.0	1	1	1	1	2,554,520	2,797,930	2,777,435	2,991,180	207,190	238,323	90,634	148,655	18.1	19.1	7.3	11.1	1.1	0.5	1.1	0.4	1.2	0.1	-1.0	0.9	1.1	0.5	1.1	0.3
				EVEQFTQVAK	2	98.6%	1																									
IPI00074829	UNKL	isoform 3 of RING finger protein unkempt-like	93.0%	8.3	1	1	1	2	2,478,570	2,771,925	2,523,155	3,194,055	302,408	242,322	261,459	155,273	27.3	19.6	23.2	10.9	1.1	0.5	1.0	0.9	1.3	0.07	-1.1	0.5	1.2	0.2	1.3	0.06
IPI00877778	UNKL	isoform 1 of RING finger protein unkempt-like	93.0%	8.2	1	1	1	2	2,478,570	2,771,925	2,523,155	3,194,055	302,408	242,322	261,459	155,273	27.3	19.6	23.2	10.9	1.1	0.5	1.0	0.9	1.3	0.07	-1.1	0.5	1.2	0.2	1.3	0.06
				QLQEELEGLGVASTLPLGR	2	93.0%	1																									
IPI00075248	CALM1	Calmodulin	100.0%	47.0	5	8	12	4	29,440,225	30,341,976	30,837,018	34,394,585	2,382,723	1,744,778	2,199,997	816,431	18.1	12.9	16.0	5.3	1.0	0.8	1.0	0.7	1.2	0.1	1.0	0.9	1.1	0.07	1.1	0.2
IPI00794543	CALM1	cDNA FLJ75174, highly similar to Homo sapiens calmodulin 1 (phosphorylase kinas	100.0%	46.1	5	8	12	4	29,440,225	30,341,976	30,837,018	34,394,585	2,382,723	1,744,778	2,199,997	816,431	18.1	12.9	16.0	5.3	1.0	0.8	1.0	0.7	1.2	0.1	1.0	0.9	1.1	0.07	1.1	0.2
IPI00916600	CALM1;CALM3;CALM	Uncharacterized protein	100.0%	35.7	5	8	12	4	29,440,225	30,341,976	30,837,018	34,394,585	2,382,723	1,744,778	2,199,997	816,431	18.1	12.9	16.0	5.3	1.0	0.8	1.0	0.7	1.2	0.1	1.0	0.9	1.1	0.07	1.1	0.2
IPI00916768	CALM1;CALM3;CALM	21 kDa protein	100.0%	37.4	5	8	12	4	29,440,225	30,341,976	30,837,018	34,394,585	2,382,723	1,744,778	2,199,997	816,431	18.1	12.9	16.0	5.3	1.0	0.8	1.0	0.7	1.2	0.1	1.0	0.9	1.1	0.07	1.1	0.2
				DTDSEEEIREAFR	3	95.4%	1																									
				EADIDGDGQVNYEEFVQMMTAK	2	99.9%	1																									
				EADIDGDGQVNYEEFVQMMTAK	3	99.9%	1																									
				EAFSLFDKDGDGTITTK	2	100.0%	2																									
				EAFSLFDKDGDGTITTK	3	100.0%	1																									
				MKDTDSEEEIREAFR	3	99.7%	2																									
				VFDKDGNGYISAAELR	2	100.0%	2																									
				VFDKDGNGYISAAELR	3	100.0%	2																									
IPI00075607	FAM192BP;FAM192A	RcNIP30 (Fragment)	99.2%	5.9	1	1	1	2	3,746,475	3,093,355	4,020,855	3,576,615	345,900	521,354	278,332	457,588	20.6	37.7	15.5	28.6	-1.2	0.3	1.1	0.6	-1.0	0.8	1.3	0.2	1.2	0.5	-1.1	0.4
IPI00178750	FAM192A	Protein FAM192A	99.2%	5.9	1	1	1	2	3,746,475	3,093,355	4,020,855	3,576,615	345,900	521,354	278,332	457,588	20.6	37.7	15.5	28.6	-1.2	0.3	1.1	0.6	-1.0	0.8	1.3	0.2	1.2	0.5	-1.1	0.4
				GLDEDETNFLDEVSR	2	99.2%	1																									
IPI00220855	H2AFJ	isoform 1 of Histone H2A.J	100.0%	28.7	3	5	8	8	8,631,774	9,143,202	8,782,009	10,745,609	825,054	389,821	716,935	432,391	21.4	9.5	18.3	9.0	1.1	0.6	1.0	0.9	1.2	0.05	-1.0	0.7	1.2	0.02	1.2	0.05
IPI00930144	H2AFJ	Histone H2A	100.0%	33.3	3	5	8	8	8,631,774	9,143,202	8,782,009	10,745,609	825,054	389,821	716,935	432,391	21.4	9.5	18.3	9.0	1.1	0.6	1.0	0.9	1.2	0.05	-1.0	0.7	1.2	0.02	1.2	0.05
IPI00255316	HIST1H2AD	Histone H2A type 1-D	100.0%	28.5	3	5	8	8	8,631,774	9,143,202	8,782,009	10,745,609	825,054	389,821	716,935	432,391	21.4	9.5	18.3	9.0	1.1	0.6	1.0	0.9	1.2	0.05	-1.0	0.7	1.2	0.02	1.2	0.05
IPI00291764	HIST1H2AI;HIST1H2A	Histone H2A type 1	100.0%	28.5	3	5	8	8	8,631,774	9,143,202	8,782,009	10,745,609	825,054	389,821	716,935	432,391	21.4	9.5	18.3	9.0	1.1	0.6	1.0	0.9	1.2	0.05	-1.0	0.7	1.2	0.02	1.2	0.05
IPI00552873	HIST1H2AI;HIST1H2A	Histone H2A type 1-J	100.0%	28.9	3	5	8	8	8,631,774	9,143,202	8,782,009	10,745,609	825,054	389,821	716,935	432,391	21.4	9.5	18.3	9.0	1.1	0.6	1.0	0.9	1.2	0.05	-1.0	0.7	1.2	0.02	1.2	0.05
IPI00081836	H2AK;HIST1H2AI;HIS	Histone H2A type 1-H	100.0%	28.9	3	5	8	8	8,631,774	9,143,202	8,782,009	10,745,609	825,054	389,821	716,935	432,391	21.4	9.5	18.3	9.0	1.1	0.6	1.0	0.9	1.2	0.05	-1.0	0.7	1.2	0.02	1.2	0.05
IPI00216457	ST2H2AA3;HIST2H2A	Histone H2A type 2-A	100.0%	28.5	3	5	8	8	8,631,774	9,143,202	8,782,009	10,745,609	825,054	389,821	716,935	432,391	21.4	9.5	18.3	9.0	1.1	0.6	1.0	0.9	1.2	0.05	-1.0	0.7	1.2	0.02	1.2	0.05
IPI00339274	HIST2H2AC	Histone H2A type 2-C	100.0%	28.7	3	5	8	8	8,631,774	9,143,202	8,782,009	10,745,609	825,054	389,821	716,935	432,391	21.4	9.5	18.3	9.0	1.1	0.6	1.0	0.9	1.2	0.05	-1.0	0.7	1.2	0.02	1.2	0.05
				HLQLAIR	2	99.9%	2																									
				NDEELNKLLGK	2	100.0%	1																									
				NDEELNKLLGK	3	99.9%	1																									
				VTIAQGGVLPNIQAVLLPK	2	100.0%	2																									
				VTIAQGGVLPNIQAVLLPK	3	100.0%	2																									
IPI00082310	KHDRBS1	isoform 3 of KH domain-containing, RNA-binding, signal transduction-associated pro	100.0%	8.4	2	2	2	1	2,882,146	3,351,577	3,214,382	3,627,833	440,327	359,095	362,239	202,341	34.2	24.0	25.2	12.5	1.2	0.4	1.1	0.6	1.3	0.2	-1.0	0.8	1.1	0.5	1.1	0.3
				DSLDPSFTHAMQLLTAEIEK	3	100.0%	1																									
				KDDEENYLDLFSHK	3	100.0%	1																									
IPI00096066	SUCLG2	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	100.0%	20.8	8	8	9	1	10,197,926	10,867,179	10,600,241	11,638,485	1,120,548	560,460	552,968	542,378	24.6	11.5	11.7	10.4	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
				ETYLAILMDR	2	99.9%	1																									
				FFVADTANEALEAAK	2	99.9%	1																									
				ILNNSGLPITSAIDLEDAAK	2	99.9%	1																									
				ILNNSGLPITSAIDLEDAAKK	3	99.9%	1																									
				INFDDNAEFR	2	99.9%	1																									
				LEGTNVQEAQK	2	99.2%	1																									
				MAENLGFVGPLK	2	100.0%	1																									
				VMVAEALDISR	2	100.0%	2																									
IPI00098769	CHST2	isoform 1 of Carbohydrate sulfotransferase 2	97.6%	3.2	1	1	1	2	3,587,140	3,485,545	3,673,845	4,142,445	196,580	179,479	257,503	216,665	12.3	11.5	15.7	11.7	-1.0	0.7	1.0	0.8	1.2	0.09	1.1	0.6	1.2	0.05	1.1	0.2
IPI00759564	CHST2	isoform 2 of Carbohydrate sulfotransferase 2	97.6%	3.5	1	1	1	2	3,587,140	3,485,545	3,673,845	4,142,445	196,580	179,479	257,503	216,665	12.3	11.5	15.7	11.7	-1.0	0.7	1.0	0.8	1.2	0.09	1.1	0.6	1.2	0.05	1.1	0.2
				CDLSVFQLYSPAGSGGR	2	97.0%	1																									
IPI00099615	HBP1	cDNA FLJ56446, highly similar to HMG box-containing protein 1	95.0%	2.5	1	1	1	5	723,592	833,292	595,202	721,162	90,476	93,427	76,137	86,366	28.0	25.1	28.6	26.8	1.2	0.4	-1.2	0.3	-1.0	1	-1.4	0.08	-1.2	0.4	1.2	0.3
IPI00550468	HBP1	isoform 2 of HMG box-containing protein 1	95.0%	2.8	1	1	1	5	723,592	833,292	595,202	721,162	90,476	93,427	76,137	86,366	28.0	25.1	28.6	26.8	1.2	0.4	-1.2	0.3	-1.0	1	-1.4	0.08	-1.2	0.4	1.2	0.3
IPI00607765	HBP1	isoform 3 of HMG box-containing protein 1	95.0%	2.5	1	1	1	5	723,592	833,292	595,202	721,162	90,476	93,427	76,137	86,366	28.0	25.1	28.6	26.8	1.2	0.4	-1.2	0.3	-1.0	1	-1.4	0.08	-1.2	0.4	1.2	0.3
IPI00910910	HBP1	cDNA FLJ55129, highly similar to HMG box-containing protein 1	95.0%	3.0	1	1	1	5	723,592	833,292	595,202	721,162	90,476	93,427	76,137	86,366	28.0	25.1	28.6	26.8	1.2	0.4	-1.2	0.3	-1.0	1	-1.4	0.08	-1.2	0.4	1.2	0.3
IPI00945567	HBP1	9 kDa protein	95.0%	15.3	1	1	1	5	723,592	833,292	595,202	721,162	90,476	93,427	76,137	86,366	28.0	25.1	28.6	26.8	1.2	0.4	-1.2	0.3	-1.0	1	-1.4	0.08	-1.2	0.4	1.2	0.3
				VEYTQMYPGKDNR	2	95.0%	1																									
IPI00099820	GPCPD1	Putative glycerophosphocholine phosphodiesterase GPCPD1	98.6%	1.8	1	1	1	1	4,505,030	4,152,230	4,283,950	4,500,090	76,065	182,233	259,108	320,941	3.8	9.8	13.5	16.0	-1.1	0.1	-1.1	0.5	-1.0	1	1.0	0.7	1.1	0.4	1.1	0.6
				TIGGPCQVIVHK	2	98.6%	1																									
IPI00100151	XRN2	isoform 1 of 5'-3' exoribonuclease 2	100.0%	8.3	5	5	5	2	6,395,687	6,519,725	6,207,161	7,311,121	521,775	141,375	349,317	218,398	18.2	4.9	12.6	6.7	1.0	0.8	-1.0	0.8	1.1	0.1	-1.1	0.4	1.1	0.02	1.2	0.03
IPI01012839	XRN2	cDNA FLJ55645, highly similar to 5'-3' exoribonuclease 2	100.0%	8.8	5	5	5	2	6,395,687	6,519,725	6,207,161	7,311,121	521,775	141,375	349,317	218,398	18.2	4.9	12.6	6.7	1.0	0.8	-1.0	0.8	1.1	0.1	-1.1	0.4	1.1	0.02	1.2	0.03
				DQPAFTPSGILTPHALGSR	3	93.8%	1																									
				NEDEMMVAIFEYIDR	2	97.2%	1																									
				NLTVILSDASAPGEGEHK	3	98.8%	1																									
				NSLGGDVLFVGK	2	99.9%	1																									
				YAWQGVALLPFVDER	2	99.9%	1																									
IPI00100154	TOLLIP	Toll-interacting protein	99.8%	8.4	2	2	3	2	3,097,328	2,910,090	2,665,161	3,167,130	266,493	247,047	158,095	223,969	19.2	19.0	13.3	15.8	-1.1	0.6	-1.2	0.2	1.0	0.8	-1.1	0.4	1.1	0.5	1.2	0.1
IPI00654582	TOLLIP	Toll interacting protein variant (Fragment)	99.8%	6.5	2	2	3	2	3,097,328	2,910,090	2,665,161	3,167,130	266,493	247,047	158,095	223,969	19.2	19.0	13.3	15.8	-1.1	0.6	-1.2	0.2	1.0	0.8	-1.1	0.4	1.1	0.5	1.2	0.1
				GPVYIGELPQDFLR	2	99.1%	2																									
				LNITVVQAK	2	99.0%	1																									
IPI00100160	CAND1	isoform 1 of Cullin-associated NEDD8-dissociated protein 1	100.0%	18.0	15	16	19	1	55,661,481	56,170,062	53,160,406	60,334,752	4,741,341	2,010,668	3,319,269	2,500,934	19.1	8.0	14.0	9.3	1.0	0.9	-1.0	0.7	1.1	0.4	-1.1	0.5	1.1	0.2	1.1	0.1
				ALTLIAGSPLK	2	99.9%	1																									
				DLLDTVLPHLYNETK	2	85.2%	1																									
				DLLDTVLPHLYNETK	3	98.8%	1																									
				EGPAVVGQFIQDVK	2	99.1%	1																									
				FMATNDLMTELQK	2	100.0%	1																									
				HEMLPEFYK	2	100.0%	2																									
				IDLRPVLGEGVPILASFLR	3	100.0%	1																									
				ISGSILNELIGLVR	2	100.0%	2																									
				ITSEALLVTQQLVK	2	98.9%	1																									
				LGTLSALDILIK	2	100.0%	2																									
				NGEVQNLAVK	2	82.4%	1																									
				QEDVSVQLEALDIMADMLSR	2	100.0%	1																									
				SPLMSEFQSQISSNPELAAIFESIQK	3	99.9%	1																									
				SVILEAFSSPSEEVK	2	94.8%	1																									
				TYIQCIAAISR	2	99.9%	1																									
				VIRPLDQPSSFDATPYIK	3	99.7%	1																									
IPI00100192	NT5C3	isoform 3 of Cytosolic 5'-nucleotidase 3	99.5%	5.2	1	1	1	4	1,297,883	1,276,023	1,146,040	1,440,938	135,545	100,118	145,859	152,318	23.4	17.5	28.5	23.6	-1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.5	1.1	0.4	1.3	0.2
IPI00619911	NT5C3	isoform 1 of Cytosolic 5'-nucleotidase 3	99.5%	5.1	1	1	1	4	1,297,883	1,276,023	1,146,040	1,440,938	135,545	100,118	145,859	152,318	23.4	17.5	28.5	23.6	-1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.5	1.1	0.4	1.3	0.2
IPI00647805	NT5C3	isoform 4 of Cytosolic 5'-nucleotidase 3	99.5%	5.3	1	1	1	4	1,297,883	1,276,023	1,146,040	1,440,938	135,545	100,118	145,859	152,318	23.4	17.5	28.5	23.6	-1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.5	1.1	0.4	1.3	0.2
IPI00807412	NT5C3	isoform 2 of Cytosolic 5'-nucleotidase 3	99.5%	4.5	1	1	1	4	1,297,883	1,276,023	1,146,040	1,440,938	135,545	100,118	145,859	152,318	23.4	17.5	28.5	23.6	-1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.5	1.1	0.4	1.3	0.2
				VVSNFMDFDETGVLK	2	99.5%	1																									
IPI00100197	NSFL1C	isoform 1 of NSFL1 cofactor p47	100.0%	23.0	7	7	7	2	10,874,193	11,618,876	10,858,492	13,081,142	871,957	352,489	834,814	513,406	17.9	6.8	17.2	8.8	1.1	0.5	-1.0	1	1.2	0.06	-1.1	0.4	1.1	0.05	1.2	0.05
IPI00397571	NSFL1C	isoform 3 of NSFL1 cofactor p47	100.0%	22.9	7	7	7	2	10,874,193	11,618,876	10,858,492	13,081,142	871,957	352,489	834,814	513,406	17.9	6.8	17.2	8.8	1.1	0.5	-1.0	1	1.2	0.06	-1.1	0.4	1.1	0.05	1.2	0.05
				ASSSILIDESEPTTNIQIR	2	100.0%	1																									
				EANLLNAVIVQR	2	100.0%	1																									
				LGAAPEEESAYVAGEK	2	99.9%	1																									
				LGAAPEEESAYVAGEKR	3	100.0%	1																									
				SGFSLDNGELR	2	99.9%	1																									
				SPNELVDDLFK	2	99.7%	1																									
				SYQDPSNAQFLESIR	2	99.5%	1																									
IPI00100559	AP1S1	isoform 2 of AP-1 complex subunit sigma-1A	99.8%	18.8	2	2	2	1	5,152,487	5,082,141	5,109,479	6,149,698	349,842	242,581	321,104	270,526	15.2	10.7	14.1	9.8	-1.0	0.9	-1.0	0.9	1.2	0.05	1.0	0.9	1.2	0.02	1.2	0.04
				ELMQVVLAR	2	87.7%	1																									
				YFGSVCELDIIFNFEK	2	98.9%	1																									
IPI00100656	TECR	isoform 1 of Trans-2,3-enoyl-CoA reductase	99.4%	3.3	1	1	1	2	3,280,330	3,107,750	3,011,230	3,562,100	321,844	172,538	200,729	211,027	21.9	12.4	14.9	13.3	-1.1	0.6	-1.1	0.5	1.1	0.5	-1.0	0.7	1.1	0.1	1.2	0.1
IPI00301279	TECR	isoform 2 of Trans-2,3-enoyl-CoA reductase	99.4%	6.4	1	1	1	2	3,280,330	3,107,750	3,011,230	3,562,100	321,844	172,538	200,729	211,027	21.9	12.4	14.9	13.3	-1.1	0.6	-1.1	0.5	1.1	0.5	-1.0	0.7	1.1	0.1	1.2	0.1
				HYEVEILDAK	2	99.4%	1																									
IPI00100716	PUF60	isoform 2 of Poly(U)-binding-splicing factor PUF60	100.0%	20.7	7	7	8	3	3,672,922	3,671,943	3,595,777	4,105,558	246,030	184,221	220,796	157,760	15.0	11.2	13.7	8.6	-1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00788826	PUF60	isoform 4 of Poly(U)-binding-splicing factor PUF60	100.0%	22.4	7	7	8	3	3,672,922	3,671,943	3,595,777	4,105,558	246,030	184,221	220,796	157,760	15.0	11.2	13.7	8.6	-1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
IPI00855912	PUF60	isoform 6 of Poly(U)-binding-splicing factor PUF60	100.0%	21.8	7	7	8	3	3,672,922	3,671,943	3,595,777	4,105,558	246,030	184,221	220,796	157,760	15.0	11.2	13.7	8.6	-1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.1
				AQSSQDAVSSMNLFDLGGQYLR	2	100.0%	1																									
				GYGFIEYEK	2	99.7%	1																									
				IYVASVHQDLSDDDIKSVFEAFGK	3	84.0%	1																									
				LGLPPLTPEQQEALQK	2	100.0%	2																									
				QGEEEDAEIIVK	2	99.9%	1																									
				QTIAHQQQQLTNLQMAAQR	3	99.9%	1																									
				VVAEVYDQER	2	99.9%	1																									
IPI00100748	HSPBP1	cDNA FLJ55382, highly similar to Hsp70-binding protein 1	91.1%	3.0	1	1	1	3	907,307	898,417	894,970	930,540	54,478	50,952	110,576	46,482	13.4	12.7	27.6	11.2	-1.0	0.9	-1.0	0.9	1.0	0.8	-1.0	1	1.0	0.7	1.0	0.8
IPI00442503	HSPBP1	isoform 2 of Hsp70-binding protein 1	91.1%	4.6	1	1	1	3	907,307	898,417	894,970	930,540	54,478	50,952	110,576	46,482	13.4	12.7	27.6	11.2	-1.0	0.9	-1.0	0.9	1.0	0.8	-1.0	1	1.0	0.7	1.0	0.8
IPI00953460	HSPBP1	Uncharacterized protein	91.1%	4.7	1	1	1	3	907,307	898,417	894,970	930,540	54,478	50,952	110,576	46,482	13.4	12.7	27.6	11.2	-1.0	0.9	-1.0	0.9	1.0	0.8	-1.0	1	1.0	0.7	1.0	0.8
				QWLQEAMSAAFR	2	91.1%	1																									
IPI00100775	C11orf67	isoform 1 of UPF0366 protein C11orf67	98.4%	17.2	2	2	2	3	3,682,267	3,845,920	3,501,200	4,085,490	227,557	435,140	242,849	315,066	13.8	25.3	15.5	17.2	1.0	0.7	-1.1	0.6	1.1	0.3	-1.1	0.5	1.1	0.7	1.2	0.2

IPI00977242	C11orf67	Uncharacterized protein	98.4%	12.5	2	2	2	3	3,682,267	3,845,920	3,501,200	4,085,490	227,557	435,140	242,849	315,066	13.8	25.3	15.5	17.2	1.0	0.7	-1.1	0.6	1.1	0.3	-1.1	0.5	1.1	0.7	1.2	0.2
IPI00980367	C11orf67	Uncharacterized protein	98.4%	14.9	2	2	2	3	3,682,267	3,845,920	3,501,200	4,085,490	227,557	435,140	242,849	315,066	13.8	25.3	15.5	17.2	1.0	0.7	-1.1	0.6	1.1	0.3	-1.1	0.5	1.1	0.7	1.2	0.2
				EYNALVAQGVR	2	89.1%	1																									
				VPSSTVEYLK	2	86.6%	1																									
IPI00100796	CHMP5	Charged multivesicular body protein 5	100.0%	15.5	2	2	2	1	6,971,870	7,711,110	7,034,940	8,424,950	798,673	372,944	758,057	300,174	25.6	10.8	24.1	8.0	1.1	0.4	1.0	1	1.2	0.1	-1.1	0.4	1.1	0.2	1.2	0.1
				APPPSLTDCIGTVDSR	2	99.6%	1																									
				NKDGVLVDEFGLPQIPAS	2	99.8%	1																									
IPI00100867	TAF1L	Transcription initiation factor TFIID subunit 1-like	97.3%	0.9	1	1	1	1	4,500,120	4,528,140	4,871,550	5,024,040	471,331	352,544	496,617	240,439	23.4	17.4	22.8	10.7	1.0	1	1.1	0.6	1.1	0.4	1.1	0.6	1.1	0.3	1.0	0.8
				RMLLVAGSAASGNNHR	3	96.0%	1																									
IPI00100933	PTER	isoform 1 of Phosphotriesterase-related protein	100.0%	9.2	2	2	2	2	4,080,099	3,222,425	3,483,484	3,718,812	396,744	493,662	490,728	358,981	21.7	34.3	31.5	21.6	-1.3	0.2	-1.2	0.4	-1.1	0.5	1.1	0.7	1.2	0.4	1.1	0.7
IPI00903152	PTER	isoform 2 of Phosphotriesterase-related protein	100.0%	10.6	2	2	2	2	4,080,099	3,222,425	3,483,484	3,718,812	396,744	493,662	490,728	358,981	21.7	34.3	31.5	21.6	-1.3	0.2	-1.2	0.4	-1.1	0.5	1.1	0.7	1.2	0.4	1.1	0.7
				AMSVEQLTDVLMNEILHGADGTSIK	3	99.9%	1																									
				APFQIIR	2	93.6%	1																									
IPI00101037	RCN3	Reticulocalbin-3	90.7%	7.9	1	1	1	1	2,016,255	2,064,640	1,978,595	2,351,110	262,773	387,133	509,189	255,983	29.1	41.9	57.5	24.4	1.0	0.9	-1.0	0.9	1.2	0.4	-1.0	0.9	1.1	0.6	1.2	0.5
				AGDGDGWVSLAELRAWIAHTQQRHIR	3	90.7%	1																									
IPI00101278	PCBP3	isoform 2 of Poly(rC)-binding protein 3	100.0%	13.0	3	3	5	2	880,616	904,386	777,755	1,018,125	91,294	41,422	55,556	46,804	23.2	10.2	16.0	10.3	1.0	0.8	-1.1	0.4	1.2	0.2	-1.2	0.1	1.1	0.1	1.3	0.01
IPI00410586	PCBP3	isoform 3 of Poly(rC)-binding protein 3	100.0%	13.0	3	3	5	2	880,616	904,386	777,755	1,018,125	91,294	41,422	55,556	46,804	23.2	10.2	16.0	10.3	1.0	0.8	-1.1	0.4	1.2	0.2	-1.2	0.1	1.1	0.1	1.3	0.01
				ESTGAQVQVAGDMLPNSTER	2	100.0%	2																									
				INISEGNCPER	2	100.0%	2																									
				LVVPASQCGSLIGK	2	100.0%	1																									
IPI00101923	SPG11	isoform 1 of Spatacsin	97.4%	0.4	1	1	1	2	1,914,670	1,749,330	1,590,385	1,883,120	387,195	62,443	120,524	109,480	45.2	8.0	17.0	13.0	-1.1	0.7	-1.2	0.5	-1.0	0.9	-1.1	0.3	1.1	0.3	1.2	0.1
IPI00798078	SPG11	spatacsin isoform 2	97.4%	0.4	1	1	1	2	1,914,670	1,749,330	1,590,385	1,883,120	387,195	62,443	120,524	109,480	45.2	8.0	17.0	13.0	-1.1	0.7	-1.2	0.5	-1.0	0.9	-1.1	0.3	1.1	0.3	1.2	0.1
				GDFNYLEEFK	2	97.4%	1																									
IPI00101968	DBNL	isoform 3 of Drebrin-like protein	100.0%	27.3	8	8	10	3	5,983,939	6,198,612	5,848,305	6,693,440	562,139	340,225	465,985	279,586	21.0	12.3	17.8	9.3	1.0	0.8	-1.0	0.9	1.1	0.3	-1.1	0.6	1.1	0.3	1.1	0.2
IPI00396437	DBNL	isoform 2 of Drebrin-like protein	100.0%	27.8	8	8	10	3	5,983,939	6,198,612	5,848,305	6,693,440	562,139	340,225	465,985	279,586	21.0	12.3	17.8	9.3	1.0	0.8	-1.0	0.9	1.1	0.3	-1.1	0.6	1.1	0.3	1.1	0.2
IPI00456925	DBNL	isoform 1 of Drebrin-like protein	100.0%	27.9	8	8	10	3	5,983,939	6,198,612	5,848,305	6,693,440	562,139	340,225	465,985	279,586	21.0	12.3	17.8	9.3	1.0	0.8	-1.0	0.9	1.1	0.3	-1.1	0.6	1.1	0.3	1.1	0.2
				AEEDVEPECIMEK	2	96.0%	1																									
				AMSTTSISSPQPGK	2	100.0%	1																									
				FQDVGPQAPVGSVYQK	2	100.0%	1																									
				FVLINWTGEGVNDVR	2	100.0%	1																									
				GYGPDGHFGMFPANYVELIE	2	100.0%	1																									
				NGPALQEAYVR	2	99.9%	2																									
				TWEQQQEVVSR	2	100.0%	2																									
				VAGTGEGGLEEMVEELNSGK	2	100.0%	1																									
IPI00101987	BABAM1	isoform 1 of BRISC and BRCA1-A complex member 1	99.1%	3.7	1	1	1	3	1,495,823	1,626,510	1,572,317	1,816,800	143,914	118,653	208,142	121,041	21.5	16.3	29.6	14.9	1.1	0.5	1.1	0.8	1.2	0.1	-1.0	0.8	1.1	0.3	1.2	0.3
IPI00910550	BABAM1	Uncharacterized protein	99.1%	4.8	1	1	1	3	1,495,823	1,626,510	1,572,317	1,816,800	143,914	118,653	208,142	121,041	21.5	16.3	29.6	14.9	1.1	0.5	1.1	0.8	1.2	0.1	-1.0	0.8	1.1	0.3	1.2	0.3
IPI01011488	BABAM1	36 kDa protein	99.1%	3.7	1	1	1	3	1,495,823	1,626,510	1,572,317	1,816,800	143,914	118,653	208,142	121,041	21.5	16.3	29.6	14.9	1.1	0.5	1.1	0.8	1.2	0.1	-1.0	0.8	1.1	0.3	1.2	0.3
				DMFAFMGSLDTK	2	99.1%	1																									
IPI00102069	EIF3M	Eukaryotic translation initiation factor 3 subunit M	100.0%	7.0	2	2	3	3	5,434,793	5,452,937	5,501,520	6,359,497	429,765	270,775	443,743	310,282	17.7	11.1	18.0	10.9	1.0	1	1.0	0.9	1.2	0.1	1.0	0.9	1.2	0.06	1.2	0.2
IPI00982537	EIF3M	25 kDa protein	100.0%	11.8	2	2	3	3	5,434,793	5,452,937	5,501,520	6,359,497	429,765	270,775	443,743	310,282	17.7	11.1	18.0	10.9	1.0	1	1.0	0.9	1.2	0.1	1.0	0.9	1.2	0.06	1.2	0.2
IPI00983383	EIF3M	cDNA FLJ54904, highly similar to Homo sapiens dendritic cell protein (hfl-B5), mRNA	100.0%	10.7	2	2	3	3	5,434,793	5,452,937	5,501,520	6,359,497	429,765	270,775	443,743	310,282	17.7	11.1	18.0	10.9	1.0	1	1.0	0.9	1.2	0.1	1.0	0.9	1.2	0.06	1.2	0.2
				LLTFMGMAVENK	2	100.0%	2																									
				QQWQQLYDTLNAWK	2	99.6%	1																									
IPI00102118	MLXIP	isoform 1 of MLX-interacting protein	90.3%	3.2	1	1	1	2	1,329,350	1,493,745	1,358,735	1,481,355	123,382	62,749	150,200	105,213	20.8	9.4	24.7	15.9	1.1	0.3	1.0	0.9	1.1	0.4	-1.1	0.4	-1.0	0.9	1.1	0.5
IPI00795813	MLXIP	isoform 2 of MLX-interacting protein	90.3%	5.5	1	1	1	2	1,329,350	1,493,745	1,358,735	1,481,355	123,382	62,749	150,200	105,213	20.8	9.4	24.7	15.9	1.1	0.3	1.0	0.9	1.1	0.4	-1.1	0.4	-1.0	0.9	1.1	0.5
				PMVLSTLRQLSTSTSILTDPAQLPEQASK	3	85.4%	1																									
IPI00102165	H2AFJ	isoform 2 of Histone H2A.J	100.0%	7.3	1	1	1	2	588,662	648,243	559,949	696,495	70,858	30,348	50,337	25,055	26.9	10.5	20.1	8.0	1.1	0.5	-1.1	0.7	1.2	0.2	-1.2	0.2	1.1	0.3	1.2	0.04
IPI01015339	H2AFJ	Histone H2A	100.0%	7.3	1	1	1	2	588,662	648,243	559,949	696,495	70,858	30,348	50,337	25,055	26.9	10.5	20.1	8.0	1.1	0.5	-1.1	0.7	1.2	0.2	-1.2	0.2	1.1	0.3	1.2	0.04
				NDEELNKLLGK	2	100.0%	1																									
IPI00102423	BIRC8	Baculoviral IAP repeat-containing protein 8	99.4%	6.8	1	1	1	1	4,445,650	4,753,840	5,651,820	5,626,650	465,729	385,322	490,298	313,286	23.4	18.1	19.4	12.5	1.1	0.6	1.3	0.1	1.3	0.07	1.2	0.2	1.2	0.1	-1.0	1
				VQCFHCGGGLANWKPK	3	99.4%	1																									
IPI00102864	HK2	Hexokinase-2	98.7%	1.2	1	1	1	2	3,140,915	3,218,470	3,203,220	3,540,230	233,343	70,436	263,414	107,155	16.6	4.9	18.4	6.8	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	1	1.1	0.04	1.1	0.3
IPI00917193	HK2	Uncharacterized protein	98.7%	1.2	1	1	1	2	3,140,915	3,218,470	3,203,220	3,540,230	233,343	70,436	263,414	107,155	16.6	4.9	18.4	6.8	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	1	1.1	0.04	1.1	0.3
				LDESFLVSWTK	2	98.7%	1																									
IPI00102936	SRP68	isoform 2 of Signal recognition particle 68 kDa protein	92.5%	5.7	2	2	2	5	2,833,545	2,856,387	2,859,533	2,768,847	265,394	138,026	328,951	217,524	20.9	10.8	25.7	17.6	1.0	0.9	1.0	1	-1.0	0.9	1.0	1	-1.0	0.7	-1.0	0.8
IPI00168388	SRP68	isoform 1 of Signal recognition particle 68 kDa protein	92.5%	5.4	2	2	2	5	2,833,545	2,856,387	2,859,533	2,768,847	265,394	138,026	328,951	217,524	20.9	10.8	25.7	17.6	1.0	0.9	1.0	1	-1.0	0.9	1.0	1	-1.0	0.7	-1.0	0.8
IPI00386885	SRP68	cDNA FLJ14414 fis, clone HEMBA1004847, highly similar to SIGNAL RECOGNITIO	92.5%	10.4	2	2	2	5	2,833,545	2,856,387	2,859,533	2,768,847	265,394	138,026	328,951	217,524	20.9	10.8	25.7	17.6	1.0	0.9	1.0	1	-1.0	0.9	1.0	1	-1.0	0.7	-1.0	0.8
IPI01009487	SRP68	cDNA FLJ44270 fis, clone TLIVE2008229, highly similar to SIGNAL RECOGNITION	92.5%	5.8	2	2	2	5	2,833,545	2,856,387	2,859,533	2,768,847	265,394	138,026	328,951	217,524	20.9	10.8	25.7	17.6	1.0	0.9	1.0	1	-1.0	0.9	1.0	1	-1.0	0.7	-1.0	0.8
IPI01015006	SRP68	cDNA FLJ14416 fis, clone HEMBA1005202, highly similar to SIGNAL RECOGNITIO	92.5%	6.5	2	2	2	5	2,833,545	2,856,387	2,859,533	2,768,847	265,394	138,026	328,951	217,524	20.9	10.8	25.7	17.6	1.0	0.9	1.0	1	-1.0	0.9	1.0	1	-1.0	0.7	-1.0	0.8
				IFLLGLADNEAAIVQAESEETKER	3	92.5%	1																									
				WSEALVLYDR	2	85.4%	1																									
IPI00103018	KIAA1217	Uncharacterized protein	100.0%	3.1	3	3	3	2	2,889,613	3,156,489	2,816,496	3,295,463	336,137	231,489	104,403	197,186	26.0	16.4	8.3	13.4	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.2	1.0	0.7	1.2	0.06
IPI00187002	KIAA1217	sickle tail protein homolog isoform 2	100.0%	3.4	3	3	3	2	2,889,613	3,156,489	2,816,496	3,295,463	336,137	231,489	104,403	197,186	26.0	16.4	8.3	13.4	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.2	1.0	0.7	1.2	0.06
				GDAPVDKVELSEDSPNSEQDLEK	3	99.5%	1																									
				GPITSYSK	2	86.5%	1																									
				SMVVPGNATIPR	2	100.0%	1																									
IPI00103142	NUDCD2	NudC domain-containing protein 2	100.0%	30.6	4	4	5	2	7,959,595	7,588,135	7,437,870	8,825,625	543,360	99,253	321,489	156,991	15.3	2.9	9.7	4.0	-1.0	0.5	-1.1	0.4	1.1	0.2	-1.0	0.7	1.2	0.0002	1.2	0.005
IPI00973891	NUDCD2	Uncharacterized protein	100.0%	36.4	4	4	5	2	7,959,595	7,588,135	7,437,870	8,825,625	543,360	99,253	321,489	156,991	15.3	2.9	9.7	4.0	-1.0	0.5	-1.1	0.4	1.1	0.2	-1.0	0.7	1.2	0.0002	1.2	0.005
				AQDIQCGLQSR	2	99.8%	1																									
				ENPGFDFSGAEISGNYTK	2	100.0%	1																									
				GGPDFSNLEK	2	97.1%	1																									
				HVALSVGGR	2	99.9%	2																									
IPI00103146	PDLIM5	isoform 3 of PDZ and LIM domain protein 5	100.0%	5.6	1	1	1	4	2,382,375	2,114,013	2,346,475	1,948,700	91,168	178,388	146,718	91,760	8.6	18.9	14.0	10.5	-1.1	0.2	-1.0	0.8	-1.2	0.01	1.1	0.3	-1.1	0.4	-1.2	0.05
IPI00942043	PDLIM5	Uncharacterized protein	100.0%	5.1	1	1	1	4	2,382,375	2,114,013	2,346,475	1,948,700	91,168	178,388	146,718	91,760	8.6	18.9	14.0	10.5	-1.1	0.2	-1.0	0.8	-1.2	0.01	1.1	0.3	-1.1	0.4	-1.2	0.05
IPI00964290	PDLIM5	isoform 2 of PDZ and LIM domain protein 5	100.0%	5.1	1	1	1	4	2,382,375	2,114,013	2,346,475	1,948,700	91,168	178,388	146,718	91,760	8.6	18.9	14.0	10.5	-1.1	0.2	-1.0	0.8	-1.2	0.01	1.1	0.3	-1.1	0.4	-1.2	0.05
IPI01013659	PDLIM5	24 kDa protein	100.0%	5.6	1	1	1	4	2,382,375	2,114,013	2,346,475	1,948,700	91,168	178,388	146,718	91,760	8.6	18.9	14.0	10.5	-1.1	0.2	-1.0	0.8	-1.2	0.01	1.1	0.3	-1.1	0.4	-1.2	0.05
				DFNMPLTISSLK	2	99.9%	1																									
IPI00103242	POF1B	isoform 1 of Protein POF1B	100.0%	10.4	5	5	5	2	10,226,755	11,130,725	11,165,783	12,690,022	665,396	513,204	562,093	596,628	14.6	10.3	11.3	10.5	1.1	0.3	1.1	0.3	1.2	0.02	1.0	1	1.1	0.08	1.1	0.1
IPI00646687	POF1B	isoform 2 of Protein POF1B	100.0%	10.5	5	5	5	2	10,226,755	11,130,725	11,165,783	12,690,022	665,396	513,204	562,093	596,628	14.6	10.3	11.3	10.5	1.1	0.3	1.1	0.3	1.2	0.02	1.0	1	1.1	0.08	1.1	0.1
				LTTYPQTTIR	2	94.6%	1																									
				MDEIGNHYTEMVK	2	98.3%	1																									
				NLEQENQNLR	2	94.0%	1																									
				QDFESTDESEDIESLIPK	2	98.2%	1																									
				YFGELLADLSR	2	99.5%	1																									
IPI00103397	MUC5AC	Mucin-5AC (Fragment)	100.0%	18.5	65	79	106	1	454,203,066	470,165,798	444,551,739	531,008,828	########	########	########	9,577,086	20.0	8.7	17.0	4.0	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.5	1.1	0.02	1.2	0.06
				ACEDHCVAGCFCPEGTVLDDIGQTGCVPVSK	3	100.0%	1																									
				ACPPLSCSLDEAR	2	100.0%	2																									
				AEACVCTYNGQR	2	100.0%	1																									
				AEDAPGVPLR	2	100.0%	2																									
				AESFPNTPLADLGQDVICSHTEGLICLNK	3	100.0%	2																									
				AESHPEVSIEHLGQVVQCSR	2	100.0%	1																									
				AESHPEVSIEHLGQVVQCSR	3	100.0%	1																									
				AFSYTEVEECGCMGR	2	100.0%	2																									
				ATSPTQSTSSWQK	2	100.0%	2																									
				CGLTDSETCLK	2	100.0%	1																									
				CLWSPWMDVSR	2	97.8%	1																									
				CLWSPWMDVSRPGR	2	99.4%	1																									
				CPAPVGCPEGAR	2	100.0%	1																									
				CPNNMQYHECR	2	97.9%	1																									
				CPNNMQYHECR	3	90.4%	1																									
				CPPEAPIFDEDK	2	92.8%	1																									
				CVQASNCPCYHR	3	94.6%	1																									
				DEGYTFCESPR	2	100.0%	1																									
				DGVCTKPMTTCPK	2	100.0%	2																									
				DPCTANPFRK	2	99.9%	1																									
				DPCTANPFRK	3	99.8%	1																									
				EQASGLCYNYQIR	2	100.0%	1																									
				FHPGDVIYHTTDGTGGCISAR	2	99.9%	1																									
				FHPGDVIYHTTDGTGGCISAR	3	100.0%	2																									
				FPGLCNYVFSEHCGAAYEDFNIQLR	3	100.0%	1																									
				GCPVTSTPVTAPSTPSGR	2	100.0%	2																									
				GGPTATSVTQGTHTTPVTR	3	98.8%	1																									
				GLEGCYPK	2	99.9%	1																									
				GNCGDSSSMYSLEGNTVEHR	3	100.0%	2																									
				GPDFCPQK	2	100.0%	1																									
				GQTCGLCGNFNSIQADDFR	2	100.0%	2																									
				GQTCGLCGNFNSIQADDFR	3	100.0%	1																									
				GSVLVNGHPVLLPFSQSGVLIQQSSSYTK	3	100.0%	1																									
				GTDSGDFDTLENLR	2	100.0%	1																									
				GTFLDDTGK	1	99.2%	1																									
				GTFLDDTGK	2	99.8%	1																									
				HQDGLVVVTTK	2	100.0%	2																									
				HQDGLVVVTTKK	2	100.0%	1																									
				HQDGLVVVTTKK	3	100.0%	1																									
				IFLGGFELK	2	99.8%	1																									
				IQCCETVNVCR	2	100.0%	2																									
				KPVHGVMTNEIIFNNK	3	100.0%	1																									
				LRGQTCGLCGNFNSIQADDFR	3	100.0%	1																									
				LSPSCPDALAPK	2	100.0%	1																									
				LTPMEFGNLQK	2	100.0%	1																									
				MCLNYEVR	2	100.0%	2																									
				NQDQQGPFK	2	100.0%	3																									
				NQLPPICYNYEIR	2	100.0%	2																									
				NSFEDPCSLSVENEK	2	100.0%	1																									
				NVTLHCTDGSSR	2	96.7%	1																									
				QCSILHGPTFAACHAHVEPAR	3	100.0%	1																									
				QCTHAGGLPQDWR	2	100.0%	1																									
				QDLCFCEDTDLLSCVCHTLAEYSR	3	99.2%	1																									
				SHPEVSIEHLGQVVQCSR	2	100.0%	1																									
				SHPEVSIEHLGQVVQCSR	3	100.0%	1																									
				SIILEYHQDR	2	100.0%	2																									
				SLIIQQQGCSSSEPVR	2	100.0%	2																									
				SLSEGDITCSVGFIPVDGCICPK	2	100.0%	2																									
				SVVGDVLEFGNSWK	2	100.0%	2																									
				SVVGDVLEFGNSWK	3	99.9%	1																									
				TCGLCGDFNGMPVVSELLSHNTK	3	100.0%	1																									
				TFDGDVFR	2	100.0%	2																									

				TGHMCPFTCPADK	2	100.0%	1																									
				TGHMCPFTCPADK	3	100.0%	1																									
				TQAACPNIR	2	99.9%	2																									
				TSIFINLSPEFK	2	100.0%	2																									
				VCGLCGNFDDIAVNDFATR	2	100.0%	2																									
				VCGLCGNFDDIAVNDFATR	3	99.5%	1																									
				VDGVVIQLTK	2	100.0%	2																									
				VEKPTCANGYPAVK	2	100.0%	1																									
				VFEPCHTVIPPLLFYEGCVFDR	3	100.0%	1																									
				VLCCETPK	1	84.8%	1																									
				VLCCETPK	2	89.5%	1																									
				VQCSPDVGLTCR	2	100.0%	2																									
				VVTENVPCGTTGTTCSK	2	100.0%	2																									
				WFDVDFPSPGPHGGDKETYNNIIR	2	100.0%	1																									
				WFDVDFPSPGPHGGDKETYNNIIR	3	100.0%	1																									
				YAQHWCSQLTDADGPFGR	2	99.9%	1																									
				YAQHWCSQLTDADGPFGR	3	100.0%	1																									
IPI00922420	-	cDNA FLJ56058, highly similar to Castor homolog 1 zinc finger protein	93.4%	1.3	1	1	1	3	2,561,350	2,616,983	2,435,120	2,721,827	175,629	210,479	174,848	146,943	15.3	18.0	16.1	12.1	1.0	0.8	-1.1	0.6	1.1	0.5	-1.1	0.5	1.0	0.7	1.1	0.2
IPI00103440	CASZ1	isoform 1 of Zinc finger protein castor homolog 1	93.4%	0.7	1	1	1	3	2,561,350	2,616,983	2,435,120	2,721,827	175,629	210,479	174,848	146,943	15.3	18.0	16.1	12.1	1.0	0.8	-1.1	0.6	1.1	0.5	-1.1	0.5	1.0	0.7	1.1	0.2
IPI00328211	CASZ1	isoform 2 of Zinc finger protein castor homolog 1	93.4%	1.1	1	1	1	3	2,561,350	2,616,983	2,435,120	2,721,827	175,629	210,479	174,848	146,943	15.3	18.0	16.1	12.1	1.0	0.8	-1.1	0.6	1.1	0.5	-1.1	0.5	1.0	0.7	1.1	0.2
				TDSITTGTVSTVK	2	88.9%	1																									
IPI00103467	ALDH1B1	Aldehyde dehydrogenase X, mitochondrial	99.5%	2.7	1	1	1	2	1,157,128	1,271,610	1,463,105	1,251,845	141,040	69,860	54,977	112,437	27.3	12.3	8.4	20.1	1.1	0.5	1.3	0.1	1.1	0.6	1.2	0.06	-1.0	0.9	-1.2	0.1
IPI01015077	ALDH1B1	cDNA FLJ51238, highly similar to Aldehyde dehydrogenase X, mitochondrial	99.5%	6.4	1	1	1	2	1,157,128	1,271,610	1,463,105	1,251,845	141,040	69,860	54,977	112,437	27.3	12.3	8.4	20.1	1.1	0.5	1.3	0.1	1.1	0.6	1.2	0.06	-1.0	0.9	-1.2	0.1
				TFVEESIYNEFLER	2	99.5%	1																									
IPI00103497	SREK1	isoform 1 of Splicing regulatory glutamine/lysine-rich protein 1	97.7%	4.3	1	1	1	1	251,166	242,679	311,200	305,943	22,282	17,714	15,629	13,414	19.8	16.3	11.2	9.8	-1.0	0.8	1.2	0.06	1.2	0.07	1.3	0.02	1.3	0.02	-1.0	0.8
				TVYVGNLNSQTTTADQLLEFFK	2	97.7%	1																									
IPI00103525	PSPC1	isoform 1 of Paraspeckle component 1	100.0%	12.4	4	4	4	3	7,457,867	6,643,490	7,971,610	7,754,663	663,356	608,132	487,341	412,316	19.9	20.5	13.7	11.9	-1.1	0.4	1.1	0.5	1.0	0.7	1.2	0.1	1.2	0.2	-1.0	0.7
IPI00395775	PSPC1	isoform 2 of Paraspeckle component 1	100.0%	16.5	4	4	4	3	7,457,867	6,643,490	7,971,610	7,754,663	663,356	608,132	487,341	412,316	19.9	20.5	13.7	11.9	-1.1	0.4	1.1	0.5	1.0	0.7	1.2	0.1	1.2	0.2	-1.0	0.7
IPI01014916	PSPC1	53 kDa protein	100.0%	14.0	4	4	4	3	7,457,867	6,643,490	7,971,610	7,754,663	663,356	608,132	487,341	412,316	19.9	20.5	13.7	11.9	-1.1	0.4	1.1	0.5	1.0	0.7	1.2	0.1	1.2	0.2	-1.0	0.7
				EKLEAEMEAAR	2	96.1%	1																									
				FAQPGTFEFEYASR	2	100.0%	1																									
				LFVGNLPTDITEEDFKR	3	99.7%	1																									
				NLSPVVSNELLEQAFSQFGPVEK	3	99.9%	1																									
IPI00103552	MUC16	Mucin-16	98.3%	0.3	2	2	2	4	1,253,222	1,296,491	1,423,318	1,487,005	150,948	63,954	77,128	67,003	26.9	11.0	12.1	10.1	1.0	0.8	1.1	0.3	1.2	0.2	1.1	0.2	1.1	0.07	1.0	0.6
IPI00646572	MUC16	1518 kDa protein	98.3%	0.4	2	2	2	4	1,253,222	1,296,491	1,423,318	1,487,005	150,948	63,954	77,128	67,003	26.9	11.0	12.1	10.1	1.0	0.8	1.1	0.3	1.2	0.2	1.1	0.2	1.1	0.07	1.0	0.6
IPI00916596	MUC16	Uncharacterized protein	98.3%	0.4	2	2	2	4	1,253,222	1,296,491	1,423,318	1,487,005	150,948	63,954	77,128	67,003	26.9	11.0	12.1	10.1	1.0	0.8	1.1	0.3	1.2	0.2	1.1	0.2	1.1	0.07	1.0	0.6
IPI01015973	MUC16	mucin-16	98.3%	0.4	2	2	2	4	1,253,222	1,296,491	1,423,318	1,487,005	150,948	63,954	77,128	67,003	26.9	11.0	12.1	10.1	1.0	0.8	1.1	0.3	1.2	0.2	1.1	0.2	1.1	0.07	1.0	0.6
				TEVTSSSRTSISGSAESTMLPEISTTRK	3	84.4%	1																									
				TSSEPETSSPPNLSSTSAEILATSEVTK	3	89.1%	1																									
IPI00103554	GATAD2B	Transcriptional repressor p66-beta	96.2%	5.2	1	1	1	1	1,529,208	1,628,420	1,768,987	1,903,800	252,913	86,921	276,507	125,960	37.0	11.9	35.0	14.8	1.1	0.7	1.2	0.5	1.2	0.2	1.1	0.6	1.2	0.1	1.1	0.7
				ENVVQKTPVVQNAASIVQPSPAHVGQQGLSK	3	94.6%	1																									
IPI00103891	MTMR14	Putative uncharacterized protein	91.5%	4.6	1	1	1	6	693,018	715,320	809,472	1,080,693	181,818	87,869	147,702	35,997	58.7	27.5	40.8	7.5	1.0	0.9	1.2	0.6	1.6	0.1	1.1	0.6	1.5	0.005	1.3	0.1
IPI00152391	MTMR14	isoform 3 of Myotubularin-related protein 14	91.5%	4.5	1	1	1	6	693,018	715,320	809,472	1,080,693	181,818	87,869	147,702	35,997	58.7	27.5	40.8	7.5	1.0	0.9	1.2	0.6	1.6	0.1	1.1	0.6	1.5	0.005	1.3	0.1
IPI00168378	MTMR14	isoform 1 of Myotubularin-related protein 14	91.5%	3.7	1	1	1	6	693,018	715,320	809,472	1,080,693	181,818	87,869	147,702	35,997	58.7	27.5	40.8	7.5	1.0	0.9	1.2	0.6	1.6	0.1	1.1	0.6	1.5	0.005	1.3	0.1
IPI00384329	MTMR14	isoform 2 of Myotubularin-related protein 14	91.5%	4.0	1	1	1	6	693,018	715,320	809,472	1,080,693	181,818	87,869	147,702	35,997	58.7	27.5	40.8	7.5	1.0	0.9	1.2	0.6	1.6	0.1	1.1	0.6	1.5	0.005	1.3	0.1
IPI00926614	MTMR14	Uncharacterized protein	91.5%	8.2	1	1	1	6	693,018	715,320	809,472	1,080,693	181,818	87,869	147,702	35,997	58.7	27.5	40.8	7.5	1.0	0.9	1.2	0.6	1.6	0.1	1.1	0.6	1.5	0.005	1.3	0.1
IPI00927299	MTMR14	Uncharacterized protein	91.5%	15.6	1	1	1	6	693,018	715,320	809,472	1,080,693	181,818	87,869	147,702	35,997	58.7	27.5	40.8	7.5	1.0	0.9	1.2	0.6	1.6	0.1	1.1	0.6	1.5	0.005	1.3	0.1
				LLLSLVNSDDDSGLLVHCISGWDR	3	91.5%	1																									
IPI00103994	LARS	Leucyl-tRNA synthetase, cytoplasmic	100.0%	16.8	14	14	15	3	19,087,147	20,603,021	18,375,753	21,847,838	1,674,918	774,645	1,168,572	590,599	19.6	8.4	14.2	6.0	1.1	0.4	-1.0	0.7	1.1	0.2	-1.1	0.2	1.1	0.2	1.2	0.03
IPI00965964	LARS	cDNA FLJ58466, highly similar to Leucyl-tRNA synthetase, cytoplasmic	100.0%	17.5	14	14	15	3	19,087,147	20,603,021	18,375,753	21,847,838	1,674,918	774,645	1,168,572	590,599	19.6	8.4	14.2	6.0	1.1	0.4	-1.0	0.7	1.1	0.2	-1.1	0.2	1.1	0.2	1.2	0.03
IPI01014989	LARS	cDNA FLJ58157, highly similar to Leucyl-tRNA synthetase, cytoplasmic	100.0%	17.2	14	14	15	3	19,087,147	20,603,021	18,375,753	21,847,838	1,674,918	774,645	1,168,572	590,599	19.6	8.4	14.2	6.0	1.1	0.4	-1.0	0.7	1.1	0.2	-1.1	0.2	1.1	0.2	1.2	0.03
				ELMGEEILGASLSAPLTSYK	2	99.9%	1																									
				EMVANWDSLRSGPASTFNDR	2	99.5%	1																									
				EVWDYVFFK	2	97.5%	1																									
				FDDPLLGPR	2	99.9%	1																									
				GFYEGIMLVDGFK	2	100.0%	1																									
				GTGVVTSVPSDSPDDIAALR	2	99.6%	1																									
				ILDLQLEFDEK	2	99.7%	1																									
				LALADAGDTVEDANFVEAMADAGILR	2	100.0%	1																									
				LHLGHTFSLSK	2	88.9%	1																									
				LYTWVEWVK	2	81.1%	1																									
				SLGLSDEEIVK	2	99.4%	1																									
				TPISEHAVFNVDLMSK	3	87.3%	1																									
				VFASELNAGIIK	2	100.0%	1																									
				VFEVNASNLEK	2	100.0%	2																									
IPI00104050	THRAP3	Thyroid hormone receptor-associated protein 3	100.0%	4.4	3	3	3	1	23,577,460	24,980,890	23,081,280	25,794,650	650,791	1,439,223	758,052	1,247,520	6.2	12.9	7.3	10.8	1.1	0.4	-1.0	0.6	1.1	0.2	-1.1	0.3	1.0	0.7	1.1	0.1
				GSFSDTGLGDGK	2	100.0%	1																									
				MDSFDEDLARPSGLLAQER	3	99.9%	1																									
				WEGLVYAPPGK	2	99.8%	1																									
IPI00104341	EPHX2	cDNA FLJ59619, highly similar to Epoxide hydrolase 2	99.1%	5.2	2	2	2	1	7,950,207	8,026,313	8,688,820	8,823,934	783,689	341,630	632,740	209,032	22.0	9.5	16.3	5.3	1.0	0.9	1.1	0.5	1.1	0.3	1.1	0.4	1.1	0.08	1.0	0.8
				GFTTAILTNTWLDDR	2	89.6%	1																									
				RHAWESHIWNQLNVK	2	91.7%	1																									
IPI00105407	AKR1B10	Aldo-keto reductase family 1 member B10	100.0%	45.6	10	12	13	1	90,710,940	100,419,105	87,664,314	107,631,367	4,730,030	5,410,165	5,991,068	3,648,556	11.7	12.1	15.3	7.6	1.1	0.2	-1.0	0.7	1.2	0.02	-1.1	0.2	1.1	0.3	1.2	0.02
				ACNVLQSSHLEDYPFNAEY	2	100.0%	1																									
				GITVTAYSPLGSPDRPWAKPEDPSLLEDPK	3	100.0%	1																									
				HIDCAYVYQNEHEVGEAIQEK	3	100.0%	1																									
				LSYLDVYLIHWPQGFK	2	99.9%	1																									
				LSYLDVYLIHWPQGFK	3	100.0%	1																									
				NVIVIPK	1	89.7%	1																									
				NVIVIPK	2	97.7%	1																									
				REDLFIVSK	2	100.0%	2																									
				SGDDLFPK	2	99.8%	1																									
				TAAQVLIR	2	96.2%	1																									
				VAIDAGYR	2	99.9%	1																									
				YKPVTNQVECHPYLTQEK	3	99.5%	1																									
IPI00105598	PSMD11	Proteasome 26S non-ATPase subunit 11 variant (Fragment)	100.0%	16.1	5	5	5	1	55,363,750	65,354,820	59,579,610	75,618,460	9,337,489	4,172,530	4,382,219	3,218,531	37.7	14.3	16.5	9.5	1.2	0.4	1.1	0.7	1.4	0.1	-1.1	0.4	1.2	0.09	1.3	0.02
				EQSILELGSLLAK	2	91.9%	1																									
				IMLNTPEDVQALVSGK	2	100.0%	1																									
				TGQAAELGGLLK	2	99.8%	1																									
				TYEAALETIQNMSK	2	100.0%	1																									
				YQEALHLGSQLLR	3	92.4%	1																									
IPI00105916	NOL3	isoform 1 of Nucleolar protein 3	100.0%	8.7	1	2	2	2	598,950	545,888	628,852	690,340	101,394	41,174	68,853	48,727	37.9	16.9	24.5	15.8	-1.1	0.6	1.0	0.8	1.2	0.4	1.2	0.3	1.3	0.05	1.1	0.5
IPI00216346	NOL3	cDNA FLJ58768, highly similar to Homo sapiens nucleolar protein 3 (apoptosis repre	100.0%	7.0	1	2	2	2	598,950	545,888	628,852	690,340	101,394	41,174	68,853	48,727	37.9	16.9	24.5	15.8	-1.1	0.6	1.0	0.8	1.2	0.4	1.2	0.3	1.3	0.05	1.1	0.5
				LVETLQADSGLLLDALLAR	2	100.0%	1																									
				LVETLQADSGLLLDALLAR	3	99.9%	1																									
IPI00106549	DPH2	Diphthamide biosynthesis protein 2	98.5%	3.9	1	1	1	4	708,770	663,170	844,713	705,245	90,655	73,162	57,525	58,866	28.6	24.7	15.2	18.7	-1.1	0.7	1.2	0.2	-1.0	1	1.3	0.09	1.1	0.7	-1.2	0.1
IPI00737502	DPH2	diphthamide biosynthesis protein 2 isoform b	98.5%	7.3	1	1	1	4	708,770	663,170	844,713	705,245	90,655	73,162	57,525	58,866	28.6	24.7	15.2	18.7	-1.1	0.7	1.2	0.2	-1.0	1	1.3	0.09	1.1	0.7	-1.2	0.1
IPI00976559	DPH2	Uncharacterized protein	98.5%	19.0	1	1	1	4	708,770	663,170	844,713	705,245	90,655	73,162	57,525	58,866	28.6	24.7	15.2	18.7	-1.1	0.7	1.2	0.2	-1.0	1	1.3	0.09	1.1	0.7	-1.2	0.1
IPI00984897	DPH2	Uncharacterized protein	98.5%	12.9	1	1	1	4	708,770	663,170	844,713	705,245	90,655	73,162	57,525	58,866	28.6	24.7	15.2	18.7	-1.1	0.7	1.2	0.2	-1.0	1	1.3	0.09	1.1	0.7	-1.2	0.1
				VALQFPDQLLGDAVAVAAR	2	98.5%	1																									
IPI00106642	SDF2L1	Dihydropyrimidinase-like 2	100.0%	23.6	9	9	14	1	9,164,044	9,604,049	10,243,038	11,121,418	640,959	200,019	594,730	295,334	15.6	4.7	13.0	5.9	1.0	0.5	1.1	0.3	1.2	0.02	1.1	0.4	1.2	0.003	1.1	0.2
				AITIANQTNCPLYITK	2	100.0%	1																									
				DIGAIAQVHAENGDIIAEEQQR	3	100.0%	2																									
				FQMPDQGMTSADDFFQGTK	2	100.0%	2																									
				GIQEEMEALVK	2	100.0%	2																									
				ILDLGITGPEGHVLSRPEEVEAEAVNR	3	100.0%	1																									
				IVNDDQSFYADIYMEDGLIK	2	100.0%	1																									
				LTHVLTGK	1	92.6%	1																									
				QIGENLIVPGGVK	2	99.9%	2																									
				SSAEVIAQAR	2	99.4%	2																									
IPI00106646	SDF4	isoform 1 of 45 kDa calcium-binding protein	99.6%	5.8	1	1	1	3	5,507,180	5,091,133	5,043,267	6,268,967	554,391	143,030	408,920	303,368	22.5	6.3	18.1	10.8	-1.1	0.5	-1.1	0.5	1.1	0.3	-1.0	0.9	1.2	0.008	1.2	0.04
IPI00930709	SDF4	isoform 2 of 45 kDa calcium-binding protein	99.6%	8.1	1	1	1	3	5,507,180	5,091,133	5,043,267	6,268,967	554,391	143,030	408,920	303,368	22.5	6.3	18.1	10.8	-1.1	0.5	-1.1	0.5	1.1	0.3	-1.0	0.9	1.2	0.008	1.2	0.04
IPI00973831	SDF4	isoform 6 of 45 kDa calcium-binding protein	99.6%	6.0	1	1	1	3	5,507,180	5,091,133	5,043,267	6,268,967	554,391	143,030	408,920	303,368	22.5	6.3	18.1	10.8	-1.1	0.5	-1.1	0.5	1.1	0.3	-1.0	0.9	1.2	0.008	1.2	0.04
				LNEELKVDEETQEVLENLKDR	3	99.6%	1																									
IPI00106668	PLIN3	perilipin-3 isoform 3	100.0%	52.6	12	13	18	1	17,214,957	18,404,398	17,760,948	20,904,654	1,597,033	873,895	1,249,550	619,289	20.7	10.6	15.7	6.6	1.1	0.5	1.0	0.8	1.2	0.08	-1.0	0.7	1.1	0.05	1.2	0.05
				DIAQQLQATCTSLGSSIQGLPTNVKDQVQQAR	3	100.0%	1																									
				DTVATQLSEAVDATR	2	100.0%	1																									
				EALDHMVEYVAQNTPVTWLVGPFAPGITEK	3	100.0%	1																									
				IATSLDGFDVASVQQQR	2	100.0%	2																									
				IATSLDGFDVASVQQQR	3	95.3%	1																									
				LGQMVLSGVDTVLGK	2	100.0%	2																									
				QEQSYFVR	2	99.9%	2																									
				QLQGPEKEPPKPEQVESR	3	99.9%	1																									
				QVEDLQATFSSIHSFQDLSSSILAQSR	3	94.0%	1																									
				SEEWADNHLPLTDAELAR	3	100.0%	1																									
				SVVTGGVQSVMGSR	2	100.0%	1																									
				TLTAAAVSGAQPILSK	2	100.0%	2																									
				VSGAQEMVSSAK	2	100.0%	2																									
IPI00106698	PELO	Protein pelota homolog	98.8%	4.7	1	1	1	1	1,005,051	826,825	944,676	943,351	109,279	100,673	158,956	176,527	24.3	27.2	37.6	41.8	-1.2	0.3	-1.1	0.8	-1.1	0.8	1.1	0.5	1.1	0.6	-1.0	1
				ANEAMAIDTLLISDELFR	2	98.8%	1																									
IPI00107104	CXorf26	UPF0368 protein Cxorf26	99.6%	6.4	1	1	2	1	2,694,280	2,759,450	2,900,550	3,026,650	231,141	102,769	173,690	163,973	19.2	8.3	13.4	12.1	1.0	0.8	1.1	0.5	1.1	0.3	1.1	0.5	1.1	0.2	1.0	0.6
				FNGIVEDFNYGTLLR	2	99.6%	2																									
IPI00107122	NUPL1	isoform 1 of Nucleoporin p58/p45	99.0%	2.2	1	1	1	7	267,211	313,793	365,571	328,257	24,351	28,375	40,123	38,397	20.4	20.2	24.5	26.2	1.2	0.2	1.4	0.07	1.2	0.2	1.2	0.3	1.0	0.8	-1.1	0.5
IPI00156037	NUPL1	Uncharacterized protein	99.0%	2.5	1	1	1	7	267,211	313,793	365,571	328,257	24,351	28,375	40,123	38,397	20.4	20.2	24.5	26.2	1.2	0.2	1.4	0.07	1.2	0.2	1.2	0.3	1.0	0.8	-1.1	0.5
IPI00550771	NUPL1	nucleoporin p58/p45 isoform b	99.0%	2.2	1	1	1	7	267,211	313,793	365,571	328,257	24,351	28,375	40,123	38,397	20.4	20.2	24.5	26.2	1.2	0.2	1.4	0.07	1.2	0.2	1.2	0.3	1.0	0.8	-1.1	0.5
IPI00552289	NUPL1	Nucleoporin like 1	99.0%	2.6	1	1	1	7	267,211	313,793	365,571	328,257	24,351	28,375	40,123	38,397	20.4	20.2	24.5	26.2	1.2	0.2	1.4	0.07	1.2	0.2	1.2	0.3	1.0	0.8	-1.1	0.5
IPI00910174	NUPL1	cDNA FLJ52820, highly similar to Nucleoporin p58/p45	99.0%	3.0	1	1	1	7	267,211	313,793	365,571	328,257	24,351	28,375	40,123	38,397	20.4	20.2	24.5	26.2	1.2	0.2	1.4	0.07	1.2	0.2	1.2	0.3	1.0	0.8	-1.1	0.5
IPI00938163	NUPL1	isoform 2 of Nucleoporin p58/p45	99.0%	2.7	1	1	1	7	267,211	313,793	365,571	328,257	24,351	28,375	40,123	38,397	20.4	20.2	24.5	26.2	1.2	0.2	1.4	0.07	1.2	0.2	1.2	0.3	1.0	0.8	-1.1	0.5
IPI01010970	NUPL1	cDNA FLJ41961 fis, clone PUAEN2004083, highly similar to Nucleoporin p58/p45	99.0%	2.3	1	1	1	7	267,211	313,793	365,571	328,257	24,351	28,375	40,123	38,397	20.4	20.2	24.5	26.2	1.2	0.2	1.4	0.07	1.2	0.2	1.2	0.3	1.0	0.8	-1.1	0.5
				MFLGDAVDVFETR	2	99.0%	1																									
IPI00107531	RAD50	isoform 3 of DNA repair protein RAD50	98.4%	2.5	2	2	2	4	4,520,747	4,534,816	4,375,404	4,756,450	230,529	143,396	243,837	155,721	11.4	7.1	12.5	7.3	1.0	1	-1.0	0.7	1.1	0.4	-1.0	0.6	1.0	0.3	1.1	0.2
IPI00305282	RAD50	isoform 1 of DNA repair protein RAD50	98.4%	2.2	2	2	2	4	4,520,747	4,534,816	4,375,404	4,756,450	230,529	143,396	243,837	155,721	11.4	7.1	12.5	7.3	1.0	1	-1.0	0.7	1.1	0.4	-1.0	0.6	1.0	0.3	1.1	0.2
IPI00549205	RAD50	isoform 2 of DNA repair protein RAD50	98.4%	2.2	2	2	2	4	4,520,747	4,534,816	4,375,404	4,756,450	230,529	143,396	243,837	155,721	11.4	7.1	12.5	7.3	1.0	1	-1.0	0.7	1.1	0.4	-1.0	0.6	1.0	0.3	1.1	0.2
IPI00658205	RAD50	Uncharacterized protein	98.4%	4.4	2	2	2	4	4,520,747	4,534,816	4,375,404	4,756,450	230,529	143,396	243,837	155,721	11.4	7.1	12.5	7.3	1.0	1	-1.0	0.7	1.1	0.4	-1.0	0.6	1.0	0.3	1.1	0.2
				DSLIQSLATQLELDGFER	2	98.4%	1																									
				KEEQLSSYEDK	2	91.6%	1																									
IPI00107555	PFN2	Profilin	100.0%	35.1	4	4	5	4	2,810,537	2,743,311	2,823,694	3,088,129	169,179	110,913	158,860	62,331	13.5	9.0	12.6	4.5	-1.0	0.7	1.0	1	1.1	0.2	1.0	0.7	1.1	0.03	1.1	0.2

IPI00219468	PFN2	isoform IIa of Profilin-2	100.0%	47.1	4	4	5	4	2,810,537	2,743,311	2,823,694	3,088,129	169,179	110,913	158,860	62,331	13.5	9.0	12.6	4.5	-1.0	0.7	1.0	1	1.1	0.2	1.0	0.7	1.1	0.03	1.1	0.2
IPI00940567	PFN2	isoform IIb of Profilin-2	100.0%	47.1	4	4	5	4	2,810,537	2,743,311	2,823,694	3,088,129	169,179	110,913	158,860	62,331	13.5	9.0	12.6	4.5	-1.0	0.7	1.0	1	1.1	0.2	1.0	0.7	1.1	0.03	1.1	0.2
IPI00947095	PFN2	Profilin	100.0%	60.0	4	4	5	4	2,810,537	2,743,311	2,823,694	3,088,129	169,179	110,913	158,860	62,331	13.5	9.0	12.6	4.5	-1.0	0.7	1.0	1	1.1	0.2	1.0	0.7	1.1	0.03	1.1	0.2
				DSLYVDGDCTMDIR	2	97.4%	1																									
				EGFFTNGLTLGAK	2	95.2%	1																									
				SQGGEPTYNVAVGR	2	100.0%	2																									
				YVWAATAGGVFQSITPIEIDMIVGK	2	100.0%	1																									
IPI00107745	LUC7L3	isoform 1 of Luc7-like protein 3	97.0%	2.6	1	1	1	5	794,328	792,792	793,964	785,402	147,991	81,143	60,695	44,910	41.7	22.9	17.1	12.8	-1.0	1	-1.0	1	-1.0	1	1.0	1	-1.0	0.9	-1.0	0.9
IPI00964696	LUC7L3	Uncharacterized protein	97.0%	6.0	1	1	1	5	794,328	792,792	793,964	785,402	147,991	81,143	60,695	44,910	41.7	22.9	17.1	12.8	-1.0	1	-1.0	1	-1.0	1	1.0	1	-1.0	0.9	-1.0	0.9
IPI00966213	LUC7L3	cDNA FLJ59548, highly similar to Cisplatin resistance-associated overexpressed pr	97.0%	3.1	1	1	1	5	794,328	792,792	793,964	785,402	147,991	81,143	60,695	44,910	41.7	22.9	17.1	12.8	-1.0	1	-1.0	1	-1.0	1	1.0	1	-1.0	0.9	-1.0	0.9
IPI00966815	LUC7L3	CROP protein (Fragment)	97.0%	4.4	1	1	1	5	794,328	792,792	793,964	785,402	147,991	81,143	60,695	44,910	41.7	22.9	17.1	12.8	-1.0	1	-1.0	1	-1.0	1	1.0	1	-1.0	0.9	-1.0	0.9
IPI00967258	LUC7L3	cDNA FLJ77715, highly similar to Homo sapiens cisplatin resistance-associated ove	97.0%	2.3	1	1	1	5	794,328	792,792	793,964	785,402	147,991	81,143	60,695	44,910	41.7	22.9	17.1	12.8	-1.0	1	-1.0	1	-1.0	1	1.0	1	-1.0	0.9	-1.0	0.9
				YLQSLLAEVER	2	96.0%	1																									
IPI00107831	PTPRF	isoform 1 of Receptor-type tyrosine-protein phosphatase F	99.9%	1.8	2	2	2	2	3,064,498	2,570,801	3,474,342	3,165,288	213,313	227,302	217,634	216,542	15.6	19.8	14.0	15.3	-1.2	0.2	1.1	0.2	1.0	0.7	1.4	0.02	1.2	0.09	-1.1	0.3
IPI00465186	PTPRF	isoform 2 of Receptor-type tyrosine-protein phosphatase F	99.9%	1.8	2	2	2	2	3,064,498	2,570,801	3,474,342	3,165,288	213,313	227,302	217,634	216,542	15.6	19.8	14.0	15.3	-1.2	0.2	1.1	0.2	1.0	0.7	1.4	0.02	1.2	0.09	-1.1	0.3
				FEVIEFDDGAGSVLR	2	99.9%	1																									
				VLAFTAVGDGPPSPTIQVK	2	81.9%	1																									
IPI00107855	HEPH	Hephaestin precursor	99.4%	1.0	1	1	1	6	180,866	208,574	200,328	190,041	23,882	10,352	19,997	16,746	29.5	11.1	22.3	19.7	1.2	0.3	1.1	0.5	1.1	0.8	-1.0	0.7	-1.1	0.4	-1.1	0.7
IPI00432025	HEPH	hephaestin isoform b	99.4%	1.4	1	1	1	6	180,866	208,574	200,328	190,041	23,882	10,352	19,997	16,746	29.5	11.1	22.3	19.7	1.2	0.3	1.1	0.5	1.1	0.8	-1.0	0.7	-1.1	0.4	-1.1	0.7
IPI00641637	HEPH	Hephaestin	99.4%	1.5	1	1	1	6	180,866	208,574	200,328	190,041	23,882	10,352	19,997	16,746	29.5	11.1	22.3	19.7	1.2	0.3	1.1	0.5	1.1	0.8	-1.0	0.7	-1.1	0.4	-1.1	0.7
IPI00924987	HEPH	hephaestin isoform c	99.4%	1.0	1	1	1	6	180,866	208,574	200,328	190,041	23,882	10,352	19,997	16,746	29.5	11.1	22.3	19.7	1.2	0.3	1.1	0.5	1.1	0.8	-1.0	0.7	-1.1	0.4	-1.1	0.7
IPI00925210	HEPH	Uncharacterized protein	99.4%	1.2	1	1	1	6	180,866	208,574	200,328	190,041	23,882	10,352	19,997	16,746	29.5	11.1	22.3	19.7	1.2	0.3	1.1	0.5	1.1	0.8	-1.0	0.7	-1.1	0.4	-1.1	0.7
IPI00982379	HEPH	hephaestin isoform a	99.4%	1.0	1	1	1	6	180,866	208,574	200,328	190,041	23,882	10,352	19,997	16,746	29.5	11.1	22.3	19.7	1.2	0.3	1.1	0.5	1.1	0.8	-1.0	0.7	-1.1	0.4	-1.1	0.7
				GEVGDILTVVFK	2	99.4%	1																									
IPI00140201	COG8;PDF	cDNA FLJ55996, highly similar to Conserved oligomeric Golgi complex component	98.4%	2.2	1	1	1	1	1,533,040	1,614,060	1,822,800	1,963,380	173,388	178,354	202,637	195,543	25.3	24.7	24.9	22.3	1.1	0.8	1.2	0.3	1.3	0.1	1.1	0.5	1.2	0.2	1.1	0.6
				VSQFLQVLETDLYR	2	98.4%	1																									
IPI00140420	SND1	Staphylococcal nuclease domain-containing protein 1	100.0%	26.8	18	18	19	2	34,664,094	35,413,091	34,903,648	40,128,754	1,737,691	1,799,064	1,982,797	744,789	11.2	11.4	12.7	4.2	1.0	0.8	1.0	0.9	1.2	0.02	-1.0	0.9	1.1	0.04	1.1	0.06
IPI01009513	SND1	cDNA FLJ39264 fis, clone OCBBF2009603, highly similar to Staphylococcal nucleas	100.0%	27.1	18	18	19	2	34,664,094	35,413,091	34,903,648	40,128,754	1,737,691	1,799,064	1,982,797	744,789	11.2	11.4	12.7	4.2	1.0	0.8	1.0	0.9	1.2	0.02	-1.0	0.9	1.1	0.04	1.1	0.06
				ADDADEFGYSR	2	99.9%	1																									
				DYVAPTANLDQK	2	100.0%	1																									
				EADGSETPEPFAAEAK	2	100.0%	1																									
				ETCLITFLLAGIECPR	2	99.9%	1																									
				EVEVEVESMDK	2	99.8%	1																									
				GDVGLGLVK	2	94.0%	1																									
				LGTLSPAFSTR	2	97.3%	1																									
				LRPLYDIPYMFEAR	2	96.8%	1																									
				MVLSGCAIIVR	2	100.0%	2																									
				NDIASHPPVEGSYAPR	3	99.9%	1																									
				NLPGLVQEGEPFSEEATLFTK	2	100.0%	1																									
				SEAVVEYVFSGSR	2	100.0%	1																									
				SLLSAEEAAK	2	99.7%	1																									
				SSHYDELLAAEAR	2	99.9%	1																									
				VADISGDTQK	2	99.9%	1																									
				VITEYLNAQESAK	2	100.0%	1																									
				VMQVLNADAIVVK	2	99.4%	1																									
				VNVTVDYIRPASPATETVPAFSER	3	99.6%	1																									
IPI00141118	EPC2	Enhancer of polycomb homolog 2	98.1%	1.5	1	1	1	1	6,149,960	5,455,370	4,653,280	5,676,570	819,755	553,126	279,322	376,203	29.8	22.7	13.4	14.8	-1.1	0.5	-1.3	0.1	-1.1	0.6	-1.2	0.2	1.0	0.7	1.2	0.06
				VTPSSAISSIAR	2	98.1%	1																									
IPI00141318	CKAP4	Cytoskeleton-associated protein 4	100.0%	6.3	3	3	3	4	11,190,820	11,645,668	11,041,348	14,560,710	1,797,346	825,725	1,489,986	926,090	35.9	15.9	30.2	14.2	1.0	0.8	-1.0	1	1.3	0.1	-1.1	0.7	1.3	0.05	1.3	0.08
IPI00604713	CKAP4	cDNA FLJ41699 fis, clone HCHON2004776, highly similar to Homo sapiens cytoske	100.0%	7.3	3	3	3	4	11,190,820	11,645,668	11,041,348	14,560,710	1,797,346	825,725	1,489,986	926,090	35.9	15.9	30.2	14.2	1.0	0.8	-1.0	1	1.3	0.1	-1.1	0.7	1.3	0.05	1.3	0.08
IPI00883950	CKAP4	Similar to cytoskeleton-associated protein 4 (Fragment)	100.0%	6.8	3	3	3	4	11,190,820	11,645,668	11,041,348	14,560,710	1,797,346	825,725	1,489,986	926,090	35.9	15.9	30.2	14.2	1.0	0.8	-1.0	1	1.3	0.1	-1.1	0.7	1.3	0.05	1.3	0.08
IPI00939370	CKAP4	CKAP4 protein (Fragment)	100.0%	6.3	3	3	3	4	11,190,820	11,645,668	11,041,348	14,560,710	1,797,346	825,725	1,489,986	926,090	35.9	15.9	30.2	14.2	1.0	0.8	-1.0	1	1.3	0.1	-1.1	0.7	1.3	0.05	1.3	0.08
				RLEEELR	2	86.6%	1																									
				SINDNIAIFTEVQKR	3	95.4%	1																									
				VQSLQATFGTFESILR	2	100.0%	1																									
IPI00143921	KDELC2	isoform 1 of KDEL motif-containing protein 2	99.9%	5.9	2	2	2	1	4,589,321	5,124,725	4,772,120	5,287,310	414,134	410,233	504,732	250,717	20.2	17.9	23.7	10.6	1.1	0.4	1.0	0.8	1.2	0.2	-1.1	0.6	1.0	0.7	1.1	0.4
				SLVWGPGLQAAVVLPVR	2	99.9%	1																									
				YQVNVDGTVAAYR	2	95.2%	1																									
IPI00147874	NANS	Sialic acid synthase	100.0%	29.0	8	9	10	1	67,938,976	74,861,429	66,507,940	80,027,806	6,088,312	3,430,174	5,804,782	5,231,144	20.0	10.3	19.5	14.6	1.1	0.4	-1.0	0.9	1.2	0.2	-1.1	0.3	1.1	0.4	1.2	0.1
				GRPMVISSGMQSMDTMK	2	98.3%	1																									
				GSDHSASLEPGELAELVR	2	100.0%	1																									
				GSDHSASLEPGELAELVR	3	100.0%	1																									
				HLEFSHDQYR	3	99.9%	1																									
				IPEGTILTMDMLTVK	2	99.9%	1																									
				LFPDIPIGYSGHETGIAISVAAVALGAK	3	99.8%	1																									
				PMVISSGMQSMDTMK	2	98.9%	1																									
				VGSGDTNNFPYLEK	2	100.0%	2																									
				VKIPEGTILTMDMLTVK	3	100.0%	1																									
IPI00148020	BRSK1	isoform 1 of BR serine/threonine-protein kinase 1	92.1%	2.1	1	1	1	2	1,842,635	1,420,675	1,687,140	1,597,120	119,960	62,405	62,429	79,035	14.6	9.8	8.3	11.1	-1.3	0.01	-1.1	0.3	-1.2	0.1	1.2	0.02	1.1	0.1	-1.1	0.4
IPI00185438	BRSK1	isoform 2 of BR serine/threonine-protein kinase 1	92.1%	2.2	1	1	1	2	1,842,635	1,420,675	1,687,140	1,597,120	119,960	62,405	62,429	79,035	14.6	9.8	8.3	11.1	-1.3	0.01	-1.1	0.3	-1.2	0.1	1.2	0.02	1.1	0.1	-1.1	0.4
				QIVSALDFCHSYSICHR	3	92.1%	1																									
IPI00148063	HEBP1	Heme-binding protein 1	100.0%	16.9	2	2	3	2	2,038,017	2,061,897	2,093,858	2,268,133	203,289	208,887	156,849	140,991	22.3	22.7	16.8	13.9	1.0	0.9	1.0	0.8	1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.4
IPI01014549	HEBP1	15 kDa protein	100.0%	24.1	2	2	3	2	2,038,017	2,061,897	2,093,858	2,268,133	203,289	208,887	156,849	140,991	22.3	22.7	16.8	13.9	1.0	0.9	1.0	0.8	1.1	0.4	1.0	0.9	1.1	0.4	1.1	0.4
				IPNQFQSDPPAPSDK	2	99.4%	1																									
				NSLFGSVETWPWQVLSK	2	99.9%	2																									
IPI00148096	H2AFY	H2A histone family, member Y isoform 2 variant (Fragment)	100.0%	15.6	2	2	2	2	2,250,860	2,210,006	2,611,736	2,626,726	193,831	147,353	235,098	111,536	19.3	14.9	20.1	9.5	-1.0	0.9	1.2	0.3	1.2	0.1	1.2	0.2	1.2	0.05	1.0	1
IPI00910098	H2AFY	Histone H2A	100.0%	15.0	2	2	2	2	2,250,860	2,210,006	2,611,736	2,626,726	193,831	147,353	235,098	111,536	19.3	14.9	20.1	9.5	-1.0	0.9	1.2	0.3	1.2	0.1	1.2	0.2	1.2	0.05	1.0	1
				EFVEAVLELR	2	99.5%	1																									
				NGPLEVAGAAVSAGHGLPAK	3	98.5%	1																									
IPI00149276	BRE	isoform 1 of BRCA1-A complex subunit BRE	98.5%	3.4	1	1	1	6	475,177	456,537	473,433	528,973	39,324	39,096	54,695	32,690	18.5	19.2	25.8	13.8	-1.0	0.7	-1.0	1	1.1	0.3	1.0	0.8	1.2	0.2	1.1	0.4
IPI00164724	BRE	isoform 2 of BRCA1-A complex subunit BRE	98.5%	3.7	1	1	1	6	475,177	456,537	473,433	528,973	39,324	39,096	54,695	32,690	18.5	19.2	25.8	13.8	-1.0	0.7	-1.0	1	1.1	0.3	1.0	0.8	1.2	0.2	1.1	0.4
IPI00446802	BRE	isoform 4 of BRCA1-A complex subunit BRE	98.5%	3.7	1	1	1	6	475,177	456,537	473,433	528,973	39,324	39,096	54,695	32,690	18.5	19.2	25.8	13.8	-1.0	0.7	-1.0	1	1.1	0.3	1.0	0.8	1.2	0.2	1.1	0.4
IPI00719447	BRE	isoform 3 of BRCA1-A complex subunit BRE	98.5%	3.7	1	1	1	6	475,177	456,537	473,433	528,973	39,324	39,096	54,695	32,690	18.5	19.2	25.8	13.8	-1.0	0.7	-1.0	1	1.1	0.3	1.0	0.8	1.2	0.2	1.1	0.4
IPI00874261	BRE	cDNA FLJ41081 fis, clone ADRGL2009755, highly similar to Homo sapiens brain an	98.5%	3.6	1	1	1	6	475,177	456,537	473,433	528,973	39,324	39,096	54,695	32,690	18.5	19.2	25.8	13.8	-1.0	0.7	-1.0	1	1.1	0.3	1.0	0.8	1.2	0.2	1.1	0.4
IPI00892695	BRE	Uncharacterized protein	98.5%	4.9	1	1	1	6	475,177	456,537	473,433	528,973	39,324	39,096	54,695	32,690	18.5	19.2	25.8	13.8	-1.0	0.7	-1.0	1	1.1	0.3	1.0	0.8	1.2	0.2	1.1	0.4
				LPVDFSNIPTYLLK	2	98.5%	1																									
IPI00150057	SMARCC2	isoform 2 of SWI/SNF complex subunit SMARCC2	99.9%	5.2	4	4	4	3	5,391,945	5,605,808	5,463,238	6,324,558	564,857	229,738	453,878	320,619	23.4	9.2	18.6	11.3	1.0	0.7	1.0	0.9	1.2	0.2	-1.0	0.8	1.1	0.1	1.2	0.2
IPI00216047	SMARCC2	isoform 1 of SWI/SNF complex subunit SMARCC2	99.9%	4.9	4	4	4	3	5,391,945	5,605,808	5,463,238	6,324,558	564,857	229,738	453,878	320,619	23.4	9.2	18.6	11.3	1.0	0.7	1.0	0.9	1.2	0.2	-1.0	0.8	1.1	0.1	1.2	0.2
IPI00793163	SMARCC2	SWI/SNF complex subunit SMARCC2 isoform c	99.9%	5.1	4	4	4	3	5,391,945	5,605,808	5,463,238	6,324,558	564,857	229,738	453,878	320,619	23.4	9.2	18.6	11.3	1.0	0.7	1.0	0.9	1.2	0.2	-1.0	0.8	1.1	0.1	1.2	0.2
				DIGEGNLSTAAAAALAAAAVK	3	93.7%	1																									
				HFEELETIMDR	2	81.3%	1																									
				SLVALLVETQMK	2	99.0%	1																									
				YYEAADTVTQFDNVR	2	99.6%	1																									
IPI00152092	KLC3	21 kDa protein	100.0%	4.6	1	1	1	5	389,421	394,214	433,767	443,894	50,611	14,350	30,614	9,546	29.1	8.1	15.8	4.8	1.0	0.9	1.1	0.5	1.1	0.3	1.1	0.3	1.1	0.02	1.0	0.8
IPI00465074	KLC3	isoform 3 of Kinesin light chain 3	100.0%	1.7	1	1	1	5	389,421	394,214	433,767	443,894	50,611	14,350	30,614	9,546	29.1	8.1	15.8	4.8	1.0	0.9	1.1	0.5	1.1	0.3	1.1	0.3	1.1	0.02	1.0	0.8
IPI00478456	KLC3	isoform 1 of Kinesin light chain 3	100.0%	1.8	1	1	1	5	389,421	394,214	433,767	443,894	50,611	14,350	30,614	9,546	29.1	8.1	15.8	4.8	1.0	0.9	1.1	0.5	1.1	0.3	1.1	0.3	1.1	0.02	1.0	0.8
IPI00736469	KLC3	isoform 2 of Kinesin light chain 3	100.0%	1.8	1	1	1	5	389,421	394,214	433,767	443,894	50,611	14,350	30,614	9,546	29.1	8.1	15.8	4.8	1.0	0.9	1.1	0.5	1.1	0.3	1.1	0.3	1.1	0.02	1.0	0.8
IPI00945465	KLC4	Uncharacterized protein	100.0%	5.6	1	1	1	5	389,421	394,214	433,767	443,894	50,611	14,350	30,614	9,546	29.1	8.1	15.8	4.8	1.0	0.9	1.1	0.5	1.1	0.3	1.1	0.3	1.1	0.02	1.0	0.8
				HLEFLGQLR	2	99.6%	1																									
IPI00152199	C1orf93	prostamide/prostaglandin F synthase isoform b	99.9%	8.3	1	1	1	7	116,430	194,083	153,222	186,750	12,274	49,109	23,602	41,876	23.6	56.6	34.4	50.1	1.7	0.2	1.3	0.2	1.6	0.2	-1.3	0.5	-1.0	0.9	1.2	0.5
IPI00383997	C1orf93	prostamide/prostaglandin F synthase isoform a	99.9%	7.7	1	1	1	7	116,430	194,083	153,222	186,750	12,274	49,109	23,602	41,876	23.6	56.6	34.4	50.1	1.7	0.2	1.3	0.2	1.6	0.2	-1.3	0.5	-1.0	0.9	1.2	0.5
IPI00643409	C1orf93	prostamide/prostaglandin F synthase isoform d	99.9%	8.9	1	1	1	7	116,430	194,083	153,222	186,750	12,274	49,109	23,602	41,876	23.6	56.6	34.4	50.1	1.7	0.2	1.3	0.2	1.6	0.2	-1.3	0.5	-1.0	0.9	1.2	0.5
IPI00908363	C1orf93	isoform 6 of Prostamide/prostaglandin F synthase	99.9%	8.5	1	1	1	7	116,430	194,083	153,222	186,750	12,274	49,109	23,602	41,876	23.6	56.6	34.4	50.1	1.7	0.2	1.3	0.2	1.6	0.2	-1.3	0.5	-1.0	0.9	1.2	0.5
IPI00910916	C1orf93	isoform 5 of Prostamide/prostaglandin F synthase	99.9%	10.0	1	1	1	7	116,430	194,083	153,222	186,750	12,274	49,109	23,602	41,876	23.6	56.6	34.4	50.1	1.7	0.2	1.3	0.2	1.6	0.2	-1.3	0.5	-1.0	0.9	1.2	0.5
IPI00976876	C1orf93	prostamide/prostaglandin F synthase isoform e	99.9%	9.9	1	1	1	7	116,430	194,083	153,222	186,750	12,274	49,109	23,602	41,876	23.6	56.6	34.4	50.1	1.7	0.2	1.3	0.2	1.6	0.2	-1.3	0.5	-1.0	0.9	1.2	0.5
IPI01008862	C1orf93	isoform 7 of Prostamide/prostaglandin F synthase	99.9%	8.2	1	1	1	7	116,430	194,083	153,222	186,750	12,274	49,109	23,602	41,876	23.6	56.6	34.4	50.1	1.7	0.2	1.3	0.2	1.6	0.2	-1.3	0.5	-1.0	0.9	1.2	0.5
				WIAQDLSSLAGLLDQHGVR	3	99.8%	1																									
IPI00152303	PIP4K2C	Phosphatidylinositol-5-phosphate 4-kinase type-2 gamma	99.0%	3.3	1	1	1	3	2,234,377	2,145,437	2,207,743	2,510,877	296,305	68,032	163,045	237,291	29.7	7.1	16.5	21.1	-1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.7	1.2	0.2	1.1	0.3
IPI00902613	PIP4K2C	cDNA PSEC0253 fis, clone NT2RP3003368, highly similar to Homo sapiens phosph	99.0%	5.3	1	1	1	3	2,234,377	2,145,437	2,207,743	2,510,877	296,305	68,032	163,045	237,291	29.7	7.1	16.5	21.1	-1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.7	1.2	0.2	1.1	0.3
IPI00929676	PIP4K2C	phosphatidylinositol-5-phosphate 4-kinase type-2 gamma isoform b	99.0%	3.5	1	1	1	3	2,234,377	2,145,437	2,207,743	2,510,877	296,305	68,032	163,045	237,291	29.7	7.1	16.5	21.1	-1.0	0.8	-1.0	0.9	1.1	0.5	1.0	0.7	1.2	0.2	1.1	0.3
				FGIDDQDYLVSLTR	2	99.0%	1																									
IPI00152316	WDR66	WD repeat-containing protein 66	98.5%	0.9	1	1	1	2	3,554,450	2,518,350	1,367,525	3,033,545	550,251	676,104	32,402	347,113	34.6	60.0	5.3	25.6	-1.4	0.3	-2.6	0.02	-1.2	0.4	-1.8	0.2	1.2	0.5	2.2	0.008
IPI00792290	WDR66	isoform 2 of WD repeat-containing protein 66	98.5%	1.1	1	1	1	2	3,554,450	2,518,350	1,367,525	3,033,545	550,251	676,104	32,402	347,113	34.6	60.0	5.3	25.6	-1.4	0.3	-2.6	0.02	-1.2	0.4	-1.8	0.2	1.2	0.5	2.2	0.008
				SNYPPDCTLK	3	98.5%	1																									
IPI00152409	AGR3	Anterior gradient protein 3 homolog	100.0%	36.1	4	6	9	1	25,567,443	25,741,073	25,158,480	28,030,567	1,676,413	923,777	1,647,321	1,197,901	14.7	8.0	14.6	9.6	1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	0.8	1.1	0.2	1.1	0.2
				DLPLLIENMK	2	100.0%	2																									
				FIMLNLMHETTDKNLSPDGQYVPR	3	99.5%	1																									
				IMFVDPSLTVR	1	94.8%	1																									
				IMFVDPSLTVR	2	100.0%	2																									
				VFAQNEEIQEMAQNK	2	100.0%	2																									
				VFAQNEEIQEMAQNK	3	100.0%	1																									
IPI00152505	SLC2A14	isoform 1 of Solute carrier family 2, facilitated glucose transporter member 14	100.0%	3.9	2	2	2	4	1,996,733	2,107,201	2,232,829	2,478,399	180,660	94,790	146,927	132,519	20.2	10.1	14.7	12.0	1.1	0.6	1.1	0.3	1.2	0.06	1.1	0.5	1.2	0.05	1.1	0.2
IPI00607720	SLC2A14	isoform 2 of Solute carrier family 2, facilitated glucose transporter member 14	100.0%	4.0	2	2	2	4	1,996,733	2,107,201	2,232,829	2,478,399	180,660	94,790	146,927	132,519	20.2	10.1	14.7	12.0	1.1	0.6	1.1	0.3	1.2	0.06	1.1	0.5	1.2	0.05	1.1	0.2
IPI00922751	SLC2A14	cDNA FLJ56136, highly similar to Solute carrier family 2, facilitated glucosetransport	100.0%	3.7	2	2	2	4	1,996,733	2,107,201	2,232,829	2,478,399	180,660	94,790	146,927	132,519	20.2	10.1	14.7	12.0	1.1	0.6	1.1	0.3	1.2	0.06	1.1	0.5	1.2	0.05	1.1	0.2
IPI01012190	SLC2A14	cDNA FLJ61499, highly similar to Solute carrier family 2, facilitated glucosetransport	100.0%	4.9	2	2	2	4	1,996,733	2,107,201	2,232,829	2,478,399	180,660	94,790	146,927	132,519	20.2	10.1	14.7	12.0	1.1	0.6	1.1	0.3	1.2	0.06	1.1	0.5	1.2	0.05	1.1	0.2
				LWGTQDVSQDIQEMK	2	100.0%	1																									
				LWGTQDVSQDIQEMKDESAR	3	100.0%	1																									
IPI00152510	DDX54	isoform 2 of ATP-dependent RNA helicase DDX54	92.1%	2.0	1	1	1	2	3,233,350	3,067,280	3,121,165	3,308,445	272,374	117,960	260,076	108,100	18.8	8.6	18.6	7.3	-1.1	0.6	-1.0	0.8	1.0	0.8	1.0	0.9	1.1	0.2	1.1	0.5
IPI00879999	DDX54	isoform 1 of ATP-dependent RNA helicase DDX54	92.1%	2.0	1	1	1	2	3,233,350	3,067,280	3,121,165	3,308,445	272,374	117,960	260,076	108,100	18.8	8.6	18.6	7.3	-1.1	0.6	-1.0	0.8	1.0	0.8	1.0	0.9	1.1	0.2	1.1	0.5
				GSDSEDGEFEIQAEDDAR	3	89.4%	1																									
IPI00152653	DNAH5	Dynein heavy chain 5, axonemal	98.1%	0.6	2	2	2	1	8,309,961	9,396,924	8,661,171	11,450,000	2,112,576	1,551,117	2,216,225	1,175,126	56.9	36.9	57.2	23.0	1.1	0.7	1.0	0.9	1.4	0.2	-1.1	0.8	1.2	0.3	1.3	0.3
				NESSAK	1	88.3%	1																									
				YGLLIAREEIDKVDTLHYAWEK	3	85.5%	1																									
IPI00152669	GAB1	CDNA FLJ23801 fis, clone HEP22544	92.5%	8.1	1	1	1	1	1,585,314	1,421,440	1,767,667	1,686,890	228,519	86,789	280,456	86,788	32.2	13.7	35.5	11.5	-1.1	0.5	1.1	0.6	1.1	0.7	1.2	0.3	1.2	0.06	-1.0	0.8
				SDPPSLSSGEGGSLR	2	92.5%	1																									
IPI00152692	DTD1	D-tyrosyl-tRNA(Tyr) deacylase 1	99.4%	7.2	1	1	1	1	1,671,200	2,281,830	1,679,560	2,260,300	203,197	76,954	224,970	145,478	27.2	7.5	30.0	14.4	1.4	0.04	1.0	1	1.4	0.05	-1.4	0.05	-1.0	0.9	1.3	0.06
				ASVTVGGEQISAIGR	2	99.4%	1																									
IPI00152695	WDR82	WD repeat-containing protein 82	99.2%	6.4	1	1	1	1	2,791,622	3,982,610	3,356,740	3,887,940	520,568	232,122	500,036	221,825	41.7	13.0	33.3	12.8	1.4	0.07	1.2	0.5	1.4	0.09	-1.2	0.3	-1.0	0.8	1.2	0.4
				VVALSMSPVDDTFISGSLDK	2	99.2%	1																									
IPI00152708	UTP15	U3 small nucleolar RNA-associated protein 15 homolog	96.2%	1.9	1	1	1	3	3,502,243	3,411,223	3,788,470	3,814,953	279,125	147,058	227,577	92,397	17.8	9.6	13.4	5.4	-1.0	0.8	1.1	0.4	1.1	0.3	1.1	0.2	1.1	0.05	1.0	0.9
IPI00967090	UTP15	cDNA FLJ57656, highly similar to U3 small nucleolar RNA-associated protein 15 hor	96.2%	2.0	1	1	1	3	3,502,243	3,411,223	3,788,470	3,814,953	279,125	147,058	227,577	92,397	17.8	9.6	13.4	5.4	-1.0	0.8	1.1	0.4	1.1	0.3	1.1	0.2	1.1	0.05	1.0	0.9
IPI00967515	UTP15	Protein	96.2%	1.8	1	1	1	3	3,502,243	3,411,223	3,788,470	3,814,953	279,125	147,058	227,577	92,397	17.8	9.6	13.4	5.4	-1.0	0.8	1.1	0.4	1.1	0.3	1.1	0.2	1.1	0.05	1.0	0.9
				TPEITVSIIK	2	93.2%	1																									
IPI00152849	CCNB3	isoform 1 of G2/mitotic-specific cyclin-B3	98.7%	0.9	1	1	1	1	4,702,160	5,405,080	5,048,230	4,649,360	868,370	643,793	591,671	800,752	41.3	26.6	26.2	38.5	1.1	0.5	1.1	0.8	-1.0	1	-1.1	0.7	-1.2	0.5	-1.1	0.7
				KLLAMQEEPSIEK	2	97.9%	1																									
IPI00152898	AP1S1	isoform 1 of AP-1 complex subunit sigma-1A	99.8%	26.0	3	3	3	2	5,547,425	5,378,816	5,433,538	6,538,684	389,184	253,457	356,126	291,960	15.7	10.5	14.7	10.0	-1.0	0.7	-1.0	0.8	1.2	0.08	1.0	0.9	1.2	0.02	1.2	0.04
IPI00927531	AP1S1	Protein	99.8%	21.5	3	3	3	2	5,547,425	5,378,816	5,433,538	6,538,684	389,184	253,457	356,126	291,960	15.7	10.5	14.7	10.0	-1.0	0.7	-1.0	0.8	1.2	0.08	1.0	0.9	1.2	0.02	1.2	0.04

				AIEQADLLQEEDESPR	2	90.7%	1																									
				ELMQVVLAR	2	87.7%	1																									
				YFGSVCELDIIFNFEK	2	98.9%	1																									
IPI00152900	LZIC	cDNA FLJ55829, highly similar to Homo sapiens leucine zipper and CTNNBIP1 dom	100.0%	15.6	2	3	4	2	6,411,601	6,857,001	6,606,729	6,940,812	809,223	617,047	721,360	199,573	28.2	20.1	24.4	6.4	1.1	0.7	1.0	0.9	1.1	0.6	-1.0	0.8	1.0	0.9	1.1	0.7
IPI01011745	LZIC	Protein LZIC	100.0%	17.4	2	3	4	2	6,411,601	6,857,001	6,606,729	6,940,812	809,223	617,047	721,360	199,573	28.2	20.1	24.4	6.4	1.1	0.7	1.0	0.9	1.1	0.6	-1.0	0.8	1.0	0.9	1.1	0.7
				ILALASFEVEK	2	99.6%	2																									
				LTADDEAFLSANAGAILSQFEK	2	100.0%	1																									
				LTADDEAFLSANAGAILSQFEK	3	100.0%	1																									
IPI00152977	PLEKHH3	isoform 1 of Pleckstrin homology domain-containing family H member 3	100.0%	2.1	1	1	1	3	1,643,337	1,633,420	1,656,700	1,896,463	148,196	162,422	123,097	185,871	20.2	22.2	16.6	21.9	-1.0	1	1.0	0.9	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.3
IPI00556551	PLEKHH3	isoform 3 of Pleckstrin homology domain-containing family H member 3	100.0%	2.4	1	1	1	3	1,643,337	1,633,420	1,656,700	1,896,463	148,196	162,422	123,097	185,871	20.2	22.2	16.6	21.9	-1.0	1	1.0	0.9	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.3
IPI00874273	PLEKHH3	isoform 2 of Pleckstrin homology domain-containing family H member 3	100.0%	2.3	1	1	1	3	1,643,337	1,633,420	1,656,700	1,896,463	148,196	162,422	123,097	185,871	20.2	22.2	16.6	21.9	-1.0	1	1.0	0.9	1.2	0.3	1.0	0.9	1.2	0.3	1.1	0.3
				EGGGGAGTAAAVLGGWK	3	99.9%	1																									
IPI00154451	MMS19	cDNA FLJ55586, highly similar to MMS19-like protein	99.3%	2.4	2	2	2	4	2,995,582	2,822,390	3,014,966	3,778,708	288,751	103,082	405,953	119,713	21.6	8.2	30.1	7.1	-1.1	0.6	1.0	1	1.3	0.04	1.1	0.7	1.3	0.0003	1.3	0.1
IPI00178649	MMS19	isoform 4 of MMS19 nucleotide excision repair protein homolog	99.3%	2.7	2	2	2	4	2,995,582	2,822,390	3,014,966	3,778,708	288,751	103,082	405,953	119,713	21.6	8.2	30.1	7.1	-1.1	0.6	1.0	1	1.3	0.04	1.1	0.7	1.3	0.0003	1.3	0.1
IPI00954146	MMS19	cDNA FLJ31682 fis, clone NT2RI2005335, highly similar to MMS19-like protein	99.3%	2.5	2	2	2	4	2,995,582	2,822,390	3,014,966	3,778,708	288,751	103,082	405,953	119,713	21.6	8.2	30.1	7.1	-1.1	0.6	1.0	1	1.3	0.04	1.1	0.7	1.3	0.0003	1.3	0.1
IPI01013156	MMS19	111 kDa protein	99.3%	2.5	2	2	2	4	2,995,582	2,822,390	3,014,966	3,778,708	288,751	103,082	405,953	119,713	21.6	8.2	30.1	7.1	-1.1	0.6	1.0	1	1.3	0.04	1.1	0.7	1.3	0.0003	1.3	0.1
				FAEFLLPLLIEK	2	99.3%	1																									
				FLNLSSSPSMAVR	2	96.1%	1																									
IPI00154509	PSMA8	isoform 1 of Proteasome subunit alpha type-7-like	100.0%	4.3	1	1	1	5	889,510	759,513	831,543	821,584	44,624	81,735	55,569	34,166	11.2	24.1	14.9	9.3	-1.2	0.2	-1.1	0.4	-1.1	0.3	1.1	0.5	1.1	0.5	-1.0	0.9
IPI00219950	PSMA8	isoform 2 of Proteasome subunit alpha type-7-like	100.0%	5.2	1	1	1	5	889,510	759,513	831,543	821,584	44,624	81,735	55,569	34,166	11.2	24.1	14.9	9.3	-1.2	0.2	-1.1	0.4	-1.1	0.3	1.1	0.5	1.1	0.5	-1.0	0.9
IPI00748423	PSMA8	isoform 3 of Proteasome subunit alpha type-7-like	100.0%	4.4	1	1	1	5	889,510	759,513	831,543	821,584	44,624	81,735	55,569	34,166	11.2	24.1	14.9	9.3	-1.2	0.2	-1.1	0.4	-1.1	0.3	1.1	0.5	1.1	0.5	-1.0	0.9
IPI01009874	PSMA8	24 kDa protein	100.0%	5.2	1	1	1	5	889,510	759,513	831,543	821,584	44,624	81,735	55,569	34,166	11.2	24.1	14.9	9.3	-1.2	0.2	-1.1	0.4	-1.1	0.3	1.1	0.5	1.1	0.5	-1.0	0.9
IPI01012067	PSMA8	PSMA8 protein	100.0%	5.2	1	1	1	5	889,510	759,513	831,543	821,584	44,624	81,735	55,569	34,166	11.2	24.1	14.9	9.3	-1.2	0.2	-1.1	0.4	-1.1	0.3	1.1	0.5	1.1	0.5	-1.0	0.9
				ALLEVVQSGGK	2	100.0%	1																									
IPI00154975	DNAJC9	DnaJ homolog subfamily C member 9	99.6%	22.3	3	3	3	1	10,001,710	12,197,840	11,570,860	14,020,865	1,938,617	886,544	1,216,715	679,030	43.3	16.3	23.5	10.8	1.2	0.3	1.2	0.5	1.4	0.1	-1.1	0.7	1.1	0.1	1.2	0.1
				AVYDEQGTVDEDSPVLTQDRDWEAYWR	3	99.6%	1																									
				ISLEDIQAFEK	2	99.3%	1																									
				NIIQQAIDAGEVPSYNAFVK	2	99.2%	1																									
IPI00155466	SUCLG2	Putative uncharacterized protein DKFZp586M2023	100.0%	32.0	7	7	8	1	9,130,696	9,943,033	9,692,308	10,580,275	1,054,367	560,004	501,366	548,303	25.8	12.6	11.6	11.6	1.1	0.5	1.1	0.6	1.2	0.3	-1.0	0.7	1.1	0.4	1.1	0.3
				ETYLAILMDR	2	99.9%	1																									
				FFVADTANEALEAAK	2	99.9%	1																									
				ILNNSGLPITSAIDLEDAAK	2	99.9%	1																									
				ILNNSGLPITSAIDLEDAAKK	3	99.9%	1																									
				LEGTNVQEAQK	2	99.2%	1																									
				MAENLGFVGPLK	2	100.0%	1																									
				VMVAEALDISR	2	100.0%	2																									
IPI00156374	IPO4	isoform 1 of Importin-4	99.5%	1.0	1	1	1	4	84,968	72,146	82,144	84,074	16,711	5,446	8,930	5,269	44.0	16.9	24.3	14.0	-1.2	0.5	-1.0	0.9	-1.0	1	1.1	0.4	1.2	0.2	1.0	0.9
IPI00398009	IPO4	isoform 2 of Importin-4	99.5%	1.0	1	1	1	4	84,968	72,146	82,144	84,074	16,711	5,446	8,930	5,269	44.0	16.9	24.3	14.0	-1.2	0.5	-1.0	0.9	-1.0	1	1.1	0.4	1.2	0.2	1.0	0.9
IPI00744488	IPO4	IPO4 protein variant (Fragment)	99.5%	1.5	1	1	1	4	84,968	72,146	82,144	84,074	16,711	5,446	8,930	5,269	44.0	16.9	24.3	14.0	-1.2	0.5	-1.0	0.9	-1.0	1	1.1	0.4	1.2	0.2	1.0	0.9
IPI01009725	IPO4	cDNA FLJ58302, highly similar to Importin-4	99.5%	1.7	1	1	1	4	84,968	72,146	82,144	84,074	16,711	5,446	8,930	5,269	44.0	16.9	24.3	14.0	-1.2	0.5	-1.0	0.9	-1.0	1	1.1	0.4	1.2	0.2	1.0	0.9
				LLGLLFPLLAR	2	99.5%	1																									
IPI00156689	VAT1	Synaptic vesicle membrane protein VAT-1 homolog	100.0%	35.1	9	10	13	1	34,809,600	34,494,231	35,389,642	38,699,827	2,389,197	1,132,514	1,705,745	1,458,983	15.4	7.3	10.8	8.4	-1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.7	1.1	0.05	1.1	0.2
				ACGLNFADLMAR	2	100.0%	1																									
				CLVLTGFGGYDK	2	99.7%	1																									
				GVDIVMDPLGGSDTAK	2	100.0%	2																									
				PAAPPAPGPGQLTLR	2	100.0%	2																									
				QGLYDRLPPLPVTPGMEGAGVVIAVGEGVSDR	3	99.3%	1																									
				RNLMALAR	2	92.0%	1																									
				TWWNQFSVTALQLLQANR	2	100.0%	1																									
				TWWNQFSVTALQLLQANR	3	100.0%	1																									
				VLLVPGPEKEN	2	100.0%	2																									
				VVTYGMANLLTGPK	2	99.9%	1																									
IPI00157176	MEA1	Male-enhanced antigen 1	97.5%	7.0	1	1	1	1	5,536,800	5,299,510	5,117,110	6,204,380	451,492	178,645	604,874	141,475	18.2	7.5	26.4	5.1	-1.0	0.6	-1.1	0.6	1.1	0.2	-1.0	0.8	1.2	0.004	1.2	0.1
				EISDAQWEDVVQK	2	97.5%	1																									
IPI00157535	EPS8L1	isoform 3 of Epidermal growth factor receptor kinase substrate 8-like protein 1	100.0%	14.5	6	6	6	1	4,830,711	4,771,986	4,775,369	5,529,968	503,463	164,078	209,471	353,428	23.3	7.7	9.8	14.3	-1.0	0.9	-1.0	0.9	1.1	0.3	1.0	1	1.2	0.09	1.2	0.1
				DLEPESEPQLESETAGK	2	100.0%	1																									
				EVDILNHVFDDVESFVSR	3	99.9%	1																									
				GPDLAVLQAER	2	99.8%	1																									
				RAAGEGLLTLR	2	95.4%	1																									
				SLLLLVCQEPER	2	98.0%	1																									
				WVLCNYDFQAR	2	99.9%	1																									
IPI00163187	FSCN1	Fascin	100.0%	8.3	2	2	2	2	2,394,800	2,573,532	2,679,633	2,769,234	256,292	120,202	290,006	96,648	23.9	10.4	24.2	7.8	1.1	0.5	1.1	0.5	1.2	0.2	1.0	0.7	1.1	0.2	1.0	0.8
IPI00747810	FSCN1	52 kDa protein	100.0%	8.7	2	2	2	2	2,394,800	2,573,532	2,679,633	2,769,234	256,292	120,202	290,006	96,648	23.9	10.4	24.2	7.8	1.1	0.5	1.1	0.5	1.2	0.2	1.0	0.7	1.1	0.2	1.0	0.8
				VGKDELFALEQSCAQVVLQAANER	3	99.4%	1																									
				YWTLTATGGVQSTASSK	2	99.5%	1																									
IPI00163230	COPS6	COP9 signalosome complex subunit 6	99.9%	7.3	2	2	2	2	10,201,193	10,347,173	10,022,060	10,877,043	316,822	298,406	445,942	275,375	6.9	6.5	10.0	5.7	1.0	0.7	-1.0	0.8	1.1	0.1	-1.0	0.6	1.1	0.2	1.1	0.1
IPI00924791	COPS6	Uncharacterized protein	99.9%	7.4	2	2	2	2	10,201,193	10,347,173	10,022,060	10,877,043	316,822	298,406	445,942	275,375	6.9	6.5	10.0	5.7	1.0	0.7	-1.0	0.8	1.1	0.1	-1.0	0.6	1.1	0.2	1.1	0.1
				QVCEIIESPLFLK	2	99.4%	1																									
				TCNTMNQFVNK	2	96.4%	1																									
IPI00163505	RBM39	isoform 1 of RNA-binding protein 39	100.0%	4.7	2	2	2	4	1,339,548	1,184,313	1,498,423	1,337,097	123,930	55,729	100,168	69,186	20.7	10.5	15.0	11.6	-1.1	0.3	1.1	0.3	-1.0	1	1.3	0.03	1.1	0.1	-1.1	0.2
IPI00215801	RBM39	isoform 2 of RNA-binding protein 39	100.0%	4.8	2	2	2	4	1,339,548	1,184,313	1,498,423	1,337,097	123,930	55,729	100,168	69,186	20.7	10.5	15.0	11.6	-1.1	0.3	1.1	0.3	-1.0	1	1.3	0.03	1.1	0.1	-1.1	0.2
IPI00514831	RBM39	cDNA FLJ59214, highly similar to RNA-binding region-containing protein 2	100.0%	4.9	2	2	2	4	1,339,548	1,184,313	1,498,423	1,337,097	123,930	55,729	100,168	69,186	20.7	10.5	15.0	11.6	-1.1	0.3	1.1	0.3	-1.0	1	1.3	0.03	1.1	0.1	-1.1	0.2
IPI01015916	RBM39	RNA-binding region (RNP1, RRM) containing 2, isoform CRA_b	100.0%	6.7	2	2	2	4	1,339,548	1,184,313	1,498,423	1,337,097	123,930	55,729	100,168	69,186	20.7	10.5	15.0	11.6	-1.1	0.3	1.1	0.3	-1.0	1	1.3	0.03	1.1	0.1	-1.1	0.2
				NSAQGNVYVK	2	99.7%	1																									
				VLGVPIIVQASQAEK	2	98.5%	1																									
IPI00164150	RAB44	Ras-related protein Rab-44	94.7%	6.0	2	2	2	1	3,755,078	3,851,531	4,032,433	4,567,923	312,521	184,104	226,006	464,125	18.6	10.7	12.5	22.7	1.0	0.8	1.1	0.5	1.2	0.2	1.0	0.6	1.2	0.2	1.1	0.3
				MQDVLEAKEREVQR	2	91.4%	1																									
				YWLDCLQDAGSDGVVILLLGNKMDCEEER	3	83.5%	1																									
IPI00164901	PTGR1	Prostaglandin reductase 1	100.0%	11.8	1	1	1	2	390,720	372,908	412,411	455,405	52,865	9,284	53,242	30,241	30.3	5.6	28.9	14.9	-1.0	0.8	1.1	0.8	1.2	0.3	1.1	0.5	1.2	0.05	1.1	0.5
IPI00643630	PTGR1	Prostaglandin reductase 1	100.0%	20.0	1	1	1	2	390,720	372,908	412,411	455,405	52,865	9,284	53,242	30,241	30.3	5.6	28.9	14.9	-1.0	0.8	1.1	0.8	1.2	0.3	1.1	0.5	1.2	0.05	1.1	0.5
				HFVGYPTNSDFELK	2	99.5%	1																									
IPI00164949	TH1L	TH1-like (Drosophila), isoform CRA_b	97.6%	2.2	1	1	1	2	1,454,695	1,536,365	1,454,605	1,720,005	285,479	147,607	235,223	143,118	43.9	21.5	36.2	18.6	1.1	0.8	-1.0	1	1.2	0.4	-1.1	0.8	1.1	0.4	1.2	0.4
IPI00759539	TH1L	isoform NELF-D of Negative elongation factor C/D	97.6%	2.2	1	1	1	2	1,454,695	1,536,365	1,454,605	1,720,005	285,479	147,607	235,223	143,118	43.9	21.5	36.2	18.6	1.1	0.8	-1.0	1	1.2	0.4	-1.1	0.8	1.1	0.4	1.2	0.4
				GALNPADITVLFK	2	97.6%	1																									
IPI00165037	DENND2D	isoform 2 of DENN domain-containing protein 2D	97.2%	3.6	1	1	1	3	926,723	1,016,467	968,433	999,560	73,531	97,252	140,218	78,321	17.7	21.4	32.4	17.5	1.1	0.5	1.0	0.8	1.1	0.5	-1.0	0.8	-1.0	0.9	1.0	0.9
IPI00641666	DENND2D	isoform 1 of DENN domain-containing protein 2D	97.2%	3.6	1	1	1	3	926,723	1,016,467	968,433	999,560	73,531	97,252	140,218	78,321	17.7	21.4	32.4	17.5	1.1	0.5	1.0	0.8	1.1	0.5	-1.0	0.8	-1.0	0.9	1.0	0.9
IPI01009392	DENND2D	cDNA FLJ54763, highly similar to DENN domain-containing protein 2D	97.2%	4.2	1	1	1	3	926,723	1,016,467	968,433	999,560	73,531	97,252	140,218	78,321	17.7	21.4	32.4	17.5	1.1	0.5	1.0	0.8	1.1	0.5	-1.0	0.8	-1.0	0.9	1.0	0.9
				LQDDILDSLGQGINELK	2	97.2%	1																									
IPI00165041	TCOF1	isoform 6 of Treacle protein	100.0%	3.9	4	4	5	7	1,967,869	2,048,390	1,851,574	2,259,687	159,982	150,940	91,141	146,657	18.2	16.5	11.0	14.5	1.0	0.7	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.3	1.2	0.05
IPI00298696	TCOF1	isoform 2 of Treacle protein	100.0%	4.0	4	4	5	7	1,967,869	2,048,390	1,851,574	2,259,687	159,982	150,940	91,141	146,657	18.2	16.5	11.0	14.5	1.0	0.7	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.3	1.2	0.05
IPI00815713	TCOF1	Uncharacterized protein	100.0%	3.7	4	4	5	7	1,967,869	2,048,390	1,851,574	2,259,687	159,982	150,940	91,141	146,657	18.2	16.5	11.0	14.5	1.0	0.7	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.3	1.2	0.05
IPI00815731	TCOF1	isoform 1 of Treacle protein	100.0%	3.8	4	4	5	7	1,967,869	2,048,390	1,851,574	2,259,687	159,982	150,940	91,141	146,657	18.2	16.5	11.0	14.5	1.0	0.7	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.3	1.2	0.05
IPI00815944	TCOF1	isoform 3 of Treacle protein	100.0%	3.8	4	4	5	7	1,967,869	2,048,390	1,851,574	2,259,687	159,982	150,940	91,141	146,657	18.2	16.5	11.0	14.5	1.0	0.7	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.3	1.2	0.05
IPI00914061	TCOF1	isoform 7 of Treacle protein	100.0%	3.9	4	4	5	7	1,967,869	2,048,390	1,851,574	2,259,687	159,982	150,940	91,141	146,657	18.2	16.5	11.0	14.5	1.0	0.7	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.3	1.2	0.05
IPI00969501	TCOF1	isoform 8 of Treacle protein	100.0%	4.0	4	4	5	7	1,967,869	2,048,390	1,851,574	2,259,687	159,982	150,940	91,141	146,657	18.2	16.5	11.0	14.5	1.0	0.7	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.3	1.2	0.05
				AGPVAVQVK	2	99.2%	1																									
				CFLAQPVTLLDIYTHWQQTSELGR	3	100.0%	1																									
				GSLGQGTAPVLPGK	2	100.0%	1																									
				VLTELLEQER	2	99.9%	2																									
IPI00165230	DAZAP1	isoform 1 of DAZ-associated protein 1	100.0%	11.6	3	3	3	2	4,757,335	4,898,495	5,090,375	5,394,960	332,599	174,567	374,255	48,362	15.6	8.0	16.4	2.0	1.0	0.7	1.1	0.5	1.1	0.1	1.0	0.7	1.1	0.04	1.1	0.5
IPI00335930	DAZAP1	isoform 2 of DAZ-associated protein 1	100.0%	12.4	3	3	3	2	4,757,335	4,898,495	5,090,375	5,394,960	332,599	174,567	374,255	48,362	15.6	8.0	16.4	2.0	1.0	0.7	1.1	0.5	1.1	0.1	1.0	0.7	1.1	0.04	1.1	0.5
				FGVVTEVVMIYDAEK	2	100.0%	1																									
				LFVGGLDWSTTQETLR	2	100.0%	1																									
				SYFSQYGEVVDCVIMK	2	100.0%	1																									
IPI00165360	MPST	3-mercaptopyruvate sulfurtransferase	100.0%	13.5	2	2	3	2	2,738,503	3,058,620	2,939,170	3,027,483	507,893	209,638	250,588	232,862	41.5	15.3	19.1	17.2	1.1	0.6	1.1	0.7	1.1	0.6	-1.0	0.7	-1.0	0.9	1.0	0.8
IPI00910977	MPST	3-mercaptopyruvate sulfurtransferase isoform 1	100.0%	12.6	2	2	3	2	2,738,503	3,058,620	2,939,170	3,027,483	507,893	209,638	250,588	232,862	41.5	15.3	19.1	17.2	1.1	0.6	1.1	0.7	1.1	0.6	-1.0	0.7	-1.0	0.9	1.0	0.8
				ALVSAQWVAEALR	2	99.9%	2																									
				DGIEPGHIPGTVNIPFTDFLSQEGLEK	3	99.6%	1																									
IPI00165393	ANP32E	Acidic leucine-rich nuclear phosphoprotein 32 family member E	100.0%	9.3	2	2	3	2	3,184,184	3,680,763	3,209,121	3,569,515	277,421	129,295	314,848	242,830	19.5	7.9	21.9	15.2	1.2	0.1	1.0	1	1.1	0.3	-1.1	0.2	-1.0	0.7	1.1	0.4
IPI00640833	ANP32E	acidic leucine-rich nuclear phosphoprotein 32 family member E isoform 3	100.0%	11.4	2	2	3	2	3,184,184	3,680,763	3,209,121	3,569,515	277,421	129,295	314,848	242,830	19.5	7.9	21.9	15.2	1.2	0.1	1.0	1	1.1	0.3	-1.1	0.2	-1.0	0.7	1.1	0.4
				CPNLTYLNLSGNK	2	99.9%	1																									
				DLSTVEALQNLK	2	99.9%	2																									
IPI00165434	YLPM1	isoform 4 of YLP motif-containing protein 1	100.0%	1.5	2	2	2	3	645,754	645,829	653,594	762,957	22,786	25,343	49,360	21,133	7.9	8.8	16.9	6.2	1.0	1	1.0	0.9	1.2	0.005	1.0	0.9	1.2	0.008	1.2	0.08
IPI00514265	YLPM1	isoform 3 of YLP motif-containing protein 1	100.0%	1.7	2	2	2	3	645,754	645,829	653,594	762,957	22,786	25,343	49,360	21,133	7.9	8.8	16.9	6.2	1.0	1	1.0	0.9	1.2	0.005	1.0	0.9	1.2	0.008	1.2	0.08
IPI00940874	YLPM1	isoform 1 of YLP motif-containing protein 1	100.0%	1.6	2	2	2	3	645,754	645,829	653,594	762,957	22,786	25,343	49,360	21,133	7.9	8.8	16.9	6.2	1.0	1	1.0	0.9	1.2	0.005	1.0	0.9	1.2	0.008	1.2	0.08
				EQHLAQLQQLQQMHQK	2	98.8%	1																									
				SDRPVYEGPSMFGGER	3	96.9%	1																									
IPI00165579	CNDP2	isoform 2 of Cytosolic non-specific dipeptidase	100.0%	23.8	6	6	6	1	8,662,739	8,985,818	8,693,144	10,112,168	633,225	350,212	823,560	325,288	16.4	8.7	21.2	7.2	1.0	0.7	1.0	1	1.2	0.08	-1.0	0.8	1.1	0.05	1.2	0.2
				EGGSIPVTLTFQEATGK	2	100.0%	1																									
				FCLEGMEESGSEGLDELIFAR	2	100.0%	1																									
				LYDDIDFDIEEFAK	2	100.0%	1																									
				MMEVAAADVK	2	100.0%	1																									
				NVMLLPVGSADDGAHSQNEK	3	96.8%	1																									
				TVFGVEPDLTR	2	99.9%	1																									
IPI00165946	MAGI1	isoform 2 of Membrane-associated guanylate kinase, WW and PDZ domain-containi	96.6%	0.8	1	1	1	7	492,214	578,026	473,377	528,521	15,566	49,190	35,262	52,977	7.1	19.0	16.7	22.4	1.2	0.2	-1.0	0.6	1.1	0.5	-1.2	0.1	-1.1	0.5	1.1	0.4
IPI00382692	MAGI1	isoform 4 of Membrane-associated guanylate kinase, WW and PDZ domain-containi	96.6%	1.0	1	1	1	7	492,214	578,026	473,377	528,521	15,566	49,190	35,262	52,977	7.1	19.0	16.7	22.4	1.2	0.2	-1.0	0.6	1.1	0.5	-1.2	0.1	-1.1	0.5	1.1	0.4
IPI00418147	MAGI1	isoform 5 of Membrane-associated guanylate kinase, WW and PDZ domain-containi	96.6%	0.9	1	1	1	7	492,214	578,026	473,377	528,521	15,566	49,190	35,262	52,977	7.1	19.0	16.7	22.4	1.2	0.2	-1.0	0.6	1.1	0.5	-1.2	0.1	-1.1	0.5	1.1	0.4
IPI00470759	MAGI1	isoform 1 of Membrane-associated guanylate kinase, WW and PDZ domain-containi	96.6%	0.7	1	1	1	7	492,214	578,026	473,377	528,521	15,566	49,190	35,262	52,977	7.1	19.0	16.7	22.4	1.2	0.2	-1.0	0.6	1.1	0.5	-1.2	0.1	-1.1	0.5	1.1	0.4
IPI00470761	MAGI1	isoform 3 of Membrane-associated guanylate kinase, WW and PDZ domain-containi	96.6%	0.9	1	1	1	7	492,214	578,026	473,377	528,521	15,566	49,190	35,262	52,977	7.1	19.0	16.7	22.4	1.2	0.2	-1.0	0.6	1.1	0.5	-1.2	0.1	-1.1	0.5	1.1	0.4
IPI00470764	MAGI1	isoform 6 of Membrane-associated guanylate kinase, WW and PDZ domain-containi	96.6%	0.8	1	1	1	7	492,214	578,026	473,377	528,521	15,566	49,190	35,262	52,977	7.1	19.0	16.7	22.4	1.2	0.2	-1.0	0.6	1.1	0.5	-1.2	0.1	-1.1	0.5	1.1	0.4
IPI00470765	MAGI1	isoform 7 of Membrane-associated guanylate kinase, WW and PDZ domain-containi	96.6%	0.8	1	1	1	7	492,214	578,026	473,377	528,521	15,566	49,190	35,262	52,977	7.1	19.0	16.7	22.4	1.2	0.2	-1.0	0.6	1.1	0.5	-1.2	0.1	-1.1	0.5	1.1	0.4
				YDVLGVIDSCK	2	89.3%	1																									
IPI00165995	SFRS18	isoform 1 of Splicing factor, arginine/serine-rich 18	94.6%	1.7	1	1	1	1	9,888,140	10,193,460	9,413,250	10,461,930	881,597	439,854	782,354	285,840	19.9	9.7	18.6	6.1	1.0	0.8	-1.1	0.7	1.1	0.6	-1.1	0.4	1.0	0.6	1.1	0.3
				IDDQRGNLSGNSHK	3	92.5%	1																									
IPI00166047	MGC45800	cDNA FLJ14238 fis, clone NT2RP4000519	95.2%	18.2	1	1	1	1	2,297,920	2,373,990	2,785,870	2,740,420	211,116	281,602	418,953	364,110	20.5	26.5	33.6	29.7	1.0	0.8	1.2	0.3	1.2	0.3	1.2	0.4	1.2	0.4	-1.0	0.9
				IPPTSTCTCTRPLGNPLAFLTTVQNQK	3	95.2%	1																									
IPI00166071	BCL6B	B-cell CLL/lymphoma 6 member B protein	90.0%	1.5	1	1	1	1	10,622,220	10,720,170	10,225,210	11,813,730	851,739	861,852	930,591	924,924	17.9	18.0	20.4	17.5	1.0	0.9	-1.0	0.8	1.1	0.4	-1.0	0.7	1.1	0.4	1.2	0.3
				CETCGSR	2	90.1%	1																									
IPI00166293	HIST3H2BB	Histone H2B type 3-B	100.0%	19.1	2	3	6	1	2,922,497	2,826,713	2,987,105	3,826,435	193,302	145,703	205,609	200,238	14.8	11.5	15.4	11.7	-1.0	0.7	1.0	0.8	1.3	0.01	1.1	0.5	1.4	0.004	1.3	0.02
				AMGIMNSFVNDIFER	2	100.0%	4																									
				AMGIMNSFVNDIFER	3	100.0%	1																									
				LLLPGELAK	1	84.1%	1																									
IPI00166396	AP2A2	Uncharacterized protein	100.0%	2.6	1	1	1	6	1,029,838	996,052	966,398	1,150,787	81,478	31,321	83,720	48,919	17.7	7.0	19.4	9.5	-1.0	0.7	-1.1	0.6	1.1	0.2	-1.0	0.8	1.2	0.03	1.2	0.09
IPI00556111	AP2A2	Adaptor-related protein complex 2, alpha 2 subunit variant (Fragment)	100.0%	8.4	1	1	1	6	1,029,838	996,052	966,398	1,150,787	81,478	31,321	83,720	48,919	17.7	7.0	19.4	9.5	-1.0	0.7	-1.1	0.6	1.1	0.2	-1.0	0.8	1.2	0.03	1.2	0.09
IPI00976074	AP2A2	Uncharacterized protein	100.0%	13.3	1	1	1	6	1,029,838	996,052	966,398	1,150,787	81,478	31,321	83,720	48,919	17.7	7.0	19.4	9.5	-1.0	0.7	-1.1	0.6	1.1	0.2	-1.0	0.8	1.2	0.03	1.2	0.09
IPI00976649	AP2A2	20 kDa protein	100.0%	6.5	1	1	1	6	1,029,838	996,052	966,398	1,150,787	81,478	31,321	83,720	48,919	17.7	7.0	19.4	9.5	-1.0	0.7	-1.1	0.6	1.1	0.2	-1.0	0.8	1.2	0.03	1.2	0.09
IPI00984039	AP2A2	Uncharacterized protein	100.0%	3.2	1	1	1	6	1,029,838	996,052	966,398	1,150,787	81,478	31,321	83,720	48,919	17.7	7.0	19.4	9.5	-1.0	0.7	-1.1	0.6	1.1	0.2	-1.0	0.8	1.2	0.03	1.2	0.09

IPI00984099	AP2A2	21 kDa protein	100.0%	6.5	1	1	1	6	1,029,838	996,052	966,398	1,150,787	81,478	31,321	83,720	48,919	17.7	7.0	19.4	9.5	-1.0	0.7	-1.1	0.6	1.1	0.2	-1.0	0.8	1.2	0.03	1.2	0.09
				EMAEAFAGEIPK	2	96.0%	1																									
IPI00166612	CMYA5	Cardiomyopathy-associated protein 5	96.3%	0.3	1	1	1	1	4,500,620	4,692,870	4,175,090	4,887,320	387,222	264,453	297,211	280,434	19.2	12.6	15.9	12.8	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.2	1.0	0.6	1.2	0.1
				SFMTTKPADVK	2	93.9%	1																									
IPI00166613	GALNTL1	isoform 1 of Putative polypeptide N-acetylgalactosaminyltransferase-like protein 1	91.6%	2.0	1	1	1	2	1,876,930	1,987,820	1,768,445	2,210,935	224,933	118,016	78,737	103,601	26.8	13.3	10.0	10.5	1.1	0.7	-1.1	0.7	1.2	0.2	-1.1	0.2	1.1	0.2	1.3	0.009
IPI00456715	GALNTL1	isoform 2 of Putative polypeptide N-acetylgalactosaminyltransferase-like protein 1	91.6%	2.0	1	1	1	2	1,876,930	1,987,820	1,768,445	2,210,935	224,933	118,016	78,737	103,601	26.8	13.3	10.0	10.5	1.1	0.7	-1.1	0.7	1.2	0.2	-1.1	0.2	1.1	0.2	1.3	0.009
				QHAFNQLESDK	2	91.6%	1																									
IPI00166996	SYVN1	isoform 1 of E3 ubiquitin-protein ligase synoviolin	98.0%	3.7	1	1	1	6	139,689	116,044	102,963	135,428	15,448	10,510	12,395	5,153	24.7	20.3	26.9	8.5	-1.2	0.2	-1.4	0.1	-1.0	0.8	-1.1	0.4	1.2	0.1	1.3	0.04
IPI00172510	SYVN1	isoform 3 of E3 ubiquitin-protein ligase synoviolin	98.0%	3.7	1	1	1	6	139,689	116,044	102,963	135,428	15,448	10,510	12,395	5,153	24.7	20.3	26.9	8.5	-1.2	0.2	-1.4	0.1	-1.0	0.8	-1.1	0.4	1.2	0.1	1.3	0.04
IPI00396584	SYVN1	isoform 2 of E3 ubiquitin-protein ligase synoviolin	98.0%	4.1	1	1	1	6	139,689	116,044	102,963	135,428	15,448	10,510	12,395	5,153	24.7	20.3	26.9	8.5	-1.2	0.2	-1.4	0.1	-1.0	0.8	-1.1	0.4	1.2	0.1	1.3	0.04
IPI00902504	SYVN1	Uncharacterized protein	98.0%	3.7	1	1	1	6	139,689	116,044	102,963	135,428	15,448	10,510	12,395	5,153	24.7	20.3	26.9	8.5	-1.2	0.2	-1.4	0.1	-1.0	0.8	-1.1	0.4	1.2	0.1	1.3	0.04
IPI00977251	SYVN1	Uncharacterized protein	98.0%	15.4	1	1	1	6	139,689	116,044	102,963	135,428	15,448	10,510	12,395	5,153	24.7	20.3	26.9	8.5	-1.2	0.2	-1.4	0.1	-1.0	0.8	-1.1	0.4	1.2	0.1	1.3	0.04
IPI00983104	SYVN1	Uncharacterized protein	98.0%	9.7	1	1	1	6	139,689	116,044	102,963	135,428	15,448	10,510	12,395	5,153	24.7	20.3	26.9	8.5	-1.2	0.2	-1.4	0.1	-1.0	0.8	-1.1	0.4	1.2	0.1	1.3	0.04
				TAVMMAASLALTGAVVAHAYYLK	3	98.0%	1																									
IPI01015830	-	18 kDa protein	94.8%	7.8	1	1	1	2	4,700,055	5,096,360	4,902,160	5,380,825	331,438	300,944	286,521	162,666	15.8	13.2	13.1	6.8	1.1	0.4	1.0	0.7	1.1	0.1	-1.0	0.7	1.1	0.4	1.1	0.2
IPI00167194	FLJ25694	cDNA FLJ25694 fis, clone TST04471	94.8%	7.8	1	1	1	2	4,700,055	5,096,360	4,902,160	5,380,825	331,438	300,944	286,521	162,666	15.8	13.2	13.1	6.8	1.1	0.4	1.0	0.7	1.1	0.1	-1.0	0.7	1.1	0.4	1.1	0.2
				LQMTCLLSVPGLR	3	94.8%	1																									
IPI00167198	PRPF31	isoform 2 of U4/U6 small nuclear ribonucleoprotein Prp31	99.6%	8.2	2	2	3	5	1,484,524	1,533,621	1,434,796	1,735,887	128,078	104,145	85,562	92,030	19.3	15.2	13.3	11.9	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.04
IPI00657750	PRPF31	Uncharacterized protein	99.6%	11.5	2	2	3	5	1,484,524	1,533,621	1,434,796	1,735,887	128,078	104,145	85,562	92,030	19.3	15.2	13.3	11.9	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.04
IPI00657783	PRPF31	Uncharacterized protein	99.6%	10.9	2	2	3	5	1,484,524	1,533,621	1,434,796	1,735,887	128,078	104,145	85,562	92,030	19.3	15.2	13.3	11.9	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.04
IPI00738596	PRPF31	cDNA FLJ59251, highly similar to U4/U6 small nuclear ribonucleoprotein Prp31	99.6%	6.7	2	2	3	5	1,484,524	1,533,621	1,434,796	1,735,887	128,078	104,145	85,562	92,030	19.3	15.2	13.3	11.9	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.04
IPI00939863	PRPF31	Uncharacterized protein	99.6%	10.6	2	2	3	5	1,484,524	1,533,621	1,434,796	1,735,887	128,078	104,145	85,562	92,030	19.3	15.2	13.3	11.9	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.04
				IMGVAGGLTNLSK	2	99.4%	2																									
				RFPELESLVPNALDYIR	2	91.5%	1																									
IPI00167202	-	64 kDa protein	97.6%	1.3	1	1	1	2	2,847,015	2,673,320	3,220,650	3,280,390	425,273	234,576	357,363	551,263	33.4	19.6	24.8	37.6	-1.1	0.7	1.1	0.5	1.2	0.6	1.2	0.2	1.2	0.3	1.0	0.9
IPI01013203	FAM187B	Protein FAM187B	97.6%	1.9	1	1	1	2	2,847,015	2,673,320	3,220,650	3,280,390	425,273	234,576	357,363	551,263	33.4	19.6	24.8	37.6	-1.1	0.7	1.1	0.5	1.2	0.6	1.2	0.2	1.2	0.3	1.0	0.9
				ENDAQWR	2	96.4%	1																									
IPI00167490	TOLLIP	cDNA FLJ39374 fis, clone PEBLM2008576, highly similar to Homo sapiens TOLLIP	99.1%	6.6	1	1	2	2	1,112,658	882,710	940,738	1,038,240	120,456	39,853	45,571	83,529	24.2	10.1	10.8	18.0	-1.3	0.1	-1.2	0.2	-1.1	0.6	1.1	0.4	1.2	0.1	1.1	0.3
IPI00979274	TOLLIP	Uncharacterized protein	99.1%	17.5	1	1	2	2	1,112,658	882,710	940,738	1,038,240	120,456	39,853	45,571	83,529	24.2	10.1	10.8	18.0	-1.3	0.1	-1.2	0.2	-1.1	0.6	1.1	0.4	1.2	0.1	1.1	0.3
				GPVYIGELPQDFLR	2	99.1%	2																									
IPI00167515	PTGR2	isoform 1 of Prostaglandin reductase 2	99.6%	6.8	2	2	2	2	4,052,105	4,299,125	3,948,970	4,542,005	583,737	177,458	235,580	237,955	32.2	9.2	13.3	11.7	1.1	0.7	-1.0	0.9	1.1	0.5	-1.1	0.3	1.1	0.4	1.2	0.1
IPI00869302	PTGR2	isoform 2 of Prostaglandin reductase 2	99.6%	13.3	2	2	2	2	4,052,105	4,299,125	3,948,970	4,542,005	583,737	177,458	235,580	237,955	32.2	9.2	13.3	11.7	1.1	0.7	-1.0	0.9	1.1	0.5	-1.1	0.3	1.1	0.4	1.2	0.1
				GDFVTSFYWPWQTK	2	97.9%	1																									
				VILDGNSLEK	2	88.3%	1																									
IPI00167572	FAM98B	Protein FAM98B	99.6%	3.9	1	1	1	2	863,225	924,665	855,570	946,780	98,812	65,293	104,229	63,420	25.6	15.8	27.2	15.0	1.1	0.6	-1.0	1	1.1	0.5	-1.1	0.6	1.0	0.8	1.1	0.5
IPI00760837	FAM98B	family with sequence similarity 98, member B isoform 1	99.6%	3.0	1	1	1	2	863,225	924,665	855,570	946,780	98,812	65,293	104,229	63,420	25.6	15.8	27.2	15.0	1.1	0.6	-1.0	1	1.1	0.5	-1.1	0.6	1.0	0.8	1.1	0.5
				MDLNSEQAEQLER	2	99.6%	1																									
IPI00167615	ABHD14B	isoform 2 of Abhydrolase domain-containing protein 14B	100.0%	12.8	1	1	1	2	1,326,214	1,423,698	1,413,762	1,539,308	136,086	58,331	129,475	75,077	22.9	9.2	20.5	10.9	1.1	0.5	1.1	0.7	1.2	0.2	-1.0	0.9	1.1	0.3	1.1	0.4
IPI00908954	ABHD14B	cDNA FLJ52511, highly similar to Abhydrolase domain-containing protein 14B	100.0%	16.9	1	1	1	2	1,326,214	1,423,698	1,413,762	1,539,308	136,086	58,331	129,475	75,077	22.9	9.2	20.5	10.9	1.1	0.5	1.1	0.7	1.2	0.2	-1.0	0.9	1.1	0.3	1.1	0.4
				TPALIVYGDQDPMGQTSFEHLK	3	100.0%	1																									
IPI00167911	PNLDC1	isoform 1 of Poly(A)-specific ribonuclease PARN-like domain-containing protein 1	98.7%	5.8	1	1	1	2	830,657	974,410	793,041	911,775	137,317	93,374	122,623	67,685	37.0	21.4	34.6	16.6	1.2	0.4	-1.0	0.8	1.1	0.6	-1.2	0.3	-1.1	0.6	1.1	0.4
IPI00797928	PNLDC1	isoform 2 of Poly(A)-specific ribonuclease PARN-like domain-containing protein 1	98.7%	5.7	1	1	1	2	830,657	974,410	793,041	911,775	137,317	93,374	122,623	67,685	37.0	21.4	34.6	16.6	1.2	0.4	-1.0	0.8	1.1	0.6	-1.2	0.3	-1.1	0.6	1.1	0.4
				IYHIDPVPESSFPQYLDVLAPYVNQVNLIR	3	98.7%	1																									
IPI00167941	MDN1	Midasin	96.9%	0.6	2	2	2	1	6,190,918	7,584,742	7,698,691	8,822,680	746,528	736,480	882,566	747,432	27.0	21.7	25.6	18.9	1.2	0.2	1.2	0.2	1.4	0.04	1.0	0.9	1.2	0.3	1.1	0.4
				DDNLDSGNSNK	3	88.8%	1																									
				GQKACPTREQLLMNALLYLR	3	96.9%	1																									
IPI00168137	ARHGEF10L	isoform 4 of Rho guanine nucleotide exchange factor 10-like protein	97.4%	1.6	1	1	1	8	47,788	44,582	41,768	47,193	10,701	5,171	5,998	1,810	50.1	25.9	32.1	8.6	-1.1	0.8	-1.1	0.6	-1.0	1	-1.1	0.7	1.1	0.7	1.1	0.4
IPI00478817	ARHGEF10L	isoform 2 of Rho guanine nucleotide exchange factor 10-like protein	97.4%	1.3	1	1	1	8	47,788	44,582	41,768	47,193	10,701	5,171	5,998	1,810	50.1	25.9	32.1	8.6	-1.1	0.8	-1.1	0.6	-1.0	1	-1.1	0.7	1.1	0.7	1.1	0.4
IPI00513819	ARHGEF10L	isoform 1 of Rho guanine nucleotide exchange factor 10-like protein	97.4%	1.3	1	1	1	8	47,788	44,582	41,768	47,193	10,701	5,171	5,998	1,810	50.1	25.9	32.1	8.6	-1.1	0.8	-1.1	0.6	-1.0	1	-1.1	0.7	1.1	0.7	1.1	0.4
IPI00642727	ARHGEF10L	Rho guanine nucleotide exchange factor (GEF) 10-like	97.4%	1.5	1	1	1	8	47,788	44,582	41,768	47,193	10,701	5,171	5,998	1,810	50.1	25.9	32.1	8.6	-1.1	0.8	-1.1	0.6	-1.0	1	-1.1	0.7	1.1	0.7	1.1	0.4
IPI00896467	ARHGEF10L	isoform 5 of Rho guanine nucleotide exchange factor 10-like protein	97.4%	1.5	1	1	1	8	47,788	44,582	41,768	47,193	10,701	5,171	5,998	1,810	50.1	25.9	32.1	8.6	-1.1	0.8	-1.1	0.6	-1.0	1	-1.1	0.7	1.1	0.7	1.1	0.4
IPI00896497	ARHGEF10L	isoform 3 of Rho guanine nucleotide exchange factor 10-like protein	97.4%	1.3	1	1	1	8	47,788	44,582	41,768	47,193	10,701	5,171	5,998	1,810	50.1	25.9	32.1	8.6	-1.1	0.8	-1.1	0.6	-1.0	1	-1.1	0.7	1.1	0.7	1.1	0.4
IPI00910632	ARHGEF10L	cDNA FLJ53192, highly similar to Homo sapiens Rho guanine nucleotide exchange	97.4%	1.5	1	1	1	8	47,788	44,582	41,768	47,193	10,701	5,171	5,998	1,810	50.1	25.9	32.1	8.6	-1.1	0.8	-1.1	0.6	-1.0	1	-1.1	0.7	1.1	0.7	1.1	0.4
IPI01009882	ARHGEF10L	cDNA FLJ53189, highly similar to Homo sapiens Rho guanine nucleotide exchange	97.4%	3.3	1	1	1	8	47,788	44,582	41,768	47,193	10,701	5,171	5,998	1,810	50.1	25.9	32.1	8.6	-1.1	0.8	-1.1	0.6	-1.0	1	-1.1	0.7	1.1	0.7	1.1	0.4
				LSLQLALTELETLAEK	2	97.4%	1																									
IPI00168165	CLASP2	CLASP2 protein	93.3%	1.1	1	1	1	2	1,262,515	991,210	923,315	1,225,780	196,024	119,964	184,311	81,145	34.7	27.1	44.6	14.8	-1.3	0.3	-1.4	0.2	-1.0	0.9	-1.1	0.8	1.2	0.1	1.3	0.2
IPI00925217	CLASP2	Uncharacterized protein	93.3%	1.1	1	1	1	2	1,262,515	991,210	923,315	1,225,780	196,024	119,964	184,311	81,145	34.7	27.1	44.6	14.8	-1.3	0.3	-1.4	0.2	-1.0	0.9	-1.1	0.8	1.2	0.1	1.3	0.2
				FDEVQSSGGMILSVCK	2	93.3%	1																									
IPI00168184	PPP2R1A	Uncharacterized protein	100.0%	33.6	14	17	19	1	15,352,589	18,203,835	15,545,613	21,371,020	2,355,996	1,337,125	1,324,386	923,907	34.3	16.4	19.1	9.7	1.2	0.3	1.0	0.9	1.4	0.06	-1.2	0.2	1.2	0.09	1.4	0.007
				DNTIEHLLPLFLAQLK	3	100.0%	1																									
				DNTIEHLLPLFLAQLKDECPEVR	3	100.0%	1																									
				ELVSDANQHVK	2	98.3%	1																									
				ENVIMSQILPCIK	2	100.0%	1																									
				LNIISNLDCVNEVIGIR	2	100.0%	1																									
				LNIISNLDCVNEVIGIR	3	99.8%	1																									
				LTQDQDVDVK	2	100.0%	2																									
				MAGDPVANVR	2	100.0%	1																									
				NLCSDDTPMVR	2	97.5%	1																									
				QLSQSLLPAIVELAEDAK	3	100.0%	1																									
				QLSQSLLPAIVELAEDAKWR	3	100.0%	1																									
				SEIIPMFSNLASDEQDSVR	2	100.0%	2																									
				TDLVPAFQNLMK	2	99.9%	1																									
				VLAMSGDPNYLHR	2	99.9%	1																									
				VLAMSGDPNYLHR	3	99.7%	1																									
				YMVADKFTELQK	2	99.9%	1																									
				YMVADKFTELQK	3	99.8%	1																									
IPI00168235	SNRNP200	isoform 2 of U5 small nuclear ribonucleoprotein 200 kDa helicase	99.0%	1.6	1	1	1	1	1,347,358	1,272,000	1,445,258	1,287,335	195,216	99,243	100,263	92,835	32.4	17.5	15.5	16.1	-1.1	0.7	1.1	0.7	-1.0	0.8	1.1	0.3	1.0	0.9	-1.1	0.3
				YAQAGFEGFK	2	99.0%	1																									
IPI00168282	NLRP5	NACHT, LRR and PYD domains-containing protein 5	93.5%	2.0	1	1	1	1	14,214,200	14,077,900	13,639,610	16,610,200	1,669,891	633,997	1,275,764	885,471	26.3	10.1	20.9	11.9	-1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.8	1.2	0.05	1.2	0.09
				LILEDCGITATGCQSLASALVSNR	3	93.5%	1																									
IPI00168399	RGAG4	Retrotransposon gag domain-containing protein 4	92.0%	2.1	1	1	1	1	6,750,180	6,539,740	6,397,890	7,217,610	571,395	363,014	569,707	464,471	18.9	12.4	19.9	14.4	-1.0	0.8	-1.1	0.7	1.1	0.5	-1.0	0.8	1.1	0.3	1.1	0.3
				GENANLGLQLGR	3	92.0%	1																									
IPI00168459	PHLDB2	isoform 2 of Pleckstrin homology-like domain family B member 2	97.2%	2.9	2	2	2	5	450,825	482,029	502,470	529,480	35,657	21,339	46,905	18,202	17.7	9.9	20.9	7.7	1.1	0.5	1.1	0.4	1.2	0.09	1.0	0.7	1.1	0.1	1.1	0.6
IPI00410259	PHLDB2	isoform 1 of Pleckstrin homology-like domain family B member 2	97.2%	2.8	2	2	2	5	450,825	482,029	502,470	529,480	35,657	21,339	46,905	18,202	17.7	9.9	20.9	7.7	1.1	0.5	1.1	0.4	1.2	0.09	1.0	0.7	1.1	0.1	1.1	0.6
IPI00657763	PHLDB2	isoform 3 of Pleckstrin homology-like domain family B member 2	97.2%	2.8	2	2	2	5	450,825	482,029	502,470	529,480	35,657	21,339	46,905	18,202	17.7	9.9	20.9	7.7	1.1	0.5	1.1	0.4	1.2	0.09	1.0	0.7	1.1	0.1	1.1	0.6
IPI00789057	PHLDB2	Putative uncharacterized protein DKFZp686P22161	97.2%	4.0	2	2	2	5	450,825	482,029	502,470	529,480	35,657	21,339	46,905	18,202	17.7	9.9	20.9	7.7	1.1	0.5	1.1	0.4	1.2	0.09	1.0	0.7	1.1	0.1	1.1	0.6
IPI00847736	PHLDB2	Uncharacterized protein	97.2%	3.1	2	2	2	5	450,825	482,029	502,470	529,480	35,657	21,339	46,905	18,202	17.7	9.9	20.9	7.7	1.1	0.5	1.1	0.4	1.2	0.09	1.0	0.7	1.1	0.1	1.1	0.6
				HKSHDNVYSLGGLEGRK	2	83.5%	1																									
				SETTELMKEKEILDHLNR	2	84.2%	1																									
IPI00168479	APOA1BP	cDNA FLJ56357, highly similar to Homo sapiens apolipoprotein A-I binding protein (	100.0%	23.5	4	4	6	3	9,038,333	9,435,366	7,462,981	9,391,514	687,756	340,897	395,881	530,331	17.0	8.1	11.9	12.6	1.0	0.6	-1.2	0.08	1.0	0.7	-1.3	0.005	-1.0	0.9	1.3	0.02
IPI00848298	APOA1BP	isoform 2 of Apolipoprotein A-I-binding protein	100.0%	38.9	4	4	6	3	9,038,333	9,435,366	7,462,981	9,391,514	687,756	340,897	395,881	530,331	17.0	8.1	11.9	12.6	1.0	0.6	-1.2	0.08	1.0	0.7	-1.3	0.005	-1.0	0.9	1.3	0.02
IPI00941988	APOA1BP	isoform 1 of Apolipoprotein A-I-binding protein	100.0%	25.0	4	4	6	3	9,038,333	9,435,366	7,462,981	9,391,514	687,756	340,897	395,881	530,331	17.0	8.1	11.9	12.6	1.0	0.6	-1.2	0.08	1.0	0.7	-1.3	0.005	-1.0	0.9	1.3	0.02
				GLTVPIASIDIPSGWDVEK	2	100.0%	2																									
				GNAGGIQPDLLISLTAPK	2	100.0%	1																									
				LFGYEPTIYYPK	2	100.0%	2																									
				SPPTVLVICGPGNNGGDGLVCAR	3	94.1%	1																									
IPI00168634	LOC439951	Putative uncharacterized protein LOC439951	92.2%	4.7	1	1	1	1	4,866,810	5,111,360	4,865,950	5,360,760	545,120	267,335	351,307	337,731	25.1	11.7	16.1	14.1	1.1	0.7	-1.0	1	1.1	0.5	-1.1	0.6	1.0	0.6	1.1	0.3
				EAGAGSPGPK	2	92.2%	1																									
IPI00168839	ST13P5	Putative protein FAM10A5	100.0%	6.8	2	2	4	1	1,773,538	1,941,079	1,706,847	1,990,375	207,472	121,644	121,876	72,319	26.2	14.0	16.0	8.1	1.1	0.5	-1.0	0.8	1.1	0.4	-1.1	0.2	1.0	0.7	1.2	0.08
				AIEINPDSAQPYK	2	100.0%	2																									
				LDYDEDASAMLK	2	100.0%	2																									
IPI00168885	DHX57	isoform 1 of Putative ATP-dependent RNA helicase DHX57	98.2%	1.4	1	1	1	2	2,056,110	1,685,140	2,328,630	2,020,575	100,356	44,949	92,653	141,471	10.9	6.0	8.9	15.7	-1.2	0.01	1.1	0.08	-1.0	0.8	1.4	0.0002	1.2	0.08	-1.2	0.1
IPI00749029	DHX57	isoform 2 of Putative ATP-dependent RNA helicase DHX57	98.2%	3.0	1	1	1	2	2,056,110	1,685,140	2,328,630	2,020,575	100,356	44,949	92,653	141,471	10.9	6.0	8.9	15.7	-1.2	0.01	1.1	0.08	-1.0	0.8	1.4	0.0002	1.2	0.08	-1.2	0.1
				SHGSGGGGGGGGGGGGNRK	2	98.2%	1																									
IPI00169280	AKR7L	isoform 1 of Aflatoxin B1 aldehyde reductase member 4	100.0%	12.4	3	3	3	2	1,877,543	1,944,651	1,934,573	2,146,611	76,822	106,156	123,695	65,862	9.2	12.2	14.3	6.9	1.0	0.6	1.0	0.7	1.1	0.03	-1.0	1	1.1	0.1	1.1	0.2
IPI00942126	AKR7L	Uncharacterized protein	100.0%	13.9	3	3	3	2	1,877,543	1,944,651	1,934,573	2,146,611	76,822	106,156	123,695	65,862	9.2	12.2	14.3	6.9	1.0	0.6	1.0	0.7	1.1	0.03	-1.0	1	1.1	0.1	1.1	0.2
				ARPATVLGAMEMGR	2	99.8%	1																									
				FYAYNPLAGGLLTGK	2	100.0%	1																									
				RMDAPTSAAVTR	2	100.0%	1																									
IPI00169307	ARHGAP21	rho GTPase-activating protein 21	97.9%	1.3	2	2	2	4	2,861,588	2,759,585	2,889,635	3,096,583	167,598	154,584	176,675	107,328	13.1	12.5	13.7	7.8	-1.0	0.7	1.0	0.9	1.1	0.3	1.0	0.6	1.1	0.1	1.1	0.3
IPI00867727	ARHGAP21	Uncharacterized protein	97.9%	2.2	2	2	2	4	2,861,588	2,759,585	2,889,635	3,096,583	167,598	154,584	176,675	107,328	13.1	12.5	13.7	7.8	-1.0	0.7	1.0	0.9	1.1	0.3	1.0	0.6	1.1	0.1	1.1	0.3
IPI00941749	ARHGAP21	cDNA FLJ54686, highly similar to Homo sapiens Rho GTPase activating protein 21 (	97.9%	2.1	2	2	2	4	2,861,588	2,759,585	2,889,635	3,096,583	167,598	154,584	176,675	107,328	13.1	12.5	13.7	7.8	-1.0	0.7	1.0	0.9	1.1	0.3	1.0	0.6	1.1	0.1	1.1	0.3
IPI00973257	ARHGAP21	Uncharacterized protein	97.9%	2.2	2	2	2	4	2,861,588	2,759,585	2,889,635	3,096,583	167,598	154,584	176,675	107,328	13.1	12.5	13.7	7.8	-1.0	0.7	1.0	0.9	1.1	0.3	1.0	0.6	1.1	0.1	1.1	0.3
				AASQSTTDYNQVVPNR	3	91.9%	1																									
				GVGSVSQFK	2	90.1%	1																									
IPI00169383	PGK1	Phosphoglycerate kinase 1	100.0%	86.1	33	51	82	1	541,738,511	539,957,237	530,601,333	626,179,086	########	########	########	########	18.6	9.8	16.8	7.1	-1.0	1	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.02	1.2	0.06
				AAVPSIK	1	98.8%	3																									
				ACANPAAGSVILLENLR	2	100.0%	3																									
				ACANPAAGSVILLENLR	3	100.0%	1																									
				AEPAKIEAFR	2	99.9%	1																									
				AGGFLMK	2	99.9%	2																									
				AHSSMVGVNLPQK	2	100.0%	2																									
				AHSSMVGVNLPQK	3	100.0%	1																									
				AKQIVWNGPVGVFEWEAFAR	3	100.0%	1																									
				ALESPERPFLAILGGAK	2	100.0%	2																									
				ALESPERPFLAILGGAK	3	100.0%	2																									
				ALMDEVVK	1	100.0%	1																									
				ALMDEVVK	2	98.9%	2																									
				DCVGPEVEK	1	98.8%	1																									
				DCVGPEVEK	2	99.1%	1																									
				DVLFLK	1	99.5%	2																									
				DVLFLK	2	98.2%	2																									
				ELNYFAK	2	87.7%	1																									
				FCLDNGAK	1	100.0%	1																									
				FCLDNGAK	2	99.4%	1																									
				FHVEEEGK	1	100.0%	1																									
				FHVEEEGK	2	99.2%	1																									
				GCITIIGGGDTATCCAK	2	100.0%	2																									
				ITLPVDFVTADKFDENAK	2	100.0%	2																									
				ITLPVDFVTADKFDENAK	3	99.8%	2																									
				KYAEAVTR	2	99.9%	1																									
				LGDVYVNDAFGTAHR	2	100.0%	2																									
				LGDVYVNDAFGTAHR	3	100.0%	2																									
				LTLDKLDVK	2	99.6%	2																									
				QIVWNGPVGVFEWEAFAR	2	100.0%	3																									
				QIVWNGPVGVFEWEAFAR	3	100.0%	1																									
				SVVLMSHLGRPDGVPMPDK	3	100.0%	2																									

				SVVLMSHLGRPDGVPMPDKYSLEPVAVELK	3	100.0%	1																									
				TGQATVASGIPAGWMGLDCGPESSK	2	100.0%	2																									
				TGQATVASGIPAGWMGLDCGPESSKK	2	100.0%	1																									
				TGQATVASGIPAGWMGLDCGPESSKK	3	100.0%	2																									
				VADKIQLINNMLDK	2	100.0%	2																									
				VADKIQLINNMLDK	3	100.0%	1																									
				VDFNVPMK	1	100.0%	1																									
				VDFNVPMK	2	99.9%	2																									
				VDFNVPMKNNQITNNQR	3	99.8%	2																									
				VLNNMEIGTSLFDEEGAK	2	100.0%	1																									
				VLNNMEIGTSLFDEEGAK	3	100.0%	1																									
				VLPGVDALSNI	1	100.0%	1																									
				VLPGVDALSNI	2	100.0%	1																									
				VNEMIIGGGMAFTFLK	2	100.0%	2																									
				VSHVSTGGGASLELLEGK	2	100.0%	2																									
				VSHVSTGGGASLELLEGK	3	100.0%	1																									
				WNTEDKVSHVSTGGGASLELLEGK	2	100.0%	2																									
				WNTEDKVSHVSTGGGASLELLEGK	3	100.0%	2																									
				YAEAVTR	1	100.0%	2																									
				YSLEPVAVELK	2	100.0%	2																									
IPI00169407	TBC1D9	Uncharacterized protein	98.9%	4.1	2	2	2	2	4,359,720	4,725,555	4,438,105	5,504,015	783,636	185,683	570,596	249,118	40.2	8.8	28.8	10.1	1.1	0.7	1.0	0.9	1.3	0.2	-1.1	0.7	1.2	0.04	1.2	0.1
IPI00848032	TBC1D9	TBC1 domain family member 9	98.9%	3.8	2	2	2	2	4,359,720	4,725,555	4,438,105	5,504,015	783,636	185,683	570,596	249,118	40.2	8.8	28.8	10.1	1.1	0.7	1.0	0.9	1.3	0.2	-1.1	0.7	1.2	0.04	1.2	0.1
				GELWLLLSGAINEK	2	95.6%	1																									
				GHAGDGGGGGGLAGLLVGTLDVVLDSSARVAPYR	3	83.1%	1																									
IPI00170692	VAPA	isoform 1 of Vesicle-associated membrane protein-associated protein A	100.0%	19.3	3	3	3	2	1,932,801	2,320,182	2,272,862	2,465,828	231,310	155,131	194,292	129,364	26.8	15.0	19.1	11.7	1.2	0.2	1.2	0.3	1.3	0.08	-1.0	0.9	1.1	0.5	1.1	0.4
IPI00374657	VAPA	isoform 2 of Vesicle-associated membrane protein-associated protein A	100.0%	16.3	3	3	3	2	1,932,801	2,320,182	2,272,862	2,465,828	231,310	155,131	194,292	129,364	26.8	15.0	19.1	11.7	1.2	0.2	1.2	0.3	1.3	0.08	-1.0	0.9	1.1	0.5	1.1	0.4
				FMVQTIFAPPNTSDMEAVWK	2	99.0%	1																									
				GPFTDVVTTNLK	2	99.9%	1																									
				VAHSDKPGSTSTASFR	3	87.9%	1																									
IPI00170786	WBP11	WW domain-binding protein 11	97.2%	1.7	1	1	1	2	6,880,820	10,128,350	7,209,805	12,272,750	2,392,929	1,539,473	926,786	732,542	77.8	34.0	28.7	13.4	1.5	0.3	1.0	0.9	1.8	0.09	-1.4	0.1	1.2	0.2	1.7	0.003
IPI00910819	WBP11	cDNA FLJ60194, highly similar to WW domain-binding protein 11	97.2%	1.8	1	1	1	2	6,880,820	10,128,350	7,209,805	12,272,750	2,392,929	1,539,473	926,786	732,542	77.8	34.0	28.7	13.4	1.5	0.3	1.0	0.9	1.8	0.09	-1.4	0.1	1.2	0.2	1.7	0.003
				AQLSQYFDAVK	2	96.7%	1																									
IPI00170935	LRRC47	Leucine-rich repeat-containing protein 47	100.0%	5.2	2	2	2	1	7,155,290	6,988,430	7,084,540	7,132,550	822,832	192,049	869,809	585,632	25.7	6.1	27.5	18.4	-1.0	0.9	-1.0	1	-1.0	1	1.0	0.9	1.0	0.8	1.0	1
				DGPSLLVVEQVR	2	99.2%	1																									
				NALGPGLSPELGPLPALR	2	99.5%	1																									
IPI00171057	SSH3	isoform 2 of Protein phosphatase Slingshot homolog 3	100.0%	4.7	2	2	2	1	2,382,230	2,459,192	2,403,723	2,626,962	298,706	206,653	253,973	81,982	28.0	18.8	23.6	7.0	1.0	0.8	1.0	1	1.1	0.5	-1.0	0.9	1.1	0.5	1.1	0.4
				EIDNFYPER	2	99.8%	1																									
				VLDVSDLESVTSK	2	99.9%	1																									
IPI00171152	ABHD11	isoform 4 of Abhydrolase domain-containing protein 11	99.0%	5.2	1	1	1	2	1,045,690	1,114,510	1,237,820	1,085,090	82,911	48,543	89,404	50,795	17.7	9.7	16.2	10.5	1.1	0.5	1.2	0.2	1.0	0.7	1.1	0.3	-1.0	0.7	-1.1	0.2
IPI00171692	ABHD11	isoform 1 of Abhydrolase domain-containing protein 11	99.0%	5.1	1	1	1	2	1,045,690	1,114,510	1,237,820	1,085,090	82,911	48,543	89,404	50,795	17.7	9.7	16.2	10.5	1.1	0.5	1.2	0.2	1.0	0.7	1.1	0.3	-1.0	0.7	-1.1	0.2
				LADEQLSSVIQDMAVR	2	99.0%	1																									
IPI00171199	PSMA3	isoform 2 of Proteasome subunit alpha type-3	100.0%	8.5	2	2	2	2	5,300,015	5,763,315	5,135,095	6,026,710	178,474	159,952	362,197	153,017	7.5	6.2	15.8	5.7	1.1	0.09	-1.0	0.7	1.1	0.01	-1.1	0.2	1.0	0.3	1.2	0.05
IPI00419249	PSMA3	isoform 1 of Proteasome subunit alpha type-3	100.0%	8.2	2	2	2	2	5,300,015	5,763,315	5,135,095	6,026,710	178,474	159,952	362,197	153,017	7.5	6.2	15.8	5.7	1.1	0.09	-1.0	0.7	1.1	0.01	-1.1	0.2	1.0	0.3	1.2	0.05
				AVENSSTAIGIR	2	99.9%	1																									
				VFQVEYAMK	2	99.9%	1																									
IPI00171411	GOLM1	Golgi membrane protein 1	98.5%	5.4	2	2	2	2	4,526,895	4,590,480	4,378,785	5,005,895	659,289	270,031	331,375	380,474	32.6	13.2	16.9	17.0	1.0	0.9	-1.0	0.8	1.1	0.5	-1.0	0.6	1.1	0.4	1.1	0.2
IPI00759659	GOLM1	isoform 2 of Golgi membrane protein 1	98.5%	5.6	2	2	2	2	4,526,895	4,590,480	4,378,785	5,005,895	659,289	270,031	331,375	380,474	32.6	13.2	16.9	17.0	1.0	0.9	-1.0	0.8	1.1	0.5	-1.0	0.6	1.1	0.4	1.1	0.2
				LQQDVLQFQK	2	98.0%	1																									
				QQLQALSEPQPR	2	92.7%	1																									
IPI00171438	TXNDC5	Thioredoxin domain-containing protein 5	100.0%	20.6	8	9	9	3	17,903,323	19,381,340	19,315,043	21,571,437	1,639,024	1,028,690	1,219,307	330,359	20.5	11.9	14.1	3.4	1.1	0.5	1.1	0.5	1.2	0.09	-1.0	1	1.1	0.1	1.1	0.1
IPI00939560	TXNDC5	thioredoxin domain-containing protein 5 isoform 3	100.0%	27.5	8	9	9	3	17,903,323	19,381,340	19,315,043	21,571,437	1,639,024	1,028,690	1,219,307	330,359	20.5	11.9	14.1	3.4	1.1	0.5	1.1	0.5	1.2	0.09	-1.0	1	1.1	0.1	1.1	0.1
IPI01012126	TXNDC5	Thioredoxin domain containing protein	100.0%	22.9	8	9	9	3	17,903,323	19,381,340	19,315,043	21,571,437	1,639,024	1,028,690	1,219,307	330,359	20.5	11.9	14.1	3.4	1.1	0.5	1.1	0.5	1.2	0.09	-1.0	1	1.1	0.1	1.1	0.1
				ALAPTWEQLALGLEHSETVK	2	100.0%	1																									
				ALAPTWEQLALGLEHSETVK	3	99.6%	1																									
				DLESLREYVESQLQR	3	100.0%	1																									
				EYVESQLQR	2	99.8%	1																									
				FVLSQAKDEL	2	98.7%	1																									
				TLAPTWEELSK	2	99.8%	1																									
				TLAPTWEELSKK	2	99.8%	1																									
				VDCTAHSDVCSAQGVR	3	99.8%	1																									
				VDCTQHYELCSGNQVR	3	100.0%	1																									
IPI00171665	NUP37	Nucleoporin Nup37	98.2%	4.9	1	1	1	1	2,827,900	3,221,370	3,031,820	3,024,420	580,494	569,666	373,820	274,327	45.9	39.5	27.6	20.3	1.1	0.6	1.1	0.8	1.1	0.8	-1.1	0.8	-1.1	0.8	-1.0	1
				VGAVAGNDWLIWDITR	2	97.7%	1																									
IPI00171844	COPS4	COP9 signalosome complex subunit 4	100.0%	23.9	7	8	8	1	12,289,676	13,280,360	12,973,672	15,061,617	1,255,038	798,136	872,983	320,386	22.8	13.4	15.1	4.8	1.1	0.5	1.1	0.7	1.2	0.09	-1.0	0.8	1.1	0.07	1.2	0.07
				AIQLSGAEQLEALK	2	99.9%	1																									
				ATTADGSSILDR	2	96.6%	1																									
				AVIEHNLLSASK	2	91.5%	1																									
				IASQMITEGR	2	99.0%	1																									
				LYNNITFEELGALLEIPAAK	2	100.0%	1																									
				LYNNITFEELGALLEIPAAK	3	99.3%	1																									
				MNGFIDQIDGIVHFETR	3	99.9%	1																									
				VISFEEQVASIR	2	98.2%	1																									
IPI00171903	HNRNPM	isoform 1 of Heterogeneous nuclear ribonucleoprotein M	100.0%	37.7	25	29	37	2	119,930,327	124,109,986	116,044,797	133,637,675	8,817,190	3,762,589	6,010,440	3,478,415	16.4	6.8	11.6	5.8	1.0	0.7	-1.0	0.7	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00383296	HNRNPM	isoform 2 of Heterogeneous nuclear ribonucleoprotein M	100.0%	39.8	25	29	37	2	119,930,327	124,109,986	116,044,797	133,637,675	8,817,190	3,762,589	6,010,440	3,478,415	16.4	6.8	11.6	5.8	1.0	0.7	-1.0	0.7	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
				AFITNIPFDVK	2	100.0%	2																									
				DKFNECGHVLYADIK	3	99.8%	1																									
				EVFSMAGVVVR	2	99.9%	1																									
				FESPEVAER	2	93.9%	2																									
				FGSGMNMGR	2	99.6%	1																									
				FNECGHVLYADIK	3	80.2%	1																									
				GCAVVEFK	2	97.5%	1																									
				GIGMGNIGPAGMGMEGIGFGINK	2	100.0%	2																									
				GIGMGNIGPAGMGMEGIGFGINK	3	100.0%	1																									
				GNFGGSFAGSFGGAGGHAPGVAR	3	99.2%	1																									
				INEILSNALK	1	81.5%	1																									
				INEILSNALK	2	100.0%	2																									
				INEILSNALKR	2	99.0%	1																									
				LGGAGMER	2	99.7%	1																									
				MGAGLGHGMDR	2	100.0%	1																									
				MGAGLGHGMDR	3	97.2%	1																									
				MGAGMGFGLER	2	100.0%	1																									
				MGLAMGGGGGASFDR	2	100.0%	1																									
				MGLSMER	2	96.2%	1																									
				MGLVMDR	2	99.1%	1																									
				MGPAIER	2	98.9%	1																									
				MGPAMGPALGAGIER	2	100.0%	2																									
				MGPGIDR	2	92.9%	1																									
				MGPLGLDHMASSIER	2	100.0%	1																									
				MGPLGLDHMASSIER	3	100.0%	1																									
				MVPAGMGAGLER	2	100.0%	2																									
				NLPFDFTWK	2	94.7%	1																									
				QGGGGGGGSVPGIER	2	100.0%	2																									
				VGEVTYVELLMDAEGK	2	100.0%	2																									
IPI00172421	SKP1	isoform 2 of S-phase kinase-associated protein 1	100.0%	26.9	3	3	3	4	7,759,493	7,715,472	7,451,261	8,597,401	623,280	334,078	564,588	362,240	18.0	9.7	16.9	9.4	-1.0	1	-1.0	0.7	1.1	0.3	-1.0	0.7	1.1	0.1	1.2	0.1
IPI00978800	SKP1	Uncharacterized protein	100.0%	42.2	3	3	3	4	7,759,493	7,715,472	7,451,261	8,597,401	623,280	334,078	564,588	362,240	18.0	9.7	16.9	9.4	-1.0	1	-1.0	0.7	1.1	0.3	-1.0	0.7	1.1	0.1	1.2	0.1
IPI00979610	SKP1	Uncharacterized protein	100.0%	30.3	3	3	3	4	7,759,493	7,715,472	7,451,261	8,597,401	623,280	334,078	564,588	362,240	18.0	9.7	16.9	9.4	-1.0	1	-1.0	0.7	1.1	0.3	-1.0	0.7	1.1	0.1	1.2	0.1
IPI00985006	SKP1	Uncharacterized protein	100.0%	27.2	3	3	3	4	7,759,493	7,715,472	7,451,261	8,597,401	623,280	334,078	564,588	362,240	18.0	9.7	16.9	9.4	-1.0	1	-1.0	0.7	1.1	0.3	-1.0	0.7	1.1	0.1	1.2	0.1
				RTDDIPVWDQEFLK	2	100.0%	1																									
				TDDIPVWDQEFLK	2	99.6%	1																									
				TMLEDLGMDDEGDDDPVPLPNVNAAILKK	3	100.0%	1																									
IPI00172460	AK2	isoform 3 of Adenylate kinase 2, mitochondrial	100.0%	23.3	4	4	6	2	3,410,102	3,701,508	3,339,967	4,060,660	257,328	186,830	294,383	211,758	16.9	11.3	19.7	11.7	1.1	0.4	-1.0	0.9	1.2	0.09	-1.1	0.3	1.1	0.2	1.2	0.08
IPI00218989	AK2	Uncharacterized protein	100.0%	23.3	4	4	6	2	3,410,102	3,701,508	3,339,967	4,060,660	257,328	186,830	294,383	211,758	16.9	11.3	19.7	11.7	1.1	0.4	-1.0	0.9	1.2	0.09	-1.1	0.3	1.1	0.2	1.2	0.08
				AMVASGSELGKK	2	99.9%	1																									
				AVLLGPPGAGK	2	99.8%	1																									
				LVSDEMVVELIEK	2	100.0%	2																									
				QAEMLDDLMEK	2	100.0%	2																									
IPI00172513	APPL2	cDNA FLJ59337, highly similar to DCC-interacting protein 13 beta	96.6%	2.1	1	1	1	2	1,173,895	1,117,530	1,135,920	1,180,840	144,417	79,398	188,674	43,598	27.5	15.9	37.1	8.3	-1.1	0.7	-1.0	0.9	1.0	1	1.0	0.9	1.1	0.5	1.0	0.8
IPI01011032	APPL2	cDNA FLJ59617, highly similar to DCC-interacting protein 13 beta	96.6%	2.3	1	1	1	2	1,173,895	1,117,530	1,135,920	1,180,840	144,417	79,398	188,674	43,598	27.5	15.9	37.1	8.3	-1.1	0.7	-1.0	0.9	1.0	1	1.0	0.9	1.1	0.5	1.0	0.8
				QLADTMVLPIIQFR	2	96.6%	1																									
IPI00172580	NUP54	Uncharacterized protein	100.0%	4.9	2	2	3	2	6,685,450	8,466,578	7,026,293	7,237,768	417,847	509,870	513,885	294,877	14.0	13.5	16.4	9.1	1.3	0.03	1.1	0.6	1.1	0.3	-1.2	0.08	-1.2	0.07	1.0	0.7
IPI00967877	NUP54	cDNA FLJ52746, highly similar to Nucleoporin p54	100.0%	5.5	2	2	3	2	6,685,450	8,466,578	7,026,293	7,237,768	417,847	509,870	513,885	294,877	14.0	13.5	16.4	9.1	1.3	0.03	1.1	0.6	1.1	0.3	-1.2	0.08	-1.2	0.07	1.0	0.7
				LDIISEDISELQK	2	99.9%	2																									
				WNQLQAFWGTGK	2	99.0%	1																									
IPI00172636	CAMK2D	isoform Delta 6 of Calcium/calmodulin-dependent protein kinase type II subunit delta	100.0%	17.8	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00430291	CAMK2D	isoform Delta 2 of Calcium/calmodulin-dependent protein kinase type II subunit delta	100.0%	17.0	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00654569	CAMK2D	isoform Delta 4 of Calcium/calmodulin-dependent protein kinase type II subunit delta	100.0%	16.4	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00827573	CAMK2D	isoform Delta 10 of Calcium/calmodulin-dependent protein kinase type II subunit delt	100.0%	17.3	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00827606	CAMK2D	isoform Delta 7 of Calcium/calmodulin-dependent protein kinase type II subunit delta	100.0%	17.4	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00827625	CAMK2D	isoform Delta 11 of Calcium/calmodulin-dependent protein kinase type II subunit delt	100.0%	16.2	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00827717	CAMK2D	isoform Delta 3 of Calcium/calmodulin-dependent protein kinase type II subunit delta	100.0%	16.7	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00828139	CAMK2D	isoform Delta 8 of Calcium/calmodulin-dependent protein kinase type II subunit delta	100.0%	17.1	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00828178	CAMK2D	isoform Delta 9 of Calcium/calmodulin-dependent protein kinase type II subunit delta	100.0%	16.6	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00876923	CAMK2D	calcium/calmodulin-dependent protein kinase type II subunit delta isoform 2	100.0%	17.8	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00965234	CAMK2D	cDNA FLJ53470, highly similar to Calcium/calmodulin-dependent protein kinase type	100.0%	16.0	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
IPI00967869	CAMK2D	Uncharacterized protein	100.0%	16.6	5	5	5	12	1,878,345	1,951,522	1,773,438	2,027,676	141,987	63,310	70,080	60,040	16.9	7.3	8.8	6.6	1.0	0.7	-1.1	0.5	1.1	0.4	-1.1	0.1	1.0	0.4	1.1	0.02
				AGAYDFPSPEWDTVTPEAK	2	100.0%	1																									
				FTDEYQLFEELGK	2	99.5%	1																									
				ICDPGLTAFEPEALGNLVEGMDFHR	3	100.0%	1																									
				STVASMMHR	2	87.2%	1																									
				VTEQLIEAINNGDFEAYTK	3	99.9%	1																									
IPI00174442	FAM98A	isoform 1 of Protein FAM98A	97.9%	2.9	1	1	1	4	1,666,675	1,754,383	1,490,183	1,802,118	213,550	92,026	127,650	77,281	28.7	11.7	19.2	9.6	1.1	0.7	-1.1	0.5	1.1	0.6	-1.2	0.1	1.0	0.7	1.2	0.07
IPI00872161	FAM98A	isoform 2 of Protein FAM98A	97.9%	2.9	1	1	1	4	1,666,675	1,754,383	1,490,183	1,802,118	213,550	92,026	127,650	77,281	28.7	11.7	19.2	9.6	1.1	0.7	-1.1	0.5	1.1	0.6	-1.2	0.1	1.0	0.7	1.2	0.07
IPI00921584	FAM98A	Uncharacterized protein	97.9%	4.8	1	1	1	4	1,666,675	1,754,383	1,490,183	1,802,118	213,550	92,026	127,650	77,281	28.7	11.7	19.2	9.6	1.1	0.7	-1.1	0.5	1.1	0.6	-1.2	0.1	1.0	0.7	1.2	0.07
IPI01009687	FAM98A	cDNA FLJ52744, highly similar to Protein FAM98A	97.9%	4.6	1	1	1	4	1,666,675	1,754,383	1,490,183	1,802,118	213,550	92,026	127,650	77,281	28.7	11.7	19.2	9.6	1.1	0.7	-1.1	0.5	1.1	0.6	-1.2	0.1	1.0	0.7	1.2	0.07
				IEAINQAIANEYEVR	2	97.9%	1																									
IPI00174771	RAB11FIP4	isoform 1 of Rab11 family-interacting protein 4	98.9%	2.5	1	1	1	2	2,170,275	2,180,615	1,965,050	2,016,895	164,074	52,963	112,798	99,870	16.9	5.4	12.8	11.1	1.0	1	-1.1	0.3	-1.1	0.4	-1.1	0.1	-1.1	0.2	1.0	0.7
IPI00556584	RAB11FIP4	isoform 2 of Rab11 family-interacting protein 4	98.9%	3.0	1	1	1	2	2,170,275	2,180,615	1,965,050	2,016,895	164,074	52,963	112,798	99,870	16.9	5.4	12.8	11.1	1.0	1	-1.1	0.3	-1.1	0.4	-1.1	0.1	-1.1	0.2	1.0	0.7

				KVTELENDSLTNGDLK	2	98.9%	1																									
IPI00174775	KRT73	isoform 1 of Keratin, type II cytoskeletal 73	94.2%	2.2	1	1	1	3	245,072	292,524	253,951	317,003	34,585	26,671	31,170	30,966	31.6	20.4	27.5	21.8	1.2	0.3	1.0	0.9	1.3	0.2	-1.2	0.4	1.1	0.6	1.2	0.2
IPI00878987	KRT73	isoform 2 of Keratin, type II cytoskeletal 73	94.2%	3.2	1	1	1	3	245,072	292,524	253,951	317,003	34,585	26,671	31,170	30,966	31.6	20.4	27.5	21.8	1.2	0.3	1.0	0.9	1.3	0.2	-1.2	0.4	1.1	0.6	1.2	0.2
IPI00329306	KRT74	Keratin, type II cytoskeletal 74	94.2%	2.3	1	1	1	3	245,072	292,524	253,951	317,003	34,585	26,671	31,170	30,966	31.6	20.4	27.5	21.8	1.2	0.3	1.0	0.9	1.3	0.2	-1.2	0.4	1.1	0.6	1.2	0.2
				FLEQQNQVLETK	2	94.2%	1																									
IPI00175079	-	Uncharacterized protein	97.7%	1.8	1	1	1	1	6,792,530	6,510,730	6,945,210	7,778,730	381,306	197,310	297,022	214,886	12.6	6.8	9.6	6.2	-1.0	0.5	1.0	0.8	1.1	0.05	1.1	0.3	1.2	0.002	1.1	0.05
				LGAPSSAR	2	96.9%	1																									
IPI00175169	ARFGAP1	isoform 1 of ADP-ribosylation factor GTPase-activating protein 1	99.6%	3.7	1	1	1	6	838,537	842,068	820,058	1,078,972	40,469	28,150	132,418	85,183	10.8	7.5	36.1	17.7	1.0	0.9	-1.0	0.9	1.3	0.03	-1.0	0.9	1.3	0.05	1.3	0.1
IPI00217354	ARFGAP1	isoform 2 of ADP-ribosylation factor GTPase-activating protein 1	99.6%	3.6	1	1	1	6	838,537	842,068	820,058	1,078,972	40,469	28,150	132,418	85,183	10.8	7.5	36.1	17.7	1.0	0.9	-1.0	0.9	1.3	0.03	-1.0	0.9	1.3	0.05	1.3	0.1
IPI00449160	ARFGAP1	isoform 3 of ADP-ribosylation factor GTPase-activating protein 1	99.6%	3.7	1	1	1	6	838,537	842,068	820,058	1,078,972	40,469	28,150	132,418	85,183	10.8	7.5	36.1	17.7	1.0	0.9	-1.0	0.9	1.3	0.03	-1.0	0.9	1.3	0.05	1.3	0.1
IPI00922590	ARFGAP1	cDNA FLJ55014, highly similar to ADP-ribosylation factor GTPase-activating protein	99.6%	5.1	1	1	1	6	838,537	842,068	820,058	1,078,972	40,469	28,150	132,418	85,183	10.8	7.5	36.1	17.7	1.0	0.9	-1.0	0.9	1.3	0.03	-1.0	0.9	1.3	0.05	1.3	0.1
IPI00973726	ARFGAP1	Uncharacterized protein	99.6%	9.8	1	1	1	6	838,537	842,068	820,058	1,078,972	40,469	28,150	132,418	85,183	10.8	7.5	36.1	17.7	1.0	0.9	-1.0	0.9	1.3	0.03	-1.0	0.9	1.3	0.05	1.3	0.1
IPI01014630	ARFGAP1	Uncharacterized protein	99.6%	4.2	1	1	1	6	838,537	842,068	820,058	1,078,972	40,469	28,150	132,418	85,183	10.8	7.5	36.1	17.7	1.0	0.9	-1.0	0.9	1.3	0.03	-1.0	0.9	1.3	0.05	1.3	0.1
				IFDDVSSGVSQLASK	2	99.6%	1																									
IPI00175193	KIF4B	Chromosome-associated kinesin KIF4B	98.1%	1.0	1	1	1	1	13,429,300	15,251,230	14,181,060	17,433,000	894,679	858,930	1,322,425	1,107,246	14.9	12.6	20.9	14.2	1.1	0.2	1.1	0.7	1.3	0.02	-1.1	0.5	1.1	0.2	1.2	0.1
				QIESLETEMELR	3	98.1%	1																									
IPI00175416	PLCH1	isoform 1 of 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase eta-1	99.4%	0.5	1	1	1	4	1,221,083	1,378,595	1,265,645	1,518,170	113,563	126,384	103,264	80,286	20.8	20.5	18.2	11.8	1.1	0.4	1.0	0.8	1.2	0.07	-1.1	0.5	1.1	0.4	1.2	0.09
IPI00783616	PLCH1	isoform 2 of 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase eta-1	99.4%	0.5	1	1	1	4	1,221,083	1,378,595	1,265,645	1,518,170	113,563	126,384	103,264	80,286	20.8	20.5	18.2	11.8	1.1	0.4	1.0	0.8	1.2	0.07	-1.1	0.5	1.1	0.4	1.2	0.09
IPI00848061	PLCH1	isoform 3 of 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase eta-1	99.4%	0.8	1	1	1	4	1,221,083	1,378,595	1,265,645	1,518,170	113,563	126,384	103,264	80,286	20.8	20.5	18.2	11.8	1.1	0.4	1.0	0.8	1.2	0.07	-1.1	0.5	1.1	0.4	1.2	0.09
IPI00889624	PLCH1	isoform 4 of 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase eta-1	99.4%	0.8	1	1	1	4	1,221,083	1,378,595	1,265,645	1,518,170	113,563	126,384	103,264	80,286	20.8	20.5	18.2	11.8	1.1	0.4	1.0	0.8	1.2	0.07	-1.1	0.5	1.1	0.4	1.2	0.09
				ILIDSIYK	2	99.4%	1																									
IPI00176637	EIF2S2P4;EIF2S2	Eukaryotic translation initiation factor 2 subunit 2-like protein	100.0%	1.8	1	1	1	1	2,103,275	1,938,280	2,023,480	2,216,325	126,237	106,576	188,844	72,784	13.4	12.3	20.9	7.3	-1.1	0.3	-1.0	0.7	1.1	0.5	1.0	0.7	1.1	0.06	1.1	0.4
				VFNIMR	2	94.1%	1																									
IPI00176698	CYCS	Cytochrome c	100.0%	13.3	1	1	1	1	643,627	751,640	731,447	772,627	46,598	53,870	81,032	21,241	16.2	16.0	24.8	6.2	1.2	0.2	1.1	0.4	1.2	0.04	-1.0	0.8	1.0	0.7	1.1	0.6
				TGQAPGYSYTAANK	2	100.0%	1																									
IPI00176903	PTRF	isoform 1 of Polymerase I and transcript release factor	96.1%	3.9	1	1	1	3	783,997	578,407	744,507	723,453	82,802	38,107	80,200	43,127	23.6	14.7	24.1	13.3	-1.4	0.05	-1.1	0.7	-1.1	0.5	1.3	0.1	1.3	0.04	-1.0	0.8
IPI00513773	PTRF	isoform 2 of Polymerase I and transcript release factor	96.1%	5.0	1	1	1	3	783,997	578,407	744,507	723,453	82,802	38,107	80,200	43,127	23.6	14.7	24.1	13.3	-1.4	0.05	-1.1	0.7	-1.1	0.5	1.3	0.1	1.3	0.04	-1.0	0.8
IPI00514023	PTRF	cDNA FLJ53495, highly similar to Polymerase I and transcript release factor	96.1%	4.1	1	1	1	3	783,997	578,407	744,507	723,453	82,802	38,107	80,200	43,127	23.6	14.7	24.1	13.3	-1.4	0.05	-1.1	0.7	-1.1	0.5	1.3	0.1	1.3	0.04	-1.0	0.8
				SDQVNGVLVLSLLDK	2	96.1%	1																									
IPI00177008	PGP	Phosphoglycolate phosphatase	99.5%	4.7	1	1	1	1	3,688,980	3,708,960	3,870,080	4,411,870	220,509	191,836	466,984	450,975	13.4	11.6	27.0	22.9	1.0	0.9	1.0	0.7	1.2	0.2	1.0	0.8	1.2	0.2	1.1	0.4
				TILTLTGVSTLGDVK	2	99.5%	1																									
IPI00177323	CDH23	FLJ00233 protein (Fragment)	95.4%	5.1	1	1	1	1	376,875	337,626	457,537	457,431	66,204	19,772	82,786	43,014	39.3	13.1	40.5	21.0	-1.1	0.6	1.2	0.5	1.2	0.3	1.4	0.2	1.4	0.04	-1.0	1
				VVASDAGTPTKSSTSTLTIHVLGCERR	3	81.9%	1																									
IPI00177728	CNDP2	isoform 1 of Cytosolic non-specific dipeptidase	100.0%	34.1	11	11	11	1	32,293,155	31,045,179	33,772,038	34,485,788	1,449,711	834,692	1,379,066	971,880	10.0	6.0	9.1	6.3	-1.0	0.5	1.0	0.5	1.1	0.2	1.1	0.1	1.1	0.03	1.0	0.7
				EGGSIPVTLTFQEATGK	2	100.0%	1																									
				FCLEGMEESGSEGLDELIFAR	2	100.0%	1																									
				GSTDDKGPVAGWINALEAYQK	3	100.0%	1																									
				LPDGSEIPLPPILLGR	2	99.3%	1																									
				LYDDIDFDIEEFAK	2	100.0%	1																									
				MMEVAAADVK	2	100.0%	1																									
				NVMLLPVGSADDGAHSQNEK	3	96.8%	1																									
				TGQEIPVNVR	2	99.6%	1																									
				TVFGVEPDLTR	2	99.9%	1																									
				WVAIQSVSAWPEKR	2	99.8%	1																									
				YNYIEGTK	2	94.9%	1																									
IPI00177817	ATP2A2	isoform 2 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	99.6%	2.5	2	2	2	6	1,619,887	1,831,053	1,709,482	1,826,990	121,131	39,796	79,106	108,906	16.7	4.9	10.4	13.3	1.1	0.2	1.1	0.6	1.1	0.2	-1.1	0.2	-1.0	1	1.1	0.4
IPI00219078	ATP2A2	isoform 1 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	99.6%	2.4	2	2	2	6	1,619,887	1,831,053	1,709,482	1,826,990	121,131	39,796	79,106	108,906	16.7	4.9	10.4	13.3	1.1	0.2	1.1	0.6	1.1	0.2	-1.1	0.2	-1.0	1	1.1	0.4
IPI00747443	ATP2A2	isoform 5 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	99.6%	2.5	2	2	2	6	1,619,887	1,831,053	1,709,482	1,826,990	121,131	39,796	79,106	108,906	16.7	4.9	10.4	13.3	1.1	0.2	1.1	0.6	1.1	0.2	-1.1	0.2	-1.0	1	1.1	0.4
IPI00914019	ATP2A2	isoform 4 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	99.6%	2.5	2	2	2	6	1,619,887	1,831,053	1,709,482	1,826,990	121,131	39,796	79,106	108,906	16.7	4.9	10.4	13.3	1.1	0.2	1.1	0.6	1.1	0.2	-1.1	0.2	-1.0	1	1.1	0.4
IPI00969023	ATP2A2	isoform 3 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	99.6%	2.5	2	2	2	6	1,619,887	1,831,053	1,709,482	1,826,990	121,131	39,796	79,106	108,906	16.7	4.9	10.4	13.3	1.1	0.2	1.1	0.6	1.1	0.2	-1.1	0.2	-1.0	1	1.1	0.4
IPI01013232	ATP2A2	110 kDa protein	99.6%	2.5	2	2	2	6	1,619,887	1,831,053	1,709,482	1,826,990	121,131	39,796	79,106	108,906	16.7	4.9	10.4	13.3	1.1	0.2	1.1	0.6	1.1	0.2	-1.1	0.2	-1.0	1	1.1	0.4
				AMGVVVATGVNTEIGK	2	91.3%	1																									
				MNVFDTELK	2	94.1%	1																									
IPI00177888	LENG8	Uncharacterized protein	97.2%	1.0	1	1	1	5	1,277,442	1,361,492	1,072,160	1,212,806	109,709	135,991	46,489	96,910	19.2	22.3	9.7	17.9	1.1	0.6	-1.2	0.1	-1.1	0.7	-1.3	0.1	-1.1	0.4	1.1	0.2
IPI00217858	LENG8	isoform 2 of Leukocyte receptor cluster member 8	97.2%	1.0	1	1	1	5	1,277,442	1,361,492	1,072,160	1,212,806	109,709	135,991	46,489	96,910	19.2	22.3	9.7	17.9	1.1	0.6	-1.2	0.1	-1.1	0.7	-1.3	0.1	-1.1	0.4	1.1	0.2
IPI00658190	LENG8	Uncharacterized protein	97.2%	2.7	1	1	1	5	1,277,442	1,361,492	1,072,160	1,212,806	109,709	135,991	46,489	96,910	19.2	22.3	9.7	17.9	1.1	0.6	-1.2	0.1	-1.1	0.7	-1.3	0.1	-1.1	0.4	1.1	0.2
IPI00852904	LENG8	Leukocyte receptor cluster (LRC) member 8	97.2%	1.1	1	1	1	5	1,277,442	1,361,492	1,072,160	1,212,806	109,709	135,991	46,489	96,910	19.2	22.3	9.7	17.9	1.1	0.6	-1.2	0.1	-1.1	0.7	-1.3	0.1	-1.1	0.4	1.1	0.2
IPI00926974	LENG8	Uncharacterized protein	97.2%	0.9	1	1	1	5	1,277,442	1,361,492	1,072,160	1,212,806	109,709	135,991	46,489	96,910	19.2	22.3	9.7	17.9	1.1	0.6	-1.2	0.1	-1.1	0.7	-1.3	0.1	-1.1	0.4	1.1	0.2
				KGQQLWNR	2	88.8%	1																									
IPI00178056	-	44 kDa protein	100.0%	5.7	2	2	2	1	12,893,200	11,797,913	13,617,477	12,838,083	276,482	584,376	399,892	466,560	4.8	11.1	6.6	8.1	-1.1	0.1	1.1	0.2	-1.0	0.9	1.2	0.03	1.1	0.2	-1.1	0.2
				HGEIDYEAIVK	2	100.0%	1																									
				LSDGFNGADLR	2	96.3%	1																									
IPI00178072	SPECC1L	Cytospin-A	98.4%	2.0	1	1	1	4	437,195	376,845	435,290	496,430	27,011	15,005	50,041	24,356	13.8	8.9	25.7	11.0	-1.2	0.09	-1.0	1	1.1	0.1	1.2	0.3	1.3	0.003	1.1	0.3
IPI00744837	SPECC1L	KIAA0376 protein variant	98.4%	2.4	1	1	1	4	437,195	376,845	435,290	496,430	27,011	15,005	50,041	24,356	13.8	8.9	25.7	11.0	-1.2	0.09	-1.0	1	1.1	0.1	1.2	0.3	1.3	0.003	1.1	0.3
IPI00879449	SPECC1L	Uncharacterized protein	98.4%	2.8	1	1	1	4	437,195	376,845	435,290	496,430	27,011	15,005	50,041	24,356	13.8	8.9	25.7	11.0	-1.2	0.09	-1.0	1	1.1	0.1	1.2	0.3	1.3	0.003	1.1	0.3
IPI01009612	SPECC1L	120 kDa protein	98.4%	2.0	1	1	1	4	437,195	376,845	435,290	496,430	27,011	15,005	50,041	24,356	13.8	8.9	25.7	11.0	-1.2	0.09	-1.0	1	1.1	0.1	1.2	0.3	1.3	0.003	1.1	0.3
				EQLLGVQQHLSNTLKMAEQDNK	3	98.4%	1																									
IPI00910924	DYNLRB1	cDNA FLJ59194, moderately similar to Dynein light chain 2A, cytoplasmic	99.9%	9.9	1	1	1	2	1,989,365	2,211,210	1,960,700	2,100,058	224,762	154,697	266,142	73,855	25.3	15.6	30.4	7.9	1.1	0.4	-1.0	0.9	1.1	0.7	-1.1	0.4	-1.1	0.5	1.1	0.6
IPI00178188	DYNLRB2	Dynein light chain roadblock-type 2	99.9%	12.5	1	1	1	2	1,989,365	2,211,210	1,960,700	2,100,058	224,762	154,697	266,142	73,855	25.3	15.6	30.4	7.9	1.1	0.4	-1.0	0.9	1.1	0.7	-1.1	0.4	-1.1	0.5	1.1	0.6
				DIDPQNDLTFLR	2	99.8%	1																									
IPI00178352	FLNC	isoform 1 of Filamin-C	100.0%	2.2	4	4	6	2	1,421,083	1,744,054	1,637,451	1,814,664	204,929	40,801	211,046	108,156	32.3	5.2	28.8	13.3	1.2	0.2	1.2	0.5	1.3	0.1	-1.1	0.6	1.0	0.6	1.1	0.5
IPI00413958	FLNC	isoform 2 of Filamin-C	100.0%	2.2	4	4	6	2	1,421,083	1,744,054	1,637,451	1,814,664	204,929	40,801	211,046	108,156	32.3	5.2	28.8	13.3	1.2	0.2	1.2	0.5	1.3	0.1	-1.1	0.6	1.0	0.6	1.1	0.5
				EAGAGGLSIAVEGPSK	2	100.0%	2																									
				GAGTGGLGLTVEGPCEAK	2	100.0%	1																									
				LIALLEVLSQK	2	100.0%	2																									
				TDTYVTDNGDGTYR	3	89.8%	1																									
IPI00178440	EEF1B2	Elongation factor 1-beta	100.0%	40.4	6	6	11	1	72,415,830	75,308,690	70,703,107	85,043,560	6,713,372	3,192,023	5,460,989	3,321,124	20.7	9.5	17.3	8.7	1.0	0.7	-1.0	0.8	1.2	0.1	-1.1	0.5	1.1	0.07	1.2	0.06
				LAQYESK	2	94.7%	1																									
				SIQADGLVWGSSK	2	100.0%	3																									
				SPAGLQVLNDYLADK	2	100.0%	3																									
				SSILLDVKPWDDETDMAK	3	100.0%	2																									
				SSILLDVKPWDDETDMAKLEECVR	3	100.0%	1																									
				SYIEGYVPSQADVAVFEAVSSPPPADLCHALR	3	99.7%	1																									
IPI00179026	MCTS1	isoform 1 of Malignant T cell-amplified sequence 1	99.6%	30.9	3	4	4	3	2,461,710	2,119,570	2,374,308	2,183,837	229,155	124,519	158,783	106,847	20.8	13.1	15.0	10.9	-1.2	0.2	-1.0	0.8	-1.1	0.3	1.1	0.2	1.0	0.7	-1.1	0.3
IPI00645446	MCTS1	malignant T cell-amplified sequence 1 isoform 2	99.6%	30.8	3	4	4	3	2,461,710	2,119,570	2,374,308	2,183,837	229,155	124,519	158,783	106,847	20.8	13.1	15.0	10.9	-1.2	0.2	-1.0	0.8	-1.1	0.3	1.1	0.2	1.0	0.7	-1.1	0.3
IPI00900380	MCTS1	isoform 2 of Malignant T cell-amplified sequence 1	99.6%	33.1	3	4	4	3	2,461,710	2,119,570	2,374,308	2,183,837	229,155	124,519	158,783	106,847	20.8	13.1	15.0	10.9	-1.2	0.2	-1.0	0.8	-1.1	0.3	1.1	0.2	1.0	0.7	-1.1	0.3
				FVLSGANIMCPGLTSPGAK	2	98.9%	1																									
				LYPAAVDTIVAIMAEGK	2	99.6%	1																									
				LYPAAVDTIVAIMAEGK	3	94.3%	1																									
				NQLIEQFPGIEPWLNQIMPK	3	94.0%	1																									
IPI00179138	SF3B3	isoform 2 of Splicing factor 3B subunit 3	100.0%	3.6	1	1	1	1	8,479,150	8,019,900	7,027,000	8,813,550	567,913	535,618	529,717	539,260	15.0	14.9	16.9	13.7	-1.1	0.6	-1.2	0.1	1.0	0.7	-1.1	0.2	1.1	0.3	1.3	0.05
				IVILEYQPSK	2	100.0%	1																									
IPI00179298	HUWE1	Uncharacterized protein	99.9%	1.2	4	4	4	3	7,046,217	7,381,344	6,838,946	8,521,195	784,300	318,568	540,959	247,349	24.9	9.7	17.7	6.5	1.0	0.7	-1.0	0.8	1.2	0.1	-1.1	0.4	1.2	0.02	1.2	0.02
IPI00445401	HUWE1	isoform 2 of E3 ubiquitin-protein ligase HUWE1	99.9%	1.2	4	4	4	3	7,046,217	7,381,344	6,838,946	8,521,195	784,300	318,568	540,959	247,349	24.9	9.7	17.7	6.5	1.0	0.7	-1.0	0.8	1.2	0.1	-1.1	0.4	1.2	0.02	1.2	0.02
IPI00643153	HUWE1	isoform 3 of E3 ubiquitin-protein ligase HUWE1	99.9%	1.2	4	4	4	3	7,046,217	7,381,344	6,838,946	8,521,195	784,300	318,568	540,959	247,349	24.9	9.7	17.7	6.5	1.0	0.7	-1.0	0.8	1.2	0.1	-1.1	0.4	1.2	0.02	1.2	0.02
				LLSLISIALPENK	2	96.0%	1																									
				LPGGVQNFPQFSALR	2	94.6%	1																									
				QVVNQVWEAADVLIK	2	98.8%	1																									
				SILTLSHEPK	2	97.5%	1																									
IPI00179326	BAIAP2L1	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	100.0%	9.0	3	3	4	1	6,953,610	8,264,045	8,969,630	8,351,179	370,586	443,634	290,702	281,621	11.9	12.0	7.3	7.5	1.2	0.05	1.3	0.003	1.2	0.02	1.1	0.2	1.0	0.9	-1.1	0.2
				SVSVATGLNMMK	2	98.2%	1																									
				TLLSFAQGDVITLLIPEEK	2	99.4%	1																									
				VNNSTGTSEDPSLQR	2	100.0%	2																									
IPI00179330	RPS27A	Ubiquitin-40S ribosomal protein S27a	100.0%	31.4	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI00798155	RPS27A	12 kDa protein	100.0%	46.2	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI00456429	UBA52	Ubiquitin-60S ribosomal protein L40	100.0%	38.3	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI00719280	UBB	Polyubiquitin-B	100.0%	21.4	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI01011805	UBB	cDNA FLJ51326, highly similar to Homo sapiens ubiquitin B (UBB), mRNA	100.0%	32.0	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI00784990	UBC	Ubiquitin C splice variant	100.0%	32.0	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI00793729	UBC	cDNA FLJ32377 fis, clone SKMUS1000014, highly similar to Polyubiquitin 9	100.0%	16.1	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI00969566	UBC	Polyubiquitin-C	100.0%	7.2	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI01009501	UBC	18 kDa protein	100.0%	30.4	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI01010419	UBC	17 kDa protein	100.0%	32.0	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI01011412	UBC	60 kDa protein	100.0%	9.2	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI01014205	UBC	15 kDa protein	100.0%	36.0	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI01014596	UBC	15 kDa protein	100.0%	36.6	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI01015113	UBC	17 kDa protein	100.0%	31.6	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI01015565	UBC	17 kDa protein	100.0%	32.9	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI01015749	UBC	cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA	100.0%	8.1	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
IPI01015985	UBC	19 kDa protein	100.0%	29.0	6	6	11	17	2,455,294	2,518,556	2,470,374	2,829,727	179,670	102,690	123,150	89,868	16.4	9.1	11.2	7.1	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.05	1.1	0.05
				ESTLHLVLR	2	99.7%	2																									
				IQDKEGIPPDQQR	2	99.9%	2																									
				TITLEVEPSDTIENVK	2	100.0%	2																									
				TITLEVEPSDTIENVKAK	3	86.9%	1																									
				TLSDYNIQK	2	100.0%	2																									
				TLSDYNIQKESTLHLVLR	3	99.3%	2																									
IPI00179357	TTN	isoform 7 of Titin	99.8%	0.2	6	6	6	2	4,727,377	4,714,110	5,354,824	5,472,781	413,730	249,450	470,592	196,141	19.6	11.8	19.7	8.0	-1.0	1	1.1	0.3	1.2	0.1	1.1	0.3	1.2	0.04	1.0	0.8
IPI00759637	TTN	isoform 4 of Titin	99.8%	0.2	6	6	6	2	4,727,377	4,714,110	5,354,824	5,472,781	413,730	249,450	470,592	196,141	19.6	11.8	19.7	8.0	-1.0	1	1.1	0.3	1.2	0.1	1.1	0.3	1.2	0.04	1.0	0.8
				AEDLSATVTDVVEGQEYSFR	3	97.1%	1																									
				ITQFLKAEASKEIAK	2	84.0%	1																									
				MPDDDGGDR	1	92.2%	1																									
				STVTIVDSKR	2	89.8%	1																									
				VLDTPGPPVNVTVK	2	90.2%	1																									
				VTGLSEGCEYFFR	3	94.3%	1																									
IPI00179415	PPP3CA	isoform 1 of Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	100.0%	5.0	1	1	1	4	457,600	490,018	616,515	536,608	41,247	41,198	80,484	37,872	20.2	18.8	29.2	15.8	1.1	0.6	1.3	0.1	1.2	0.2	1.3	0.2	1.1	0.4	-1.1	0.4
IPI00747748	PPP3CA	isoform 2 of Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	100.0%	5.1	1	1	1	4	457,600	490,018	616,515	536,608	41,247	41,198	80,484	37,872	20.2	18.8	29.2	15.8	1.1	0.6	1.3	0.1	1.2	0.2	1.3	0.2	1.1	0.4	-1.1	0.4
IPI00966317	PPP3CA	Serine/threonine-protein phosphatase	100.0%	5.7	1	1	1	4	457,600	490,018	616,515	536,608	41,247	41,198	80,484	37,872	20.2	18.8	29.2	15.8	1.1	0.6	1.3	0.1	1.2	0.2	1.3	0.2	1.1	0.4	-1.1	0.4
IPI00910825	PPP3CA	serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform isoform 3	100.0%	5.5	1	1	1	4	457,600	490,018	616,515	536,608	41,247	41,198	80,484	37,872	20.2	18.8	29.2	15.8	1.1	0.6	1.3	0.1	1.2	0.2	1.3	0.2	1.1	0.4	-1.1	0.4
				FKEPPAYGPMCDILWSDPLEDFGNEK	3	99.9%	1																									
IPI00879205	-	Tyrosine-protein kinase receptor	99.6%	3.2	1	1	1	6	224,312	229,093	245,001	266,847	24,906	14,349	26,134	29,893	24.8	14.0	23.9	25.1	1.0	0.9	1.1	0.6	1.2	0.3	1.1	0.6	1.2	0.3	1.1	0.6
IPI00179473	SQSTM1	isoform 1 of Sequestosome-1	99.6%	5.9	1	1	1	6	224,312	229,093	245,001	266,847	24,906	14,349	26,134	29,893	24.8	14.0	23.9	25.1	1.0	0.9	1.1	0.6	1.2	0.3	1.1	0.6	1.2	0.3	1.1	0.6
IPI00784104	SQSTM1	isoform 2 of Sequestosome-1	99.6%	7.3	1	1	1	6	224,312	229,093	245,001	266,847	24,906	14,349	26,134	29,893	24.8	14.0	23.9	25.1	1.0	0.9	1.1	0.6	1.2	0.3	1.1	0.6	1.2	0.3	1.1	0.6
IPI00908710	SQSTM1	cDNA FLJ52854, highly similar to Sequestosome-1	99.6%	8.8	1	1	1	6	224,312	229,093	245,001	266,847	24,906	14,349	26,134	29,893	24.8	14.0	23.9	25.1	1.0	0.9	1.1	0.6	1.2	0.3	1.1	0.6	1.2	0.3	1.1	0.6
IPI00965064	SQSTM1	Uncharacterized protein	99.6%	6.9	1	1	1	6	224,312	229,093	245,001	266,847	24,906	14,349	26,134	29,893	24.8	14.0	23.9	25.1	1.0	0.9	1.1	0.6	1.2	0.3	1.1	0.6	1.2	0.3	1.1	0.6
IPI01012876	SQSTM1	Uncharacterized protein	99.6%	15.6	1	1	1	6	224,312	229,093	245,001	266,847	24,906	14,349	26,134	29,893	24.8	14.0	23.9	25.1	1.0	0.9	1.1	0.6	1.2	0.3	1.1	0.6	1.2	0.3	1.1	0.6
				AGEARPGPTAESASGPSEDPSVNFLK	3	99.6%	1																									
IPI00179700	HMGA1	isoform HMG-I of High mobility group protein HMG-I/HMG-Y	99.6%	23.4	1	1	2	3	814,103	881,653	787,767	1,004,210	86,617	111,487	103,408	91,021	23.8	28.3	29.4	20.3	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.4	1.3	0.2

IPI00744851	HMGA1	cDNA FLJ54188, moderately similar to High mobility group protein HMG-I/HMG-Y	99.6%	7.6	1	1	2	3	814,103	881,653	787,767	1,004,210	86,617	111,487	103,408	91,021	23.8	28.3	29.4	20.3	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.4	1.3	0.2
IPI00746310	HMGA1	isoform HMG-R of High mobility group protein HMG-I/HMG-Y	99.6%	14.0	1	1	2	3	814,103	881,653	787,767	1,004,210	86,617	111,487	103,408	91,021	23.8	28.3	29.4	20.3	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.4	1.3	0.2
				KQPPVSPGTALVGSQKEPSEVPTPK	3	99.6%	2																									
IPI00179709	TUBA3D;TUBA3C	isoform 1 of Tubulin alpha-3C/D chain	100.0%	3.3	1	1	1	1	4,702,730	4,733,120	4,421,560	5,681,420	503,049	231,452	369,966	353,383	23.9	10.9	18.7	13.9	1.0	1	-1.1	0.7	1.2	0.2	-1.1	0.5	1.2	0.06	1.3	0.04
				AVFVDLEPTVVDEVR	3	87.1%	1																									
IPI00179713	IGF2BP2	isoform 1 of Insulin-like growth factor 2 mRNA-binding protein 2	100.0%	18.5	8	8	8	3	10,044,298	10,714,339	10,295,287	11,704,828	892,594	423,719	655,949	346,615	19.9	8.8	14.3	6.6	1.1	0.5	1.0	0.8	1.2	0.1	-1.0	0.6	1.1	0.1	1.1	0.09
IPI00180983	IGF2BP2	isoform 2 of Insulin-like growth factor 2 mRNA-binding protein 2	100.0%	20.0	8	8	8	3	10,044,298	10,714,339	10,295,287	11,704,828	892,594	423,719	655,949	346,615	19.9	8.8	14.3	6.6	1.1	0.5	1.0	0.8	1.2	0.1	-1.0	0.6	1.1	0.1	1.1	0.09
IPI00953576	IGF2BP2	isoform 4 of Insulin-like growth factor 2 mRNA-binding protein 2	100.0%	18.4	8	8	8	3	10,044,298	10,714,339	10,295,287	11,704,828	892,594	423,719	655,949	346,615	19.9	8.8	14.3	6.6	1.1	0.5	1.0	0.8	1.2	0.1	-1.0	0.6	1.1	0.1	1.1	0.09
				DQTPDENEEVIVR	2	99.9%	1																									
				IAPAEGPDVSER	2	99.9%	1																									
				ISYIPDEEVSSPSPPQR	3	91.1%	1																									
				ITISSLQDLSIYNPER	2	99.0%	1																									
				KLPLAGQVLLK	3	94.7%	1																									
				SGYAFVDYPDQNWAIR	2	100.0%	1																									
				TVNELQNLTSAEVIVPR	3	99.5%	1																									
				YPQGVASQR	2	95.8%	1																									
IPI00179953	NASP	isoform 1 of Nuclear autoantigenic sperm protein	100.0%	11.7	5	6	7	3	4,805,188	4,814,594	4,957,948	5,169,140	170,407	180,725	348,077	254,409	7.9	8.4	15.7	11.0	1.0	1	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.3	1.0	0.6
IPI00219821	NASP	isoform 2 of Nuclear autoantigenic sperm protein	100.0%	20.5	5	6	7	3	4,805,188	4,814,594	4,957,948	5,169,140	170,407	180,725	348,077	254,409	7.9	8.4	15.7	11.0	1.0	1	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.3	1.0	0.6
IPI00332499	NASP	isoform 3 of Nuclear autoantigenic sperm protein	100.0%	11.7	5	6	7	3	4,805,188	4,814,594	4,957,948	5,169,140	170,407	180,725	348,077	254,409	7.9	8.4	15.7	11.0	1.0	1	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.3	1.0	0.6
				HLVMGDIPAAVNAFQEAASLLGK	3	100.0%	1																									
				LLAETHYQLGLAYGYNSQYDEAVAQFSK	3	100.0%	1																									
				MAVLNEQVK	2	94.3%	1																									
				SIEVIENR	2	83.7%	1																									
				SLQENEEEEIGNLELAWDMLDLAK	2	100.0%	2																									
				SLQENEEEEIGNLELAWDMLDLAK	3	99.9%	1																									
IPI00179964	PTBP1	isoform 1 of Polypyrimidine tract-binding protein 1	100.0%	32.2	11	14	20	3	24,839,827	25,710,907	24,942,187	28,388,553	2,037,609	828,133	1,780,810	1,031,795	18.3	7.2	16.0	8.1	1.0	0.7	1.0	1	1.1	0.2	-1.0	0.7	1.1	0.08	1.1	0.1
IPI00183626	PTBP1	polypyrimidine tract-binding protein 1 isoform a	100.0%	30.7	11	14	20	3	24,839,827	25,710,907	24,942,187	28,388,553	2,037,609	828,133	1,780,810	1,031,795	18.3	7.2	16.0	8.1	1.0	0.7	1.0	1	1.1	0.2	-1.0	0.7	1.1	0.08	1.1	0.1
IPI00334175	PTBP1	isoform 2 of Polypyrimidine tract-binding protein 1	100.0%	31.1	11	14	20	3	24,839,827	25,710,907	24,942,187	28,388,553	2,037,609	828,133	1,780,810	1,031,795	18.3	7.2	16.0	8.1	1.0	0.7	1.0	1	1.1	0.2	-1.0	0.7	1.1	0.08	1.1	0.1
				DYGNSPLHR	2	95.1%	1																									
				DYGNSPLHR	3	99.7%	1																									
				ENALVQMADGNQAQLAMSHLNGHK	3	100.0%	1																									
				HQNVQLPR	2	99.9%	2																									
				IAIPGLAGAGNSVLLVSNLNPER	2	100.0%	2																									
				KLPIDVTEGEVISLGLPFGK	2	100.0%	2																									
				KLPIDVTEGEVISLGLPFGK	3	100.0%	1																									
				LPIDVTEGEVISLGLPFGK	2	100.0%	2																									
				LSLDGQNIYNACCTLR	2	97.6%	2																									
				MDGIVPDIAVGTK	2	95.8%	1																									
				NFQNIFPPSATLHLSNIPPSVSEEDLK	3	100.0%	1																									
				NNQFQALLQYADPVSAQHAK	2	100.0%	1																									
				NNQFQALLQYADPVSAQHAK	3	100.0%	2																									
				VLFSSNGGVVK	2	99.9%	1																									
IPI00180121	CLCN6	isoform A of Chloride transport protein 6	99.9%	3.5	1	1	1	3	907,737	871,177	675,827	1,038,887	156,795	80,142	69,652	157,509	38.6	20.6	23.1	33.9	-1.0	0.8	-1.3	0.2	1.1	0.6	-1.3	0.1	1.2	0.4	1.5	0.07
IPI00642888	CLCN6	isoform E of Chloride transport protein 6	99.9%	3.2	1	1	1	3	907,737	871,177	675,827	1,038,887	156,795	80,142	69,652	157,509	38.6	20.6	23.1	33.9	-1.0	0.8	-1.3	0.2	1.1	0.6	-1.3	0.1	1.2	0.4	1.5	0.07
IPI01012707	CLCN6	95 kDa protein	99.9%	3.5	1	1	1	3	907,737	871,177	675,827	1,038,887	156,795	80,142	69,652	157,509	38.6	20.6	23.1	33.9	-1.0	0.8	-1.3	0.2	1.1	0.6	-1.3	0.1	1.2	0.4	1.5	0.07
				MIVDVTPYMNPSPFTVSPNTHVSQVFNLFR	3	97.5%	1																									
IPI00180128	BZW1	isoform 2 of Basic leucine zipper and W2 domain-containing protein 1	99.7%	8.5	3	3	3	1	6,250,402	6,241,000	5,892,155	7,468,204	569,056	338,863	389,195	387,506	20.4	12.1	14.8	11.6	-1.0	1	-1.1	0.6	1.2	0.1	-1.1	0.5	1.2	0.04	1.3	0.02
				AEVLSEEPILK	2	89.0%	1																									
				EGVSAAFAVK	2	92.4%	1																									
				LMELFPANK	2	99.5%	1																									
IPI00816288	TMSB4XP1	Similar to Thymosin beta-4	100.0%	33.9	3	3	4	10	4,038,607	4,289,794	3,879,715	4,763,171	300,965	126,329	243,067	313,820	16.7	6.6	14.0	14.7	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
IPI00220828	TMSB4X	Thymosin beta-4	100.0%	43.2	3	3	4	10	4,038,607	4,289,794	3,879,715	4,763,171	300,965	126,329	243,067	313,820	16.7	6.6	14.0	14.7	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
IPI00815642	TMSB4X	TMSB4X protein (Fragment)	100.0%	27.1	3	3	4	10	4,038,607	4,289,794	3,879,715	4,763,171	300,965	126,329	243,067	313,820	16.7	6.6	14.0	14.7	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
IPI01011913	TMSB4X	TMSB4X protein (Fragment)	100.0%	30.2	3	3	4	10	4,038,607	4,289,794	3,879,715	4,763,171	300,965	126,329	243,067	313,820	16.7	6.6	14.0	14.7	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
IPI01012854	TMSB4X	TMSB4X protein (Fragment)	100.0%	27.5	3	3	4	10	4,038,607	4,289,794	3,879,715	4,763,171	300,965	126,329	243,067	313,820	16.7	6.6	14.0	14.7	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
IPI01013265	TMSB4X	TMSB4X protein (Fragment)	100.0%	27.5	3	3	4	10	4,038,607	4,289,794	3,879,715	4,763,171	300,965	126,329	243,067	313,820	16.7	6.6	14.0	14.7	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
IPI01014272	TMSB4X	TMSB4X protein (Fragment)	100.0%	29.2	3	3	4	10	4,038,607	4,289,794	3,879,715	4,763,171	300,965	126,329	243,067	313,820	16.7	6.6	14.0	14.7	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
IPI00180240	TMSL3	Thymosin beta-4-like protein 3	100.0%	43.2	3	3	4	10	4,038,607	4,289,794	3,879,715	4,763,171	300,965	126,329	243,067	313,820	16.7	6.6	14.0	14.7	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
IPI01015569	TMSL3	8 kDa protein	100.0%	27.5	3	3	4	10	4,038,607	4,289,794	3,879,715	4,763,171	300,965	126,329	243,067	313,820	16.7	6.6	14.0	14.7	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
IPI00719405	TMSL6	TMSL6 protein	100.0%	43.2	3	3	4	10	4,038,607	4,289,794	3,879,715	4,763,171	300,965	126,329	243,067	313,820	16.7	6.6	14.0	14.7	1.1	0.5	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
				NPLPSKETIEQEK	3	94.8%	1																									
				TETQEKNPLPSK	2	100.0%	2																									
				TETQEKNPLPSKETIEQEK	3	100.0%	1																									
IPI00180386	GYG1	isoform GN-1L of Glycogenin-1	100.0%	6.9	2	2	2	3	6,731,560	6,954,840	6,925,553	8,707,980	506,281	665,406	1,162,124	529,848	16.8	21.4	37.5	13.6	1.0	0.8	1.0	0.9	1.3	0.03	-1.0	1	1.3	0.07	1.3	0.2
IPI00556308	GYG1	isoform GN-1 of Glycogenin-1	100.0%	7.2	2	2	2	3	6,731,560	6,954,840	6,925,553	8,707,980	506,281	665,406	1,162,124	529,848	16.8	21.4	37.5	13.6	1.0	0.8	1.0	0.9	1.3	0.03	-1.0	1	1.3	0.07	1.3	0.2
IPI00794444	GYG1	isoform GN-1S of Glycogenin-1	100.0%	9.2	2	2	2	3	6,731,560	6,954,840	6,925,553	8,707,980	506,281	665,406	1,162,124	529,848	16.8	21.4	37.5	13.6	1.0	0.8	1.0	0.9	1.3	0.03	-1.0	1	1.3	0.07	1.3	0.2
				LVVLATPQVSDSMR	2	98.5%	1																									
				RPELGVTLTK	2	97.4%	1																									
IPI00180672	MOCS1	isoform 2 of Molybdenum cofactor biosynthesis protein 1	91.2%	7.5	1	1	1	7	207,003	253,718	178,980	249,440	18,013	40,439	47,468	27,653	19.5	35.6	59.3	24.8	1.2	0.3	-1.2	0.6	1.2	0.2	-1.4	0.3	-1.0	0.9	1.4	0.2
IPI00289462	MOCS1	isoform MOCS1B of Molybdenum cofactor biosynthesis protein 1	91.2%	4.6	1	1	1	7	207,003	253,718	178,980	249,440	18,013	40,439	47,468	27,653	19.5	35.6	59.3	24.8	1.2	0.3	-1.2	0.6	1.2	0.2	-1.4	0.3	-1.0	0.9	1.4	0.2
IPI00289463	MOCS1	isoform 6 of Molybdenum cofactor biosynthesis protein 1	91.2%	4.7	1	1	1	7	207,003	253,718	178,980	249,440	18,013	40,439	47,468	27,653	19.5	35.6	59.3	24.8	1.2	0.3	-1.2	0.6	1.2	0.2	-1.4	0.3	-1.0	0.9	1.4	0.2
IPI00413557	MOCS1	isoform 3 of Molybdenum cofactor biosynthesis protein 1	91.2%	8.2	1	1	1	7	207,003	253,718	178,980	249,440	18,013	40,439	47,468	27,653	19.5	35.6	59.3	24.8	1.2	0.3	-1.2	0.6	1.2	0.2	-1.4	0.3	-1.0	0.9	1.4	0.2
IPI00746947	MOCS1	isoform 7 of Molybdenum cofactor biosynthesis protein 1	91.2%	5.4	1	1	1	7	207,003	253,718	178,980	249,440	18,013	40,439	47,468	27,653	19.5	35.6	59.3	24.8	1.2	0.3	-1.2	0.6	1.2	0.2	-1.4	0.3	-1.0	0.9	1.4	0.2
IPI00925345	MOCS1	isoform 8 of Molybdenum cofactor biosynthesis protein 1	91.2%	4.6	1	1	1	7	207,003	253,718	178,980	249,440	18,013	40,439	47,468	27,653	19.5	35.6	59.3	24.8	1.2	0.3	-1.2	0.6	1.2	0.2	-1.4	0.3	-1.0	0.9	1.4	0.2
IPI00926940	MOCS1	isoform 4 of Molybdenum cofactor biosynthesis protein 1	91.2%	10.3	1	1	1	7	207,003	253,718	178,980	249,440	18,013	40,439	47,468	27,653	19.5	35.6	59.3	24.8	1.2	0.3	-1.2	0.6	1.2	0.2	-1.4	0.3	-1.0	0.9	1.4	0.2
				VNCVVMRGLNEDELLDFAALTEGLPLDVR	3	92.0%	1																									
IPI00180851	SYT6	isoform 1 of Synaptotagmin-6	99.5%	4.7	1	1	1	2	3,817,080	4,550,030	5,135,795	5,694,280	706,959	628,750	1,074,509	486,124	41.4	30.9	46.8	19.1	1.2	0.5	1.3	0.3	1.5	0.06	1.1	0.7	1.3	0.2	1.1	0.6
IPI00903166	SYT6	isoform 2 of Synaptotagmin-6	99.5%	5.7	1	1	1	2	3,817,080	4,550,030	5,135,795	5,694,280	706,959	628,750	1,074,509	486,124	41.4	30.9	46.8	19.1	1.2	0.5	1.3	0.3	1.5	0.06	1.1	0.7	1.3	0.2	1.1	0.6
				KTLNPTFDENFHFPVPYEELADRK	3	99.2%	1																									
IPI00180954	CIRBP	Cold-inducible RNA-binding protein	100.0%	18.6	2	3	5	1	1,342,331	1,319,712	1,222,117	1,558,540	134,477	40,764	91,115	17,989	22.4	6.9	16.7	2.6	-1.0	0.9	-1.1	0.5	1.2	0.2	-1.1	0.4	1.2	0.0007	1.3	0.02
				LFVGGLSFDTNEQSLEQVFSK	2	100.0%	2																									
				LFVGGLSFDTNEQSLEQVFSK	3	100.0%	1																									
				YGQISEVVVVK	2	100.0%	2																									
IPI00181265	CCDC120	cDNA FLJ56060, weakly similar to FERM domain-containing protein 4B	90.4%	3.7	1	1	1	4	1,284,453	975,378	1,262,598	998,423	79,121	73,215	65,759	71,563	13.8	16.8	11.7	16.0	-1.3	0.02	-1.0	0.8	-1.3	0.03	1.3	0.02	1.0	0.8	-1.3	0.03
IPI00942201	CCDC120	Coiled-coil domain-containing protein 120	90.4%	4.1	1	1	1	4	1,284,453	975,378	1,262,598	998,423	79,121	73,215	65,759	71,563	13.8	16.8	11.7	16.0	-1.3	0.02	-1.0	0.8	-1.3	0.03	1.3	0.02	1.0	0.8	-1.3	0.03
IPI00943718	CCDC120	coiled-coil domain-containing protein 120 isoform 4	90.4%	4.2	1	1	1	4	1,284,453	975,378	1,262,598	998,423	79,121	73,215	65,759	71,563	13.8	16.8	11.7	16.0	-1.3	0.02	-1.0	0.8	-1.3	0.03	1.3	0.02	1.0	0.8	-1.3	0.03
IPI00943897	CCDC120	coiled-coil domain-containing protein 120 isoform 2	90.4%	4.0	1	1	1	4	1,284,453	975,378	1,262,598	998,423	79,121	73,215	65,759	71,563	13.8	16.8	11.7	16.0	-1.3	0.02	-1.0	0.8	-1.3	0.03	1.3	0.02	1.0	0.8	-1.3	0.03
				DGLLTMLPGPPPVYAADSNSPLLRTK	3	86.6%	1																									
IPI00181283	PLCB3	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3 isoform 2	100.0%	3.3	2	3	3	1	424,172	463,166	496,458	518,422	33,100	13,848	55,944	23,599	17.5	6.7	25.2	10.2	1.1	0.3	1.2	0.3	1.2	0.05	1.1	0.6	1.1	0.08	1.0	0.7
				DDLIASILSEVAPTPLDELR	2	97.6%	1																									
				SFDPFTEVIVDGIVANALR	2	100.0%	1																									
				SFDPFTEVIVDGIVANALR	3	99.9%	1																									
IPI00181352	DNM2	dynamin-2 isoform 4	100.0%	22.1	13	13	13	3	22,363,649	22,828,587	23,337,544	26,310,493	2,194,041	1,103,186	1,898,498	715,673	21.9	10.8	18.2	6.1	1.0	0.9	1.0	0.7	1.2	0.1	1.0	0.8	1.2	0.03	1.1	0.2
IPI00514550	DNM2	dynamin-2 isoform 2	100.0%	22.0	13	13	13	3	22,363,649	22,828,587	23,337,544	26,310,493	2,194,041	1,103,186	1,898,498	715,673	21.9	10.8	18.2	6.1	1.0	0.9	1.0	0.7	1.2	0.1	1.0	0.8	1.2	0.03	1.1	0.2
IPI01015103	DNM2	98 kDa protein	100.0%	22.0	13	13	13	3	22,363,649	22,828,587	23,337,544	26,310,493	2,194,041	1,103,186	1,898,498	715,673	21.9	10.8	18.2	6.1	1.0	0.9	1.0	0.7	1.2	0.1	1.0	0.8	1.2	0.03	1.1	0.2
				AGVYPEKDQAENEDGAQENTFSMDPQLER	3	99.9%	1																									
				ALLQMVQQFGVDFEK	2	100.0%	1																									
				ALLQMVQQFGVDFEKR	3	100.0%	1																									
				ESSLILAVTPANMDLANSDALK	2	100.0%	1																									
				GISPVPINLR	2	84.2%	1																									
				GMEELIPLVNK	2	99.7%	1																									
				GWLTINNISLMK	2	99.4%	1																									
				IEGSGDQVDTLELSGGAR	2	100.0%	1																									
				LDLMDEGTDARDVLENK	3	84.1%	1																									
				NLVDSYVAIINK	2	100.0%	1																									
				SSVLENFVGR	2	99.9%	1																									
				VPVGDQPPDIEYQIK	2	100.0%	1																									
				VYSPHVLNLTLIDLPGITK	3	100.0%	1																									
IPI00181833	EPS8L3	isoform 1 of Epidermal growth factor receptor kinase substrate 8-like protein 3	99.9%	4.6	2	2	2	3	3,844,503	3,914,897	3,960,660	4,239,040	412,701	207,861	359,956	120,937	24.0	11.9	20.3	6.4	1.0	0.9	1.0	0.8	1.1	0.4	1.0	0.9	1.1	0.2	1.1	0.5
IPI00256752	EPS8L3	isoform 3 of Epidermal growth factor receptor kinase substrate 8-like protein 3	99.9%	4.6	2	2	2	3	3,844,503	3,914,897	3,960,660	4,239,040	412,701	207,861	359,956	120,937	24.0	11.9	20.3	6.4	1.0	0.9	1.0	0.8	1.1	0.4	1.0	0.9	1.1	0.2	1.1	0.5
IPI00302864	EPS8L3	isoform 2 of Epidermal growth factor receptor kinase substrate 8-like protein 3	99.9%	4.8	2	2	2	3	3,844,503	3,914,897	3,960,660	4,239,040	412,701	207,861	359,956	120,937	24.0	11.9	20.3	6.4	1.0	0.9	1.0	0.8	1.1	0.4	1.0	0.9	1.1	0.2	1.1	0.5
				IRPGELQMLCPQEAPR	3	96.8%	1																									
				VWSQDLILQVR	2	98.0%	1																									
IPI00182126	FKBP9	Peptidyl-prolyl cis-trans isomerase FKBP9	98.8%	5.1	2	2	2	2	1,823,680	1,959,040	1,588,161	2,101,369	234,755	172,099	209,809	145,563	28.8	19.6	29.5	15.5	1.1	0.7	-1.1	0.5	1.2	0.3	-1.2	0.2	1.1	0.5	1.3	0.08
IPI00922428	FKBP9	cDNA FLJ51089, highly similar to FK506-binding protein 9	98.8%	4.7	2	2	2	2	1,823,680	1,959,040	1,588,161	2,101,369	234,755	172,099	209,809	145,563	28.8	19.6	29.5	15.5	1.1	0.7	-1.1	0.5	1.2	0.3	-1.2	0.2	1.1	0.5	1.3	0.08
				TYDTYVGIGWLIPGMDK	2	98.8%	1																									
				YHYVGTFPDGQK	2	92.5%	1																									
IPI00182293	GUK1	Guanylate kinase	100.0%	17.3	3	3	3	9	1,544,077	1,568,769	1,596,443	1,765,587	116,671	94,153	107,463	97,901	16.9	13.4	15.1	12.4	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.3
IPI00470394	GUK1	Putative uncharacterized protein DKFZp666D023	100.0%	19.9	3	3	3	9	1,544,077	1,568,769	1,596,443	1,765,587	116,671	94,153	107,463	97,901	16.9	13.4	15.1	12.4	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.3
IPI00513820	GUK1	Guanylate kinase 1	100.0%	17.1	3	3	3	9	1,544,077	1,568,769	1,596,443	1,765,587	116,671	94,153	107,463	97,901	16.9	13.4	15.1	12.4	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.3
IPI00514021	GUK1	Uncharacterized protein	100.0%	11.9	3	3	3	9	1,544,077	1,568,769	1,596,443	1,765,587	116,671	94,153	107,463	97,901	16.9	13.4	15.1	12.4	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.3
IPI00514083	GUK1	Guanylate kinase 1	100.0%	14.1	3	3	3	9	1,544,077	1,568,769	1,596,443	1,765,587	116,671	94,153	107,463	97,901	16.9	13.4	15.1	12.4	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.3
IPI00514494	GUK1	Guanylate kinase 1	100.0%	15.6	3	3	3	9	1,544,077	1,568,769	1,596,443	1,765,587	116,671	94,153	107,463	97,901	16.9	13.4	15.1	12.4	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.3
IPI00514926	GUK1	Guanylate kinase 1	100.0%	13.4	3	3	3	9	1,544,077	1,568,769	1,596,443	1,765,587	116,671	94,153	107,463	97,901	16.9	13.4	15.1	12.4	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.3
IPI00515106	GUK1	Guanylate kinase 1	100.0%	14.1	3	3	3	9	1,544,077	1,568,769	1,596,443	1,765,587	116,671	94,153	107,463	97,901	16.9	13.4	15.1	12.4	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.3
IPI00644488	GUK1	guanylate kinase isoform a	100.0%	15.6	3	3	3	9	1,544,077	1,568,769	1,596,443	1,765,587	116,671	94,153	107,463	97,901	16.9	13.4	15.1	12.4	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.3
				ICVLDVDLQGVR	2	99.9%	1																									
				NTETEESLVKR	2	99.0%	1																									
				VAVQAVQAMNR	2	99.4%	1																									
IPI00182313	SEC61A2	protein transport protein Sec61 subunit alpha isoform 2 isoform b	93.8%	5.1	1	1	1	4	236,195	323,518	283,760	326,747	20,800	28,656	31,580	17,437	19.7	19.8	24.9	11.9	1.4	0.04	1.2	0.2	1.4	0.01	-1.1	0.4	1.0	0.9	1.2	0.3
IPI00414427	SEC61A2	isoform 1 of Protein transport protein Sec61 subunit alpha isoform 2	93.8%	4.8	1	1	1	4	236,195	323,518	283,760	326,747	20,800	28,656	31,580	17,437	19.7	19.8	24.9	11.9	1.4	0.04	1.2	0.2	1.4	0.01	-1.1	0.4	1.0	0.9	1.2	0.3
IPI00414428	SEC61A2	isoform 2 of Protein transport protein Sec61 subunit alpha isoform 2	93.8%	5.3	1	1	1	4	236,195	323,518	283,760	326,747	20,800	28,656	31,580	17,437	19.7	19.8	24.9	11.9	1.4	0.04	1.2	0.2	1.4	0.01	-1.1	0.4	1.0	0.9	1.2	0.3
IPI00982948	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae), isoform CRA_d	93.8%	5.5	1	1	1	4	236,195	323,518	283,760	326,747	20,800	28,656	31,580	17,437	19.7	19.8	24.9	11.9	1.4	0.04	1.2	0.2	1.4	0.01	-1.1	0.4	1.0	0.9	1.2	0.3
				FSGNFLVNLLGQWADVSGGGPAR	3	93.8%	1																									
IPI00182373	P4HA2	isoform IIa of Prolyl 4-hydroxylase subunit alpha-2	100.0%	21.2	7	7	7	1	15,046,916	16,939,693	17,355,343	18,934,703	968,805	904,024	696,653	752,078	14.4	11.9	9.0	8.9	1.1	0.2	1.2	0.09	1.3	0.01	1.0	0.7	1.1	0.1	1.1	0.2
				LATFLNYMSDVEAGGATVFPDLGAAIWPK	3	99.5%	1																									
				QFFPTDEDEIGAAK	2	99.7%	1																									
				SQVLDYLSYAVFQLGDLHR	3	93.8%	1																									
				SSWLEEDDDPVVAR	2	100.0%	1																									
				TGVLTVASYR	2	99.2%	1																									
				YQAMLSVDDCFGMGR	2	97.7%	1																									
				YYDVMSDEEIER	2	100.0%	1																									
IPI00182383	MST4	serine/threonine-protein kinase MST4 isoform 3	100.0%	7.6	2	2	2	4	1,735,548	1,613,991	1,543,748	1,815,053	217,790	58,772	42,533	116,461	28.1	8.1	6.2	14.4	-1.1	0.6	-1.1	0.4	1.0	0.8	-1.0	0.4	1.1	0.2	1.2	0.08
IPI00292827	MST4	Serine/threonine-protein kinase MST4	100.0%	6.5	2	2	2	4	1,735,548	1,613,991	1,543,748	1,815,053	217,790	58,772	42,533	116,461	28.1	8.1	6.2	14.4	-1.1	0.6	-1.1	0.4	1.0	0.8	-1.0	0.4	1.1	0.2	1.2	0.08
IPI00760722	MST4	serine/threonine-protein kinase MST4 isoform 2	100.0%	8.0	2	2	2	4	1,735,548	1,613,991	1,543,748	1,815,053	217,790	58,772	42,533	116,461	28.1	8.1	6.2	14.4	-1.1	0.6	-1.1	0.4	1.0	0.8	-1.0	0.4	1.1	0.2	1.2	0.08
IPI00945940	MST4	cDNA, FLJ79036, highly similar to Serine/threonine-protein kinase MST4	100.0%	6.2	2	2	2	4	1,735,548	1,613,991	1,543,748	1,815,053	217,790	58,772	42,533	116,461	28.1	8.1	6.2	14.4	-1.1	0.6	-1.1	0.4	1.0	0.8	-1.0	0.4	1.1	0.2	1.2	0.08
				LADFGVAGQLTDTQIKR	3	99.9%	1																									

				TSYLTELIDR	2	99.8%	1																									
IPI00182469	CTNND1	isoform 1AB of Catenin delta-1	100.0%	14.0	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00219725	CTNND1	isoform 2AB of Catenin delta-1	100.0%	14.9	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00219726	CTNND1	isoform 2AC of Catenin delta-1	100.0%	15.3	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00219728	CTNND1	isoform 2A of Catenin delta-1	100.0%	15.4	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00219733	CTNND1	isoform 3ABC of Catenin delta-1	100.0%	15.6	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00219734	CTNND1	isoform 3AB of Catenin delta-1	100.0%	15.7	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00219735	CTNND1	isoform 3AC of Catenin delta-1	100.0%	16.1	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00219738	CTNND1	isoform 3A of Catenin delta-1	100.0%	16.2	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00219870	CTNND1	isoform 1A of Catenin delta-1	100.0%	14.5	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00219875	CTNND1	isoform 2ABC of Catenin delta-1	100.0%	14.8	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00942869	CTNND1	isoform 1ABC of Catenin delta-1	100.0%	14.0	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
IPI00983022	CTNND1	Uncharacterized protein	100.0%	14.4	11	12	13	12	1,773,720	1,890,715	1,763,836	2,078,575	131,897	69,040	154,588	44,184	16.6	8.2	19.6	4.8	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.5	1.1	0.05	1.2	0.1
				AAALVLQTIWGYK	2	100.0%	2																									
				GYELLFQPEVVR	2	100.0%	1																									
				HAIPNLVK	2	100.0%	1																									
				NLAVDAR	1	83.0%	1																									
				QDVYGPQPQVR	2	100.0%	1																									
				QPELPEVIAMLGFR	2	99.9%	1																									
				SDFQVNLNNASR	2	99.9%	1																									
				SLDNNYSTPNER	2	99.7%	1																									
				SQSSHSYDDSTLPLIDR	2	94.8%	1																									
				SQSSHSYDDSTLPLIDR	3	99.4%	1																									
				TPAILEASAGAIQNLCAGR	3	98.3%	1																									
				VGGSSVDLHR	2	99.7%	1																									
IPI00182540	CTNND1	Uncharacterized protein	100.0%	13.0	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219727	CTNND1	isoform 2BC of Catenin delta-1	100.0%	13.8	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219730	CTNND1	isoform 2B of Catenin delta-1	100.0%	13.9	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219731	CTNND1	isoform 2C of Catenin delta-1	100.0%	14.2	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219732	CTNND1	isoform 2 of Catenin delta-1	100.0%	14.3	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219737	CTNND1	isoform 3BC of Catenin delta-1	100.0%	14.5	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219739	CTNND1	isoform 3B of Catenin delta-1	100.0%	14.6	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219741	CTNND1	isoform 3C of Catenin delta-1	100.0%	15.0	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219742	CTNND1	isoform 3 of Catenin delta-1	100.0%	15.2	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219869	CTNND1	isoform 1BC of Catenin delta-1	100.0%	13.0	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219872	CTNND1	isoform 1B of Catenin delta-1	100.0%	13.1	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00219873	CTNND1	isoform 1C of Catenin delta-1	100.0%	13.4	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00419482	CTNND1	catenin delta-1 isoform 1B	100.0%	13.1	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00845519	CTNND1	isoform 1 of Catenin delta-1	100.0%	13.5	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00977746	CTNND1	99 kDa protein	100.0%	13.9	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
IPI00979192	CTNND1	catenin delta-1 isoform 3B	100.0%	14.6	10	11	12	16	1,627,859	1,702,477	1,606,251	1,880,900	122,938	70,146	146,336	45,261	16.9	9.2	20.4	5.4	1.0	0.6	-1.0	0.9	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.1
				AAALVLQTIWGYK	2	100.0%	2																									
				GYELLFQPEVVR	2	100.0%	1																									
				HAIPNLVK	2	100.0%	1																									
				NLAVDAR	1	83.0%	1																									
				QDVYGPQPQVR	2	100.0%	1																									
				QPELPEVIAMLGFR	2	99.9%	1																									
				SDFQVNLNNASR	2	99.9%	1																									
				SQSSHSYDDSTLPLIDR	2	94.8%	1																									
				SQSSHSYDDSTLPLIDR	3	99.4%	1																									
				TPAILEASAGAIQNLCAGR	3	98.3%	1																									
				VGGSSVDLHR	2	99.7%	1																									
IPI00182728	VPS4B	Vacuolar protein sorting-associated protein 4B	94.7%	6.3	2	2	2	1	5,107,295	5,303,630	5,477,640	5,842,135	478,632	283,447	570,099	298,355	21.0	12.0	23.3	11.4	1.0	0.7	1.1	0.6	1.1	0.2	1.0	0.8	1.1	0.2	1.1	0.6
				LQNQLQGAIVIERPNVK	3	93.8%	1																									
				WSDVAGLEGAK	2	94.7%	1																									
IPI00182757	KIAA1967	isoform 1 of Protein KIAA1967	100.0%	13.4	8	8	8	2	16,497,215	18,122,137	17,555,235	21,323,587	1,918,031	853,849	1,367,984	640,473	26.0	10.5	17.4	6.7	1.1	0.5	1.1	0.7	1.3	0.06	-1.0	0.7	1.2	0.02	1.2	0.04
IPI00873406	KIAA1967	isoform 2 of Protein KIAA1967	100.0%	13.4	8	8	8	2	16,497,215	18,122,137	17,555,235	21,323,587	1,918,031	853,849	1,367,984	640,473	26.0	10.5	17.4	6.7	1.1	0.5	1.1	0.7	1.3	0.06	-1.0	0.7	1.2	0.02	1.2	0.04
				FAEFQYLQPGPPR	2	99.3%	1																									
				KEEEAVLVGGEWSPSLDGLDPQADPQVLVR	3	100.0%	1																									
				LTPLQLEIQR	2	93.9%	1																									
				QGILGAQPQLIFQPHR	3	100.0%	1																									
				TLAAEMQELR	2	99.4%	1																									
				VHLTPYTVDSPICDFLELQR	3	98.3%	1																									
				VLLLSSPGLEELYR	2	98.5%	1																									
				VQTLSNQPLLK	2	99.7%	1																									
IPI00182938	AHCYL1	isoform 1 of Putative adenosylhomocysteinase 2	99.8%	7.0	2	2	2	2	8,219,280	8,471,775	7,643,275	8,749,025	938,618	976,401	554,246	270,993	25.5	25.8	16.2	6.9	1.0	0.9	-1.1	0.6	1.1	0.6	-1.1	0.5	1.0	0.8	1.1	0.1
IPI00479201	AHCYL1	isoform 2 of Putative adenosylhomocysteinase 2	99.8%	7.7	2	2	2	2	8,219,280	8,471,775	7,643,275	8,749,025	938,618	976,401	554,246	270,993	25.5	25.8	16.2	6.9	1.0	0.9	-1.1	0.6	1.1	0.6	-1.1	0.5	1.0	0.8	1.1	0.1
				SISQSSTDSYSSAASYTDSSDDEVSPREK	3	93.9%	1																									
				TPELTWER	2	97.2%	1																									
IPI00183002	PPP1R12A	isoform 1 of Protein phosphatase 1 regulatory subunit 12A	100.0%	3.5	2	2	2	4	525,001	489,515	544,822	693,982	43,406	39,072	45,275	19,520	18.5	17.9	18.6	6.3	-1.1	0.6	1.0	0.8	1.3	0.008	1.1	0.4	1.4	0.002	1.3	0.02
IPI00397730	PPP1R12A	isoform 4 of Protein phosphatase 1 regulatory subunit 12A	100.0%	3.7	2	2	2	4	525,001	489,515	544,822	693,982	43,406	39,072	45,275	19,520	18.5	17.9	18.6	6.3	-1.1	0.6	1.0	0.8	1.3	0.008	1.1	0.4	1.4	0.002	1.3	0.02
IPI00413191	PPP1R12A	isoform 3 of Protein phosphatase 1 regulatory subunit 12A	100.0%	3.7	2	2	2	4	525,001	489,515	544,822	693,982	43,406	39,072	45,275	19,520	18.5	17.9	18.6	6.3	-1.1	0.6	1.0	0.8	1.3	0.008	1.1	0.4	1.4	0.002	1.3	0.02
IPI01015009	PPP1R12A	115 kDa protein	100.0%	3.5	2	2	2	4	525,001	489,515	544,822	693,982	43,406	39,072	45,275	19,520	18.5	17.9	18.6	6.3	-1.1	0.6	1.0	0.8	1.3	0.008	1.1	0.4	1.4	0.002	1.3	0.02
				TGSYGALAEITASK	2	96.0%	1																									
				VGQTAFDVADEDILGYLEELQK	3	100.0%	1																									
IPI00183274	SNX1	sorting nexin-1 isoform c	100.0%	4.4	2	2	2	2	9,434,735	10,703,383	9,622,318	11,154,413	622,905	394,958	750,994	295,191	14.8	8.3	17.5	5.9	1.1	0.1	1.0	0.9	1.2	0.04	-1.1	0.2	1.0	0.4	1.2	0.1
IPI00220527	SNX1	isoform 1A of Sorting nexin-1	100.0%	4.6	2	2	2	2	9,434,735	10,703,383	9,622,318	11,154,413	622,905	394,958	750,994	295,191	14.8	8.3	17.5	5.9	1.1	0.1	1.0	0.9	1.2	0.04	-1.1	0.2	1.0	0.4	1.2	0.1
				ELALNTAQFAK	2	92.5%	1																									
				YWEAFLPEAK	2	99.9%	1																									
IPI00183294	NUP214	isoform 1 of Nuclear pore complex protein Nup214	99.5%	1.5	2	2	2	5	1,254,303	1,177,610	1,219,118	1,343,403	71,371	53,107	51,863	52,188	12.7	10.1	9.5	8.7	-1.1	0.4	-1.0	0.7	1.1	0.3	1.0	0.6	1.1	0.06	1.1	0.1
IPI00646361	NUP214	isoform 5 of Nuclear pore complex protein Nup214	99.5%	1.5	2	2	2	5	1,254,303	1,177,610	1,219,118	1,343,403	71,371	53,107	51,863	52,188	12.7	10.1	9.5	8.7	-1.1	0.4	-1.0	0.7	1.1	0.3	1.0	0.6	1.1	0.06	1.1	0.1
IPI00900318	NUP214	isoform 2 of Nuclear pore complex protein Nup214	99.5%	1.5	2	2	2	5	1,254,303	1,177,610	1,219,118	1,343,403	71,371	53,107	51,863	52,188	12.7	10.1	9.5	8.7	-1.1	0.4	-1.0	0.7	1.1	0.3	1.0	0.6	1.1	0.06	1.1	0.1
IPI00900325	NUP214	isoform 3 of Nuclear pore complex protein Nup214	99.5%	1.5	2	2	2	5	1,254,303	1,177,610	1,219,118	1,343,403	71,371	53,107	51,863	52,188	12.7	10.1	9.5	8.7	-1.1	0.4	-1.0	0.7	1.1	0.3	1.0	0.6	1.1	0.06	1.1	0.1
IPI00900331	NUP214	isoform 4 of Nuclear pore complex protein Nup214	99.5%	1.5	2	2	2	5	1,254,303	1,177,610	1,219,118	1,343,403	71,371	53,107	51,863	52,188	12.7	10.1	9.5	8.7	-1.1	0.4	-1.0	0.7	1.1	0.3	1.0	0.6	1.1	0.06	1.1	0.1
				QSDQINWESWLLEDSSR	2	99.5%	1																									
				TTLLEGFAGVEEAR	3	91.8%	1																									
IPI00878175	-	30 kDa protein	99.9%	8.7	2	2	2	2	2,928,692	3,065,145	3,008,935	3,038,653	261,839	96,730	99,436	61,910	20.0	7.1	7.4	4.6	1.0	0.6	1.0	0.8	1.0	0.7	-1.0	0.7	-1.0	0.8	1.0	0.8
IPI00183508	TWF1	twinfilin-1	99.9%	6.0	2	2	2	2	2,928,692	3,065,145	3,008,935	3,038,653	261,839	96,730	99,436	61,910	20.0	7.1	7.4	4.6	1.0	0.6	1.0	0.8	1.0	0.7	-1.0	0.7	-1.0	0.8	1.0	0.8
				EIFARARNGK	2	80.8%	1																									
				INEVQTDVGVDTK	2	100.0%	1																									
IPI00183530	SNX1	cDNA FLJ46302 fis, clone TESTI4036048, highly similar to Sorting nexin 1	94.1%	2.0	1	1	1	1	3,547,610	3,801,233	3,473,793	3,724,913	126,889	34,537	348,204	99,559	8.0	2.0	22.4	6.0	1.1	0.1	-1.0	0.8	1.0	0.3	-1.1	0.4	-1.0	0.5	1.1	0.5
				ELALNTAQFAK	2	92.5%	1																									
IPI00183572	DOCK7	isoform 2 of Dedicator of cytokinesis protein 7	98.0%	0.7	1	1	1	7	293,960	284,840	312,029	314,914	29,905	20,273	25,054	21,816	22.8	15.9	18.0	15.5	-1.0	0.8	1.1	0.7	1.1	0.6	1.1	0.4	1.1	0.3	1.0	0.9
IPI00513791	DOCK7	isoform 1 of Dedicator of cytokinesis protein 7	98.0%	0.7	1	1	1	7	293,960	284,840	312,029	314,914	29,905	20,273	25,054	21,816	22.8	15.9	18.0	15.5	-1.0	0.8	1.1	0.7	1.1	0.6	1.1	0.4	1.1	0.3	1.0	0.9
IPI00807434	DOCK7	isoform 3 of Dedicator of cytokinesis protein 7	98.0%	0.7	1	1	1	7	293,960	284,840	312,029	314,914	29,905	20,273	25,054	21,816	22.8	15.9	18.0	15.5	-1.0	0.8	1.1	0.7	1.1	0.6	1.1	0.4	1.1	0.3	1.0	0.9
IPI00815633	DOCK7	isoform 6 of Dedicator of cytokinesis protein 7	98.0%	0.7	1	1	1	7	293,960	284,840	312,029	314,914	29,905	20,273	25,054	21,816	22.8	15.9	18.0	15.5	-1.0	0.8	1.1	0.7	1.1	0.6	1.1	0.4	1.1	0.3	1.0	0.9
IPI00815886	DOCK7	isoform 5 of Dedicator of cytokinesis protein 7	98.0%	0.7	1	1	1	7	293,960	284,840	312,029	314,914	29,905	20,273	25,054	21,816	22.8	15.9	18.0	15.5	-1.0	0.8	1.1	0.7	1.1	0.6	1.1	0.4	1.1	0.3	1.0	0.9
IPI00816106	DOCK7	isoform 4 of Dedicator of cytokinesis protein 7	98.0%	0.7	1	1	1	7	293,960	284,840	312,029	314,914	29,905	20,273	25,054	21,816	22.8	15.9	18.0	15.5	-1.0	0.8	1.1	0.7	1.1	0.6	1.1	0.4	1.1	0.3	1.0	0.9
IPI01008893	DOCK7	cDNA FLJ56240, highly similar to Dedicator of cytokinesis protein 7	98.0%	1.5	1	1	1	7	293,960	284,840	312,029	314,914	29,905	20,273	25,054	21,816	22.8	15.9	18.0	15.5	-1.0	0.8	1.1	0.7	1.1	0.6	1.1	0.4	1.1	0.3	1.0	0.9
				DSNPVDKCKLDPNK	2	98.0%	1																									
IPI00183603	OSTC	Oligosaccharyltransferase complex subunit OSTC	99.1%	8.1	1	1	1	2	3,791,610	3,789,425	3,471,380	3,956,255	186,062	120,789	220,987	116,516	11.0	7.1	14.2	6.6	-1.0	1	-1.1	0.3	1.0	0.5	-1.1	0.2	1.0	0.3	1.1	0.09
IPI00968228	OSTCL;OSTC	Uncharacterized protein	99.1%	7.0	1	1	1	2	3,791,610	3,789,425	3,471,380	3,956,255	186,062	120,789	220,987	116,516	11.0	7.1	14.2	6.6	-1.0	1	-1.1	0.3	1.0	0.5	-1.1	0.2	1.0	0.3	1.1	0.09
				VPFLVLECPNLK	2	99.1%	1																									
IPI00183695	S100A10	Protein S100-A10	100.0%	33.0	2	2	2	1	17,958,160	16,450,000	13,761,780	17,992,200	1,861,112	1,409,591	1,364,753	1,692,078	23.2	19.2	22.2	21.0	-1.1	0.5	-1.3	0.1	1.0	1	-1.2	0.2	1.1	0.5	1.3	0.09
				FAGDKGYLTK	2	99.7%	1																									
				VLMEKEFPGFLENQKDPLAVDK	3	97.2%	1																									
IPI00183879	ITPRIPL2	Inositol 1,4,5-triphosphate receptor-interacting protein-like 2	93.6%	1.9	1	1	1	1	6,708,220	7,505,700	6,674,820	7,899,310	948,805	461,651	654,801	393,876	31.6	13.8	21.9	11.2	1.1	0.5	-1.0	1	1.2	0.3	-1.1	0.3	1.1	0.5	1.2	0.1
				LEGHAAFSSR	2	93.6%	1																									
IPI00184160	RNF180	isoform 2 of E3 ubiquitin-protein ligase RNF180	97.0%	3.1	1	1	1	2	3,315,705	3,255,405	3,211,135	3,451,610	180,667	118,634	104,560	293,237	12.2	8.2	7.3	19.0	-1.0	0.8	-1.0	0.6	1.0	0.7	-1.0	0.8	1.1	0.6	1.1	0.5
IPI00784453	RNF180	isoform 1 of E3 ubiquitin-protein ligase RNF180	97.0%	2.2	1	1	1	2	3,315,705	3,255,405	3,211,135	3,451,610	180,667	118,634	104,560	293,237	12.2	8.2	7.3	19.0	-1.0	0.8	-1.0	0.6	1.0	0.7	-1.0	0.8	1.1	0.6	1.1	0.5
				LMRPSVKYLSHPR	3	97.0%	1																									
IPI00184262	ESRP1	isoform 3 of Epithelial splicing regulatory protein 1	96.5%	2.2	1	1	1	9	493,368	521,042	444,122	555,333	46,033	20,011	52,411	24,953	20.9	8.6	26.4	10.1	1.1	0.6	-1.1	0.5	1.1	0.3	-1.2	0.2	1.1	0.3	1.3	0.09
IPI00654821	ESRP1	isoform 4 of Epithelial splicing regulatory protein 1	96.5%	2.3	1	1	1	9	493,368	521,042	444,122	555,333	46,033	20,011	52,411	24,953	20.9	8.6	26.4	10.1	1.1	0.6	-1.1	0.5	1.1	0.3	-1.2	0.2	1.1	0.3	1.3	0.09
IPI00789651	ESRP1	isoform 2 of Epithelial splicing regulatory protein 1	96.5%	2.5	1	1	1	9	493,368	521,042	444,122	555,333	46,033	20,011	52,411	24,953	20.9	8.6	26.4	10.1	1.1	0.6	-1.1	0.5	1.1	0.3	-1.2	0.2	1.1	0.3	1.3	0.09
IPI00797684	ESRP1	isoform 1 of Epithelial splicing regulatory protein 1	96.5%	2.2	1	1	1	9	493,368	521,042	444,122	555,333	46,033	20,011	52,411	24,953	20.9	8.6	26.4	10.1	1.1	0.6	-1.1	0.5	1.1	0.3	-1.2	0.2	1.1	0.3	1.3	0.09
IPI00889667	ESRP1	epithelial splicing regulatory protein 1 isoform 5	96.5%	2.5	1	1	1	9	493,368	521,042	444,122	555,333	46,033	20,011	52,411	24,953	20.9	8.6	26.4	10.1	1.1	0.6	-1.1	0.5	1.1	0.3	-1.2	0.2	1.1	0.3	1.3	0.09
IPI00889741	ESRP1	epithelial splicing regulatory protein 1 isoform 3	96.5%	2.3	1	1	1	9	493,368	521,042	444,122	555,333	46,033	20,011	52,411	24,953	20.9	8.6	26.4	10.1	1.1	0.6	-1.1	0.5	1.1	0.3	-1.2	0.2	1.1	0.3	1.3	0.09
IPI00981412	ESRP1	Protein	96.5%	3.0	1	1	1	9	493,368	521,042	444,122	555,333	46,033	20,011	52,411	24,953	20.9	8.6	26.4	10.1	1.1	0.6	-1.1	0.5	1.1	0.3	-1.2	0.2	1.1	0.3	1.3	0.09
IPI01010529	ESRP1	71 kDa protein	96.5%	2.4	1	1	1	9	493,368	521,042	444,122	555,333	46,033	20,011	52,411	24,953	20.9	8.6	26.4	10.1	1.1	0.6	-1.1	0.5	1.1	0.3	-1.2	0.2	1.1	0.3	1.3	0.09
IPI01011591	ESRP1	58 kDa protein	96.5%	2.9	1	1	1	9	493,368	521,042	444,122	555,333	46,033	20,011	52,411	24,953	20.9	8.6	26.4	10.1	1.1	0.6	-1.1	0.5	1.1	0.3	-1.2	0.2	1.1	0.3	1.3	0.09
				IAGGTSNEVAQFLSK	2	96.5%	1																									
IPI00184376	SCAI	isoform 2 of Protein SCAI	96.4%	1.9	1	1	1	3	27,914,500	30,986,833	31,183,567	33,292,267	4,329,694	2,528,199	2,578,943	1,110,107	34.7	18.2	18.5	7.5	1.1	0.6	1.1	0.5	1.2	0.3	1.0	1	1.1	0.4	1.1	0.5
IPI00646433	SCAI	isoform 1 of Protein SCAI	96.4%	2.0	1	1	1	3	27,914,500	30,986,833	31,183,567	33,292,267	4,329,694	2,528,199	2,578,943	1,110,107	34.7	18.2	18.5	7.5	1.1	0.6	1.1	0.5	1.2	0.3	1.0	1	1.1	0.4	1.1	0.5
IPI00946202	SCAI	C9orf126 protein	96.4%	2.5	1	1	1	3	27,914,500	30,986,833	31,183,567	33,292,267	4,329,694	2,528,199	2,578,943	1,110,107	34.7	18.2	18.5	7.5	1.1	0.6	1.1	0.5	1.2	0.3	1.0	1	1.1	0.4	1.1	0.5
				ELSDEIEDYTHR	2	96.4%	1																									
IPI00184402	VAT1	Uncharacterized protein	100.0%	6.2	1	1	2	3	1,061,185	1,197,800	1,137,005	1,286,358	89,709	70,757	85,823	43,232	18.9	13.2	16.9	7.5	1.1	0.3	1.1	0.6	1.2	0.05	-1.1	0.6	1.1	0.3	1.1	0.2
IPI00789469	VAT1	22 kDa protein	100.0%	7.2	1	1	2	3	1,061,185	1,197,800	1,137,005	1,286,358	89,709	70,757	85,823	43,232	18.9	13.2	16.9	7.5	1.1	0.3	1.1	0.6	1.2	0.05	-1.1	0.6	1.1	0.3	1.1	0.2
IPI00797605	VAT1	15 kDa protein	100.0%	10.3	1	1	2	3	1,061,185	1,197,800	1,137,005	1,286,358	89,709	70,757	85,823	43,232	18.9	13.2	16.9	7.5	1.1	0.3	1.1	0.6	1.2	0.05	-1.1	0.6	1.1	0.3	1.1	0.2
				PAAPPAPGPGQLTLR	2	100.0%	2																									
IPI00184821	COASY	isoform 1 of Bifunctional coenzyme A synthase	97.6%	2.1	1	1	1	3	900,330	1,035,739	967,890	1,039,763	102,630	196,222	96,128	115,801	25.5	42.4	22.2	24.9	1.2	0.6	1.1	0.6	1.2	0.4	-1.1	0.8	1.0	1	1.1	0.6
IPI00783178	COASY	bifunctional coenzyme A synthase isoform b	97.6%	4.5	1	1	1	3	900,330	1,035,739	967,890	1,039,763	102,630	196,222	96,128	115,801	25.5	42.4	22.2	24.9	1.2	0.6	1.1	0.6	1.2	0.4	-1.1	0.8	1.0	1	1.1	0.6
IPI00909064	COASY	isoform 2 of Bifunctional coenzyme A synthase	97.6%	2.0	1	1	1	3	900,330	1,035,739	967,890	1,039,763	102,630	196,222	96,128	115,801	25.5	42.4	22.2	24.9	1.2	0.6	1.1	0.6	1.2	0.4	-1.1	0.8	1.0	1	1.1	0.6
				ILTDIMWPIIAK	2	97.6%	1																									
IPI00185146	IPO9	Importin-9	92.1%	2.9	1	1	1	1	316,984	345,183	456,302	514,733	64,378	75,662	62,525	57,470	45.4	49.0	30.6	25.0	1.1	0.8	1.4	0.2	1.6	0.05	1.3	0.3	1.5	0.1	1.1	0.5
				FTVAMSPELIQQFLQATVSGLHETQPPSVR	3	92.1%	1																									
IPI00185217	RAB1A	isoform 3 of Ras-related protein Rab-1A	100.0%	27.9	2	3	4	2	2,895,495	2,874,018	3,307,535	3,193,071	337,418	240,260	325,036	117,073	26.1	18.7	22.0	8.2	-1.0	1	1.1	0.4	1.1	0.4	1.2	0.3	1.1	0.3	-1.0	0.8
IPI00937805	RAB1A	14 kDa protein	100.0%	27.9	2	3	4	2	2,895,495	2,874,018	3,307,535	3,193,071	337,418	240,260	325,036	117,073	26.1	18.7	22.0	8.2	-1.0	1	1.1	0.4	1.1	0.4	1.2	0.3	1.1	0.3	-1.0	0.8
				FADDTYTESYISTIGVDFK	2	100.0%	2																									
				FADDTYTESYISTIGVDFK	3	100.0%	1																									
				NATNVEQSFMTMAAEIK	3	100.0%	1																									
IPI00185374	PSMD12	26S proteasome non-ATPase regulatory subunit 12	100.0%	14.5	5	5	6	1	17,128,811	18,370,880	16,357,582	18,767,186	1,450,838	939,429	922,564	1,133,290	18.9	11.4	12.6	13.5	1.1	0.5	-1.0	0.7	1.1	0.4	-1.1	0.2	1.0	0.8	1.1	0.1
				DPNNLLNDWSQK	2	99.6%	1																									
				EWDLLNENIMLLSK	2	100.0%	1																									
				INTKFFQEENTEKLK	2	89.8%	1																									
				LQEVIETLLSLEK	2	100.0%	2																									
				MEVDYSATVDQR	2	87.0%	1																									
IPI00185574	CALB2	Uncharacterized protein	100.0%	21.2	4	4	5	2	19,877,010	19,783,847	19,009,947	21,933,330	1,401,835	925,174	1,326,758	446,716	15.8	10.5	15.6	4.6	-1.0	1	-1.0	0.7	1.1	0.2	-1.0	0.6	1.1	0.07	1.2	0.09

IPI00413067	CALB2	calretinin isoform 22k	100.0%	19.8	4	4	5	2	19,877,010	19,783,847	19,009,947	21,933,330	1,401,835	925,174	1,326,758	446,716	15.8	10.5	15.6	4.6	-1.0	1	-1.0	0.7	1.1	0.2	-1.0	0.6	1.1	0.07	1.2	0.09
				ELENFFQELEK	2	99.9%	2																									
				LGLSEMSR	2	99.0%	1																									
				LQEYTQTILR	2	99.1%	1																									
				MFDLNGDGK	2	99.9%	1																									
IPI00185919	LARP1	isoform 1 of La-related protein 1	99.3%	2.8	2	2	2	3	10,784,360	10,419,580	9,880,368	11,631,033	619,536	476,664	503,622	281,533	12.9	10.2	11.4	5.4	-1.0	0.7	-1.1	0.3	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.02
IPI00411690	LARP1	isoform 2 of La-related protein 1	99.3%	3.0	2	2	2	3	10,784,360	10,419,580	9,880,368	11,631,033	619,536	476,664	503,622	281,533	12.9	10.2	11.4	5.4	-1.0	0.7	-1.1	0.3	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.02
IPI00977919	LARP1	Uncharacterized protein	99.3%	5.1	2	2	2	3	10,784,360	10,419,580	9,880,368	11,631,033	619,536	476,664	503,622	281,533	12.9	10.2	11.4	5.4	-1.0	0.7	-1.1	0.3	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.02
				FQQVPTDALANK	2	98.2%	1																									
				FSHLTSLPQQLPSQQLMSK	3	99.0%	1																									
IPI00186008	STARD10	PCTP-like protein	100.0%	36.1	7	7	9	1	10,048,055	10,607,700	10,406,887	11,996,288	525,853	331,501	677,007	628,646	11.7	7.0	14.6	11.7	1.1	0.4	1.0	0.7	1.2	0.04	-1.0	0.8	1.1	0.09	1.2	0.1
				AGVSVWVQAVEMDR	2	95.9%	1																									
				AVSIQTGYLIQSTGPK	2	100.0%	2																									
				ESVQVPDDQDFR	2	99.9%	2																									
				MECCDVPAETLYDVLHDIEYR	3	99.4%	1																									
				MGGAGGEGSDDDTSLT	3	93.9%	1																									
				SCVITYLAQVDPK	2	99.5%	1																									
				WDSNVIETFDIAR	2	99.2%	1																									
IPI00186290	EEF2	Elongation factor 2	100.0%	41.7	31	36	49	1	373,573,205	386,916,838	391,438,045	442,081,079	########	########	########	########	20.3	9.6	16.4	5.8	1.0	0.7	1.0	0.7	1.2	0.1	1.0	0.9	1.1	0.03	1.1	0.1
				AGIIASAR	2	98.4%	1																									
				ALLELQLEPEELYQTFQR	2	100.0%	2																									
				ALLELQLEPEELYQTFQR	3	100.0%	2																									
				ARPFPDGLAEDIDKGEVSAR	3	100.0%	2																									
				AYLPVNESFGFTADLR	2	100.0%	2																									
				CELLYEGPPDDEAAMGIK	2	100.0%	1																									
				EDLYLKPIQR	2	95.6%	1																									
				EGALCEENMR	2	99.9%	1																									
				EGIPALDNFLDK	2	99.6%	1																									
				EGIPALDNFLDKL	2	100.0%	3																									
				FSVSPVVR	2	99.8%	1																									
				GGGQIIPTAR	2	94.6%	1																									
				GHVFEESQVAGTPMFVVK	2	100.0%	1																									
				GHVFEESQVAGTPMFVVK	3	87.7%	1																									
				GVQYLNEIK	2	99.9%	1																									
				GVQYLNEIKDSVVAGFQWATK	3	95.8%	1																									
				IMGPNYTPGK	2	95.9%	1																									
				IWCFGPDGTGPNILTDITK	2	100.0%	2																									
				KEDLYLKPIQR	2	92.3%	1																									
				KIWCFGPDGTGPNILTDITK	3	100.0%	2																									
				KVEDMMK	2	99.8%	2																									
				NMSVIAHVDHGK	2	100.0%	1																									
				NPADLPK	1	98.6%	1																									
				PSQVVAETR	2	95.2%	1																									
				QFAEMYVAK	2	99.0%	1																									
				SDPVVSYR	2	100.0%	1																									
				STAISLFYELSENDLNFIK	2	100.0%	2																									
				STAISLFYELSENDLNFIK	3	100.0%	1																									
				TFCQLILDPIFK	2	100.0%	2																									
				VFSGLVSTGLK	2	100.0%	1																									
				WLPAGDALLQMITIHLPSPVTAQK	2	96.4%	1																									
				WLPAGDALLQMITIHLPSPVTAQK	3	100.0%	1																									
				YEWDVAEAR	2	100.0%	2																									
				YLAEKYEWDVAEAR	2	99.7%	1																									
				YLAEKYEWDVAEAR	3	100.0%	1																									
				YVEPIEDVPCGNIVGLVGVDQFLVK	2	100.0%	2																									
IPI00186338	C100505506;LOC645	barrier-to-autointegration factor-like	100.0%	41.9	2	3	4	1	6,013,385	5,687,179	5,905,496	6,621,170	472,888	196,064	546,907	86,031	17.6	7.7	20.7	2.9	-1.1	0.5	-1.0	0.9	1.1	0.3	1.0	0.7	1.2	0.002	1.1	0.3
				AYVVLGQFLVLK	2	100.0%	2																									
				DFVAEPMGEKPVGSLAGIGEVLGK	2	100.0%	1																									
				DFVAEPMGEKPVGSLAGIGEVLGK	3	100.0%	1																									
IPI00827972	PARF	Putative GTP-binding protein Parf	100.0%	9.2	3	3	5	2	1,650,152	1,721,505	1,650,367	2,021,771	78,312	102,013	61,920	130,073	10.6	13.3	8.4	14.4	1.0	0.6	1.0	1	1.2	0.04	-1.0	0.6	1.2	0.1	1.2	0.03
IPI00983976	C9orf86	54 kDa protein	100.0%	9.9	3	3	5	2	1,650,152	1,721,505	1,650,367	2,021,771	78,312	102,013	61,920	130,073	10.6	13.3	8.4	14.4	1.0	0.6	1.0	1	1.2	0.04	-1.0	0.6	1.2	0.1	1.2	0.03
				FFNIPFLQLQR	2	100.0%	2																									
				NIPAGLQSMNQALQR	2	100.0%	2																									
				PFVEEYIPTQEIQVTSIHWSYK	3	99.8%	1																									
IPI00186946	COL25A1	isoform 1 of Collagen alpha-1(XXV) chain	93.5%	5.1	1	1	1	5	677,404	728,006	780,400	766,508	18,617	20,690	71,028	34,759	6.2	6.4	20.4	10.1	1.1	0.1	1.2	0.2	1.1	0.05	1.1	0.5	1.1	0.4	-1.0	0.9
IPI00852938	COL25A1	Uncharacterized protein	93.5%	5.1	1	1	1	5	677,404	728,006	780,400	766,508	18,617	20,690	71,028	34,759	6.2	6.4	20.4	10.1	1.1	0.1	1.2	0.2	1.1	0.05	1.1	0.5	1.1	0.4	-1.0	0.9
IPI00942774	COL25A1	isoform 2 of Collagen alpha-1(XXV) chain	93.5%	5.1	1	1	1	5	677,404	728,006	780,400	766,508	18,617	20,690	71,028	34,759	6.2	6.4	20.4	10.1	1.1	0.1	1.2	0.2	1.1	0.05	1.1	0.5	1.1	0.4	-1.0	0.9
IPI00953070	COL25A1	isoform 3 of Collagen alpha-1(XXV) chain	93.5%	5.7	1	1	1	5	677,404	728,006	780,400	766,508	18,617	20,690	71,028	34,759	6.2	6.4	20.4	10.1	1.1	0.1	1.2	0.2	1.1	0.05	1.1	0.5	1.1	0.4	-1.0	0.9
IPI01010812	COL25A1	65 kDa protein	93.5%	5.0	1	1	1	5	677,404	728,006	780,400	766,508	18,617	20,690	71,028	34,759	6.2	6.4	20.4	10.1	1.1	0.1	1.2	0.2	1.1	0.05	1.1	0.5	1.1	0.4	-1.0	0.9
				GEQGSPGIPGMDGEQGLKGSKGDMGDPGMTGEK	3	93.5%	1																									
IPI00186966	BIN1	isoform IIA of Myc box-dependent-interacting protein 1	100.0%	12.0	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
IPI00220586	BIN1	isoform BIN1-13 of Myc box-dependent-interacting protein 1	100.0%	16.8	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
IPI00220587	BIN1	isoform BIN1+12A of Myc box-dependent-interacting protein 1	100.0%	14.3	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
IPI00220996	BIN1	isoform IIB of Myc box-dependent-interacting protein 1	100.0%	13.7	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
IPI00220997	BIN1	isoform IIC1 of Myc box-dependent-interacting protein 1	100.0%	14.0	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
IPI00220998	BIN1	isoform II2 of Myc box-dependent-interacting protein 1	100.0%	14.7	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
IPI00220999	BIN1	isoform II3 of Myc box-dependent-interacting protein 1	100.0%	16.2	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
IPI00221000	BIN1	isoform BIN1 of Myc box-dependent-interacting protein 1	100.0%	15.6	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
IPI00221001	BIN1	isoform BIN1-10-13 of Myc box-dependent-interacting protein 1	100.0%	17.4	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
IPI00329733	BIN1	isoform IIC2 of Myc box-dependent-interacting protein 1	100.0%	15.0	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
IPI00395680	BIN1	isoform IID of Myc box-dependent-interacting protein 1	100.0%	12.9	4	5	6	11	2,750,586	2,984,444	3,040,311	3,346,138	186,978	202,691	197,399	199,406	15.2	15.2	14.5	13.3	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.8	1.1	0.2	1.1	0.3
				LNQNLNDVLVGLEK	2	99.9%	2																									
				LVDQALLTMDTYLGQFPDIK	2	100.0%	1																									
				LVDQALLTMDTYLGQFPDIK	3	100.0%	1																									
				VNHEPEPAGGATPGATLPK	3	100.0%	1																									
				VQAQHDYTATDTDELQLK	3	99.5%	1																									
IPI00480056	RAB4A	RAB4A, member RAS oncogene family variant	93.6%	6.4	1	1	1	3	2,543,707	1,945,297	2,810,730	2,255,630	139,022	172,054	102,694	179,619	12.2	19.8	8.2	17.8	-1.3	0.03	1.1	0.2	-1.1	0.2	1.4	0.003	1.2	0.2	-1.2	0.03
IPI00477489	RAB4B;MIA	isoform 1 of Ras-related protein Rab-4B	93.6%	6.6	1	1	1	3	2,543,707	1,945,297	2,810,730	2,255,630	139,022	172,054	102,694	179,619	12.2	19.8	8.2	17.8	-1.3	0.03	1.1	0.2	-1.1	0.2	1.4	0.003	1.2	0.2	-1.2	0.03
IPI00187143	RAB4B	isoform 2 of Ras-related protein Rab-4B	93.6%	5.7	1	1	1	3	2,543,707	1,945,297	2,810,730	2,255,630	139,022	172,054	102,694	179,619	12.2	19.8	8.2	17.8	-1.3	0.03	1.1	0.2	-1.1	0.2	1.4	0.003	1.2	0.2	-1.2	0.03
				GAAGALLVYDITSR	2	93.6%	1																									
IPI00187145	CDK5RAP3	isoform 3 of CDK5 regulatory subunit-associated protein 3	98.6%	5.0	1	1	1	1	971,473	1,010,437	1,054,027	1,176,687	102,085	97,464	90,402	67,882	23.5	21.6	19.2	12.9	1.0	0.8	1.1	0.6	1.2	0.1	1.0	0.8	1.2	0.2	1.1	0.3
				GPDALTLLEYTETR	2	98.6%	1																									
IPI00215637	DDX3X	ATP-dependent RNA helicase DDX3X	100.0%	12.2	6	6	6	3	5,230,339	4,826,019	4,593,485	5,191,586	368,490	196,330	303,390	107,726	15.8	9.1	14.8	4.6	-1.1	0.4	-1.1	0.2	-1.0	0.9	-1.1	0.5	1.1	0.1	1.1	0.1
IPI00984839	DDX3X	ATP-dependent RNA helicase DDX3X isoform 2	100.0%	12.3	6	6	6	3	5,230,339	4,826,019	4,593,485	5,191,586	368,490	196,330	303,390	107,726	15.8	9.1	14.8	4.6	-1.1	0.4	-1.1	0.2	-1.0	0.9	-1.1	0.5	1.1	0.1	1.1	0.1
IPI00985384	DDX3X	ATP-dependent RNA helicase DDX3X isoform 3	100.0%	12.5	6	6	6	3	5,230,339	4,826,019	4,593,485	5,191,586	368,490	196,330	303,390	107,726	15.8	9.1	14.8	4.6	-1.1	0.4	-1.1	0.2	-1.0	0.9	-1.1	0.5	1.1	0.1	1.1	0.1
				EIQMLAR	2	87.7%	1																									
				LEQELFSGGNTGINFEK	2	92.8%	1																									
				MLDMGFEPQIR	2	100.0%	1																									
				QYPISLVLAPTR	2	95.9%	1																									
				SFLLDLLNATGK	2	100.0%	1																									
				TAAFLLPILSQIYSDGPGEALR	3	100.0%	1																									
IPI00215719	RPL18	60S ribosomal protein L18	100.0%	12.8	2	2	2	1	5,941,005	5,719,485	5,616,920	6,559,105	439,068	233,550	336,272	460,255	16.5	9.1	13.4	15.7	-1.0	0.7	-1.1	0.6	1.1	0.4	-1.0	0.8	1.1	0.1	1.2	0.1
				TAVVVGTITDDVR	2	100.0%	1																									
				TNSTFNQVVLK	2	99.9%	1																									
IPI00215743	RRBP1	isoform 3 of Ribosome-binding protein 1	100.0%	31.6	33	34	39	2	42,305,188	45,286,325	43,212,600	49,665,577	3,612,905	1,938,828	3,194,133	1,575,204	19.1	9.6	16.5	7.1	1.1	0.5	1.0	0.9	1.2	0.1	-1.0	0.6	1.1	0.1	1.1	0.1
IPI00856098	RRBP1	p180/ribosome receptor	100.0%	28.9	33	34	39	2	42,305,188	45,286,325	43,212,600	49,665,577	3,612,905	1,938,828	3,194,133	1,575,204	19.1	9.6	16.5	7.1	1.1	0.5	1.0	0.9	1.2	0.1	-1.0	0.6	1.1	0.1	1.1	0.1
				AAILETAPK	2	89.4%	1																									
				AGIIQDTWHK	3	96.7%	1																									
				AQEQQQQMAELHSK	3	100.0%	2																									
				EHTSHLEAELEK	2	99.9%	1																									
				EQEITAVQAR	2	100.0%	1																									
				EVPMVVVPPVGAK	2	99.4%	1																									
				HLEEIVEK	2	100.0%	2																									
				HPPAPAEPSSDLASK	2	100.0%	1																									
				KKGEPGPPDADGPLYLPYK	3	85.1%	1																									
				KLTSDLGR	2	81.1%	1																									
				LKELESQVSGLEK	2	99.9%	1																									
				LKGELESSDQVR	3	99.9%	1																									
				LLATEQEDAAVAK	2	100.0%	2																									
				LQQENSILR	2	98.0%	1																									
				LQSSEAEVR	2	89.3%	1																									
				LREAEETQSTLQAECDQYR	3	98.3%	1																									
				LTAEFEEAQTSACR	2	99.9%	1																									
				NTDVAQSPEAPKQEAPAK	3	91.3%	1																									
				QLLLESQSQLDAAK	2	100.0%	2																									
				QSDELALVR	2	88.6%	1																									
				QVLQLQASHR	2	88.0%	1																									
				SHVEDGDIAGAPASSPEAPPAEQDPVQLK	3	100.0%	1																									
				SIEALLEAGQAR	2	99.9%	1																									
				SILAETEGMLR	2	100.0%	2																									
				SKCEELSGLHGQLQEAR	3	80.4%	1																									
				SVEEEEQVWR	2	100.0%	1																									
				TAGPLESSETEEASQLKER	3	98.7%	1																									
				TLQEQLENGPNTQLAR	2	100.0%	1																									
				TLVSTVGSMVFNEGEAQR	2	100.0%	1																									
				TQLEWTEAILEDEQTQR	3	100.0%	1																									
				VDTTPNQGKK	2	89.4%	1																									
				VEPAVSSVVNSIQVLTSK	2	99.9%	1																									
				VEPAVSSVVNSIQVLTSK	3	100.0%	1																									
				VGAAEEELQK	2	98.3%	1																									
IPI00215780	RPS19	40S ribosomal protein S19	100.0%	17.2	3	3	3	1	18,128,080	19,921,310	18,514,210	21,550,280	1,292,960	919,115	1,588,870	955,276	16.0	10.3	19.2	9.9	1.1	0.3	1.0	0.9	1.2	0.07	-1.1	0.5	1.1	0.3	1.2	0.1
				ELAPYDENWFYTR	2	99.7%	1																									
				HKELAPYDENWFYTR	3	99.9%	1																									
				NGVMPSHFSR	2	95.5%	1																									
IPI00215861	USH1C	isoform 2 of Harmonin	97.7%	1.7	1	1	1	5	1,501,286	1,788,704	1,583,132	1,849,090	114,269	102,179	142,464	48,694	17.0	12.8	20.1	5.9	1.2	0.1	1.1	0.7	1.2	0.02	-1.1	0.3	1.0	0.6	1.2	0.1
IPI00218195	USH1C	Similar to Harmonin isoform b3	97.7%	1.4	1	1	1	5	1,501,286	1,788,704	1,583,132	1,849,090	114,269	102,179	142,464	48,694	17.0	12.8	20.1	5.9	1.2	0.1	1.1	0.7	1.2	0.02	-1.1	0.3	1.0	0.6	1.2	0.1
IPI00412105	USH1C	harmonin isoform b3	97.7%	1.0	1	1	1	5	1,501,286	1,788,704	1,583,132	1,849,090	114,269	102,179	142,464	48,694	17.0	12.8	20.1	5.9	1.2	0.1	1.1	0.7	1.2	0.02	-1.1	0.3	1.0	0.6	1.2	0.1

IPI00478105	USH1C	isoform 4 of Harmonin	97.7%	1.7	1	1	1	5	1,501,286	1,788,704	1,583,132	1,849,090	114,269	102,179	142,464	48,694	17.0	12.8	20.1	5.9	1.2	0.1	1.1	0.7	1.2	0.02	-1.1	0.3	1.0	0.6	1.2	0.1
IPI00910900	USH1C	cDNA FLJ51329, highly similar to Harmonin	97.7%	1.9	1	1	1	5	1,501,286	1,788,704	1,583,132	1,849,090	114,269	102,179	142,464	48,694	17.0	12.8	20.1	5.9	1.2	0.1	1.1	0.7	1.2	0.02	-1.1	0.3	1.0	0.6	1.2	0.1
				VVVSAVYER	2	97.7%	1																									
IPI00215884	SRSF1	isoform ASF-1 of Serine/arginine-rich splicing factor 1	100.0%	40.7	8	9	18	1	18,193,910	19,246,890	18,731,256	21,840,572	1,217,624	534,476	1,052,515	547,776	15.0	6.2	12.6	5.6	1.1	0.5	1.0	0.7	1.2	0.03	-1.0	0.7	1.1	0.01	1.2	0.03
				DGTGVVEFVR	2	99.9%	2																									
				DGYDYDGYR	2	100.0%	2																									
				EAGDVCYADVYR	2	100.0%	2																									
				GGPPFAFVEFEDPRDAEDAVYGR	3	99.9%	2																									
				IYVGNLPPDIR	2	100.0%	3																									
				SHEGETAYIR	2	100.0%	3																									
				TKDIEDVFYK	2	100.0%	2																									
				TKDIEDVFYK	3	96.5%	1																									
				VVVSGLPPSGSWQDLK	2	99.5%	1																									
IPI00215888	SRP72	Signal recognition particle 72 kDa protein	97.9%	1.5	1	1	1	2	3,435,565	3,325,190	3,733,210	3,751,370	123,484	271,166	84,862	205,336	8.0	18.2	5.1	12.2	-1.0	0.7	1.1	0.08	1.1	0.2	1.1	0.2	1.1	0.2	1.0	0.9
IPI00966751	SRP72	CaM kinase II isoform	97.9%	1.6	1	1	1	2	3,435,565	3,325,190	3,733,210	3,751,370	123,484	271,166	84,862	205,336	8.0	18.2	5.1	12.2	-1.0	0.7	1.1	0.08	1.1	0.2	1.1	0.2	1.1	0.2	1.0	0.9
				LTNAEGVEFK	2	97.9%	1																									
IPI00215901	AK2	isoform 1 of Adenylate kinase 2, mitochondrial	100.0%	44.4	8	8	10	2	7,876,957	8,051,182	9,073,140	8,929,527	560,761	480,728	543,547	388,828	15.9	13.4	13.4	9.7	1.0	0.8	1.2	0.2	1.1	0.2	1.1	0.2	1.1	0.2	-1.0	0.8
IPI00218988	AK2	isoform 2 of Adenylate kinase 2, mitochondrial	100.0%	45.7	8	8	10	2	7,876,957	8,051,182	9,073,140	8,929,527	560,761	480,728	543,547	388,828	15.9	13.4	13.4	9.7	1.0	0.8	1.2	0.2	1.1	0.2	1.1	0.2	1.1	0.2	-1.0	0.8
				AMVASGSELGKK	2	99.9%	1																									
				AVLLGPPGAGK	2	99.8%	1																									
				EKLDSVIEFSIPDSLLIR	2	98.9%	1																									
				GIHSAIDASQTPDVVFASILAAFSK	3	100.0%	1																									
				LDSVIEFSIPDSLLIR	2	99.9%	1																									
				LQAYHTQTTPLIEYYR	3	100.0%	1																									
				LVSDEMVVELIEK	2	100.0%	2																									
				QAEMLDDLMEK	2	100.0%	2																									
IPI00215911	APEX1	DNA-(apurinic or apyrimidinic site) lyase	100.0%	23.0	6	6	7	1	20,772,772	22,251,173	21,486,800	24,736,790	3,434,317	1,095,049	2,243,221	1,194,427	37.0	11.0	23.3	10.8	1.1	0.7	1.0	0.9	1.2	0.3	-1.0	0.8	1.1	0.2	1.2	0.2
				GAVAEDGDELRTEPEAK	2	88.2%	1																									
				GLDWVKEEAPDILCLQETK	3	99.4%	1																									
				ICSWNVDGLR	2	99.9%	2																									
				KGAVAEDGDELRTEPEAK	3	97.4%	1																									
				NAGFTPQER	2	94.3%	1																									
				QGFGELLQAVPLADSFR	2	100.0%	1																									
IPI00215914	ARF1	ADP-ribosylation factor 1	100.0%	43.7	6	7	10	2	9,378,106	9,533,708	10,044,075	10,278,027	595,782	257,460	546,045	241,366	14.2	6.0	12.2	5.3	1.0	0.8	1.1	0.4	1.1	0.2	1.1	0.4	1.1	0.07	1.0	0.7
IPI00215917	ARF3	ADP-ribosylation factor 3	100.0%	43.7	6	7	10	2	9,378,106	9,533,708	10,044,075	10,278,027	595,782	257,460	546,045	241,366	14.2	6.0	12.2	5.3	1.0	0.8	1.1	0.4	1.1	0.2	1.1	0.4	1.1	0.07	1.0	0.7
				ILMVGLDAAGK	2	100.0%	1																									
				LGEIVTTIPTIGFNVETVEYK	2	100.0%	2																									
				LGEIVTTIPTIGFNVETVEYK	3	100.0%	1																									
				MLAEDELR	2	88.1%	1																									
				MLAEDELRDAVLLVFANK	2	100.0%	2																									
				NISFTVWDVGGQDK	2	100.0%	1																									
				QDLPNAMNAAEITDK	2	100.0%	2																									
IPI00215918	ARF4	ADP-ribosylation factor 4	100.0%	51.7	6	7	8	1	16,985,909	18,054,760	19,455,116	19,573,331	1,546,952	854,087	1,489,283	493,406	20.4	10.6	17.1	5.6	1.1	0.6	1.1	0.3	1.2	0.2	1.1	0.4	1.1	0.2	1.0	0.9
				ILMVGLDAAGK	2	100.0%	1																									
				IQEVADELQK	2	99.9%	1																									
				LGEIVTTIPTIGFNVETVEYK	2	100.0%	2																									
				LGEIVTTIPTIGFNVETVEYK	3	100.0%	1																									
				MLLVDELR	2	94.7%	1																									
				QDLPNAMAISEMTDK	2	99.9%	1																									
				TWYVQATCATQGTGLYEGLDWLSNELSK	3	97.9%	1																									
IPI00215919	ARF5	ADP-ribosylation factor 5	100.0%	26.1	3	4	6	2	4,158,738	4,150,021	4,213,868	4,416,992	389,502	243,047	445,975	137,699	20.9	13.1	23.7	7.0	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9	1.1	0.4	1.0	0.7
IPI00853337	ARF5	Uncharacterized protein	100.0%	31.3	3	4	6	2	4,158,738	4,150,021	4,213,868	4,416,992	389,502	243,047	445,975	137,699	20.9	13.1	23.7	7.0	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9	1.1	0.4	1.0	0.7
				ILMVGLDAAGK	2	100.0%	1																									
				LGEIVTTIPTIGFNVETVEYK	2	100.0%	2																									
				LGEIVTTIPTIGFNVETVEYK	3	100.0%	1																									
				QDMPNAMPVSELTDK	2	100.0%	2																									
IPI00215920	ARF6	ADP-ribosylation factor 6	97.7%	6.3	1	1	1	1	5,266,760	6,288,500	6,250,720	8,295,160	762,833	704,598	533,096	424,286	32.4	25.1	19.1	11.4	1.2	0.4	1.2	0.3	1.6	0.008	-1.0	1	1.3	0.04	1.3	0.02
				FNVWDVGGQDK	2	97.7%	1																									
IPI00215928	CETN2	Centrin-2	98.9%	7.6	1	1	1	1	1,668,110	1,869,490	1,670,511	2,076,780	139,721	130,867	44,914	171,736	18.7	15.7	6.0	18.5	1.1	0.3	1.0	1	1.2	0.1	-1.1	0.2	1.1	0.4	1.2	0.08
				MNFGDFLTVMTQK	2	98.9%	1																									
IPI00215948	CTNNA1	isoform 1 of Catenin alpha-1	100.0%	36.1	22	22	25	1	57,721,049	64,212,178	55,815,127	67,938,381	8,905,029	4,436,543	5,489,000	3,527,309	34.5	15.5	22.0	11.6	1.1	0.5	-1.0	0.9	1.2	0.3	-1.2	0.3	1.1	0.5	1.2	0.1
				AAAGEFADDPCSSVK	2	92.7%	1																									
				AEVQNLGGELVVSGVDSAMSLIQAAK	3	100.0%	2																									
				AHVLAASVEQATENFLEK	3	99.1%	1																									
				AIMAQLPQEQK	2	98.7%	1																									
				ALLSAVTR	2	85.8%	1																									
				AVMDHVSDSFLETNVPLLVLIEAAK	3	99.9%	1																									
				IAEQVASFQEEK	2	100.0%	1																									
				IVAECNAVR	2	99.0%	1																									
				KAVMDHVSDSFLETNVPLLVLIEAAKNGNEK	3	96.7%	1																									
				LESIISGAALMADSSCTR	2	100.0%	1																									
				LLEPLVTQVTTLVNTNSK	2	89.9%	1																									
				LLILADMADVYK	2	100.0%	1																									
				LLSNTVMPR	2	85.6%	1																									
				MSASQLEALCPQVINAALALAAKPQSK	3	99.5%	1																									
				NAGNEQDLGIQYK	2	100.0%	2																									
				NLMNAVVQTVK	2	100.0%	1																									
				QIIVDPLSFSEER	2	100.0%	2																									
				SDALNSAIDK	2	97.4%	1																									
				SKLDAEVSKWDDSGNDIIVLAK	3	85.5%	1																									
				SQGMASLNLPAVSWK	2	100.0%	1																									
				VLTDAVDDITSIDDFLAVSENHILEDVNK	3	100.0%	1																									
				WDDSGNDIIVLAK	2	100.0%	1																									
IPI00215952	ENTPD5	Ectonucleoside triphosphate diphosphohydrolase 5	90.4%	2.8	1	1	1	1	1,566,080	1,809,050	1,735,940	2,103,860	276,823	149,865	76,617	115,144	39.5	18.5	9.9	12.2	1.2	0.5	1.1	0.6	1.3	0.1	-1.0	0.7	1.2	0.2	1.2	0.03
				WLEAEWIFGGVK	2	90.4%	1																									
IPI00215965	HNRNPA1	isoform A1-B of Heterogeneous nuclear ribonucleoprotein A1	100.0%	36.6	11	12	15	2	14,540,667	14,702,665	14,621,508	15,868,547	1,037,156	506,732	750,659	327,764	16.0	7.7	11.5	4.6	1.0	0.9	1.0	1	1.1	0.3	-1.0	0.9	1.1	0.09	1.1	0.2
IPI00465365	HNRNPA1	isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	100.0%	42.5	11	12	15	2	14,540,667	14,702,665	14,621,508	15,868,547	1,037,156	506,732	750,659	327,764	16.0	7.7	11.5	4.6	1.0	0.9	1.0	1	1.1	0.3	-1.0	0.9	1.1	0.09	1.1	0.2
				EDSQRPGAHLTVK	2	90.2%	1																									
				GFAFVTFDDHDSVDK	3	100.0%	1																									
				GFGFVTYATVEEVDAAMNAR	3	100.0%	2																									
				GGGFGGNDNFGR	2	98.0%	1																									
				KLFIGGLSFETTDESLR	2	100.0%	1																									
				KLFIGGLSFETTDESLR	3	99.5%	1																									
				LFIGGLSFETTDESLR	2	100.0%	3																									
				NQGGYGGSSSSSSYGSGR	2	100.0%	1																									
				SESPKEPEQLRK	3	99.9%	1																									
				SHFEQWGTLTDCVVMR	2	100.0%	1																									
				SSGPYGGGGQYFAK	2	100.0%	1																									
				WGTLTDCVVMR	2	99.9%	1																									
IPI00215975	ACIN1	isoform 2 of Apoptotic chromatin condensation inducer in the nucleus	100.0%	10.4	6	6	7	2	13,380,826	13,492,746	12,578,554	14,328,658	1,184,798	672,843	814,196	493,461	19.8	11.2	14.5	7.7	1.0	0.9	-1.1	0.6	1.1	0.5	-1.1	0.4	1.1	0.3	1.1	0.1
IPI00297991	ACIN1	isoform 3 of Apoptotic chromatin condensation inducer in the nucleus	100.0%	11.0	6	6	7	2	13,380,826	13,492,746	12,578,554	14,328,658	1,184,798	672,843	814,196	493,461	19.8	11.2	14.5	7.7	1.0	0.9	-1.1	0.6	1.1	0.5	-1.1	0.4	1.1	0.3	1.1	0.1
				AAPCIYWLPLTDSQIVQK	2	96.2%	1																									
				GLLVDRPSETK	2	96.8%	1																									
				KVTLGDTLTR	2	88.8%	1																									
				SGVSITIDDPVR	2	98.0%	2																									
				TGTLVEEAFWIDK	2	99.9%	1																									
				VTLGDTLTR	2	87.0%	1																									
IPI00215997	CD9	CD9 antigen	97.6%	4.4	1	1	1	3	1,086,610	909,417	984,780	1,100,023	197,010	93,231	83,452	127,951	40.5	22.9	19.0	26.0	-1.2	0.4	-1.1	0.6	1.0	1	1.1	0.6	1.2	0.3	1.1	0.5
IPI00657796	CD9	Uncharacterized protein	97.6%	6.3	1	1	1	3	1,086,610	909,417	984,780	1,100,023	197,010	93,231	83,452	127,951	40.5	22.9	19.0	26.0	-1.2	0.4	-1.1	0.6	1.0	1	1.1	0.6	1.2	0.3	1.1	0.5
IPI01012333	CD9	25 kDa protein	97.6%	4.4	1	1	1	3	1,086,610	909,417	984,780	1,100,023	197,010	93,231	83,452	127,951	40.5	22.9	19.0	26.0	-1.2	0.4	-1.1	0.6	1.0	1	1.1	0.6	1.2	0.3	1.1	0.5
				KDVLETFTVK	2	97.6%	1																									
IPI00216008	G6PD	isoform Long of Glucose-6-phosphate 1-dehydrogenase	99.9%	3.0	2	2	2	4	3,571,705	3,829,085	3,513,643	3,935,628	287,506	164,514	227,167	149,890	18.0	9.6	14.5	8.5	1.1	0.5	-1.0	0.9	1.1	0.3	-1.1	0.3	1.0	0.6	1.1	0.2
IPI00289800	G6PD	isoform Short of Glucose-6-phosphate 1-dehydrogenase	99.9%	3.3	2	2	2	4	3,571,705	3,829,085	3,513,643	3,935,628	287,506	164,514	227,167	149,890	18.0	9.6	14.5	8.5	1.1	0.5	-1.0	0.9	1.1	0.3	-1.1	0.3	1.0	0.6	1.1	0.2
IPI00853547	G6PD	isoform 3 of Glucose-6-phosphate 1-dehydrogenase	99.9%	3.1	2	2	2	4	3,571,705	3,829,085	3,513,643	3,935,628	287,506	164,514	227,167	149,890	18.0	9.6	14.5	8.5	1.1	0.5	-1.0	0.9	1.1	0.3	-1.1	0.3	1.0	0.6	1.1	0.2
IPI00884082	G6PD	Uncharacterized protein	99.9%	3.3	2	2	2	4	3,571,705	3,829,085	3,513,643	3,935,628	287,506	164,514	227,167	149,890	18.0	9.6	14.5	8.5	1.1	0.5	-1.0	0.9	1.1	0.3	-1.1	0.3	1.0	0.6	1.1	0.2
				EMVQNLMVLR	2	94.7%	1																									
				RNELVIR	2	98.8%	1																									
IPI00216049	HNRNPK	isoform 1 of Heterogeneous nuclear ribonucleoprotein K	100.0%	51.0	21	24	36	2	38,675,250	39,835,750	38,318,324	45,149,108	3,064,704	1,635,164	2,931,525	1,459,189	17.7	9.2	17.1	7.2	1.0	0.7	-1.0	0.9	1.2	0.09	-1.0	0.7	1.1	0.04	1.2	0.07
IPI00514561	HNRNPK	cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K	100.0%	55.1	21	24	36	2	38,675,250	39,835,750	38,318,324	45,149,108	3,064,704	1,635,164	2,931,525	1,459,189	17.7	9.2	17.1	7.2	1.0	0.7	-1.0	0.9	1.2	0.09	-1.0	0.7	1.1	0.04	1.2	0.07
				AQPYDPNFYDETYDYGGFTMMFDDR	2	100.0%	1																									
				DYDDMSPR	2	83.0%	1																									
				GGDLMAYDRR	3	93.3%	1																									
				GSDFDCELR	2	100.0%	2																									
				GSYGDLGGPIITTQVTIPK	2	100.0%	2																									
				IDEPLEGSEDR	2	99.9%	1																									
				IILDLISESPIK	2	100.0%	2																									
				IITITGTQDQIQNAQYLLQNSVK	2	100.0%	2																									
				IITITGTQDQIQNAQYLLQNSVK	3	100.0%	1																									
				ILLQSK	1	94.3%	1																									
				ILSISADIETIGEILK	2	100.0%	1																									
				ILSISADIETIGEILKK	2	100.0%	1																									
				ILSISADIETIGEILKK	3	99.9%	1																									
				LFQECCPHSTDR	2	100.0%	1																									
				LLIHQSLAGGIIGVK	2	100.0%	2																									
				LLIHQSLAGGIIGVK	3	100.0%	1																									
				NLPLPPPPPPR	2	99.9%	3																									
				NTDEMVELR	2	100.0%	2																									
				RPAEDMEEEQAFK	2	100.0%	2																									
				RPAEDMEEEQAFKR	3	100.0%	2																									
				SRNTDEMVELR	2	99.7%	1																									
				TDYNASVSVPDSSGPER	2	100.0%	2																									
				VVECIK	2	94.2%	1																									
				VVLIGGKPDR	2	99.4%	2																									
IPI00216057	SORD	Sorbitol dehydrogenase	100.0%	33.6	8	8	10	1	45,731,421	48,262,536	50,759,802	53,798,768	4,699,682	2,483,322	2,264,007	1,597,665	23.0	11.5	10.0	6.6	1.1	0.6	1.1	0.4	1.2	0.2	1.1	0.5	1.1	0.1	1.1	0.3
				ALEAFETFKK	2	91.3%	1																									
				EIGADLVLQISK	2	100.0%	1																									
				KPMVLGHEASGTVEK	2	99.8%	1																									

				LENYPIPEPGPNEVLLR	2	100.0%	2																									
				LPDNVTFEEGALIEPLSVGIHACR	3	100.0%	2																									
				VAIEPGAPR	2	91.9%	1																									
				VLVCGAGPIGMVTLLVAK	2	95.9%	1																									
				YCNTWPVAISMLASK	2	89.3%	1																									
IPI00216085	COX6B1	Cytochrome c oxidase subunit 6B1	100.0%	47.7	3	3	4	2	6,842,111	6,632,800	6,655,940	7,760,295	427,351	417,559	638,954	283,837	14.0	14.1	21.5	8.2	-1.0	0.7	-1.0	0.8	1.1	0.1	1.0	1	1.2	0.06	1.2	0.2
IPI00797738	COX6B1	12 kDa protein	100.0%	39.8	3	3	4	2	6,842,111	6,632,800	6,655,940	7,760,295	427,351	417,559	638,954	283,837	14.0	14.1	21.5	8.2	-1.0	0.7	-1.0	0.8	1.1	0.1	1.0	1	1.2	0.06	1.2	0.2
				GGDISVCEWYQR	2	100.0%	2																									
				NCWQNYLDFHR	3	99.9%	1																									
				VYQSLCPTSWVTDWDEQR	2	100.0%	1																									
IPI00216088	CRABP2	Cellular retinoic acid-binding protein 2	100.0%	44.9	6	6	7	1	29,726,168	30,969,725	30,071,111	33,627,270	2,393,811	1,432,447	1,963,175	1,335,175	18.0	10.3	14.6	8.9	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.1	0.2
				ELTNDGELILTMTADDVVCTR	2	100.0%	1																									
				SENFEELLK	2	99.9%	2																									
				TTEINFK	2	93.2%	1																									
				VGEEFEEQTVDGR	2	100.0%	1																									
				VGEEFEEQTVDGRPCK	3	99.7%	1																									
				VLGVNVMLR	2	100.0%	1																									
IPI00216106	OLA1	isoform 3 of Obg-like ATPase 1	100.0%	14.8	3	3	4	1	3,026,474	3,230,001	2,633,603	3,438,567	360,440	229,918	210,369	249,351	26.6	15.9	17.9	16.2	1.1	0.6	-1.1	0.4	1.1	0.4	-1.2	0.09	1.1	0.6	1.3	0.04
				FYHDWNDKEIEVLNK	3	96.4%	1																									
				IGIVGLPNVGK	2	99.9%	1																									
				IPAFLNVVDIAGLVK	2	100.0%	2																									
IPI00216125	SRP9	signal recognition particle 9 kDa protein isoform 1	100.0%	11.0	1	1	1	2	1,549,657	2,155,080	2,190,563	1,903,720	119,479	111,442	286,206	90,904	17.2	11.6	29.2	10.7	1.4	0.006	1.4	0.07	1.2	0.05	1.0	0.9	-1.1	0.1	-1.2	0.4
IPI00419797	SRP9	Uncharacterized protein	100.0%	13.6	1	1	1	2	1,549,657	2,155,080	2,190,563	1,903,720	119,479	111,442	286,206	90,904	17.2	11.6	29.2	10.7	1.4	0.006	1.4	0.07	1.2	0.05	1.0	0.9	-1.1	0.1	-1.2	0.4
				HSDGNLCVK	2	99.7%	1																									
IPI00216134	TPM1	tropomyosin alpha-1 chain isoform 7	100.0%	23.4	6	6	10	5	2,494,766	2,605,056	2,556,987	3,005,176	131,271	111,404	102,924	77,910	11.8	9.6	9.0	5.8	1.0	0.5	1.0	0.7	1.2	0.01	-1.0	0.8	1.2	0.02	1.2	0.008
IPI00384369	TPM1	Tropomyosin 1 alpha variant 6	100.0%	23.4	6	6	10	5	2,494,766	2,605,056	2,556,987	3,005,176	131,271	111,404	102,924	77,910	11.8	9.6	9.0	5.8	1.0	0.5	1.0	0.7	1.2	0.01	-1.0	0.8	1.2	0.02	1.2	0.008
IPI00921977	TPM1	cDNA FLJ54760, highly similar to Rattus norvegicus tropomyosin 1, alpha (Tpm1), tr	100.0%	23.4	6	6	10	5	2,494,766	2,605,056	2,556,987	3,005,176	131,271	111,404	102,924	77,910	11.8	9.6	9.0	5.8	1.0	0.5	1.0	0.7	1.2	0.01	-1.0	0.8	1.2	0.02	1.2	0.008
IPI00940084	TPM1	TPM1 protein variant (Fragment)	100.0%	19.1	6	6	10	5	2,494,766	2,605,056	2,556,987	3,005,176	131,271	111,404	102,924	77,910	11.8	9.6	9.0	5.8	1.0	0.5	1.0	0.7	1.2	0.01	-1.0	0.8	1.2	0.02	1.2	0.008
IPI01012191	TPM1	isoform 5 of Tropomyosin alpha-1 chain	100.0%	23.7	6	6	10	5	2,494,766	2,605,056	2,556,987	3,005,176	131,271	111,404	102,924	77,910	11.8	9.6	9.0	5.8	1.0	0.5	1.0	0.7	1.2	0.01	-1.0	0.8	1.2	0.02	1.2	0.008
				AQKDEEKMEIQEIQLK	3	92.3%	1																									
				ETAEADVASLNR	2	100.0%	2																									
				IQLVEEELDR	2	100.0%	2																									
				LATALQK	1	96.5%	2																									
				RIQLVEEELDR	2	100.0%	2																									
				SLQEQADAAEER	2	100.0%	1																									
IPI00216139	SEP6	isoform I of Septin-6	97.9%	2.6	1	1	1	7	334,620	300,513	295,661	301,009	17,466	25,218	25,630	19,197	11.7	18.8	19.4	14.3	-1.1	0.3	-1.1	0.2	-1.1	0.2	-1.0	0.9	1.0	1	1.0	0.9
IPI00376992	SEP6	cDNA FLJ59732, highly similar to Septin-6	97.9%	2.6	1	1	1	7	334,620	300,513	295,661	301,009	17,466	25,218	25,630	19,197	11.7	18.8	19.4	14.3	-1.1	0.3	-1.1	0.2	-1.1	0.2	-1.0	0.9	1.0	1	1.0	0.9
IPI00550119	SEP6	cDNA FLJ58821, highly similar to Septin-6	97.9%	2.4	1	1	1	7	334,620	300,513	295,661	301,009	17,466	25,218	25,630	19,197	11.7	18.8	19.4	14.3	-1.1	0.3	-1.1	0.2	-1.1	0.2	-1.0	0.9	1.0	1	1.0	0.9
IPI00644857	SEP6	Septin 6, isoform CRA_b	97.9%	2.6	1	1	1	7	334,620	300,513	295,661	301,009	17,466	25,218	25,630	19,197	11.7	18.8	19.4	14.3	-1.1	0.3	-1.1	0.2	-1.1	0.2	-1.0	0.9	1.0	1	1.0	0.9
IPI00744597	SEP6	isoform V of Septin-6	97.9%	2.6	1	1	1	7	334,620	300,513	295,661	301,009	17,466	25,218	25,630	19,197	11.7	18.8	19.4	14.3	-1.1	0.3	-1.1	0.2	-1.1	0.2	-1.0	0.9	1.0	1	1.0	0.9
IPI00941331	SEP6	isoform II of Septin-6	97.9%	2.5	1	1	1	7	334,620	300,513	295,661	301,009	17,466	25,218	25,630	19,197	11.7	18.8	19.4	14.3	-1.1	0.3	-1.1	0.2	-1.1	0.2	-1.0	0.9	1.0	1	1.0	0.9
IPI00978128	SEP6	isoform IV of Septin-6	97.9%	4.1	1	1	1	7	334,620	300,513	295,661	301,009	17,466	25,218	25,630	19,197	11.7	18.8	19.4	14.3	-1.1	0.3	-1.1	0.2	-1.1	0.2	-1.0	0.9	1.0	1	1.0	0.9
				STLMDTLFNTK	2	97.9%	1																									
IPI00216159	GFPT2	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2	100.0%	2.1	1	1	2	2	302,451	345,327	353,537	406,375	36,901	13,601	12,679	32,682	27.3	8.8	8.0	18.0	1.1	0.3	1.2	0.2	1.3	0.07	1.0	0.7	1.2	0.1	1.1	0.2
IPI00974350	GFPT2	Uncharacterized protein	100.0%	6.5	1	1	2	2	302,451	345,327	353,537	406,375	36,901	13,601	12,679	32,682	27.3	8.8	8.0	18.0	1.1	0.3	1.2	0.2	1.3	0.07	1.0	0.7	1.2	0.1	1.1	0.2
				VIQQLEGAFALVFK	2	100.0%	2																									
IPI00216171	ENO2	Gamma-enolase	100.0%	55.3	14	19	24	2	77,185,555	81,385,672	81,994,610	90,355,773	7,868,426	3,545,758	6,186,043	1,956,685	22.8	9.7	16.9	4.8	1.1	0.6	1.1	0.6	1.2	0.2	1.0	0.9	1.1	0.06	1.1	0.3
IPI00791564	ENO2	Enolase	100.0%	61.4	14	19	24	2	77,185,555	81,385,672	81,994,610	90,355,773	7,868,426	3,545,758	6,186,043	1,956,685	22.8	9.7	16.9	4.8	1.1	0.6	1.1	0.6	1.2	0.2	1.0	0.9	1.1	0.06	1.1	0.3
				AAVPSGASTGIYEALELR	2	100.0%	2																									
				AAVPSGASTGIYEALELR	3	100.0%	1																									
				DATNVGDEGGFAPNILENSEALELVK	2	100.0%	2																									
				DATNVGDEGGFAPNILENSEALELVK	3	100.0%	1																									
				DGKYDLDFK	3	98.7%	1																									
				DYPVVSIEDPFDQDDWAAWSK	3	99.1%	1																									
				FGANAILGVSLAVCK	2	100.0%	1																									
				FTANVGIQIVGDDLTVTNPK	2	83.4%	1																									
				GLFRAAVPSGASTGIYEALELR	3	99.9%	1																									
				GNPTVEVDLYTAK	2	97.6%	1																									
				HIAQLAGNSDLILPVPAFNVINGGSHAGNK	3	99.9%	1																									
				IVIGMDVAASEFYR	2	100.0%	2																									
				IVIGMDVAASEFYR	3	93.3%	1																									
				LAMQEFMILPVGAESFR	2	100.0%	2																									
				LAMQEFMILPVGAESFR	3	100.0%	1																									
				SGETEDTFIADLVVGLCTGQIK	2	100.0%	2																									
				SGETEDTFIADLVVGLCTGQIK	3	100.0%	1																									
				VNQIGSVTEAIQACK	2	100.0%	1																									
				YITGDQLGALYQDFVR	3	100.0%	1																									
IPI00216184	PICALM	isoform 2 of Phosphatidylinositol-binding clathrin assembly protein	100.0%	19.5	7	8	9	4	7,622,331	8,201,016	8,008,217	9,038,885	411,107	296,662	350,689	282,547	12.1	8.1	9.8	7.0	1.1	0.3	1.1	0.5	1.2	0.02	-1.0	0.7	1.1	0.08	1.1	0.05
IPI00290738	PICALM	isoform 1 of Phosphatidylinositol-binding clathrin assembly protein	100.0%	18.9	7	8	9	4	7,622,331	8,201,016	8,008,217	9,038,885	411,107	296,662	350,689	282,547	12.1	8.1	9.8	7.0	1.1	0.3	1.1	0.5	1.2	0.02	-1.0	0.7	1.1	0.08	1.1	0.05
IPI00400849	PICALM	isoform 3 of Phosphatidylinositol-binding clathrin assembly protein	100.0%	20.2	7	8	9	4	7,622,331	8,201,016	8,008,217	9,038,885	411,107	296,662	350,689	282,547	12.1	8.1	9.8	7.0	1.1	0.3	1.1	0.5	1.2	0.02	-1.0	0.7	1.1	0.08	1.1	0.05
IPI00984627	PICALM	PICALM variant protein	100.0%	19.1	7	8	9	4	7,622,331	8,201,016	8,008,217	9,038,885	411,107	296,662	350,689	282,547	12.1	8.1	9.8	7.0	1.1	0.3	1.1	0.5	1.2	0.02	-1.0	0.7	1.1	0.08	1.1	0.05
				ATTLSNAVSSLASTGLSLTK	2	99.9%	1																									
				GDIPDLSQAPSSLLDALEQHLASLEGK	3	97.3%	1																									
				ITAAQHSVTGSAVSK	2	100.0%	1																									
				ITAAQHSVTGSAVSK	3	97.7%	1																									
				LFAAYNEGIINLLEK	2	99.3%	2																									
				LVSDDLDSSLANLVGNLGIGNGTTK	2	100.0%	1																									
				NDVNWSQPGEK	2	99.5%	1																									
				QAALEEEQAR	2	97.0%	1																									
IPI00216219	TJP1	isoform Long of Tight junction protein ZO-1	100.0%	3.2	4	4	4	5	7,137,014	7,206,440	6,800,406	7,762,116	543,643	246,101	368,251	213,500	17.0	7.6	12.1	6.2	1.0	0.9	-1.0	0.6	1.1	0.3	-1.1	0.4	1.1	0.1	1.1	0.05
IPI00335824	TJP1	isoform Short of Tight junction protein ZO-1	100.0%	3.4	4	4	4	5	7,137,014	7,206,440	6,800,406	7,762,116	543,643	246,101	368,251	213,500	17.0	7.6	12.1	6.2	1.0	0.9	-1.0	0.6	1.1	0.3	-1.1	0.4	1.1	0.1	1.1	0.05
IPI00795990	TJP1	Putative uncharacterized protein DKFZp686A1195	100.0%	3.3	4	4	4	5	7,137,014	7,206,440	6,800,406	7,762,116	543,643	246,101	368,251	213,500	17.0	7.6	12.1	6.2	1.0	0.9	-1.0	0.6	1.1	0.3	-1.1	0.4	1.1	0.1	1.1	0.05
IPI00941530	TJP1	187 kDa protein	100.0%	3.4	4	4	4	5	7,137,014	7,206,440	6,800,406	7,762,116	543,643	246,101	368,251	213,500	17.0	7.6	12.1	6.2	1.0	0.9	-1.0	0.6	1.1	0.3	-1.1	0.4	1.1	0.1	1.1	0.05
IPI01013569	TJP1	Tight junction protein ZO-1	100.0%	3.2	4	4	4	5	7,137,014	7,206,440	6,800,406	7,762,116	543,643	246,101	368,251	213,500	17.0	7.6	12.1	6.2	1.0	0.9	-1.0	0.6	1.1	0.3	-1.1	0.4	1.1	0.1	1.1	0.05
				APGFGFGIAISGGR	2	99.6%	1																									
				DGNIQEGDVVLK	2	85.3%	1																									
				EAGFLRPVTIFGPIADVAR	3	89.6%	1																									
				YQINNISTVPK	2	80.8%	1																									
IPI00216230	TMPO	Lamina-associated polypeptide 2, isoform alpha	99.9%	8.7	3	3	3	1	1,669,038	1,537,945	1,751,424	1,723,015	80,081	25,545	124,548	86,313	10.7	3.7	15.9	11.2	-1.1	0.2	1.0	0.6	1.0	0.7	1.1	0.2	1.1	0.1	-1.0	0.9
				NRPPLPAGTNSK	2	99.0%	1																									
				QEDKDDLDVTELTNEDLLDQLVK	3	98.2%	1																									
				SSSSSSQPEHSAMLVSTAASPSLIK	2	95.2%	1																									
IPI00216237	RPL36	60S ribosomal protein L36	96.7%	19.1	2	2	3	1	16,762,260	18,034,120	17,204,280	19,828,460	947,155	665,777	1,118,679	503,665	12.6	8.3	14.5	5.7	1.1	0.3	1.0	0.8	1.2	0.02	-1.0	0.5	1.1	0.06	1.2	0.06
				EELSNVLAAMR	2	95.3%	1																									
				YPMAVGLNK	2	96.7%	2																									
IPI00216245	TJP2	isoform C1 of Tight junction protein ZO-2	100.0%	8.6	7	7	7	1	9,376,748	9,800,135	8,629,616	10,603,194	726,655	212,058	654,302	521,427	17.3	4.8	17.0	11.0	1.0	0.6	-1.1	0.5	1.1	0.2	-1.1	0.2	1.1	0.2	1.2	0.05
				AEQMASVQNAQR	2	99.9%	1																									
				AFEVMDEFDGR	2	100.0%	1																									
				GEMVTILAQSR	2	99.9%	1																									
				MEELIWEQYTVTLQK	2	89.8%	1																									
				MSYLTAMGADYLSCDSR	2	99.9%	1																									
				RPVVLFGPIADIAMEK	2	85.0%	1																									
				TFLRPSPEDEAIYGPNTK	3	100.0%	1																									
IPI00216246	TJP2	isoform C2 of Tight junction protein ZO-2	100.0%	9.8	7	7	7	1	9,376,748	9,800,135	8,629,616	10,603,194	726,655	212,058	654,302	521,427	17.3	4.8	17.0	11.0	1.0	0.6	-1.1	0.5	1.1	0.2	-1.1	0.2	1.1	0.2	1.2	0.05
				AEQMASVQNAQR	2	99.9%	1																									
				AFEVMDEFDGR	2	100.0%	1																									
				GEMVTILAQSR	2	99.9%	1																									
				MEELIWEQYTVTLQK	2	89.8%	1																									
				MSYLTAMGADYLSCDSR	2	99.9%	1																									
				RPVVLFGPIADIAMEK	2	85.0%	1																									
				TFLRPSPEDEAIYGPNTK	3	100.0%	1																									
IPI00216247	PSMD4	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 4, isoform CRA_b	100.0%	13.2	4	4	6	1	7,236,648	8,240,358	7,544,522	9,229,951	647,137	546,811	434,220	572,710	20.0	14.8	12.9	13.9	1.1	0.3	1.0	0.7	1.3	0.05	-1.1	0.3	1.1	0.2	1.2	0.05
				LTAFVNTLNGK	2	99.9%	2																									
				MTISQQEFGR	2	99.9%	2																									
				NAMGSLASQATK	2	97.4%	1																									
				VNVDIINFGEEEVNTEK	2	100.0%	1																									
IPI00216293	TST	Thiosulfate sulfurtransferase	100.0%	10.4	2	2	2	2	10,152,850	10,052,400	10,166,200	11,306,210	1,010,988	510,787	613,855	198,360	22.3	11.4	13.5	3.9	-1.0	0.9	1.0	1	1.1	0.3	1.0	0.9	1.1	0.07	1.1	0.1
IPI00878140	TST	cDNA FLJ57870, highly similar to Thiosulfate sulfurtransferase	100.0%	12.7	2	2	2	2	10,152,850	10,052,400	10,166,200	11,306,210	1,010,988	510,787	613,855	198,360	22.3	11.4	13.5	3.9	-1.0	0.9	1.0	1	1.1	0.3	1.0	0.9	1.1	0.07	1.1	0.1
				FLGTEPEPDAVGLDSGHIR	3	100.0%	1																									
				TYEQVLENLESK	2	99.5%	1																									
IPI00216298	TXN	Thioredoxin	100.0%	65.7	8	11	13	1	67,972,960	72,511,530	73,782,846	80,130,048	5,383,689	2,639,603	5,320,755	1,482,275	17.7	8.1	16.1	4.1	1.1	0.5	1.1	0.5	1.2	0.09	1.0	0.8	1.1	0.04	1.1	0.3
				CMPTFQFFK	2	100.0%	1																									
				EKLEATINELV	2	99.5%	2																									
				LVVVDFSATWCGPCK	2	100.0%	1																									
				MIKPFFHSLSEK	2	100.0%	1																									
				MIKPFFHSLSEK	3	99.5%	1																									
				TAFQEALDAAGDK	2	100.0%	2																									
				TAFQEALDAAGDKLVVVDFSATWCGPCK	3	100.0%	1																									
				VGEFSGANK	1	100.0%	1																									
				VGEFSGANK	2	100.0%	1																									
				VGEFSGANKEK	2	99.3%	1																									
				VGEFSGANKEK	3	97.1%	1																									
IPI00216308	VDAC1	Voltage-dependent anion-selective channel protein 1	100.0%	26.9	5	6	7	1	12,895,398	13,634,443	12,825,170	14,926,177	1,679,653	812,461	1,011,563	770,084	29.1	13.3	17.6	11.5	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.6	1.1	0.3	1.2	0.1
				TDEFQLHTNVNDGTEFGGSIYQK	3	100.0%	2																									
				VTQSNFAVGYK	2	99.8%	1																									
				WNTDNTLGTEITVEDQLAR	2	96.7%	1																									
				WNTDNTLGTEITVEDQLAR	3	99.6%	1																									
				WTEYGLTFTEK	2	99.9%	1																									
				YQIDPDACFSAK	2	98.9%	1																									
IPI00216318	YWHAB	isoform Long of 14-3-3 protein beta/alpha	100.0%	46.3	9	11	16	2	21,320,611	22,792,180	21,744,912	25,141,408	1,628,559	772,819	1,363,266	521,088	17.1	7.6	14.0	4.6	1.1	0.4	1.0	0.8	1.2	0.08	-1.0	0.5	1.1	0.04	1.2	0.07
IPI00759832	YWHAB	isoform Short of 14-3-3 protein beta/alpha	100.0%	46.7	9	11	16	2	21,320,611	22,792,180	21,744,912	25,141,408	1,628,559	772,819	1,363,266	521,088	17.1	7.6	14.0	4.6	1.1	0.4	1.0	0.8	1.2	0.08	-1.0	0.5	1.1	0.04	1.2	0.07
				AVTEQGHELSNEER	2	100.0%	2																									
				AVTEQGHELSNEER	3	100.0%	1																									
				DNLTLWTSENQGDEGDAGEGEN	2	100.0%	2																									
				LAEQAERYDDMAAAMK	3	99.6%	1																									
				QTTVSNSQQAYQEAFEISK	2	100.0%	2																									
				QTTVSNSQQAYQEAFEISKK	3	99.9%	1																									

				TAFDEAIAELDTLNEESYK	2	100.0%	2																									
				TAFDEAIAELDTLNEESYK	3	100.0%	1																									
				YDDMAAAMK	2	100.0%	1																									
				YLIPNATQPESK	2	100.0%	2																									
				YLSEVASGDNKQTTVSNSQQAYQEAFEISK	3	100.0%	1																									
IPI00216319	YWHAH	14-3-3 protein eta	100.0%	14.2	3	3	3	1	12,187,990	13,744,520	13,513,969	15,800,570	1,233,806	660,512	1,047,125	940,717	22.6	10.8	17.3	13.3	1.1	0.3	1.1	0.4	1.3	0.05	-1.0	0.9	1.1	0.1	1.2	0.1
				AVTELNEPLSNEDR	2	100.0%	1																									
				NSVVEASEAAYK	2	100.0%	1																									
				YDDMASAMK	2	89.7%	1																									
IPI00216320	PDXK	isoform 2 of Pyridoxal kinase	100.0%	27.1	5	5	5	1	7,409,069	7,353,252	7,275,495	8,309,683	620,694	229,912	320,855	176,006	18.7	7.0	9.9	4.7	-1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.01	1.1	0.02
				AQAGEGVRPSPMQLELR	3	99.6%	1																									
				GQVLNSDELQELYEGLR	3	99.9%	1																									
				RNPAGSVVMER	2	82.5%	1																									
				TVSTLHHVLQR	2	99.7%	1																									
				VVPLADIITPNQFEAELLSGR	2	99.8%	1																									
IPI00216348	DYNC1I2	isoform 2C of Cytoplasmic dynein 1 intermediate chain 2	99.6%	6.7	2	2	2	7	918,440	975,921	815,328	960,369	71,185	36,330	80,636	40,370	17.3	8.3	22.1	9.4	1.1	0.5	-1.1	0.4	1.0	0.6	-1.2	0.1	-1.0	0.8	1.2	0.1
IPI00302712	DYNC1I2	isoform 2B of Cytoplasmic dynein 1 intermediate chain 2	99.6%	6.5	2	2	2	7	918,440	975,921	815,328	960,369	71,185	36,330	80,636	40,370	17.3	8.3	22.1	9.4	1.1	0.5	-1.1	0.4	1.0	0.6	-1.2	0.1	-1.0	0.8	1.2	0.1
IPI00744015	DYNC1I2	isoform 2A of Cytoplasmic dynein 1 intermediate chain 2	99.6%	6.4	2	2	2	7	918,440	975,921	815,328	960,369	71,185	36,330	80,636	40,370	17.3	8.3	22.1	9.4	1.1	0.5	-1.1	0.4	1.0	0.6	-1.2	0.1	-1.0	0.8	1.2	0.1
IPI00827813	DYNC1I2	isoform 2F of Cytoplasmic dynein 1 intermediate chain 2	99.6%	6.7	2	2	2	7	918,440	975,921	815,328	960,369	71,185	36,330	80,636	40,370	17.3	8.3	22.1	9.4	1.1	0.5	-1.1	0.4	1.0	0.6	-1.2	0.1	-1.0	0.8	1.2	0.1
IPI00827859	DYNC1I2	isoform 2E of Cytoplasmic dynein 1 intermediate chain 2	99.6%	6.4	2	2	2	7	918,440	975,921	815,328	960,369	71,185	36,330	80,636	40,370	17.3	8.3	22.1	9.4	1.1	0.5	-1.1	0.4	1.0	0.6	-1.2	0.1	-1.0	0.8	1.2	0.1
IPI00915993	DYNC1I2	cDNA, FLJ79018, highly similar to Cytoplasmic dynein 1 intermediate chain 2	99.6%	6.5	2	2	2	7	918,440	975,921	815,328	960,369	71,185	36,330	80,636	40,370	17.3	8.3	22.1	9.4	1.1	0.5	-1.1	0.4	1.0	0.6	-1.2	0.1	-1.0	0.8	1.2	0.1
IPI01015321	DYNC1I2	71 kDa protein	99.6%	6.4	2	2	2	7	918,440	975,921	815,328	960,369	71,185	36,330	80,636	40,370	17.3	8.3	22.1	9.4	1.1	0.5	-1.1	0.4	1.0	0.6	-1.2	0.1	-1.0	0.8	1.2	0.1
				EAVAPVQEESDLEK	2	99.4%	1																									
				LDLWNLNNDTEVPTASISVEGNPALNR	3	99.4%	1																									
IPI00216470	PIP4K2B	isoform 1 of Phosphatidylinositol-5-phosphate 4-kinase type-2 beta	96.1%	1.4	1	1	1	1	1,344,360	1,281,766	1,406,046	1,504,510	104,535	144,731	93,359	77,043	17.4	25.3	14.9	11.5	-1.0	0.7	1.0	0.7	1.1	0.3	1.1	0.5	1.2	0.2	1.1	0.4
				KNFLEK	1	82.6%	1																									
IPI00216492	HNRNPH3	isoform 2 of Heterogeneous nuclear ribonucleoprotein H3	100.0%	30.2	6	8	12	1	8,937,836	9,171,195	8,364,285	10,122,480	865,346	393,065	558,998	551,744	21.7	9.6	14.9	12.2	1.0	0.8	-1.1	0.6	1.1	0.3	-1.1	0.3	1.1	0.2	1.2	0.06
				ATENDIANFFSPLNPIR	2	100.0%	2																									
				ATENDIANFFSPLNPIR	3	100.0%	1																									
				ATGEADVEFVTHEDAVAAMSK	3	100.0%	1																									
				DGMDNQGGYGSVGR	2	100.0%	2																									
				STGEAFVQFASK	2	100.0%	2																									
				VHIDIGADGR	2	100.0%	2																									
				VHIDIGADGR	3	99.8%	1																									
				YIELFLNSTPGGGSGMGGSGMGGYGR	2	100.0%	1																									
IPI00216494	HNRNPH3	isoform 4 of Heterogeneous nuclear ribonucleoprotein H3	100.0%	28.8	4	5	8	2	4,740,533	4,910,093	4,170,477	5,415,053	436,446	245,447	373,726	288,108	20.6	11.2	20.0	11.9	1.0	0.7	-1.1	0.4	1.1	0.2	-1.2	0.1	1.1	0.2	1.3	0.03
IPI00908651	HNRNPH3	cDNA FLJ57726, highly similar to Heterogeneous nuclear ribonucleoprotein H3	100.0%	26.1	4	5	8	2	4,740,533	4,910,093	4,170,477	5,415,053	436,446	245,447	373,726	288,108	20.6	11.2	20.0	11.9	1.0	0.7	-1.1	0.4	1.1	0.2	-1.2	0.1	1.1	0.2	1.3	0.03
				ATENDIANFFSPLNPIR	2	100.0%	2																									
				ATENDIANFFSPLNPIR	3	100.0%	1																									
				ATGEADVEFVTHEDAVAAMSK	3	100.0%	1																									
				DGMDNQGGYGSVGR	2	100.0%	2																									
				VHIDIGADGR	2	100.0%	2																									
IPI00216495	HNRNPH3	isoform 5 of Heterogeneous nuclear ribonucleoprotein H3	100.0%	26.2	2	2	3	2	1,036,957	1,085,909	1,078,557	1,158,911	86,671	66,583	58,117	40,384	18.7	13.7	12.1	7.8	1.0	0.7	1.0	0.7	1.1	0.2	-1.0	0.9	1.1	0.4	1.1	0.3
IPI00216496	HNRNPH3	isoform 6 of Heterogeneous nuclear ribonucleoprotein H3	100.0%	27.3	2	2	3	2	1,036,957	1,085,909	1,078,557	1,158,911	86,671	66,583	58,117	40,384	18.7	13.7	12.1	7.8	1.0	0.7	1.0	0.7	1.1	0.2	-1.0	0.9	1.1	0.4	1.1	0.3
				ATENDIANFFSPLNPIR	2	100.0%	2																									
				ATGEADVEFVTHEDAVAAMSK	3	100.0%	1																									
IPI00216508	SNX3	isoform 2 of Sorting nexin-3	99.0%	18.5	2	2	2	3	4,353,753	3,698,053	4,430,803	4,502,843	133,489	173,867	150,847	193,222	6.9	10.5	7.6	9.6	-1.2	0.02	1.0	0.7	1.0	0.5	1.2	0.01	1.2	0.01	1.0	0.8
IPI00552276	SNX3	isoform 4 of Sorting nexin-3	99.0%	17.1	2	2	2	3	4,353,753	3,698,053	4,430,803	4,502,843	133,489	173,867	150,847	193,222	6.9	10.5	7.6	9.6	-1.2	0.02	1.0	0.7	1.0	0.5	1.2	0.01	1.2	0.01	1.0	0.8
IPI00815770	SNX3	isoform 1 of Sorting nexin-3	99.0%	14.8	2	2	2	3	4,353,753	3,698,053	4,430,803	4,502,843	133,489	173,867	150,847	193,222	6.9	10.5	7.6	9.6	-1.2	0.02	1.0	0.7	1.0	0.5	1.2	0.01	1.2	0.01	1.0	0.8
				GDDGIFDDNFIEER	2	91.6%	1																									
				KQGLEQFINK	2	99.0%	1																									
IPI00216547	CITED2	Uncharacterized protein	99.1%	13.6	1	1	1	1	1,575,207	1,521,910	1,532,815	1,519,080	238,143	93,551	174,345	108,769	33.8	13.8	25.4	16.0	-1.0	0.8	-1.0	0.9	-1.0	0.8	1.0	1	-1.0	1	-1.0	0.9
				DCNPPNVIDTDFIDEEVLMSLVIEMGLDR	3	98.7%	1																									
IPI00216587	RPS8	40S ribosomal protein S8	100.0%	24.5	4	4	6	2	9,052,045	10,296,050	9,416,640	11,665,170	1,127,936	803,681	1,132,609	379,918	27.9	17.5	26.9	7.3	1.1	0.4	1.0	0.8	1.3	0.08	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00645201	RPS8	40S ribosomal protein S8	100.0%	27.1	4	4	6	2	9,052,045	10,296,050	9,416,640	11,665,170	1,127,936	803,681	1,132,609	379,918	27.9	17.5	26.9	7.3	1.1	0.4	1.0	0.8	1.3	0.08	-1.1	0.5	1.1	0.2	1.2	0.1
				IIDVVYNASNNELVR	2	99.9%	1																									
				ISSLLEEQFQQGK	2	100.0%	2																									
				LTPEEEEILNK	2	99.5%	2																									
				NCIVLIDSTPYR	2	99.9%	1																									
IPI00216592	HNRNPC	isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2	100.0%	33.1	9	12	16	2	19,452,830	19,366,963	18,694,287	22,166,052	1,813,016	788,162	1,233,763	906,126	20.8	9.1	14.8	9.1	-1.0	1	-1.0	0.7	1.1	0.2	-1.0	0.7	1.1	0.05	1.2	0.05
IPI00909232	HNRNPC	cDNA FLJ53542, highly similar to Heterogeneous nuclear ribonucleoproteins C	100.0%	33.7	9	12	16	2	19,452,830	19,366,963	18,694,287	22,166,052	1,813,016	788,162	1,233,763	906,126	20.8	9.1	14.8	9.1	-1.0	1	-1.0	0.7	1.1	0.2	-1.0	0.7	1.1	0.05	1.2	0.05
				GFAFVQYVNER	2	100.0%	2																									
				KSDVEAIFSK	2	100.0%	1																									
				KSDVEAIFSK	3	96.8%	1																									
				LKGDDLQAIKK	2	99.8%	1																									
				MIAGQVLDINLAAEPK	2	100.0%	1																									
				MIAGQVLDINLAAEPK	3	99.1%	1																									
				SAAEMYGSSFDLDYDFQR	2	100.0%	2																									
				SAAEMYGSSFDLDYDFQR	3	100.0%	1																									
				SDVEAIFSK	2	100.0%	1																									
				VDSLLENLEK	2	100.0%	2																									
				VFIGNLNTLVVK	2	100.0%	2																									
				VPPPPPIAR	2	88.7%	1																									
IPI00216613	SFPQ	isoform Short of Splicing factor, proline- and glutamine-rich	100.0%	22.6	11	13	15	1	50,001,474	52,613,464	48,797,049	58,555,210	4,416,870	2,002,841	4,032,871	1,182,180	19.8	8.5	18.5	4.5	1.1	0.6	-1.0	0.8	1.2	0.1	-1.1	0.4	1.1	0.03	1.2	0.07
				AELDDTPMR	2	99.8%	1																									
				FAQHGTFEYEYSQR	3	95.5%	1																									
				FATHAAALSVR	3	100.0%	1																									
				ISDSEGFK	2	91.0%	1																									
				LFVGNLPADITEDEFKR	2	100.0%	1																									
				LFVGNLPADITEDEFKR	3	99.0%	1																									
				MGGGGAMNMGDPYGSGGQK	2	100.0%	1																									
				NLSPYVSNELLEEAFSQFGPIER	2	100.0%	1																									
				PVIVEPLEQLDDEDGLPEK	2	100.0%	1																									
				PVIVEPLEQLDDEDGLPEK	3	100.0%	1																									
				REEEMMIR	2	90.0%	1																									
				RMEELHNQEMQK	3	100.0%	2																									
				YGEPGEVFINK	2	100.0%	2																									
IPI00216654	NOLC1	isoform Beta of Nucleolar and coiled-body phosphoprotein 1	100.0%	3.5	2	3	4	2	2,511,851	2,196,322	2,100,041	2,730,379	465,817	150,866	174,946	324,615	41.5	15.4	18.6	26.6	-1.1	0.5	-1.2	0.4	1.1	0.7	-1.0	0.7	1.2	0.2	1.3	0.1
IPI00292387	NOLC1	isoform Alpha of Nucleolar and coiled-body phosphoprotein 1	100.0%	3.6	2	3	4	2	2,511,851	2,196,322	2,100,041	2,730,379	465,817	150,866	174,946	324,615	41.5	15.4	18.6	26.6	-1.1	0.5	-1.2	0.4	1.1	0.7	-1.0	0.7	1.2	0.2	1.3	0.1
				DNQLSEVANK	2	99.4%	1																									
				VVPSDLYPLVLGFLR	2	100.0%	2																									
				VVPSDLYPLVLGFLR	3	100.0%	1																									
IPI00216682	CNN3	Calponin-3	100.0%	11.6	3	3	3	3	5,381,127	5,368,837	4,871,173	5,671,660	437,429	369,447	340,630	335,835	18.2	15.4	15.6	13.2	-1.0	1	-1.1	0.4	1.1	0.6	-1.1	0.4	1.1	0.6	1.2	0.1
IPI00642542	CNN3	cDNA, FLJ79297, highly similar to Calponin-3	100.0%	13.2	3	3	3	3	5,381,127	5,368,837	4,871,173	5,671,660	437,429	369,447	340,630	335,835	18.2	15.4	15.6	13.2	-1.0	1	-1.1	0.4	1.1	0.6	-1.1	0.4	1.1	0.6	1.2	0.1
IPI00909623	CNN3	cDNA FLJ53072, highly similar to Calponin-3	100.0%	13.4	3	3	3	3	5,381,127	5,368,837	4,871,173	5,671,660	437,429	369,447	340,630	335,835	18.2	15.4	15.6	13.2	-1.0	1	-1.1	0.4	1.1	0.6	-1.1	0.4	1.1	0.6	1.2	0.1
				AGQSVIGLQMGTNK	2	99.9%	1																									
				DGIILCELINK	2	99.8%	1																									
				GASQAGMLAPGTR	2	95.4%	1																									
IPI00216689	PCBP2	Poly(rC)-binding protein 2	100.0%	25.5	7	8	11	5	3,567,780	3,720,023	3,451,571	4,143,626	411,895	123,220	172,204	212,122	25.8	7.4	11.2	11.5	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.1	1.2	0.04
IPI00788837	PCBP2	cDNA FLJ54752, highly similar to Poly(rC)-binding protein 2	100.0%	33.0	7	8	11	5	3,567,780	3,720,023	3,451,571	4,143,626	411,895	123,220	172,204	212,122	25.8	7.4	11.2	11.5	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.1	1.2	0.04
IPI00791223	PCBP2	poly(rC)-binding protein 2 isoform f	100.0%	27.8	7	8	11	5	3,567,780	3,720,023	3,451,571	4,143,626	411,895	123,220	172,204	212,122	25.8	7.4	11.2	11.5	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.1	1.2	0.04
IPI00796337	PCBP2	poly(rC)-binding protein 2 isoform a	100.0%	25.4	7	8	11	5	3,567,780	3,720,023	3,451,571	4,143,626	411,895	123,220	172,204	212,122	25.8	7.4	11.2	11.5	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.1	1.2	0.04
IPI00900327	PCBP2	cDNA FLJ58339, highly similar to Poly(rC)-binding protein 2	100.0%	28.9	7	8	11	5	3,567,780	3,720,023	3,451,571	4,143,626	411,895	123,220	172,204	212,122	25.8	7.4	11.2	11.5	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.1	1.2	0.04
				AFAMIIDK	2	94.2%	1																									
				AITIAGIPQSIIECVK	2	100.0%	2																									
				ESTGAQVQVAGDMLPNSTER	2	100.0%	2																									
				ESTGAQVQVAGDMLPNSTER	3	99.9%	1																									
				IANPVEGSTDR	2	100.0%	1																									
				IITLAGPTNAIFK	2	99.8%	1																									
				INISEGNCPER	2	100.0%	2																									
				LVVPASQCGSLIGK	2	100.0%	1																									
IPI00216691	PFN1	Profilin-1	100.0%	73.6	11	13	21	1	156,629,000	161,471,180	155,189,590	177,475,760	########	5,882,913	########	6,785,886	16.8	8.2	15.6	8.6	1.0	0.7	-1.0	0.9	1.1	0.2	-1.0	0.6	1.1	0.1	1.1	0.1
				CYEMASHLR	2	100.0%	1																									
				DSLLQDGEFSMDLR	2	100.0%	2																									
				DSLLQDGEFSMDLR	3	100.0%	1																									
				DSPSVWAAVPGK	2	100.0%	2																									
				EGVHGGLINK	2	99.9%	2																									
				KCYEMASHLR	2	95.8%	1																									
				KCYEMASHLR	3	95.9%	1																									
				SSFYVNGLTLGGQK	2	100.0%	2																									
				STGGAPTFNVTVTK	2	100.0%	2																									
				TDKTLVLLMGK	2	100.0%	2																									
				TFVNITPAEVGVLVGK	2	100.0%	2																									
				TFVNITPAEVGVLVGKDR	3	99.8%	1																									
				TLVLLMGK	2	100.0%	2																									
IPI00216694	PLS3	Plastin-3	100.0%	19.8	9	9	10	1	12,530,966	12,541,492	12,481,859	14,463,024	1,350,972	597,608	941,874	670,200	24.1	10.7	16.9	10.4	1.0	1	-1.0	1	1.2	0.2	-1.0	1	1.2	0.06	1.2	0.1
				AESMLQQADK	2	98.7%	1																									
				ANDDIIVNWVNR	2	99.9%	1																									
				IDINMSGFNETDDLKR	2	99.9%	1																									
				ISFDEFVYIFQEVK	2	100.0%	1																									
				LNLAFVANLFNK	2	100.0%	1																									
				QFVTPADVVSGNPK	2	100.0%	2																									
				VDLNSNGFICDYELHELFK	2	99.3%	1																									
				VYALPEDLVEVKPK	3	96.0%	1																									
				YTLNVLEDLGDGQK	2	100.0%	1																									
IPI00216730	HIST2H2AB	Histone H2A type 2-B	100.0%	35.4	5	7	11	1	23,163,952	22,578,889	23,657,654	26,494,462	1,986,897	606,497	1,163,481	616,128	19.2	6.0	11.0	5.2	-1.0	0.8	1.0	0.8	1.1	0.2	1.0	0.4	1.2	0.002	1.1	0.06
				AGLQFPVGR	2	100.0%	2																									
				HLQLAVR	2	96.2%	1																									
				LLGGVTIAQGGVLPNIQAVLLPK	2	100.0%	2																									
				LLGGVTIAQGGVLPNIQAVLLPK	3	100.0%	1																									
				NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	3	100.0%	1																									
				VTIAQGGVLPNIQAVLLPK	2	100.0%	2																									
				VTIAQGGVLPNIQAVLLPK	3	100.0%	2																									
IPI00216746	HNRNPK	isoform 2 of Heterogeneous nuclear ribonucleoprotein K	100.0%	52.2	21	25	38	2	41,694,847	42,519,530	40,709,269	48,272,415	3,340,348	1,719,810	3,042,777	1,541,516	17.9	9.0	16.7	7.1	1.0	0.8	-1.0	0.8	1.2	0.1	-1.0	0.6	1.1	0.04	1.2	0.06
IPI00807545	HNRNPK	isoform 3 of Heterogeneous nuclear ribonucleoprotein K	100.0%	55.0	21	25	38	2	41,694,847	42,519,530	40,709,269	48,272,415	3,340,348	1,719,810	3,042,777	1,541,516	17.9	9.0	16.7	7.1	1.0	0.8	-1.0	0.8	1.2	0.1	-1.0	0.6	1.1	0.04	1.2	0.06
				AQPYDPNFYDETYDYGGFTMMFDDR	2	100.0%	1																									
				DYDDMSPR	2	83.0%	1																									

				GGDLMAYDRR	2	80.1%	1																									
				GGDLMAYDRR	3	93.3%	1																									
				GSDFDCELR	2	100.0%	2																									
				GSYGDLGGPIITTQVTIPK	2	100.0%	2																									
				IDEPLEGSEDR	2	99.9%	1																									
				IILDLISESPIK	2	100.0%	2																									
				IITITGTQDQIQNAQYLLQNSVK	2	100.0%	2																									
				IITITGTQDQIQNAQYLLQNSVK	3	100.0%	1																									
				ILLQSK	1	94.3%	1																									
				ILSISADIETIGEILK	2	100.0%	1																									
				ILSISADIETIGEILKK	2	100.0%	1																									
				ILSISADIETIGEILKK	3	99.9%	1																									
				LFQECCPHSTDR	2	100.0%	1																									
				LLIHQSLAGGIIGVK	2	100.0%	2																									
				LLIHQSLAGGIIGVK	3	100.0%	1																									
				NLPLPPPPPPR	2	99.9%	3																									
				NTDEMVELR	2	100.0%	2																									
				QYADVEGF	1	98.5%	2																									
				RPAEDMEEEQAFK	2	100.0%	2																									
				RPAEDMEEEQAFKR	3	100.0%	2																									
				TDYNASVSVPDSSGPER	2	100.0%	2																									
				VVECIK	2	94.2%	1																									
				VVLIGGKPDR	2	99.4%	2																									
IPI00216770	PSMC4	isoform 2 of 26S protease regulatory subunit 6B	100.0%	19.4	5	6	6	1	13,462,255	12,626,012	12,543,681	14,741,419	1,320,351	176,554	771,103	318,582	21.9	3.1	13.8	4.8	-1.1	0.6	-1.1	0.6	1.1	0.4	-1.0	0.9	1.2	0.0004	1.2	0.03
				ENAPAIIFIDEIDAIATK	3	99.9%	1																									
				ENAPAIIFIDEIDAIATKR	3	99.9%	1																									
				ILLELLNQMDGFDQNVNVK	2	100.0%	1																									
				ILLELLNQMDGFDQNVNVK	3	100.0%	1																									
				ISGADINSICQESGMLAVR	2	100.0%	1																									
				MNLSEEVDLEDYVARPDK	3	99.3%	1																									
IPI00216773	ALB	Uncharacterized protein	100.0%	3.8	2	2	4	1	766,557	976,231	767,044	1,182,938	233,765	134,351	76,006	83,015	68.2	30.8	22.2	15.7	1.3	0.5	1.0	1	1.5	0.2	-1.3	0.2	1.2	0.2	1.5	0.006
				KVPQVSTPTLVEVSR	2	100.0%	2																									
				VPQVSTPTLVEVSR	2	100.0%	2																									
IPI00216951	DARS	Aspartyl-tRNA synthetase, cytoplasmic	100.0%	20.8	9	9	9	1	24,137,977	26,017,793	24,383,113	27,260,449	1,909,593	1,146,428	1,689,881	811,117	17.7	9.9	15.5	6.7	1.1	0.4	1.0	0.9	1.1	0.2	-1.1	0.4	1.0	0.4	1.1	0.2
				ADEVVWVR	2	82.3%	1																									
				ESIVDVEGVVR	2	99.9%	1																									
				FQTEIQTVNK	2	98.6%	1																									
				LEYCEALAMLR	2	100.0%	1																									
				LLGHLVK	2	95.9%	1																									
				LPLQLDDAVRPEAEGEEEGR	3	99.9%	1																									
				NNAYLAQSPQLYK	2	100.0%	1																									
				TSTSQAVFR	2	92.4%	1																									
				YGISSMIQSQEKPDR	3	100.0%	1																									
IPI00216975	TPM4	isoform 2 of Tropomyosin alpha-4 chain	100.0%	26.4	8	9	12	1	20,708,360	21,479,916	20,159,777	22,885,284	1,273,176	627,820	1,225,251	677,314	13.8	6.5	13.6	6.6	1.0	0.6	-1.0	0.8	1.1	0.2	-1.1	0.4	1.1	0.2	1.1	0.09
				ASDAEGDVAALNR	2	95.7%	1																									
				CGDLEEELKNVTNNLK	3	99.9%	1																									
				IQLVEEELDR	2	100.0%	2																									
				KLVILEGELER	2	99.9%	1																									
				KLVILEGELER	3	99.8%	1																									
				LATALQK	1	96.5%	2																									
				RIQLVEEELDR	2	100.0%	2																									
				RIQLVEEELDRAQER	3	99.2%	1																									
				YSEKEDKYEEEIK	3	99.2%	1																									
IPI00217013	SMEK1	isoform 1 of Serine/threonine-protein phosphatase 4 regulatory subunit 3A	100.0%	2.9	2	2	2	3	3,134,383	3,094,830	2,968,141	3,281,518	172,434	112,470	139,253	146,663	12.3	8.1	10.5	10.0	-1.0	0.9	-1.1	0.5	1.0	0.5	-1.0	0.5	1.1	0.3	1.1	0.2
IPI00384714	SMEK1	isoform 4 of Serine/threonine-protein phosphatase 4 regulatory subunit 3A	100.0%	4.0	2	2	2	3	3,134,383	3,094,830	2,968,141	3,281,518	172,434	112,470	139,253	146,663	12.3	8.1	10.5	10.0	-1.0	0.9	-1.1	0.5	1.0	0.5	-1.0	0.5	1.1	0.3	1.1	0.2
IPI00479778	SMEK1	isoform 2 of Serine/threonine-protein phosphatase 4 regulatory subunit 3A	100.0%	2.9	2	2	2	3	3,134,383	3,094,830	2,968,141	3,281,518	172,434	112,470	139,253	146,663	12.3	8.1	10.5	10.0	-1.0	0.9	-1.1	0.5	1.0	0.5	-1.0	0.5	1.1	0.3	1.1	0.2
				AESDGSLLLESK	2	99.9%	1																									
				SLTAHVIENYWK	1	98.6%	1																									
IPI00217030	RPS4X	40S ribosomal protein S4, X isoform	100.0%	31.6	7	7	9	1	29,665,273	26,966,571	29,290,260	32,148,047	1,579,028	1,422,106	2,007,762	1,964,319	11.9	11.8	15.3	13.7	-1.1	0.2	-1.0	0.9	1.1	0.4	1.1	0.4	1.2	0.07	1.1	0.3
				ECLPLIIFLR	2	99.3%	1																									
				FDTGNLCMVTGGANLGR	2	100.0%	1																									
				GNKPWISLPR	3	92.7%	1																									
				TDITYPAGFMDVISIDK	2	100.0%	2																									
				VNDTIQIDLETGK	2	100.0%	2																									
				VNDTIQIDLETGKITDFIK	3	99.5%	1																									
				YALTGDEVKK	3	81.7%	1																									
IPI00217053	PRRC1	isoform 3 of Protein PRRC1	100.0%	10.0	3	3	5	3	3,100,777	3,172,668	3,157,249	3,707,180	223,855	119,575	324,039	98,135	16.1	8.4	23.0	5.9	1.0	0.8	1.0	0.9	1.2	0.04	-1.0	1	1.2	0.009	1.2	0.2
IPI00744319	PRRC1	isoform 2 of Protein PRRC1	100.0%	9.9	3	3	5	3	3,100,777	3,172,668	3,157,249	3,707,180	223,855	119,575	324,039	98,135	16.1	8.4	23.0	5.9	1.0	0.8	1.0	0.9	1.2	0.04	-1.0	1	1.2	0.009	1.2	0.2
IPI00868973	PRRC1	isoform 1 of Protein PRRC1	100.0%	10.3	3	3	5	3	3,100,777	3,172,668	3,157,249	3,707,180	223,855	119,575	324,039	98,135	16.1	8.4	23.0	5.9	1.0	0.8	1.0	0.9	1.2	0.04	-1.0	1	1.2	0.009	1.2	0.2
				GQDEASAGGIWGFIK	2	100.0%	2																									
				QTAVSVENFIAELLPDK	2	99.7%	1																									
				WSGLLVTVGEVLEK	2	100.0%	2																									
IPI00217121	C19orf21	Uncharacterized protein C19orf21	100.0%	4.3	3	3	3	1	17,191,520	15,591,390	16,080,400	18,530,830	1,168,282	576,826	934,816	936,256	15.2	8.3	13.0	11.3	-1.1	0.3	-1.1	0.5	1.1	0.4	1.0	0.7	1.2	0.03	1.2	0.1
				LSLITAPR	2	99.1%	1																									
				WAVIQGQAVR	2	99.7%	1																									
				YPILGIPQAHR	3	99.3%	1																									
IPI00217131	MAPKAPK5	isoform 2 of MAP kinase-activated protein kinase 5	97.3%	3.8	1	1	1	1	2,975,870	2,695,090	3,050,270	3,629,470	484,034	76,888	275,510	301,503	36.4	6.4	20.2	18.6	-1.1	0.6	1.0	0.9	1.2	0.3	1.1	0.3	1.3	0.03	1.2	0.2
				DVIAQCILPQAGENEDEK	3	97.3%	1																									
IPI00217143	SDHA	Uncharacterized protein	100.0%	15.2	5	5	6	1	7,001,451	6,510,322	6,711,486	7,588,514	345,337	203,236	404,991	216,378	11.0	7.0	13.5	6.4	-1.1	0.3	-1.0	0.6	1.1	0.2	1.0	0.7	1.2	0.007	1.1	0.09
				GEGGILINSQGER	2	100.0%	1																									
				HTLSYVDVGTGK	2	100.0%	1																									
				LGANSLLDLVVFGR	2	100.0%	2																									
				VGSVLQEGCGK	2	99.9%	1																									
				VSDSISAQYPVVDHEFDAVVVGAGGAGLR	3	93.8%	1																									
IPI00217182	DSP	isoform DPII of Desmoplakin	100.0%	9.6	15	16	22	1	44,455,873	45,166,143	43,353,403	50,041,947	3,287,881	1,200,163	3,949,945	2,112,510	16.5	5.9	20.4	9.4	1.0	0.8	-1.0	0.8	1.1	0.2	-1.0	0.7	1.1	0.08	1.2	0.2
				AELIVQPELK	2	99.9%	1																									
				AITGFDDPFSGK	2	100.0%	2																									
				FLEFQYLTGGLVDPEVHGR	3	100.0%	2																									
				GYFNEELSEILSDPSDDTK	2	100.0%	2																									
				LLEAQIASGGVVDPVNSVFLPK	2	100.0%	2																									
				LLEAQIASGGVVDPVNSVFLPK	3	100.0%	1																									
				LSLQDAVSQGVIDQDMATR	2	100.0%	1																									
				LTVDSAIAR	2	99.9%	2																									
				QLQNIIQATSR	2	100.0%	1																									
				SAIYQLEEEYENLLK	2	100.0%	1																									
				SGSLSLTQFADMISLK	2	100.0%	2																									
				SMVEDITGLR	2	98.3%	1																									
				SRELDECFAQANDQMEILDSLIR	3	100.0%	1																									
				TIADLELHYQEFIR	2	99.9%	1																									
				VLLQEEGTR	2	99.5%	1																									
				YGDGIQLTR	2	99.9%	1																									
IPI00217223	PAICS	Multifunctional protein ADE2	100.0%	15.7	6	6	6	1	10,926,201	10,580,586	10,828,144	11,736,514	729,798	352,972	983,821	407,707	14.9	7.5	20.3	7.8	-1.0	0.7	-1.0	0.9	1.1	0.4	1.0	0.8	1.1	0.06	1.1	0.4
				ACGNFGIPCELR	2	98.4%	1																									
				ASILNTWISLK	2	100.0%	1																									
				EIVLADVIDNDSWR	2	99.7%	1																									
				EVTPEGLQMVK	2	98.5%	1																									
				ITSCIFQLLQEAGIK	2	100.0%	1																									
				NFEWVAER	2	99.9%	1																									
IPI00217232	SUCLA2	isoform 2 of Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	99.9%	5.0	2	2	2	4	2,738,515	2,727,738	2,660,333	2,868,485	239,795	134,678	304,881	190,523	19.6	11.0	25.6	14.9	-1.0	1	-1.0	0.8	1.0	0.7	-1.0	0.8	1.1	0.6	1.1	0.6
IPI00464979	SUCLA2	isoform 1 of Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	99.9%	4.8	2	2	2	4	2,738,515	2,727,738	2,660,333	2,868,485	239,795	134,678	304,881	190,523	19.6	11.0	25.6	14.9	-1.0	1	-1.0	0.8	1.0	0.7	-1.0	0.8	1.1	0.6	1.1	0.6
IPI01013225	SUCLA2	cDNA, FLJ78940, highly similar to Succinyl-CoA ligase (ADP-forming) beta-chain, m	99.9%	6.7	2	2	2	4	2,738,515	2,727,738	2,660,333	2,868,485	239,795	134,678	304,881	190,523	19.6	11.0	25.6	14.9	-1.0	1	-1.0	0.8	1.0	0.7	-1.0	0.8	1.1	0.6	1.1	0.6
IPI01013597	SUCLA2	Putative uncharacterized protein DKFZp564P2062	99.9%	7.6	2	2	2	4	2,738,515	2,727,738	2,660,333	2,868,485	239,795	134,678	304,881	190,523	19.6	11.0	25.6	14.9	-1.0	1	-1.0	0.8	1.0	0.7	-1.0	0.8	1.1	0.6	1.1	0.6
				ILACDDLDEAAR	2	93.4%	1																									
				INFDSNSAYR	2	98.7%	1																									
IPI00217236	TBCA	Tubulin-specific chaperone A	100.0%	44.4	5	5	5	3	12,125,957	11,849,539	11,333,918	13,718,711	862,539	525,119	548,930	374,913	15.9	9.9	10.8	6.1	-1.0	0.8	-1.1	0.5	1.1	0.1	-1.0	0.5	1.2	0.02	1.2	0.007
IPI00973811	TBCA	Uncharacterized protein	100.0%	40.3	5	5	5	3	12,125,957	11,849,539	11,333,918	13,718,711	862,539	525,119	548,930	374,913	15.9	9.9	10.8	6.1	-1.0	0.8	-1.1	0.5	1.1	0.1	-1.0	0.5	1.2	0.02	1.2	0.007
IPI00981739	TBCA	Uncharacterized protein	100.0%	57.1	5	5	5	3	12,125,957	11,849,539	11,333,918	13,718,711	862,539	525,119	548,930	374,913	15.9	9.9	10.8	6.1	-1.0	0.8	-1.1	0.5	1.1	0.1	-1.0	0.5	1.2	0.02	1.2	0.007
				ILENEKDLEEAEEYKEAR	3	99.9%	1																									
				LEAAYLDLQR	2	98.9%	1																									
				LVLDSVKLEA	2	96.8%	1																									
				QAEILQESR	2	85.8%	1																									
				RLEAAYLDLQR	2	99.9%	1																									
IPI00217253	GCHFR	GTP cyclohydrolase 1 feedback regulatory protein	100.0%	48.8	2	2	2	1	10,929,210	10,791,290	10,920,460	12,045,640	659,509	566,597	680,201	628,888	13.5	11.7	13.9	11.7	-1.0	0.9	-1.0	1	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.3
				ALGNNFYEYYVDDPPR	2	99.8%	1																									
				MEVGPTMVGDEQSDPELMQHLGASK	3	100.0%	1																									
IPI00217296	PPP2R4	isoform 3 of Serine/threonine-protein phosphatase 2A activator	96.7%	4.4	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
IPI00293102	PPP2R4	isoform 2 of Serine/threonine-protein phosphatase 2A activator	96.7%	3.6	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
IPI00640101	PPP2R4	Protein phosphatase 2A activator, regulatory subunit 4	96.7%	5.2	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
IPI00853207	PPP2R4	Protein phosphatase 2A activator, regulatory subunit 4	96.7%	10.1	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
IPI00853351	PPP2R4	Protein phosphatase 2A activator, regulatory subunit 4	96.7%	7.4	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
IPI00880122	PPP2R4	Protein phosphatase 2A activator, regulatory subunit 4	96.7%	20.3	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
IPI00893197	PPP2R4	Protein phosphatase 2A, regulatory subunit B' isoform b	96.7%	3.5	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
IPI00893753	PPP2R4	Uncharacterized protein	96.7%	9.9	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
IPI00910771	PPP2R4	cDNA FLJ54705, highly similar to Serine/threonine-protein phosphatase 2A regulato	96.7%	3.5	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
IPI00935879	PPP2R4	Protein phosphatase 2A activator, regulatory subunit 4	96.7%	4.0	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
IPI00941236	PPP2R4	serine/threonine-protein phosphatase 2A activator isoform e	96.7%	4.5	1	1	1	11	108,851	102,120	105,754	108,551	6,566	8,669	19,564	8,151	13.5	19.0	41.4	16.8	-1.1	0.6	-1.0	0.9	-1.0	1	1.0	0.9	1.1	0.6	1.0	0.9
				WIDETPPVDQPSR	2	96.7%	1																									
IPI00217343	CD302	CD302 antigen	90.9%	8.6	1	1	1	2	436,159	422,620	414,341	542,295	72,954	45,431	44,547	74,325	37.4	24.0	24.0	30.7	-1.0	0.9	-1.1	0.8	1.2	0.3	-1.0	0.9	1.3	0.2	1.3	0.2
IPI00975529	CD302	CD302 antigen isoform 3 precursor	90.9%	10.3	1	1	1	2	436,159	422,620	414,341	542,295	72,954	45,431	44,547	74,325	37.4	24.0	24.0	30.7	-1.0	0.9	-1.1	0.8	1.2	0.3	-1.0	0.9	1.3	0.2	1.3	0.2
				WTDQDDDEDLVDTCAFLHIK	3	90.9%	1																									
IPI00217357	CCAR1	isoform 1 of Cell division cycle and apoptosis regulator protein 1	97.8%	3.9	3	3	3	5	1,922,777	1,874,206	1,870,090	2,092,544	131,607	144,163	87,322	39,209	15.3	17.2	10.4	4.2	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.05
IPI00939119	CCAR1	isoform 2 of Cell division cycle and apoptosis regulator protein 1	97.8%	4.0	3	3	3	5	1,922,777	1,874,206	1,870,090	2,092,544	131,607	144,163	87,322	39,209	15.3	17.2	10.4	4.2	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.05
IPI01009122	CCAR1	64 kDa protein	97.8%	7.9	3	3	3	5	1,922,777	1,874,206	1,870,090	2,092,544	131,607	144,163	87,322	39,209	15.3	17.2	10.4	4.2	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.05
IPI01010531	CCAR1	88 kDa protein	97.8%	5.8	3	3	3	5	1,922,777	1,874,206	1,870,090	2,092,544	131,607	144,163	87,322	39,209	15.3	17.2	10.4	4.2	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.05
IPI01011002	CCAR1	120 kDa protein	97.8%	4.3	3	3	3	5	1,922,777	1,874,206	1,870,090	2,092,544	131,607	144,163	87,322	39,209	15.3	17.2	10.4	4.2	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.05
				FSLDCPSCDMMELR	2	97.8%	1																									
				IQTLPNQNQSQTQPLLK	2	97.3%	1																									

				VLVEATYNPNMPFK	2	97.5%	1																									
IPI00217437	TTBK2	Tau-tubulin kinase	97.6%	2.6	2	2	2	1	7,995,869	9,362,155	7,834,135	8,569,484	324,997	271,052	352,748	304,846	9.1	6.5	10.1	8.0	1.2	0.01	-1.0	0.7	1.1	0.2	-1.2	0.009	-1.1	0.09	1.1	0.2
				DHSATTEPLDVTK	2	88.8%	1																									
				NKISKDDDIMSEDLPGHQGDLSTFLHQEGK	3	92.9%	1																									
IPI00217469	HIST1H1A	Histone H1.1	99.5%	5.1	1	1	1	5	1,353,238	1,328,812	1,493,284	1,500,548	61,274	108,171	33,945	82,135	10.1	18.2	5.1	12.2	-1.0	0.8	1.1	0.08	1.1	0.2	1.1	0.2	1.1	0.2	1.0	0.9
IPI00217465	HIST1H1C	Histone H1.2	99.5%	5.2	1	1	1	5	1,353,238	1,328,812	1,493,284	1,500,548	61,274	108,171	33,945	82,135	10.1	18.2	5.1	12.2	-1.0	0.8	1.1	0.08	1.1	0.2	1.1	0.2	1.1	0.2	1.0	0.9
IPI00217466	HIST1H1D	Histone H1.3	99.5%	5.0	1	1	1	5	1,353,238	1,328,812	1,493,284	1,500,548	61,274	108,171	33,945	82,135	10.1	18.2	5.1	12.2	-1.0	0.8	1.1	0.08	1.1	0.2	1.1	0.2	1.1	0.2	1.0	0.9
IPI00217467	HIST1H1E	Histone H1.4	99.5%	5.0	1	1	1	5	1,353,238	1,328,812	1,493,284	1,500,548	61,274	108,171	33,945	82,135	10.1	18.2	5.1	12.2	-1.0	0.8	1.1	0.08	1.1	0.2	1.1	0.2	1.1	0.2	1.0	0.9
IPI00419983	HIST1H1T	Histone H1/H5 domain containing protein	99.5%	5.0	1	1	1	5	1,353,238	1,328,812	1,493,284	1,500,548	61,274	108,171	33,945	82,135	10.1	18.2	5.1	12.2	-1.0	0.8	1.1	0.08	1.1	0.2	1.1	0.2	1.1	0.2	1.0	0.9
				ALAAAGYDVEK	2	99.5%	1																									
IPI00217468	HIST1H1B	Histone H1.5	99.8%	5.3	1	1	2	1	24,944,500	25,460,400	22,018,100	25,855,200	2,459,272	1,244,362	720,472	1,950,610	22.1	10.9	7.3	16.9	1.0	0.9	-1.1	0.3	1.0	0.8	-1.2	0.04	1.0	0.9	1.2	0.1
				ATGPPVSELITK	2	99.8%	2																									
IPI00217471	HBE1	Hemoglobin subunit epsilon	99.9%	14.3	2	2	3	1	15,880,405	20,979,999	16,685,394	18,896,956	3,383,356	2,124,355	1,674,152	1,143,339	47.6	22.6	22.4	13.5	1.3	0.2	1.1	0.8	1.2	0.4	-1.3	0.2	-1.1	0.4	1.1	0.3
				LLVVYPWTQR	2	99.8%	2																									
				NMDNLKPAFAK	2	89.7%	1																									
IPI00374293	HMGB3P22	high mobility group protein B3-like isoform 1, partial	99.5%	7.1	1	1	1	7	478,317	693,140	526,453	610,379	27,187	65,341	41,916	63,635	12.7	21.1	17.8	23.3	1.4	0.02	1.1	0.4	1.3	0.09	-1.3	0.06	-1.1	0.4	1.2	0.3
IPI00376756	HMGB3P24	high mobility group protein B3-like	99.5%	6.3	1	1	1	7	478,317	693,140	526,453	610,379	27,187	65,341	41,916	63,635	12.7	21.1	17.8	23.3	1.4	0.02	1.1	0.4	1.3	0.09	-1.3	0.06	-1.1	0.4	1.2	0.3
IPI00888596	HMGB3P24	high mobility group protein B3-like	99.5%	6.3	1	1	1	7	478,317	693,140	526,453	610,379	27,187	65,341	41,916	63,635	12.7	21.1	17.8	23.3	1.4	0.02	1.1	0.4	1.3	0.09	-1.3	0.06	-1.1	0.4	1.2	0.3
IPI00217477	HMGB3	High mobility group protein B3	99.5%	6.5	1	1	1	7	478,317	693,140	526,453	610,379	27,187	65,341	41,916	63,635	12.7	21.1	17.8	23.3	1.4	0.02	1.1	0.4	1.3	0.09	-1.3	0.06	-1.1	0.4	1.2	0.3
IPI00411540	HMGB3	Uncharacterized protein	99.5%	8.5	1	1	1	7	478,317	693,140	526,453	610,379	27,187	65,341	41,916	63,635	12.7	21.1	17.8	23.3	1.4	0.02	1.1	0.4	1.3	0.09	-1.3	0.06	-1.1	0.4	1.2	0.3
IPI00640781	HMGB3	Uncharacterized protein	99.5%	6.7	1	1	1	7	478,317	693,140	526,453	610,379	27,187	65,341	41,916	63,635	12.7	21.1	17.8	23.3	1.4	0.02	1.1	0.4	1.3	0.09	-1.3	0.06	-1.1	0.4	1.2	0.3
IPI00643317	HMGB3	Uncharacterized protein	99.5%	6.9	1	1	1	7	478,317	693,140	526,453	610,379	27,187	65,341	41,916	63,635	12.7	21.1	17.8	23.3	1.4	0.02	1.1	0.4	1.3	0.09	-1.3	0.06	-1.1	0.4	1.2	0.3
				STNPGISIGDVAK	2	99.5%	1																									
IPI00217519	RALA	Ras-related protein Ral-A	100.0%	16.5	2	2	2	2	983,465	954,264	881,983	1,146,529	23,275	93,572	58,615	113,771	5.3	21.9	14.9	22.2	-1.0	0.8	-1.1	0.1	1.2	0.2	-1.1	0.5	1.2	0.2	1.3	0.07
IPI00927712	RALA	Protein	100.0%	20.7	2	2	2	2	983,465	954,264	881,983	1,146,529	23,275	93,572	58,615	113,771	5.3	21.9	14.9	22.2	-1.0	0.8	-1.1	0.1	1.2	0.2	-1.1	0.5	1.2	0.2	1.3	0.07
				AEQWNVNYVETSAK	2	100.0%	1																									
				SALTLQFMYDEFVEDYEPTK	2	100.0%	1																									
IPI00217540	KDM1A	isoform 2 of Lysine-specific histone demethylase 1A	100.0%	2.9	2	2	2	3	5,739,283	6,729,390	5,801,717	6,567,673	685,681	225,260	590,579	321,651	26.7	7.5	22.8	11.0	1.2	0.2	1.0	0.9	1.1	0.3	-1.2	0.2	-1.0	0.7	1.1	0.3
IPI00456631	KDM1A	isoform 1 of Lysine-specific histone demethylase 1A	100.0%	2.9	2	2	2	3	5,739,283	6,729,390	5,801,717	6,567,673	685,681	225,260	590,579	321,651	26.7	7.5	22.8	11.0	1.2	0.2	1.0	0.9	1.1	0.3	-1.2	0.2	-1.0	0.7	1.1	0.3
IPI01015618	KDM1A	95 kDa protein	100.0%	2.9	2	2	2	3	5,739,283	6,729,390	5,801,717	6,567,673	685,681	225,260	590,579	321,651	26.7	7.5	22.8	11.0	1.2	0.2	1.0	0.9	1.1	0.3	-1.2	0.2	-1.0	0.7	1.1	0.3
				TLQLWLDNPK	2	99.9%	1																									
				VIIIGSGVSGLAAAR	2	99.9%	1																									
IPI00217561	ITGB1	isoform Beta-1C of Integrin beta-1	100.0%	3.4	2	2	2	4	1,895,330	1,837,515	1,842,897	2,070,962	249,265	48,060	179,677	94,099	29.4	5.9	21.8	10.2	-1.0	0.8	-1.0	0.9	1.1	0.5	1.0	1	1.1	0.06	1.1	0.3
IPI00217562	ITGB1	isoform Beta-1C-2 of Integrin beta-1	100.0%	3.4	2	2	2	4	1,895,330	1,837,515	1,842,897	2,070,962	249,265	48,060	179,677	94,099	29.4	5.9	21.8	10.2	-1.0	0.8	-1.0	0.9	1.1	0.5	1.0	1	1.1	0.06	1.1	0.3
IPI00293305	ITGB1	isoform Beta-1B of Integrin beta-1	100.0%	3.6	2	2	2	4	1,895,330	1,837,515	1,842,897	2,070,962	249,265	48,060	179,677	94,099	29.4	5.9	21.8	10.2	-1.0	0.8	-1.0	0.9	1.1	0.5	1.0	1	1.1	0.06	1.1	0.3
IPI00549336	ITGB1	isoform Beta-1D of Integrin beta-1	100.0%	3.5	2	2	2	4	1,895,330	1,837,515	1,842,897	2,070,962	249,265	48,060	179,677	94,099	29.4	5.9	21.8	10.2	-1.0	0.8	-1.0	0.9	1.1	0.5	1.0	1	1.1	0.06	1.1	0.3
				LKPEDITQIQPQQLVLR	3	99.1%	1																									
				SLGTDLMNEMR	2	100.0%	1																									
IPI00217563	ITGB1	isoform Beta-1A of Integrin beta-1	100.0%	4.8	3	3	3	1	6,013,640	5,885,755	5,728,587	6,358,542	512,926	220,632	354,640	394,062	19.1	8.4	13.8	13.9	-1.0	0.8	-1.0	0.7	1.1	0.6	-1.0	0.7	1.1	0.3	1.1	0.3
				LKPEDITQIQPQQLVLR	3	99.1%	1																									
				SLGTDLMNEMR	2	100.0%	1																									
				WDTGENPIYK	2	94.3%	1																									
IPI00217661	RAVER1	ribonucleoprotein PTB-binding 1	99.5%	4.1	1	1	1	2	935,328	905,270	1,013,050	1,063,630	95,549	68,703	133,635	43,234	22.8	17.0	29.5	9.1	-1.0	0.8	1.1	0.6	1.1	0.3	1.1	0.5	1.2	0.09	1.0	0.7
IPI00217670	RAVER1	isoform 1 of Ribonucleoprotein PTB-binding 1	99.5%	5.1	1	1	1	2	935,328	905,270	1,013,050	1,063,630	95,549	68,703	133,635	43,234	22.8	17.0	29.5	9.1	-1.0	0.8	1.1	0.6	1.1	0.3	1.1	0.5	1.2	0.09	1.0	0.7
				GFAVLEYETAEMAEEAQQQADGLSLGGSHLR	3	99.5%	1																									
IPI00217751	NAGLT1	Sodium-dependent glucose transporter 1	90.4%	2.3	1	1	1	1	25,463,800	25,544,600	22,951,300	30,955,600	1,904,629	860,182	3,272,992	1,140,594	16.7	7.5	31.9	8.2	1.0	1	-1.1	0.5	1.2	0.04	-1.1	0.5	1.2	0.005	1.3	0.07
				NISSLSFIFVGR	2	90.4%	1																									
IPI00217766	SCARB2	Lysosome membrane protein 2	100.0%	17.0	5	5	5	1	12,564,715	13,487,514	12,109,455	14,579,731	562,127	496,569	671,780	255,904	10.0	8.2	12.4	3.9	1.1	0.3	-1.0	0.6	1.2	0.01	-1.1	0.1	1.1	0.09	1.2	0.02
				FVSAIEGMHPNQEDHETFVDINPLTGIILK	3	99.8%	1																									
				KLDDFVETGDIR	2	96.2%	1																									
				TLNIPVLTVIEWSQVHFLR	3	97.3%	1																									
				TSLDWWITDK	2	98.7%	1																									
				VEEVGPYTYR	2	80.1%	1																									
IPI00217802	FAM186B	Protein FAM186B	95.0%	1.5	1	1	1	3	3,401,470	3,579,077	3,813,737	3,793,377	240,558	206,098	392,829	399,779	15.8	12.9	23.0	23.6	1.1	0.6	1.1	0.4	1.1	0.4	1.1	0.6	1.1	0.6	-1.0	1
IPI00797620	FAM186B	60 kDa protein	95.0%	2.6	1	1	1	3	3,401,470	3,579,077	3,813,737	3,793,377	240,558	206,098	392,829	399,779	15.8	12.9	23.0	23.6	1.1	0.6	1.1	0.4	1.1	0.4	1.1	0.6	1.1	0.6	-1.0	1
IPI01014964	FAM186B	cDNA FLJ57285	95.0%	1.7	1	1	1	3	3,401,470	3,579,077	3,813,737	3,793,377	240,558	206,098	392,829	399,779	15.8	12.9	23.0	23.6	1.1	0.6	1.1	0.4	1.1	0.4	1.1	0.6	1.1	0.6	-1.0	1
				AQNLYIFLENIDR	2	95.0%	1																									
IPI00217872	PGM1	isoform 2 of Phosphoglucomutase-1	100.0%	26.6	11	11	13	1	55,210,700	57,940,882	57,525,910	68,073,940	6,953,663	4,840,632	6,615,004	4,260,869	28.2	18.7	25.7	14.0	1.0	0.8	1.0	0.8	1.2	0.2	-1.0	1	1.2	0.2	1.2	0.2
				ADNFEYSDPVDGSISR	2	100.0%	1																									
				AIGGIILTASHNPGGPNGDFGIK	3	100.0%	1																									
				FNISNGGPAPEAITDK	2	100.0%	1																									
				IALYETPTGWK	2	100.0%	2																									
				IDAMHGVVGPYVK	3	94.5%	1																									
				LSGTGSAGATIR	2	100.0%	2																									
				LYIDSYEKDVAK	2	94.3%	1																									
				SGEHDFGAAFDGDGDRNMILGK	3	98.4%	1																									
				SIFDFSALK	2	91.5%	1																									
				TIEEYAVCPDLK	2	100.0%	1																									
				VDLGVLGK	2	99.6%	1																									
IPI00217906	GNAI2	isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2	99.1%	8.6	2	2	2	6	1,466,285	1,513,002	1,370,653	1,633,830	120,949	66,852	111,261	50,170	18.4	9.9	18.2	6.9	1.0	0.7	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.06
IPI00748145	GNAI2	isoform 1 of Guanine nucleotide-binding protein G(i) subunit alpha-2	99.1%	8.2	2	2	2	6	1,466,285	1,513,002	1,370,653	1,633,830	120,949	66,852	111,261	50,170	18.4	9.9	18.2	6.9	1.0	0.7	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.06
IPI00924427	GNAI2	cDNA FLJ61561, highly similar to Guanine nucleotide-binding protein G(i), alpha-2 s	99.1%	9.6	2	2	2	6	1,466,285	1,513,002	1,370,653	1,633,830	120,949	66,852	111,261	50,170	18.4	9.9	18.2	6.9	1.0	0.7	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.06
IPI00925504	GNAI2	cDNA FLJ39276 fis, clone OCBBF2010843, highly similar to Guanine nucleotide-bin	99.1%	8.6	2	2	2	6	1,466,285	1,513,002	1,370,653	1,633,830	120,949	66,852	111,261	50,170	18.4	9.9	18.2	6.9	1.0	0.7	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.06
IPI00926935	GNAI2	Galphai2 protein	99.1%	7.9	2	2	2	6	1,466,285	1,513,002	1,370,653	1,633,830	120,949	66,852	111,261	50,170	18.4	9.9	18.2	6.9	1.0	0.7	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.06
IPI01015661	GNAI2	guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 2	99.1%	9.1	2	2	2	6	1,466,285	1,513,002	1,370,653	1,633,830	120,949	66,852	111,261	50,170	18.4	9.9	18.2	6.9	1.0	0.7	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.06
				AMGNLQIDFADPSR	2	98.7%	1																									
				IAQSDYIPTQQDVLR	2	99.1%	1																									
IPI00217920	ALDH16A1	isoform 1 of Aldehyde dehydrogenase family 16 member A1	95.7%	1.4	1	1	1	4	2,034,520	1,984,663	1,868,103	2,200,430	114,253	117,741	96,459	91,890	12.6	13.3	11.6	9.3	-1.0	0.8	-1.1	0.3	1.1	0.3	-1.1	0.5	1.1	0.2	1.2	0.04
IPI00910572	ALDH16A1	aldehyde dehydrogenase family 16 member A1 isoform 2	95.7%	1.5	1	1	1	4	2,034,520	1,984,663	1,868,103	2,200,430	114,253	117,741	96,459	91,890	12.6	13.3	11.6	9.3	-1.0	0.8	-1.1	0.3	1.1	0.3	-1.1	0.5	1.1	0.2	1.2	0.04
IPI01009162	ALDH16A1	cDNA FLJ51525, highly similar to Homo sapiens aldehyde dehydrogenase 16 family	95.7%	1.7	1	1	1	4	2,034,520	1,984,663	1,868,103	2,200,430	114,253	117,741	96,459	91,890	12.6	13.3	11.6	9.3	-1.0	0.8	-1.1	0.3	1.1	0.3	-1.1	0.5	1.1	0.2	1.2	0.04
IPI01016080	ALDH16A1	67 kDa protein	95.7%	1.7	1	1	1	4	2,034,520	1,984,663	1,868,103	2,200,430	114,253	117,741	96,459	91,890	12.6	13.3	11.6	9.3	-1.0	0.8	-1.1	0.3	1.1	0.3	-1.1	0.5	1.1	0.2	1.2	0.04
				GLDGAVDMGAR	2	95.7%	1																									
IPI00217937	C1orf101	isoform 1 of Uncharacterized protein C1orf101	99.9%	2.9	2	2	2	3	2,618,963	3,207,037	2,665,328	3,355,266	272,339	164,149	310,418	91,497	23.3	11.5	26.0	6.1	1.2	0.1	1.0	0.9	1.3	0.05	-1.2	0.2	1.0	0.5	1.3	0.09
IPI00514357	C1orf101	Uncharacterized protein	99.9%	3.2	2	2	2	3	2,618,963	3,207,037	2,665,328	3,355,266	272,339	164,149	310,418	91,497	23.3	11.5	26.0	6.1	1.2	0.1	1.0	0.9	1.3	0.05	-1.2	0.2	1.0	0.5	1.3	0.09
IPI00645983	C1orf101	isoform 2 of Uncharacterized protein C1orf101	99.9%	3.4	2	2	2	3	2,618,963	3,207,037	2,665,328	3,355,266	272,339	164,149	310,418	91,497	23.3	11.5	26.0	6.1	1.2	0.1	1.0	0.9	1.3	0.05	-1.2	0.2	1.0	0.5	1.3	0.09
				KIFLVIYNEDTK	2	99.8%	1																									
				YLFVESSHTCFLWYYR	3	94.4%	1																									
IPI00217952	GFPT1	isoform 1 of Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	100.0%	17.6	10	10	14	2	22,609,151	21,299,762	23,373,037	23,507,210	1,475,343	731,311	734,591	1,341,739	14.6	7.7	7.0	12.8	-1.1	0.4	1.0	0.7	1.0	0.7	1.1	0.08	1.1	0.2	1.0	0.9
IPI00299506	GFPT1	isoform 2 of Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	100.0%	18.1	10	10	14	2	22,609,151	21,299,762	23,373,037	23,507,210	1,475,343	731,311	734,591	1,341,739	14.6	7.7	7.0	12.8	-1.1	0.4	1.0	0.7	1.0	0.7	1.1	0.08	1.1	0.2	1.0	0.9
				AVQTLQMELQQIMK	2	99.8%	1																									
				CQNALQQVVAR	2	99.7%	1																									
				EIFEQPESVVNTMR	2	100.0%	3																									
				ESQDTSFTTLVER	2	100.0%	2																									
				GNFSSFMQK	2	99.4%	1																									
				GYDFESETDTETIAK	2	100.0%	1																									
				GYDVDFPR	2	100.0%	1																									
				HGPLALVDK	2	89.9%	1																									
				VIFLEDDDVAAVVDGR	2	100.0%	1																									
				VIQQLEGAFALVFK	2	100.0%	2																									
IPI00217975	LMNB1	Lamin-B1	100.0%	43.5	21	24	31	1	92,714,515	95,399,578	92,876,670	108,008,064	5,651,842	2,667,208	4,700,457	3,539,022	13.6	6.3	11.3	7.3	1.0	0.7	1.0	1	1.2	0.05	-1.0	0.7	1.1	0.02	1.2	0.03
				ALYETELADAR	2	100.0%	1																									
				CQSLTEDLEFR	2	99.7%	1																									
				DAALATALGDKK	2	100.0%	2																									
				DAALATALGDKK	3	99.7%	1																									
				DQMQQQLNDYEQLLDVK	2	100.0%	2																									
				DQMQQQLNDYEQLLDVK	3	100.0%	1																									
				IESLSSQLSNLQK	2	100.0%	2																									
				IGDTSVSYK	2	96.0%	1																									
				IQELEDLLAK	2	99.9%	1																									
				KIGDTSVSYK	2	99.6%	1																									
				KQLADETLLK	2	99.1%	1																									
				LAVYIDK	2	99.3%	1																									
				LSSEMNTSTVNSAR	2	100.0%	2																									
				LSSEMNTSTVNSAREELMESR	3	91.4%	1																									
				LYKEELEQTYHAK	3	99.0%	1																									
				NQNSWGTGEDVK	2	100.0%	1																									
				NTSEQDQPMGGWEMIR	2	100.0%	1																									
				QIEYEYK	2	99.1%	1																									
				SLEGDLEDLKDQIAQLEASLAAAK	2	100.0%	2																									
				SLEGDLEDLKDQIAQLEASLAAAK	3	100.0%	2																									
				SLETENSALQLQVTER	2	100.0%	1																									
				SLETENSALQLQVTEREEVR	3	97.9%	1																									
				SMYEEEINETR	2	100.0%	2																									
				TTIPEEEEEEEEAAGVVVEEELFHQQGTPR	3	100.0%	1																									
IPI00217979	MLL5	Uncharacterized protein	92.8%	1.7	1	1	1	7	200,628	204,383	208,581	192,721	13,590	18,216	36,793	19,582	15.2	19.9	39.4	22.7	1.0	0.9	1.0	0.8	-1.0	0.7	1.0	0.9	-1.1	0.7	-1.1	0.7
IPI00337726	MLL5	isoform 1 of Histone-lysine N-methyltransferase MLL5	92.8%	1.7	1	1	1	7	200,628	204,383	208,581	192,721	13,590	18,216	36,793	19,582	15.2	19.9	39.4	22.7	1.0	0.9	1.0	0.8	-1.0	0.7	1.0	0.9	-1.1	0.7	-1.1	0.7
IPI00384449	MLL5	isoform 5 of Histone-lysine N-methyltransferase MLL5	92.8%	1.9	1	1	1	7	200,628	204,383	208,581	192,721	13,590	18,216	36,793	19,582	15.2	19.9	39.4	22.7	1.0	0.9	1.0	0.8	-1.0	0.7	1.0	0.9	-1.1	0.7	-1.1	0.7
IPI00647901	MLL5	isoform 7 of Histone-lysine N-methyltransferase MLL5	92.8%	1.7	1	1	1	7	200,628	204,383	208,581	192,721	13,590	18,216	36,793	19,582	15.2	19.9	39.4	22.7	1.0	0.9	1.0	0.8	-1.0	0.7	1.0	0.9	-1.1	0.7	-1.1	0.7
IPI00895784	MLL5	isoform 6 of Histone-lysine N-methyltransferase MLL5	92.8%	1.9	1	1	1	7	200,628	204,383	208,581	192,721	13,590	18,216	36,793	19,582	15.2	19.9	39.4	22.7	1.0	0.9	1.0	0.8	-1.0	0.7	1.0	0.9	-1.1	0.7	-1.1	0.7
IPI00895932	MLL5	isoform 2 of Histone-lysine N-methyltransferase MLL5	92.8%	1.7	1	1	1	7	200,628	204,383	208,581	192,721	13,590	18,216	36,793	19,582	15.2	19.9	39.4	22.7	1.0	0.9	1.0	0.8	-1.0	0.7	1.0	0.9	-1.1	0.7	-1.1	0.7
IPI00983907	MLL5	cDNA FLJ14026 fis, clone HEMBA1003679, weakly similar to SIALIDASE	92.8%	5.3	1	1	1	7	200,628	204,383	208,581	192,721	13,590	18,216	36,793	19,582	15.2	19.9	39.4	22.7	1.0	0.9	1.0	0.8	-1.0	0.7	1.0	0.9	-1.1	0.7	-1.1	0.7
				IFTKPDPQWDSTVSASEAENGVHLKTELQQK	3	92.8%	1																									
IPI00218038	ST13P4	Putative protein FAM10A4	100.0%	12.5	2	2	3	1	3,553,111	3,977,049	3,371,167	3,847,955	253,692	496,280	83,723	180,213	16.0	27.9	5.6	10.5	1.1	0.5	-1.1	0.5	1.1	0.4	-1.2	0.3	-1.0	0.8	1.1	0.04
				AIEINPDSAQPYK	2	100.0%	2																									
				LLGHWEEAAHDLALACK	3	100.0%	1																									
IPI00218070	GRB2	isoform GRB3-3 of Growth factor receptor-bound protein 2	100.0%	27.3	4	5	5	1	9,100,232	9,058,933	9,161,755	10,161,733	725,952	396,031	485,350	572,164	17.8	9.8	11.9	12.6	-1.0	1	1.0	0.9	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.2
				GACHGQTGMFPR	2	97.0%	1																									
				NQQIFLR	2	89.4%	1																									
				RGDFIHVMDNSDPNWWK	3	100.0%	1																									
				VLNEECDQNWYK	2	100.0%	1																									
				VLNEECDQNWYK	3	80.4%	1																									
IPI00218097	SPAG9	Uncharacterized protein	99.3%	1.5	2	2	2	8	899,259	1,018,343	911,966	1,064,709	130,898	88,619	82,109	68,107	32.6	19.5	20.1	14.3	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.4	1.0	0.7	1.2	0.2
IPI00384432	SPAG9	isoform 2 of C-Jun-amino-terminal kinase-interacting protein 4	99.3%	1.5	2	2	2	8	899,259	1,018,343	911,966	1,064,709	130,898	88,619	82,109	68,107	32.6	19.5	20.1	14.3	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.4	1.0	0.7	1.2	0.2
IPI00479676	SPAG9	isoform 4 of C-Jun-amino-terminal kinase-interacting protein 4	99.3%	1.5	2	2	2	8	899,259	1,018,343	911,966	1,064,709	130,898	88,619	82,109	68,107	32.6	19.5	20.1	14.3	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.4	1.0	0.7	1.2	0.2
IPI00744288	SPAG9	isoform 5 of C-Jun-amino-terminal kinase-interacting protein 4	99.3%	2.2	2	2	2	8	899,259	1,018,343	911,966	1,064,709	130,898	88,619	82,109	68,107	32.6	19.5	20.1	14.3	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.4	1.0	0.7	1.2	0.2
IPI00744648	SPAG9	isoform 1 of C-Jun-amino-terminal kinase-interacting protein 4	99.3%	1.5	2	2	2	8	899,259	1,018,343	911,966	1,064,709	130,898	88,619	82,109	68,107	32.6	19.5	20.1	14.3	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.4	1.0	0.7	1.2	0.2
IPI00745406	SPAG9	Uncharacterized protein	99.3%	1.5	2	2	2	8	899,259	1,018,343	911,966	1,064,709	130,898	88,619	82,109	68,107	32.6	19.5	20.1	14.3	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.4	1.0	0.7	1.2	0.2

IPI00879552	SPAG9	isoform 3 of C-Jun-amino-terminal kinase-interacting protein 4	99.3%	2.1	2	2	2	8	899,259	1,018,343	911,966	1,064,709	130,898	88,619	82,109	68,107	32.6	19.5	20.1	14.3	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.4	1.0	0.7	1.2	0.2
IPI01011459	SPAG9	cDNA FLJ59325, highly similar to C-jun-amino-terminal kinase-interacting protein 4	99.3%	1.7	2	2	2	8	899,259	1,018,343	911,966	1,064,709	130,898	88,619	82,109	68,107	32.6	19.5	20.1	14.3	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.4	1.0	0.7	1.2	0.2
				HIEVQVAQETR	2	99.3%	1																									
				LMELQEAVR	2	92.1%	1																									
IPI00218106	TCEA1	isoform 2 of Transcription elongation factor A protein 1	91.6%	5.4	1	1	1	1	1,602,300	1,837,375	2,094,700	1,866,430	134,837	120,910	207,446	74,708	18.8	14.7	22.1	9.0	1.1	0.2	1.3	0.08	1.2	0.1	1.1	0.3	1.0	0.8	-1.1	0.3
				MTAEEMASDELKEMR	3	91.6%	1																									
IPI00218130	PYGM	Glycogen phosphorylase, muscle form	100.0%	5.5	3	4	6	2	8,155,445	8,162,642	8,292,452	8,758,661	497,989	356,575	233,981	331,568	13.7	9.8	6.3	8.5	1.0	1	1.0	0.8	1.1	0.3	1.0	0.8	1.1	0.3	1.1	0.3
IPI01009320	PYGM	Phosphorylase	100.0%	5.5	3	4	6	2	8,155,445	8,162,642	8,292,452	8,758,661	497,989	356,575	233,981	331,568	13.7	9.8	6.3	8.5	1.0	1	1.0	0.8	1.1	0.3	1.0	0.8	1.1	0.3	1.1	0.3
				VIPAADLSEQISTAGTEASGTGNMK	2	100.0%	1																									
				VIPAADLSEQISTAGTEASGTGNMK	3	100.0%	1																									
				VLYPNDNFFEGK	2	100.0%	2																									
				YEFGIFNQK	2	100.0%	2																									
IPI00218200	BCAP31	B-cell receptor-associated protein 31	95.5%	3.7	1	1	1	2	3,303,325	3,500,725	3,414,000	3,490,545	218,711	110,255	118,518	151,981	14.8	7.0	7.8	9.7	1.1	0.4	1.0	0.7	1.1	0.5	-1.0	0.6	-1.0	1	1.0	0.7
IPI01009955	BCAP31	B-cell receptor-associated protein 31 isoform a	95.5%	2.9	1	1	1	2	3,303,325	3,500,725	3,414,000	3,490,545	218,711	110,255	118,518	151,981	14.8	7.0	7.8	9.7	1.1	0.4	1.0	0.7	1.1	0.5	-1.0	0.6	-1.0	1	1.0	0.7
				AENQVLAMR	2	95.5%	1																									
IPI00218236	PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	100.0%	23.6	7	7	9	1	10,044,656	11,349,948	10,724,849	12,305,966	557,684	660,445	765,016	224,741	12.4	13.0	16.0	4.1	1.1	0.2	1.1	0.5	1.2	0.006	-1.1	0.6	1.1	0.2	1.1	0.1
				EIFLSQPILLELEAPLK	2	100.0%	2																									
				GVSFTFGADVVSK	2	99.4%	1																									
				HDLDLICR	2	99.9%	2																									
				IVQMTEAEVR	2	99.9%	1																									
				IYGFYDECK	2	99.2%	1																									
				SREIFLSQPILLELEAPLK	3	98.3%	1																									
				TFTDCFNCLPIAAIVDEK	2	100.0%	1																									
IPI00218251	TGM2	isoform 2 of Protein-glutamine gamma-glutamyltransferase 2	100.0%	4.0	1	1	1	2	285,713	262,827	361,386	270,469	33,574	42,969	33,550	22,807	26.3	36.6	20.8	18.9	-1.1	0.7	1.3	0.1	-1.1	0.7	1.4	0.1	1.0	0.9	-1.3	0.06
IPI00218252	TGM2	isoform 3 of Protein-glutamine gamma-glutamyltransferase 2	100.0%	6.3	1	1	1	2	285,713	262,827	361,386	270,469	33,574	42,969	33,550	22,807	26.3	36.6	20.8	18.9	-1.1	0.7	1.3	0.1	-1.1	0.7	1.4	0.1	1.0	0.9	-1.3	0.06
				WDNNYGDGVSPMSWIGSVDILR	2	99.9%	1																									
IPI00218292	UFD1L	isoform Short of Ubiquitin fusion degradation protein 1 homolog	99.6%	3.9	1	1	1	4	599,415	564,948	585,380	700,750	118,452	23,541	57,883	58,281	44.2	9.3	22.1	18.6	-1.1	0.8	-1.0	0.9	1.2	0.5	1.0	0.8	1.2	0.06	1.2	0.2
IPI00654779	UFD1L	Uncharacterized protein	99.6%	4.1	1	1	1	4	599,415	564,948	585,380	700,750	118,452	23,541	57,883	58,281	44.2	9.3	22.1	18.6	-1.1	0.8	-1.0	0.9	1.2	0.5	1.0	0.8	1.2	0.06	1.2	0.2
IPI00655754	UFD1L	isoform Long of Ubiquitin fusion degradation protein 1 homolog	99.6%	3.5	1	1	1	4	599,415	564,948	585,380	700,750	118,452	23,541	57,883	58,281	44.2	9.3	22.1	18.6	-1.1	0.8	-1.0	0.9	1.2	0.5	1.0	0.8	1.2	0.06	1.2	0.2
IPI00873326	UFD1L	Uncharacterized protein	99.6%	3.5	1	1	1	4	599,415	564,948	585,380	700,750	118,452	23,541	57,883	58,281	44.2	9.3	22.1	18.6	-1.1	0.8	-1.0	0.9	1.2	0.5	1.0	0.8	1.2	0.06	1.2	0.2
				FVAFSGEGQSLR	2	99.6%	1																									
IPI00218319	TPM3	isoform 2 of Tropomyosin alpha-3 chain	100.0%	30.7	10	11	15	1	51,417,759	48,522,406	46,278,776	53,931,790	3,325,611	2,664,932	2,219,224	1,498,895	14.5	12.3	10.7	6.2	-1.1	0.5	-1.1	0.2	1.0	0.5	-1.0	0.5	1.1	0.1	1.2	0.02
				ALKDEEKMELQEIQLK	3	100.0%	1																									
				IQLVEEELDR	2	100.0%	2																									
				IQVLQQQADDAEER	2	100.0%	2																									
				KIQVLQQQADDAEER	3	100.0%	1																									
				LATALQK	1	96.5%	2																									
				LMDQNLK	2	91.3%	1																									
				LVIIEGDLER	2	99.0%	1																									
				MELQEIQLK	2	86.0%	1																									
				RIQLVEEELDR	2	100.0%	2																									
				TIDDLEDKLK	2	99.7%	1																									
				TIDDLEDKLK	3	86.7%	1																									
IPI00218342	MTHFD1	C-1-tetrahydrofolate synthase, cytoplasmic	100.0%	21.0	15	15	17	1	57,146,235	61,173,372	58,007,791	70,725,580	5,484,238	2,725,759	4,272,579	2,635,203	21.5	10.0	16.5	8.3	1.1	0.5	1.0	0.9	1.2	0.06	-1.1	0.5	1.2	0.04	1.2	0.04
				AYIQENLELVEK	2	100.0%	1																									
				EIGLLSEEVELYGETK	2	99.9%	1																									
				GALALAQAVQR	2	100.0%	1																									
				IYGADDIELLPEAQHK	2	97.1%	1																									
				KVVGDVAYDEAK	2	89.3%	1																									
				LAILQVGNR	2	94.1%	1																									
				LDIDPETITWQR	2	100.0%	2																									
				LVGPEGFVVTEAGFGADIGMEK	3	96.4%	1																									
				QGFGNLPICMAK	2	100.0%	1																									
				QPSQGPTFGIK	2	87.3%	1																									
				TDPTTLTDEEINR	2	100.0%	2																									
				TDTESELDLISR	2	100.0%	1																									
				TPVPSDIDISR	2	99.0%	1																									
				WMIQYNNLNLK	2	94.1%	1																									
				YVVVTGITPTPLGEGK	2	100.0%	1																									
IPI00218343	TUBA1C	Tubulin alpha-1C chain	100.0%	55.5	19	27	44	1	251,222,941	255,445,899	243,545,018	285,464,328	########	########	########	########	13.6	9.0	14.8	8.6	1.0	0.8	-1.0	0.7	1.1	0.1	-1.0	0.6	1.1	0.08	1.2	0.06
				AVCMLSNTTAVAEAWAR	2	100.0%	1																									
				AVFVDLEPTVIDEVR	2	100.0%	3																									
				AVFVDLEPTVIDEVR	3	100.0%	1																									
				DVNAAIATIK	1	100.0%	2																									
				DVNAAIATIK	2	100.0%	2																									
				EIIDLVLDR	2	100.0%	2																									
				FDGALNVDLTEFQTNLVPYPR	2	100.0%	2																									
				FDLMYAK	2	99.9%	2																									
				IHFPLATYAPVISAEK	2	100.0%	3																									
				IHFPLATYAPVISAEK	3	100.0%	1																									
				LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	3	100.0%	1																									
				LDHKFDLMYAK	2	99.9%	1																									
				LDHKFDLMYAK	3	100.0%	1																									
				LISQIVSSITASLR	2	100.0%	2																									
				LISQIVSSITASLR	3	100.0%	2																									
				LSVDYGK	2	91.2%	1																									
				LSVDYGKK	2	91.7%	1																									
				NLDIERPTYTNLNR	2	99.2%	2																									
				NLDIERPTYTNLNR	3	100.0%	1																									
				QLFHPEQLITGKEDAANNYAR	3	100.0%	2																									
				RNLDIERPTYTNLNR	3	99.6%	1																									
				TIGGGDDSFNTFFSETGAGK	2	100.0%	2																									
				TIGGGDDSFNTFFSETGAGK	3	99.9%	1																									
				TIQFVDWCPTGFK	2	100.0%	2																									
				VGINYQPPTVVPGGDLAK	2	100.0%	2																									
				VGINYQPPTVVPGGDLAK	3	85.0%	1																									
				YMACCLLYR	2	100.0%	2																									
IPI00218371	PRPS1L1	Ribose-phosphate pyrophosphokinase 3	98.1%	5.4	1	1	1	1	444,953	441,700	445,406	437,686	49,141	34,875	30,214	32,779	24.7	17.7	15.2	16.8	-1.0	1	1.0	1	-1.0	0.9	1.0	0.9	-1.0	0.9	-1.0	0.9
				VYAILTHGIFSGPAISR	2	98.1%	1																									
IPI00218372	PSMA7	isoform 2 of Proteasome subunit alpha type-7	100.0%	19.1	2	2	3	1	1,159,120	1,116,982	1,223,894	1,268,943	116,138	38,093	81,925	77,791	22.4	7.6	15.0	13.7	-1.0	0.7	1.1	0.7	1.1	0.5	1.1	0.3	1.1	0.1	1.0	0.7
				NYTDEAIETDDLTIK	2	100.0%	2																									
				RPFGISALIVGFDFDGTPR	3	99.5%	1																									
IPI00218407	ALDOB	Fructose-bisphosphate aldolase B	97.5%	6.6	1	1	1	2	8,040,500	8,250,100	8,252,590	11,087,600	1,568,116	605,516	1,165,388	606,712	43.6	16.4	31.6	12.2	1.0	0.9	1.0	0.9	1.4	0.1	1.0	1	1.3	0.01	1.3	0.06
IPI00942961	ALDOB	Fructose-bisphosphate aldolase	97.5%	8.1	1	1	1	2	8,040,500	8,250,100	8,252,590	11,087,600	1,568,116	605,516	1,165,388	606,712	43.6	16.4	31.6	12.2	1.0	0.9	1.0	0.9	1.4	0.1	1.0	1	1.3	0.01	1.3	0.06
				GQYVHTGSSGAASTQSLFTACYTY	3	97.5%	1																									
IPI00218408	GART	isoform Short of Trifunctional purine biosynthetic protein adenosine-3	100.0%	5.3	2	2	2	2	2,381,990	2,884,434	2,544,263	2,757,471	260,925	75,801	111,067	119,458	24.5	5.9	9.8	9.7	1.2	0.1	1.1	0.6	1.2	0.2	-1.1	0.04	-1.0	0.4	1.1	0.2
IPI00879865	GART	GARS protein	100.0%	5.3	2	2	2	2	2,381,990	2,884,434	2,544,263	2,757,471	260,925	75,801	111,067	119,458	24.5	5.9	9.8	9.7	1.2	0.1	1.1	0.6	1.2	0.2	-1.1	0.04	-1.0	0.4	1.1	0.2
				AIAFLQQPR	2	96.8%	1																									
				FGDPECQVILPLLK	2	100.0%	1																									
IPI00218486	SSH3	isoform 1 of Protein phosphatase Slingshot homolog 3	100.0%	5.6	3	3	3	2	3,127,039	3,210,833	3,544,490	3,627,464	272,374	179,401	270,789	116,171	19.5	12.5	17.1	7.2	1.0	0.8	1.1	0.3	1.2	0.1	1.1	0.3	1.1	0.09	1.0	0.8
IPI00655638	SSH3	isoform 3 of Protein phosphatase Slingshot homolog 3	100.0%	7.2	3	3	3	2	3,127,039	3,210,833	3,544,490	3,627,464	272,374	179,401	270,789	116,171	19.5	12.5	17.1	7.2	1.0	0.8	1.1	0.3	1.2	0.1	1.1	0.3	1.1	0.09	1.0	0.8
				EIDNFYPER	2	99.8%	1																									
				QLQIYQGILTASR	2	99.4%	1																									
				QSVVTLQGSAVVANR	2	99.1%	1																									
IPI00218493	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	100.0%	22.5	4	4	5	1	9,208,670	9,854,282	10,123,363	11,385,875	575,997	338,645	583,957	234,844	14.0	7.7	12.9	4.6	1.1	0.4	1.1	0.3	1.2	0.008	1.0	0.7	1.2	0.006	1.1	0.08
				DLNHVCVISETGK	2	87.4%	1																									
				FFADLLDYIK	2	100.0%	1																									
				NVLIVEDIIDTGK	2	100.0%	1																									
				VIGGDDLSTLTGK	2	100.0%	2																									
IPI00218539	COL11A1	isoform B of Collagen alpha-1(XI) chain	90.9%	1.5	1	1	1	5	603,898	593,834	600,866	701,168	55,339	28,534	42,633	55,236	20.5	10.7	15.9	17.6	-1.0	0.9	-1.0	1	1.2	0.2	1.0	0.9	1.2	0.1	1.2	0.2
IPI00218540	COL11A1	isoform C of Collagen alpha-1(XI) chain	90.9%	1.5	1	1	1	5	603,898	593,834	600,866	701,168	55,339	28,534	42,633	55,236	20.5	10.7	15.9	17.6	-1.0	0.9	-1.0	1	1.2	0.2	1.0	0.9	1.2	0.1	1.2	0.2
IPI00295575	COL11A1	isoform A of Collagen alpha-1(XI) chain	90.9%	1.5	1	1	1	5	603,898	593,834	600,866	701,168	55,339	28,534	42,633	55,236	20.5	10.7	15.9	17.6	-1.0	0.9	-1.0	1	1.2	0.2	1.0	0.9	1.2	0.1	1.2	0.2
IPI00844199	COL11A1	cDNA FLJ57066, highly similar to Collagen alpha-1(XI) chain	90.9%	2.6	1	1	1	5	603,898	593,834	600,866	701,168	55,339	28,534	42,633	55,236	20.5	10.7	15.9	17.6	-1.0	0.9	-1.0	1	1.2	0.2	1.0	0.9	1.2	0.1	1.2	0.2
IPI00965543	COL11A1	collagen alpha-1(XI) chain isoform C preproprotein	90.9%	1.6	1	1	1	5	603,898	593,834	600,866	701,168	55,339	28,534	42,633	55,236	20.5	10.7	15.9	17.6	-1.0	0.9	-1.0	1	1.2	0.2	1.0	0.9	1.2	0.1	1.2	0.2
				GEPGEAGNPGPPGEAGVGGPKGERGEK	3	90.9%	1																									
IPI00218568	PCBD1	Pterin-4-alpha-carbinolamine dehydratase	99.4%	23.1	2	2	3	1	45,498,850	44,527,230	40,640,330	53,178,940	5,206,966	1,757,177	5,007,246	3,090,535	25.6	8.8	27.6	13.0	-1.0	0.9	-1.1	0.5	1.2	0.2	-1.1	0.5	1.2	0.04	1.3	0.07
				AVGWNELEGR	2	99.4%	2																									
				LSAEERDQLLPNLR	3	99.1%	1																									
IPI01014727	PGAM1	cDNA FLJ51983, highly similar to Phosphoglycerate mutase 1	100.0%	8.4	2	2	3	2	4,824,809	4,797,127	4,841,338	5,304,425	334,211	232,770	274,347	133,300	15.5	10.9	12.7	5.6	-1.0	0.9	1.0	1	1.1	0.2	1.0	0.9	1.1	0.1	1.1	0.2
IPI00218570	PGAM2	Phosphoglycerate mutase 2	100.0%	7.9	2	2	3	2	4,824,809	4,797,127	4,841,338	5,304,425	334,211	232,770	274,347	133,300	15.5	10.9	12.7	5.6	-1.0	0.9	1.0	1	1.1	0.2	1.0	0.9	1.1	0.1	1.1	0.2
				AMEAVAAQGK	1	100.0%	1																									
				HYGGLTGLNK	2	99.9%	2																									
IPI00218591	SRSF1	isoform ASF-2 of Serine/arginine-rich splicing factor 1	100.0%	31.2	7	7	14	2	10,821,569	11,677,378	11,369,468	12,869,387	837,403	304,000	835,398	300,461	17.3	5.8	16.4	5.2	1.1	0.4	1.1	0.7	1.2	0.07	-1.0	0.7	1.1	0.02	1.1	0.2
IPI00218592	SRSF1	isoform ASF-3 of Serine/arginine-rich splicing factor 1	100.0%	45.3	7	7	14	2	10,821,569	11,677,378	11,369,468	12,869,387	837,403	304,000	835,398	300,461	17.3	5.8	16.4	5.2	1.1	0.4	1.1	0.7	1.2	0.07	-1.0	0.7	1.1	0.02	1.1	0.2
				DGTGVVEFVR	2	99.9%	2																									
				DGYDYDGYR	2	100.0%	2																									
				EAGDVCYADVYR	2	100.0%	2																									
				GGPPFAFVEFEDPRDAEDAVYGR	3	99.9%	2																									
				IYVGNLPPDIR	2	100.0%	3																									
				TKDIEDVFYK	2	100.0%	2																									
				VVVSGLPPSGSWQDLK	2	99.5%	1																									
IPI00218638	MYO1F	Myosin-If	94.1%	0.8	1	1	1	2	10,342,750	12,253,550	9,774,500	14,553,000	1,996,668	1,186,540	1,309,457	951,999	43.2	21.7	30.0	14.6	1.2	0.4	-1.1	0.8	1.4	0.09	-1.3	0.2	1.2	0.2	1.5	0.02
IPI00736464	MYO1F	FLJ00395 protein (Fragment)	94.1%	0.8	1	1	1	2	10,342,750	12,253,550	9,774,500	14,553,000	1,996,668	1,186,540	1,309,457	951,999	43.2	21.7	30.0	14.6	1.2	0.4	-1.1	0.8	1.4	0.09	-1.3	0.2	1.2	0.2	1.5	0.02
				VDFADSVTK	2	94.1%	1																									
IPI00218682	P4HA1	isoform 2 of Prolyl 4-hydroxylase subunit alpha-1	100.0%	33.7	15	17	22	2	28,336,990	29,370,820	28,198,383	32,369,660	2,579,884	1,211,881	1,431,102	1,083,712	20.4	9.2	11.4	7.5	1.0	0.7	-1.0	1	1.1	0.2	-1.0	0.5	1.1	0.1	1.1	0.05
IPI00916535	P4HA1	prolyl 4-hydroxylase subunit alpha-1 isoform 3 precursor	100.0%	34.9	15	17	22	2	28,336,990	29,370,820	28,198,383	32,369,660	2,579,884	1,211,881	1,431,102	1,083,712	20.4	9.2	11.4	7.5	1.0	0.7	-1.0	1	1.1	0.2	-1.0	0.5	1.1	0.1	1.1	0.05
				AEEDKLEQIKK	3	88.5%	1																									
				DPEGFVGHPVNAFK	2	100.0%	1																									
				DPEGFVGHPVNAFK	3	99.9%	1																									
				FHDIISDAEIEIVK	2	100.0%	1																									
				FILAPAKQEDEWDKPR	3	100.0%	1																									
				HAACPVLVGNK	2	100.0%	2																									
				KDEPDAFKELGTGNR	3	100.0%	1																									
				LLELDPEHQR	2	99.2%	1																									
				LLELDPEHQR	3	92.9%	1																									
				LNTEWSELENLVLK	2	100.0%	2																									
				LQDTYNLDTDTISK	2	100.0%	2																									

				LTSTATKDPEGFVGHPVNAFK	3	100.0%	1																									
				QLDEGEISTIDK	2	88.8%	1																									
				QYFPNDEDQVGAAK	2	100.0%	2																									
				RLNTEWSELENLVLK	2	99.9%	1																									
				SAWLSGYENPVVSR	2	100.0%	2																									
				SFLTAEDCFELGK	2	99.9%	1																									
IPI00218687	CACNA1G	isoform 10 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00218688	CACNA1G	isoform 11 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00218689	CACNA1G	isoform 12 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00218690	CACNA1G	isoform 13 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00219390	CACNA1G	isoform 1 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00219391	CACNA1G	isoform 2 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.5	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00219393	CACNA1G	isoform 3 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00219394	CACNA1G	isoform 4 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.5	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00219395	CACNA1G	isoform 6 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00219396	CACNA1G	isoform 7 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00219397	CACNA1G	isoform 8 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00219398	CACNA1G	isoform 9 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00299037	CACNA1G	isoform 5 of Voltage-dependent T-type calcium channel subunit alpha-1G	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00794872	CACNA1G	voltage-dependent T-type calcium channel subunit alpha-1G isoform 15	92.6%	0.6	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00964039	CACNA1G	T calcium channel alpha 1G subunit variant 137	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00964592	CACNA1G	T calcium channel alpha 1G subunit variant 33	92.6%	0.6	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00964641	CACNA1G	T calcium channel alpha 1G subunit variant 473	92.6%	0.5	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00965139	CACNA1G	T calcium channel alpha 1G subunit variant 177	92.6%	0.6	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00965676	CACNA1G	T calcium channel alpha 1G subunit variant 477	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00966179	CACNA1G	T calcium channel alpha 1G subunit variant 49	92.6%	0.6	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00966310	CACNA1G	T calcium channel alpha 1G subunit variant 184	92.6%	0.5	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00966433	CACNA1G	T calcium channel alpha 1G subunit variant 441	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00966790	CACNA1G	T calcium channel alpha 1G subunit variant 409	92.6%	0.5	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00966975	CACNA1G	T calcium channel alpha 1G subunit variant 216	92.6%	0.5	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00966996	CACNA1G	T calcium channel alpha 1G subunit variant 223	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00967763	CACNA1G	T calcium channel alpha 1G subunit variant 209	92.6%	0.6	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00967839	CACNA1G	T calcium channel alpha 1G subunit variant 145	92.6%	0.6	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00968035	CACNA1G	T calcium channel alpha 1G subunit variant 169	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI00968099	CACNA1G	38 kDa protein	92.6%	3.0	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI01009819	CACNA1G	T calcium channel alpha 1G subunit variant 313	92.6%	0.5	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI01010803	CACNA1G	T calcium channel alpha 1G subunit variant 249	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI01012623	CACNA1G	T calcium channel alpha 1G subunit variant 157	92.6%	0.4	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
IPI01013285	CACNA1G	T calcium channel alpha 1G subunit variant 17	92.6%	0.6	1	1	1	33	75,372	89,939	83,146	99,423	4,586	8,615	14,013	11,274	13.6	21.4	37.7	25.4	1.2	0.2	1.1	0.6	1.3	0.08	-1.1	0.7	1.1	0.5	1.2	0.4
				FFVCQGEDTR	2	92.6%	1																									
IPI00218693	APRT	Adenine phosphoribosyltransferase	100.0%	75.0	10	11	17	1	43,920,573	45,845,906	45,617,158	51,053,699	5,587,011	2,599,439	3,996,320	1,516,225	28.4	12.7	19.6	6.6	1.0	0.8	1.0	0.8	1.2	0.3	-1.0	1	1.1	0.1	1.1	0.3
				AAIGLLAR	2	99.0%	2																									
				AELEIQKDALEPGQR	2	99.8%	1																									
				DISPVLKDPASFR	2	100.0%	2																									
				DISPVLKDPASFR	3	98.0%	1																									
				EKLAPVPFFSLLQYE	2	99.4%	1																									
				GFLFGPSLAQELGLGCVLIR	3	100.0%	2																									
				IDYIAGLDSR	2	100.0%	2																									
				LAPVPFFSLLQYE	2	99.9%	1																									
				LQAEVLECVSLVELTSLK	3	100.0%	1																									
				SFPDFPTPGVVFR	2	100.0%	2																									
				VVVVDDLLATGGTMNAACELLGR	2	100.0%	2																									
IPI00218725	LAMA2	laminin subunit alpha-2 isoform b precursor	98.0%	0.3	1	1	1	4	1,707,943	1,798,473	1,700,408	1,886,890	77,766	68,860	70,309	79,299	10.2	8.6	9.3	9.4	1.1	0.4	-1.0	0.9	1.1	0.1	-1.1	0.3	1.0	0.4	1.1	0.1
IPI00479834	LAMA2	Uncharacterized protein	98.0%	0.3	1	1	1	4	1,707,943	1,798,473	1,700,408	1,886,890	77,766	68,860	70,309	79,299	10.2	8.6	9.3	9.4	1.1	0.4	-1.0	0.9	1.1	0.1	-1.1	0.3	1.0	0.4	1.1	0.1
IPI00873889	LAMA2	Uncharacterized protein	98.0%	0.3	1	1	1	4	1,707,943	1,798,473	1,700,408	1,886,890	77,766	68,860	70,309	79,299	10.2	8.6	9.3	9.4	1.1	0.4	-1.0	0.9	1.1	0.1	-1.1	0.3	1.0	0.4	1.1	0.1
IPI00940615	LAMA2	Uncharacterized protein	98.0%	0.3	1	1	1	4	1,707,943	1,798,473	1,700,408	1,886,890	77,766	68,860	70,309	79,299	10.2	8.6	9.3	9.4	1.1	0.4	-1.0	0.9	1.1	0.1	-1.1	0.3	1.0	0.4	1.1	0.1
				NTWWQSPSIK	2	98.0%	1																									
IPI00218728	PAFAH1B1	isoform 1 of Platelet-activating factor acetylhydrolase IB subunit alpha	99.4%	3.7	1	1	1	3	1,111,627	1,399,207	1,192,437	1,369,200	85,973	78,772	138,854	77,717	17.3	12.6	26.0	12.7	1.3	0.04	1.1	0.6	1.2	0.06	-1.2	0.2	-1.0	0.8	1.1	0.3
IPI00873228	PAFAH1B1	cDNA FLJ51164, highly similar to Platelet-activating factor acetylhydrolase IB alpha	99.4%	6.3	1	1	1	3	1,111,627	1,399,207	1,192,437	1,369,200	85,973	78,772	138,854	77,717	17.3	12.6	26.0	12.7	1.3	0.04	1.1	0.6	1.2	0.06	-1.2	0.2	-1.0	0.8	1.1	0.3
IPI00909586	PAFAH1B1	cDNA FLJ52123, highly similar to Platelet-activating factor acetylhydrolase IB alpha	99.4%	7.3	1	1	1	3	1,111,627	1,399,207	1,192,437	1,369,200	85,973	78,772	138,854	77,717	17.3	12.6	26.0	12.7	1.3	0.04	1.1	0.6	1.2	0.06	-1.2	0.2	-1.0	0.8	1.1	0.3
				TAPYVVTGSVDQTVK	2	99.4%	1																									
IPI00218733	SOD1	Superoxide dismutase [Cu-Zn]	100.0%	16.9	2	2	3	1	8,883,040	9,186,070	8,159,000	9,824,565	748,133	291,779	510,663	598,219	18.8	7.1	14.0	13.6	1.0	0.7	-1.1	0.4	1.1	0.4	-1.1	0.1	1.1	0.4	1.2	0.07
				GDGPVQGIINFEQK	2	100.0%	2																									
				HVGDLGNVTADK	2	99.8%	1																									
IPI00218775	FKBP5	Peptidyl-prolyl cis-trans isomerase FKBP5	94.7%	2.0	1	1	1	4	806,125	881,860	865,998	970,065	69,510	56,502	81,491	86,212	19.3	14.3	21.0	19.9	1.1	0.4	1.1	0.6	1.2	0.2	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00443474	FKBP5	cDNA FLJ46716 fis, clone TRACH3018108, highly similar to 51 kDa FK506-binding	94.7%	2.0	1	1	1	4	806,125	881,860	865,998	970,065	69,510	56,502	81,491	86,212	19.3	14.3	21.0	19.9	1.1	0.4	1.1	0.6	1.2	0.2	-1.0	0.9	1.1	0.4	1.1	0.4
IPI01010266	FKBP5	cDNA FLJ57237, highly similar to FK506-binding protein 5	94.7%	3.2	1	1	1	4	806,125	881,860	865,998	970,065	69,510	56,502	81,491	86,212	19.3	14.3	21.0	19.9	1.1	0.4	1.1	0.6	1.2	0.2	-1.0	0.9	1.1	0.4	1.1	0.4
IPI01015705	FKBP5	cDNA FLJ58213, highly similar to FK506-binding protein 5	94.7%	2.1	1	1	1	4	806,125	881,860	865,998	970,065	69,510	56,502	81,491	86,212	19.3	14.3	21.0	19.9	1.1	0.4	1.1	0.6	1.2	0.2	-1.0	0.9	1.1	0.4	1.1	0.4
				VLEVNPQNK	2	94.7%	1																									
IPI00218782	CAPZB	cDNA FLJ60094, highly similar to F-actin capping protein subunit beta	100.0%	36.1	12	12	18	2	18,713,704	19,820,477	18,650,307	22,394,983	1,512,903	731,402	1,402,086	507,282	18.1	8.3	16.8	5.1	1.1	0.5	-1.0	1	1.2	0.07	-1.1	0.5	1.1	0.02	1.2	0.05
IPI00642256	CAPZB	isoform 2 of F-actin-capping protein subunit beta	100.0%	44.5	12	12	18	2	18,713,704	19,820,477	18,650,307	22,394,983	1,512,903	731,402	1,402,086	507,282	18.1	8.3	16.8	5.1	1.1	0.5	-1.0	1	1.2	0.07	-1.1	0.5	1.1	0.02	1.2	0.05
				DYLLCDYNR	2	100.0%	2																									
				KLEVEANNAFDQYR	2	100.0%	1																									
				LEVEANNAFDQYR	2	100.0%	1																									
				LVEDMENK	2	99.7%	1																									
				NDLVEALKR	2	99.9%	2																									
				QMEKDETVSDCSPHIANIGR	3	99.9%	1																									
				RLPPQQIEK	2	99.9%	2																									
				SGSGTMNLGGSLTR	2	100.0%	2																									
				SPWSNKYDPPLEDGAMPSAR	3	100.0%	1																									
				STLNEIYFGK	2	100.0%	2																									
				SVQTFADK	2	99.9%	2																									
				YDPPLEDGAMPSAR	2	98.2%	1																									
IPI00218820	TPM2	isoform 3 of Tropomyosin beta chain	100.0%	12.5	4	4	7	1	1,692,695	1,709,541	2,033,639	2,011,302	168,417	40,343	182,506	134,419	22.3	5.3	20.1	14.9	1.0	0.9	1.2	0.2	1.2	0.2	1.2	0.2	1.2	0.09	-1.0	0.9
				IQLVEEELDR	2	100.0%	2																									
				LATALQK	1	96.5%	2																									
				LEEAEKAADESER	2	98.5%	1																									
				RIQLVEEELDR	2	100.0%	2																									
IPI00218829	GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	100.0%	10.4	4	4	4	1	4,329,230	4,275,106	4,169,961	4,894,857	323,879	187,753	229,724	303,906	16.7	9.8	12.3	13.9	-1.0	0.9	-1.0	0.7	1.1	0.2	-1.0	0.7	1.1	0.1	1.2	0.09
				GQQLVMMPNK	2	100.0%	1																									
				HFTILDAPGHK	3	99.2%	1																									
				HLIVLINK	2	95.5%	1																									
				SFVPNMIGGASQADLAVLVISAR	2	99.8%	1																									
IPI00218847	ACP1	isoform 2 of Low molecular weight phosphotyrosine protein phosphatase	100.0%	12.7	2	2	3	2	2,988,227	3,031,963	2,845,903	3,280,390	396,500	147,173	166,614	74,397	29.7	10.9	13.1	5.1	1.0	0.9	-1.1	0.7	1.1	0.5	-1.1	0.4	1.1	0.2	1.2	0.04
IPI00410615	ACP1	isoform 3 of Low molecular weight phosphotyrosine protein phosphatase	100.0%	16.1	2	2	3	2	2,988,227	3,031,963	2,845,903	3,280,390	396,500	147,173	166,614	74,397	29.7	10.9	13.1	5.1	1.0	0.9	-1.1	0.7	1.1	0.5	-1.1	0.4	1.1	0.2	1.2	0.04
				IELLGSYDPQK	2	99.9%	2																									
				SPIAEAVFR	2	99.9%	1																									
IPI00218852	VIL1	Villin-1	100.0%	23.8	16	19	22	1	111,745,111	106,155,355	103,661,365	121,596,380	########	4,973,229	6,145,870	4,109,954	20.7	10.5	13.3	7.6	-1.1	0.6	-1.1	0.5	1.1	0.4	-1.0	0.8	1.1	0.04	1.2	0.04
				DPETPIIVVK	2	99.8%	1																									
				DWSQITAEVTSPK	2	100.0%	2																									
				EVQGNESEAFR	2	100.0%	1																									
				GSLNITTPGLQIWR	2	100.0%	1																									
				IENLELVPVDSK	2	100.0%	1																									
				LMEVMNHVLGK	2	99.8%	1																									
				LMEVMNHVLGK	3	98.3%	1																									
				LQEENLVITPR	2	100.0%	2																									
				LYHVSDSEGNLVVR	2	100.0%	1																									
				LYHVSDSEGNLVVR	3	100.0%	1																									
				MVADTISR	2	92.9%	1																									
				MVDDGSGEVQVWR	2	100.0%	2																									
				MVVYQGGTSR	2	99.2%	1																									
				NVVAGEVEMSWK	2	100.0%	1																									
				QGHEPPTFTGWFLAWDPFK	3	99.7%	1																									
				QVVVEGQEPANFWMALGGK	2	99.6%	1																									
				QVVVEGQEPANFWMALGGK	3	99.9%	1																									
				TNNLETGPSTR	2	99.9%	1																									
				YNGEPVQIR	2	94.9%	1																									
IPI00218914	ALDH1A1	Retinal dehydrogenase 1	100.0%	35.1	13	13	16	1	60,189,694	59,727,398	55,795,333	67,139,589	5,490,768	2,757,158	4,658,195	2,906,139	20.4	10.3	18.7	9.7	-1.0	0.9	-1.1	0.6	1.1	0.3	-1.1	0.5	1.1	0.1	1.2	0.07
				ANNTFYGLSAGVFTK	2	99.6%	1																									
				EAGFPPGVVNIVPGYGPTAGAAISSHMDIDK	3	100.0%	1																									
				EEIFGPVQQIMK	2	97.6%	1																									
				GYFVQPTVFSNVTDEMR	2	100.0%	1																									
				IFVEESIYDEFVR	2	100.0%	1																									
				LADLIER	2	91.9%	1																									
				LECGGGPWGNK	2	99.2%	1																									
				LLLATMESMNGGK	2	100.0%	1																									
				LYSNAYLNDLAGCIK	2	100.0%	2																									
				QAFQIGSPWR	2	99.9%	2																									
				RANNTFYGLSAGVFTK	3	82.3%	1																									
				SLDDVIKR	2	89.1%	1																									
				YILGNPLTPGVTQGPQIDKEQYDK	3	99.9%	2																									
IPI00218918	ANXA1	Annexin A1	100.0%	57.5	15	17	25	1	127,423,415	130,746,309	130,384,942	147,850,444	########	5,623,207	9,170,794	3,901,430	18.9	9.6	15.7	5.9	1.0	0.8	1.0	0.8	1.2	0.1	-1.0	1	1.1	0.04	1.1	0.1
				AAYLQETGKPLDETLKK	3	100.0%	2																									
				ALTGHLEEVVLALLK	2	99.7%	1																									
				ALTGHLEEVVLALLK	3	100.0%	1																									
				ALYEAGER	2	97.3%	1																									
				CLTAIVK	2	82.9%	1																									
				DITSDTSGDFR	2	100.0%	2																									
				GDRSEDFGVNEDLADSDAR	3	100.0%	1																									
				GGPGSAVSPYPTFNPSSDVAALHK	3	100.0%	2																									
				GLGTDEDTLIEILASR	2	100.0%	2																									
				GLGTDEDTLIEILASR	3	100.0%	1																									
				GVDEATIIDILTK	2	100.0%	2																									
				MYGISLCQAILDETKGDYEK	3	100.0%	1																									
				QAWFIENEEQEYVQTVK	2	100.0%	2																									
				SEDFGVNEDLADSDAR	2	100.0%	2																									
				SEIDMNDIK	2	100.0%	1																									

				TPAQFDADELR	2	100.0%	2																									
				VLDLELKGDIEK	2	98.7%	1																									
IPI00218919	ATP4A	Potassium-transporting ATPase alpha chain 1	98.3%	2.6	1	1	1	1	1,655,366	1,656,090	1,577,940	1,762,480	239,345	241,293	141,386	154,032	32.3	32.6	20.0	19.5	1.0	1	-1.0	0.8	1.1	0.7	-1.0	0.8	1.1	0.7	1.1	0.4
				LASKNCVVKNLEAVETLGSTSVICSDK	3	98.3%	1																									
IPI00218993	HSPH1	isoform Beta of Heat shock protein 105 kDa	100.0%	18.7	11	12	13	3	18,044,403	19,331,808	18,055,456	22,429,019	2,299,262	844,972	1,368,230	1,037,277	28.5	9.8	16.9	10.3	1.1	0.6	1.0	1	1.2	0.1	-1.1	0.5	1.2	0.05	1.2	0.03
IPI00513743	HSPH1	isoform 3 of Heat shock protein 105 kDa	100.0%	18.6	11	12	13	3	18,044,403	19,331,808	18,055,456	22,429,019	2,299,262	844,972	1,368,230	1,037,277	28.5	9.8	16.9	10.3	1.1	0.6	1.0	1	1.2	0.1	-1.1	0.5	1.2	0.05	1.2	0.03
IPI00939163	HSPH1	isoform Alpha of Heat shock protein 105 kDa	100.0%	17.7	11	12	13	3	18,044,403	19,331,808	18,055,456	22,429,019	2,299,262	844,972	1,368,230	1,037,277	28.5	9.8	16.9	10.3	1.1	0.6	1.0	1	1.2	0.1	-1.1	0.5	1.2	0.05	1.2	0.03
				AFNDPFIQK	2	97.4%	1																									
				AGGIETIANEFSDR	2	100.0%	1																									
				DISTTLNADEAVAR	2	99.5%	1																									
				DLLNMYIETEGK	2	100.0%	2																									
				FVVQNVSAQK	2	96.6%	1																									
				IEVPLYSLLEQTHLK	3	100.0%	1																									
				LLTETEDWLYEEGEDQAK	2	100.0%	1																									
				NAVEEYVYEFR	2	99.6%	1																									
				SQFEELCAELLQK	2	93.7%	1																									
				SVNEVMEWMNNVMNAQAK	3	94.3%	1																									
				VVNVELPIEANLVWQLGK	2	100.0%	1																									
				VVNVELPIEANLVWQLGK	3	99.9%	1																									
IPI00219005	FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4	100.0%	10.2	5	5	5	1	12,543,446	13,495,257	12,494,160	15,217,907	1,740,365	1,046,317	1,349,593	629,102	31.0	17.3	24.2	9.2	1.1	0.7	-1.0	1	1.2	0.2	-1.1	0.6	1.1	0.2	1.2	0.1
				FDSSLDRK	2	90.8%	1																									
				LQAFSAAIESCNK	2	100.0%	1																									
				LYANMFER	2	99.6%	1																									
				TQLAVCQQR	2	99.9%	1																									
				VLQLYPNNK	2	99.8%	1																									
IPI00219018	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	100.0%	50.5	18	28	46	1	350,881,674	374,485,481	339,111,538	416,590,690	########	########	########	########	20.9	9.7	18.5	9.2	1.1	0.5	-1.0	0.8	1.2	0.1	-1.1	0.3	1.1	0.1	1.2	0.05
				AENGKLVINGNPITIFQER	3	99.9%	1																									
				AENGKLVINGNPITIFQERDPSK	3	99.9%	1																									
				GALQNIIPASTGAAK	1	100.0%	1																									
				GALQNIIPASTGAAK	2	100.0%	2																									
				IISNASCTTNCLAPLAK	2	100.0%	2																									
				IISNASCTTNCLAPLAK	3	100.0%	1																									
				IKWGDAGAEYVVESTGVFTTMEK	3	99.9%	1																									
				LISWYDNEFGYSNR	2	100.0%	3																									
				LISWYDNEFGYSNR	3	100.0%	1																									
				LTGMAFR	2	100.0%	2																									
				LVINGNPITIFQER	2	100.0%	2																									
				LVINGNPITIFQER	3	100.0%	1																									
				LVINGNPITIFQERDPSK	2	100.0%	2																									
				LVINGNPITIFQERDPSK	3	100.0%	2																									
				RVIISAPSADAPMFVMGVNHEK	3	100.0%	1																									
				VGVNGFGR	1	89.5%	1																									
				VGVNGFGR	2	100.0%	2																									
				VIISAPSADAPMFVMGVNHEK	2	100.0%	2																									
				VIISAPSADAPMFVMGVNHEK	3	100.0%	2																									
				VIPELNGK	1	98.0%	1																									
				VPTANVSVVDLTCR	2	100.0%	4																									
				VPTANVSVVDLTCR	3	99.9%	1																									
				VVDLMAHMASK	3	99.2%	1																									
				VVDLMAHMASKE	2	100.0%	2																									
				VVDLMAHMASKE	3	99.8%	2																									
				WGDAGAEYVVESTGVFTTMEK	2	100.0%	2																									
				WGDAGAEYVVESTGVFTTMEK	3	100.0%	2																									
				YDNSLK	1	99.3%	1																									
IPI00219025	GLRX	Glutaredoxin-1	100.0%	38.7	3	3	5	1	8,636,047	9,115,460	9,388,907	10,569,369	754,453	429,721	665,961	316,362	19.5	10.5	15.9	6.7	1.1	0.6	1.1	0.5	1.2	0.05	1.0	0.7	1.2	0.03	1.1	0.1
				AQEILSQLPIK	2	99.9%	1																									
				QGLLEFVDITATNHTNEIQDYLQQLTGAR	3	100.0%	2																									
				RAQEILSQLPIK	2	98.4%	2																									
IPI00219029	GOT1	Aspartate aminotransferase, cytoplasmic	100.0%	38.7	13	15	18	1	35,786,608	35,873,352	35,478,021	40,997,079	2,867,808	1,158,253	2,543,060	889,409	17.9	7.2	16.0	4.9	1.0	1	-1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.008	1.2	0.1
				FLFPFFDSAYQGFASGNLER	2	100.0%	2																									
				FLFPFFDSAYQGFASGNLER	3	100.0%	1																									
				HIYLLPSGR	2	97.6%	1																									
				IANDNSLNHEYLPILGLAEFR	3	100.0%	1																									
				IGADFLAR	2	99.9%	1																									
				INVSGLTTK	2	83.5%	1																									
				ITWSNPPAQGAR	2	99.7%	1																									
				IVASTLSNPELFEEWTGNVK	2	100.0%	2																									
				IVASTLSNPELFEEWTGNVK	3	100.0%	1																									
				KVNLGVGAYR	2	89.6%	1																									
				LALGDDSPALK	2	99.9%	1																									
				QVEYLVNEK	2	98.1%	1																									
				VGNLTVVGKEPESILQVLSQMEK	3	93.8%	1																									
				VNLGVGAYR	2	98.1%	1																									
				WYNGTNNK	2	99.8%	2																									
IPI00219036	DICER1	Endoribonuclease Dicer	95.6%	1.2	1	1	1	2	21,522,000	21,750,800	21,572,000	24,520,250	2,022,094	1,692,516	1,751,920	1,129,998	21.0	17.4	18.2	10.3	1.0	0.9	1.0	1	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.2
IPI00977554	DICER1	endoribonuclease Dicer isoform 2	95.6%	1.3	1	1	1	2	21,522,000	21,750,800	21,572,000	24,520,250	2,022,094	1,692,516	1,751,920	1,129,998	21.0	17.4	18.2	10.3	1.0	0.9	1.0	1	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.2
				YEEELDLHDEEETSVPGRPGSTK	2	82.9%	1																									
IPI00219065	AGL	isoform 5 of Glycogen debranching enzyme	99.7%	1.4	2	2	2	3	7,139,797	7,099,430	7,151,783	7,620,987	816,156	418,605	615,384	349,754	25.6	13.2	19.2	10.3	-1.0	1	1.0	1	1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.5
IPI00219066	AGL	isoform 6 of Glycogen debranching enzyme	99.7%	1.4	2	2	2	3	7,139,797	7,099,430	7,151,783	7,620,987	816,156	418,605	615,384	349,754	25.6	13.2	19.2	10.3	-1.0	1	1.0	1	1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.5
IPI00514126	AGL	isoform 1 of Glycogen debranching enzyme	99.7%	1.4	2	2	2	3	7,139,797	7,099,430	7,151,783	7,620,987	816,156	418,605	615,384	349,754	25.6	13.2	19.2	10.3	-1.0	1	1.0	1	1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.5
				IPFASLASR	2	91.7%	1																									
				SGDWMIDYVSNR	2	96.2%	1																									
IPI00219077	LTA4H	isoform 1 of Leukotriene A-4 hydrolase	100.0%	23.2	9	9	10	2	12,832,117	12,435,573	13,646,668	14,284,453	1,336,642	548,856	945,103	921,431	23.3	9.9	15.5	14.4	-1.0	0.8	1.1	0.6	1.1	0.4	1.1	0.3	1.1	0.1	1.0	0.6
IPI00514090	LTA4H	isoform 2 of Leukotriene A-4 hydrolase	100.0%	26.4	9	9	10	2	12,832,117	12,435,573	13,646,668	14,284,453	1,336,642	548,856	945,103	921,431	23.3	9.9	15.5	14.4	-1.0	0.8	1.1	0.6	1.1	0.4	1.1	0.3	1.1	0.1	1.0	0.6
				AILPCQDTPSVK	2	99.9%	1																									
				EDDLNSFNATDLK	2	100.0%	1																									
				GSPMEISLPIALSK	2	99.9%	1																									
				HFNALGGWGELQNSVK	2	98.8%	1																									
				LVVDLTDIDPDVAYSSVPYEK	2	100.0%	1																									
				MQEVYNFNAINNSEIR	2	100.0%	1																									
				SAYEFSETESMLK	2	100.0%	2																									
				SLSNVIAHEISHSWTGNLVTNK	3	100.0%	1																									
				SSALQWLTPEQTSGK	2	99.9%	1																									
IPI00219084	RELA	isoform 2 of Transcription factor p65	99.7%	5.2	2	2	2	6	1,957,232	2,074,252	1,785,305	2,155,052	173,627	129,152	161,295	198,132	19.8	13.9	20.2	20.6	1.1	0.6	-1.1	0.5	1.1	0.5	-1.2	0.2	1.0	0.7	1.2	0.2
IPI00386448	RELA	isoform 1 of Transcription factor p65	99.7%	5.1	2	2	2	6	1,957,232	2,074,252	1,785,305	2,155,052	173,627	129,152	161,295	198,132	19.8	13.9	20.2	20.6	1.1	0.6	-1.1	0.5	1.1	0.5	-1.2	0.2	1.0	0.7	1.2	0.2
IPI00479470	RELA	isoform 3 of Transcription factor p65	99.7%	5.2	2	2	2	6	1,957,232	2,074,252	1,785,305	2,155,052	173,627	129,152	161,295	198,132	19.8	13.9	20.2	20.6	1.1	0.6	-1.1	0.5	1.1	0.5	-1.2	0.2	1.0	0.7	1.2	0.2
IPI00883897	RELA	RELA protein	99.7%	7.4	2	2	2	6	1,957,232	2,074,252	1,785,305	2,155,052	173,627	129,152	161,295	198,132	19.8	13.9	20.2	20.6	1.1	0.6	-1.1	0.5	1.1	0.5	-1.2	0.2	1.0	0.7	1.2	0.2
IPI00884950	RELA	isoform 4 of Transcription factor p65	99.7%	5.1	2	2	2	6	1,957,232	2,074,252	1,785,305	2,155,052	173,627	129,152	161,295	198,132	19.8	13.9	20.2	20.6	1.1	0.6	-1.1	0.5	1.1	0.5	-1.2	0.2	1.0	0.7	1.2	0.2
IPI00984552	RELA	cDNA FLJ57698, highly similar to Transcription factor p65	99.7%	6.6	2	2	2	6	1,957,232	2,074,252	1,785,305	2,155,052	173,627	129,152	161,295	198,132	19.8	13.9	20.2	20.6	1.1	0.6	-1.1	0.5	1.1	0.5	-1.2	0.2	1.0	0.7	1.2	0.2
				SPFSGPTDPRPPPR	3	82.0%	1																									
				TPPYADPSLQAPVR	2	99.3%	1																									
IPI00219097	HMGB2	High mobility group protein B2	100.0%	17.2	5	5	5	1	46,923,760	47,920,460	43,898,020	49,473,720	2,960,139	1,858,945	1,624,391	2,098,835	14.1	8.7	8.3	9.5	1.0	0.8	-1.1	0.4	1.1	0.5	-1.1	0.1	1.0	0.6	1.1	0.07
				IKSEHPGLSIGDTAK	3	100.0%	1																									
				KLGEMWSEQSAK	2	100.0%	1																									
				LGEMWSEQSAK	2	99.8%	1																									
				SEHPGLSIGDTAK	2	100.0%	1																									
				YEKDIAAYR	3	92.5%	1																									
IPI00219114	DCTN1	isoform p135 of Dynactin subunit 1	100.0%	2.1	2	2	2	7	2,057,311	2,162,207	2,077,401	2,244,183	78,724	103,006	102,254	123,363	8.6	10.7	11.0	12.3	1.1	0.4	1.0	0.9	1.1	0.2	-1.0	0.6	1.0	0.6	1.1	0.3
IPI00872359	DCTN1	Uncharacterized protein	100.0%	1.9	2	2	2	7	2,057,311	2,162,207	2,077,401	2,244,183	78,724	103,006	102,254	123,363	8.6	10.7	11.0	12.3	1.1	0.4	1.0	0.9	1.1	0.2	-1.0	0.6	1.0	0.6	1.1	0.3
IPI00873712	DCTN1	Uncharacterized protein	100.0%	1.9	2	2	2	7	2,057,311	2,162,207	2,077,401	2,244,183	78,724	103,006	102,254	123,363	8.6	10.7	11.0	12.3	1.1	0.4	1.0	0.9	1.1	0.2	-1.0	0.6	1.0	0.6	1.1	0.3
IPI00914026	DCTN1	dynactin subunit 1 isoform 4	100.0%	2.1	2	2	2	7	2,057,311	2,162,207	2,077,401	2,244,183	78,724	103,006	102,254	123,363	8.6	10.7	11.0	12.3	1.1	0.4	1.0	0.9	1.1	0.2	-1.0	0.6	1.0	0.6	1.1	0.3
IPI00916757	DCTN1	dynactin subunit 1 isoform 5	100.0%	1.9	2	2	2	7	2,057,311	2,162,207	2,077,401	2,244,183	78,724	103,006	102,254	123,363	8.6	10.7	11.0	12.3	1.1	0.4	1.0	0.9	1.1	0.2	-1.0	0.6	1.0	0.6	1.1	0.3
IPI00917681	DCTN1	dynactin subunit 1 isoform 6	100.0%	1.9	2	2	2	7	2,057,311	2,162,207	2,077,401	2,244,183	78,724	103,006	102,254	123,363	8.6	10.7	11.0	12.3	1.1	0.4	1.0	0.9	1.1	0.2	-1.0	0.6	1.0	0.6	1.1	0.3
IPI00935906	DCTN1	dynactin subunit 1 isoform 3	100.0%	1.9	2	2	2	7	2,057,311	2,162,207	2,077,401	2,244,183	78,724	103,006	102,254	123,363	8.6	10.7	11.0	12.3	1.1	0.4	1.0	0.9	1.1	0.2	-1.0	0.6	1.0	0.6	1.1	0.3
				ELTNQQEASVER	2	97.9%	1																									
				VDELTTDLEILK	2	97.8%	1																									
IPI00219129	NQO2	Ribosyldihydronicotinamide dehydrogenase [quinone]	99.3%	7.8	1	1	1	2	975,005	1,059,035	1,017,610	1,057,880	38,414	70,528	80,856	61,468	8.8	14.9	17.8	13.0	1.1	0.3	1.0	0.6	1.1	0.3	-1.0	0.7	-1.0	1	1.0	0.7
IPI00515016	NQO2	NAD(P)H dehydrogenase, quinone 2	99.3%	9.3	1	1	1	2	975,005	1,059,035	1,017,610	1,057,880	38,414	70,528	80,856	61,468	8.8	14.9	17.8	13.0	1.1	0.3	1.0	0.6	1.1	0.3	-1.0	0.7	-1.0	1	1.0	0.7
				VLAPQISFAPEIASEEER	2	99.3%	1																									
IPI00219153	RPL22	60S ribosomal protein L22	100.0%	42.2	3	3	4	1	5,278,500	5,945,627	5,368,790	6,086,993	381,363	282,711	332,994	244,220	16.2	10.6	13.9	9.0	1.1	0.2	1.0	0.9	1.2	0.1	-1.1	0.2	1.0	0.7	1.1	0.1
				AGNLGGGVVTIER	2	100.0%	1																									
				FTLDCTHPVEDGIMDAANFEQFLQER	3	100.0%	2																									
				YFQINQDEEEEEDED	2	100.0%	1																									
IPI00219155	RPL27	60S ribosomal protein L27	99.8%	14.7	2	2	2	2	2,704,135	2,732,515	2,799,540	3,154,205	112,510	119,029	142,908	155,550	9.3	9.7	11.4	11.0	1.0	0.9	1.0	0.6	1.2	0.05	1.0	0.7	1.2	0.06	1.1	0.1
IPI00790294	RPL27	60S ribosomal protein L27	99.8%	25.0	2	2	2	2	2,704,135	2,732,515	2,799,540	3,154,205	112,510	119,029	142,908	155,550	9.3	9.7	11.4	11.0	1.0	0.9	1.0	0.6	1.2	0.05	1.0	0.7	1.2	0.06	1.1	0.1
				VYNYNHLMPTR	2	90.1%	1																									
				YSVDIPLDK	2	99.7%	1																									
IPI00219156	RPL30	60S ribosomal protein L30	100.0%	34.8	3	3	4	2	7,178,643	7,526,840	7,867,288	8,216,128	639,388	517,459	605,431	396,901	19.9	15.4	17.2	10.8	1.0	0.7	1.1	0.5	1.1	0.2	1.0	0.7	1.1	0.3	1.0	0.6
IPI00983316	RPL30	Uncharacterized protein	100.0%	35.1	3	3	4	2	7,178,643	7,526,840	7,867,288	8,216,128	639,388	517,459	605,431	396,901	19.9	15.4	17.2	10.8	1.0	0.7	1.1	0.5	1.1	0.2	1.0	0.7	1.1	0.3	1.0	0.6
				KSEIEYYAMLAK	2	96.6%	1																									
				LVILANNCPALR	2	100.0%	2																									
				VCTLAIIDPGDSDIIR	2	99.7%	1																									
IPI00219217	LDHB	L-lactate dehydrogenase B chain	100.0%	55.1	18	22	33	1	179,385,028	181,710,743	174,097,120	205,447,270	########	5,540,279	########	5,110,799	15.4	6.8	18.2	5.6	1.0	0.9	-1.0	0.8	1.1	0.09	-1.0	0.6	1.1	0.01	1.2	0.09
				FIIPQIVK	2	94.2%	1																									
				GLTSVINQK	2	100.0%	2																									
				GMYGIENEVFLSLPCILNAR	2	100.0%	2																									
				GMYGIENEVFLSLPCILNAR	3	93.4%	1																									
				IHPVSTMVK	2	87.1%	1																									
				ITVVGVGQVGMACAISILGK	3	100.0%	1																									
				IVADKDYSVTANSK	2	100.0%	2																									
				IVADKDYSVTANSK	3	100.0%	2																									
				IVVVTAGVR	2	100.0%	1																									
				LIAPVAEEEATVPNNK	2	100.0%	2																									
				LKDDEVAQLK	2	91.8%	1																									
				LKDDEVAQLKK	2	100.0%	2																									
				LNLVQR	2	97.8%	1																									
				MVVESAYEVIK	2	100.0%	2																									

				NVNVFK	2	96.9%	1																									
				SADTLWDIQK	2	100.0%	2																									
				SLADELALVDVLEDK	2	100.0%	2																									
				SLADELALVDVLEDKLK	2	100.0%	1																									
				SLADELALVDVLEDKLK	3	99.9%	1																									
				VIGSGCNLDSAR	1	99.4%	1																									
				VIGSGCNLDSAR	2	100.0%	3																									
				YLMAEK	1	98.0%	1																									
IPI00219229	LSM3	U6 snRNA-associated Sm-like protein LSm3	97.0%	11.8	1	1	1	1	6,173,650	4,485,710	5,129,100	5,361,680	424,525	471,305	469,212	535,101	15.4	23.5	20.5	22.3	-1.4	0.03	-1.2	0.1	-1.2	0.3	1.1	0.4	1.2	0.3	1.0	0.8
				GDGVVLVAPPLR	2	97.0%	1																									
IPI00219249	CNTNAP1	Contactin-associated protein 1	98.5%	0.6	1	1	1	1	2,779,630	2,643,420	2,862,510	2,983,990	285,404	109,807	111,349	364,820	23.0	9.3	8.7	27.3	-1.1	0.7	1.0	0.8	1.1	0.7	1.1	0.2	1.1	0.4	1.0	0.8
				YNLQSALR	2	93.5%	1																									
IPI00219299	TLN2	Talin-2	99.7%	1.8	2	2	2	1	9,085,720	8,981,150	9,762,300	10,828,530	1,048,702	1,024,491	513,680	428,394	25.8	25.5	11.8	8.9	-1.0	0.9	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.1	1.1	0.1
				DIEQASLAAVSQSLATR	3	98.9%	1																									
				QADETLDFEEQILEAAKSIAAATSALVK	3	99.7%	1																									
IPI00219301	MARCKS	Myristoylated alanine-rich C-kinase substrate	100.0%	30.7	5	5	5	1	10,278,168	10,845,720	10,177,922	11,926,067	668,553	464,879	1,192,862	379,606	14.5	9.6	26.2	7.1	1.1	0.5	-1.0	0.9	1.2	0.06	-1.1	0.6	1.1	0.1	1.2	0.2
				AEDGATPSPSNETPK	2	99.5%	1																									
				EAPAEGEAAEPGSPTAAEGEAASAASSTSSPK	3	100.0%	1																									
				EEPAAAGSGAASPSAAEK	3	97.0%	1																									
				GEAAAERPGEAAVASSPSK	3	99.9%	1																									
				GEPAAAAAPEAGASPVEK	2	99.3%	1																									
IPI00219330	ILF3	isoform 5 of Interleukin enhancer-binding factor 3	100.0%	26.8	16	16	19	4	20,680,258	20,068,348	19,124,179	23,417,719	1,403,554	973,209	1,241,997	1,195,969	15.2	10.8	14.5	11.4	-1.0	0.7	-1.1	0.4	1.1	0.2	-1.0	0.6	1.2	0.06	1.2	0.04
IPI00298789	ILF3	isoform 2 of Interleukin enhancer-binding factor 3	100.0%	26.4	16	16	19	4	20,680,258	20,068,348	19,124,179	23,417,719	1,403,554	973,209	1,241,997	1,195,969	15.2	10.8	14.5	11.4	-1.0	0.7	-1.1	0.4	1.1	0.2	-1.0	0.6	1.2	0.06	1.2	0.04
IPI00414335	ILF3	isoform 3 of Interleukin enhancer-binding factor 3	100.0%	24.2	16	16	19	4	20,680,258	20,068,348	19,124,179	23,417,719	1,403,554	973,209	1,241,997	1,195,969	15.2	10.8	14.5	11.4	-1.0	0.7	-1.1	0.4	1.1	0.2	-1.0	0.6	1.2	0.06	1.2	0.04
IPI00556173	ILF3	isoform 6 of Interleukin enhancer-binding factor 3	100.0%	26.2	16	16	19	4	20,680,258	20,068,348	19,124,179	23,417,719	1,403,554	973,209	1,241,997	1,195,969	15.2	10.8	14.5	11.4	-1.0	0.7	-1.1	0.4	1.1	0.2	-1.0	0.6	1.2	0.06	1.2	0.04
				AEPPQAMNALMR	2	98.0%	1																									
				AVSDWIDEQEK	2	99.9%	1																									
				AYAALAALEK	2	99.8%	1																									
				EDITQSAQHALR	2	96.0%	1																									
				FVMEVEVDGQK	2	100.0%	1																									
				GDLDLELVLLCK	2	100.0%	1																									
				HSSVYPTQEELEAVQNMVSHTER	3	100.0%	2																									
				IFVNDDR	2	89.9%	1																									
				LAAFGQLHK	2	96.3%	1																									
				LNQLKPGLQYK	2	99.9%	1																									
				QQREDITQSAQHALR	3	80.8%	1																									
				VLAGETLSVNDPPDVLDR	2	100.0%	2																									
				VLGMDPLPSK	2	99.9%	1																									
				VLQDMGLPTGAEGR	2	100.0%	2																									
				VPTWGPLR	2	95.4%	1																									
				YELISETGGSHDKR	2	100.0%	1																									
IPI00219358	MPI	isoform 1 of Mannose-6-phosphate isomerase	100.0%	25.3	7	7	7	1	8,193,171	8,387,484	8,565,362	9,281,000	754,599	443,934	478,764	260,579	20.6	11.8	12.5	6.3	1.0	0.8	1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.1	1.1	0.2
				FIDVPTLCEMLSYTPSSSK	2	100.0%	1																									
				SQEDPYLSIYDPPVPDFTIMK	2	100.0%	1																									
				TEVPGSVTEYK	2	80.4%	1																									
				TLSQWIAENQDSLGSK	2	100.0%	1																									
				VFPLSCAVQQYAWGK	2	100.0%	1																									
				VKDTFNGNLPFLFK	2	87.5%	1																									
				VVVEQLNLLVK	2	99.8%	1																									
IPI00219365	MSN	Moesin	100.0%	39.5	18	22	28	1	108,727,757	109,571,722	110,898,738	121,765,132	6,351,433	2,679,241	5,507,917	4,796,540	13.1	5.5	11.1	8.8	1.0	0.9	1.0	0.8	1.1	0.1	1.0	0.8	1.1	0.06	1.1	0.2
				ALELEQER	2	96.8%	1																									
				ALTSELANAR	2	100.0%	2																									
				APDFVFYAPR	2	100.0%	2																									
				AQMVQEDLEK	2	99.9%	1																									
				EALLQASRDQKK	3	89.8%	1																									
				ERQEAEEAKEALLQASR	3	99.9%	1																									
				EVWFFGLQYQDTK	2	100.0%	1																									
				FVIKPIDKK	2	87.7%	1																									
				FVIKPIDKK	3	97.1%	1																									
				FYPEDVSEELIQDITQR	2	100.0%	1																									
				FYPEDVSEELIQDITQR	3	100.0%	1																									
				GSELWLGVDALGLNIYEQNDR	2	99.9%	1																									
				IGFPWSEIR	2	100.0%	2																									
				ISQLEMAR	2	86.7%	1																									
				LFFLQVK	2	92.1%	1																									
				NISFNDKK	2	99.8%	2																									
				RKPDTIEVQQMK	2	100.0%	2																									
				RKPDTIEVQQMK	3	100.0%	1																									
				TAMSTPHVAEPAENEQDEQDENGAEASADLR	3	100.0%	1																									
				TQEQLALEMAELTAR	2	100.0%	1																									
				VTTMDAELEFAIQPNTTGK	2	100.0%	2																									
				VTTMDAELEFAIQPNTTGK	3	99.8%	1																									
IPI00219420	SMC3	Structural maintenance of chromosomes protein 3	100.0%	1.8	2	2	2	1	9,411,805	10,339,039	9,104,440	11,089,174	588,962	609,628	585,074	441,398	14.0	13.2	14.4	8.9	1.1	0.3	-1.0	0.7	1.2	0.05	-1.1	0.2	1.1	0.3	1.2	0.03
				INQMATAPDSQR	2	99.9%	1																									
				SMEVSTQLAR	2	90.6%	1																									
IPI00219446	PEBP1	Phosphatidylethanolamine-binding protein 1	100.0%	44.9	6	9	11	1	57,676,750	58,378,825	54,538,480	64,180,820	3,930,245	2,938,576	3,746,575	1,040,993	15.2	11.3	15.4	3.6	1.0	0.9	-1.1	0.6	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.06
				APVAGTCYQAEWDDYVPK	2	100.0%	2																									
				APVAGTCYQAEWDDYVPK	3	99.9%	1																									
				CDEPILSNR	2	99.9%	1																									
				GNDISSGTVLSDYVGSGPPK	2	100.0%	2																									
				GNDISSGTVLSDYVGSGPPK	3	100.0%	1																									
				LYEQLSGK	2	99.8%	1																									
				LYTLVLTDPDAPSR	2	100.0%	1																									
				NRPTSISWDGLDSGK	2	100.0%	1																									
				NRPTSISWDGLDSGK	3	100.0%	1																									
IPI00219483	SNRNP70	isoform 2 of U1 small nuclear ribonucleoprotein 70 kDa	100.0%	6.1	2	2	2	2	4,115,738	3,898,950	3,974,185	4,809,857	360,139	204,441	251,316	266,641	19.6	11.7	14.1	12.4	-1.1	0.6	-1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.03	1.2	0.05
IPI00290204	SNRNP70	isoform 1 of U1 small nuclear ribonucleoprotein 70 kDa	100.0%	6.0	2	2	2	2	4,115,738	3,898,950	3,974,185	4,809,857	360,139	204,441	251,316	266,641	19.6	11.7	14.1	12.4	-1.1	0.6	-1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.03	1.2	0.05
				MWDPHNDPNAQGDAFK	3	100.0%	1																									
				RLGGGLGGTR	2	96.7%	1																									
IPI00219484	SNRNP70	isoform 3 of U1 small nuclear ribonucleoprotein 70 kDa	100.0%	9.6	1	1	1	1	1,447,683	1,210,760	1,366,650	1,702,667	194,502	113,253	153,109	120,082	30.0	20.9	25.1	15.8	-1.2	0.3	-1.1	0.8	1.2	0.3	1.1	0.4	1.4	0.02	1.2	0.1
				MWDPHNDPNAQGDAFK	3	100.0%	1																									
IPI00219512	UCHL5	isoform 2 of Ubiquitin carboxyl-terminal hydrolase isozyme L5	95.9%	6.0	2	2	2	8	830,956	833,525	755,698	821,192	78,493	41,547	63,627	31,435	21.1	11.2	18.8	8.6	1.0	1	-1.1	0.5	-1.0	0.9	-1.1	0.3	-1.0	0.8	1.1	0.4
IPI00219513	UCHL5	isoform 3 of Ubiquitin carboxyl-terminal hydrolase isozyme L5	95.9%	5.8	2	2	2	8	830,956	833,525	755,698	821,192	78,493	41,547	63,627	31,435	21.1	11.2	18.8	8.6	1.0	1	-1.1	0.5	-1.0	0.9	-1.1	0.3	-1.0	0.8	1.1	0.4
IPI00299313	UCHL5	isoform 1 of Ubiquitin carboxyl-terminal hydrolase isozyme L5	95.9%	5.8	2	2	2	8	830,956	833,525	755,698	821,192	78,493	41,547	63,627	31,435	21.1	11.2	18.8	8.6	1.0	1	-1.1	0.5	-1.0	0.9	-1.1	0.3	-1.0	0.8	1.1	0.4
IPI00549253	UCHL5	Uncharacterized protein	95.9%	6.0	2	2	2	8	830,956	833,525	755,698	821,192	78,493	41,547	63,627	31,435	21.1	11.2	18.8	8.6	1.0	1	-1.1	0.5	-1.0	0.9	-1.1	0.3	-1.0	0.8	1.1	0.4
IPI00549820	UCHL5	isoform 4 of Ubiquitin carboxyl-terminal hydrolase isozyme L5	95.9%	5.8	2	2	2	8	830,956	833,525	755,698	821,192	78,493	41,547	63,627	31,435	21.1	11.2	18.8	8.6	1.0	1	-1.1	0.5	-1.0	0.9	-1.1	0.3	-1.0	0.8	1.1	0.4
IPI00549849	UCHL5	Ubiquitin carboxyl-terminal hydrolase L5	95.9%	5.4	2	2	2	8	830,956	833,525	755,698	821,192	78,493	41,547	63,627	31,435	21.1	11.2	18.8	8.6	1.0	1	-1.1	0.5	-1.0	0.9	-1.1	0.3	-1.0	0.8	1.1	0.4
IPI00641843	UCHL5	cDNA, FLJ78963, highly similar to Ubiquitin carboxyl-terminal hydrolase isozyme L5	95.9%	9.8	2	2	2	8	830,956	833,525	755,698	821,192	78,493	41,547	63,627	31,435	21.1	11.2	18.8	8.6	1.0	1	-1.1	0.5	-1.0	0.9	-1.1	0.3	-1.0	0.8	1.1	0.4
IPI00642374	UCHL5	Ubiquitin carboxyl-terminal hydrolase L5	95.9%	5.2	2	2	2	8	830,956	833,525	755,698	821,192	78,493	41,547	63,627	31,435	21.1	11.2	18.8	8.6	1.0	1	-1.1	0.5	-1.0	0.9	-1.1	0.3	-1.0	0.8	1.1	0.4
				LYELDGLR	2	95.5%	1																									
				NQMLIEEEVQK	2	95.9%	1																									
IPI00219518	ARL1	ADP-ribosylation factor-like protein 1	100.0%	16.6	2	2	2	3	3,672,102	3,691,176	3,628,140	3,907,247	241,234	183,828	278,848	171,804	14.7	11.1	17.2	9.8	1.0	1	-1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.4	1.1	0.4
IPI00791961	ARL1	cDNA FLJ50309, highly similar to ADP-ribosylation factor-like protein 1	100.0%	22.2	2	2	2	3	3,672,102	3,691,176	3,628,140	3,907,247	241,234	183,828	278,848	171,804	14.7	11.1	17.2	9.8	1.0	1	-1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.4	1.1	0.4
IPI01011723	ARL1	cDNA FLJ51704, highly similar to ADP-ribosylation factor-like protein 1	100.0%	18.3	2	2	2	3	3,672,102	3,691,176	3,628,140	3,907,247	241,234	183,828	278,848	171,804	14.7	11.1	17.2	9.8	1.0	1	-1.0	0.9	1.1	0.5	-1.0	0.9	1.1	0.4	1.1	0.4
				GTGLDEAMEWLVETLK	3	100.0%	1																									
				SELVAMLEEEELRK	2	99.2%	1																									
IPI00219525	PGD	6-phosphogluconate dehydrogenase, decarboxylating	100.0%	18.4	7	8	11	2	13,773,303	14,067,563	13,934,740	15,522,790	1,052,686	1,024,275	815,903	705,948	17.1	16.3	13.1	10.2	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.3	1.1	0.2
IPI01012504	PGD	6-phosphogluconate dehydrogenase, decarboxylating	100.0%	18.9	7	8	11	2	13,773,303	14,067,563	13,934,740	15,522,790	1,052,686	1,024,275	815,903	705,948	17.1	16.3	13.1	10.2	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.3	1.1	0.2
				AGQAVDDFIEK	2	100.0%	2																									
				FQFDGDKK	2	97.1%	1																									
				GILFVGSGVSGGEEGAR	2	100.0%	2																									
				LVPLLDTGDIIIDGGNSEYR	2	100.0%	2																									
				LVPLLDTGDIIIDGGNSEYR	3	99.8%	1																									
				NPELQNLLLDDFFK	2	86.2%	1																									
				SFLEDIRK	2	98.6%	1																									
				YGPSLMPGGNK	2	99.4%	1																									
IPI00219526	PGM1	isoform 1 of Phosphoglucomutase-1	100.0%	37.7	15	15	17	1	62,124,569	65,724,777	64,808,313	76,126,374	7,650,825	4,973,727	6,643,318	4,149,823	27.5	16.9	22.9	12.2	1.1	0.7	1.0	0.8	1.2	0.1	-1.0	0.9	1.2	0.1	1.2	0.2
				ADNFEYSDPVDGSISR	2	100.0%	1																									
				AIGGIILTASHNPGGPNGDFGIK	3	100.0%	1																									
				FNISNGGPAPEAITDK	2	100.0%	1																									
				FNISNGGPAPEAITDKIFQISK	3	97.0%	1																									
				IAAANGIGR	2	99.8%	1																									
				IALYETPTGWK	2	100.0%	2																									
				IDAMHGVVGPYVK	3	94.5%	1																									
				INQDPQVMLAPLISIALK	3	99.5%	1																									
				LSGTGSAGATIR	2	100.0%	2																									
				LYIDSYEKDVAK	2	94.3%	1																									
				SGEHDFGAAFDGDGDRNMILGK	3	98.4%	1																									
				SIFDFSALK	2	91.5%	1																									
				TIEEYAVCPDLK	2	100.0%	1																									
				VDLGVLGK	2	99.6%	1																									
				VFQSSANYAENFIQSIISTVEPAQR	3	99.9%	1																									
IPI00219568	PGK2	Phosphoglycerate kinase 2	100.0%	13.0	5	8	13	1	70,133,248	69,396,882	67,133,972	81,172,748	5,637,452	3,468,083	4,372,869	2,756,247	18.0	11.2	14.6	7.6	-1.0	0.9	-1.0	0.7	1.2	0.1	-1.0	0.7	1.2	0.03	1.2	0.03
				ACANPAPGSVILLENLR	3	99.9%	1																									
				DVLFLK	1	99.5%	2																									
				DVLFLK	2	98.2%	2																									
				FHVEEEGK	2	99.2%	1																									
				LGDVYVNDAFGTAHR	2	100.0%	2																									
				LGDVYVNDAFGTAHR	3	100.0%	2																									
				VDFNVPMK	1	100.0%	1																									
				VDFNVPMK	2	99.9%	2																									
IPI00219585	PFKM	isoform 2 of 6-phosphofructokinase, muscle type	96.8%	1.6	1	1	1	3	817,497	924,757	950,087	960,197	50,847	83,334	58,459	79,038	13.9	20.2	13.8	18.4	1.1	0.3	1.2	0.1	1.2	0.2	1.0	0.8	1.0	0.8	1.0	0.9
IPI00465179	PFKM	6-phosphofructokinase, muscle type isoform 1	96.8%	1.4	1	1	1	3	817,497	924,757	950,087	960,197	50,847	83,334	58,459	79,038	13.9	20.2	13.8	18.4	1.1	0.3	1.2	0.1	1.2	0.2	1.0	0.8	1.0	0.8	1.0	0.9
IPI00743142	PFKM	isoform 1 of 6-phosphofructokinase, muscle type	96.8%	1.5	1	1	1	3	817,497	924,757	950,087	960,197	50,847	83,334	58,459	79,038	13.9	20.2	13.8	18.4	1.1	0.3	1.2	0.1	1.2	0.2	1.0	0.8	1.0	0.8	1.0	0.9
				SEWSDLLSDLQK	2	96.8%	1																									
IPI00219604	MAP2K1	isoform 1 of Dual specificity mitogen-activated protein kinase kinase 1	100.0%	5.6	1	2	2	3	610,455	592,349	631,862	661,033	45,805	23,022	32,099	19,777	16.8	8.7	11.4	6.7	-1.0	0.7	1.0	0.7	1.1	0.3	1.1	0.3	1.1	0.05	1.0	0.5
IPI00797850	MAP2K1	isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1	100.0%	6.0	1	2	2	3	610,455	592,349	631,862	661,033	45,805	23,022	32,099	19,777	16.8	8.7	11.4	6.7	-1.0	0.7	1.0	0.7	1.1	0.3	1.1	0.3	1.1	0.05	1.0	0.5

IPI00795187	MAP2K2	cDNA FLJ35806 fis, clone TESTI2005987, highly similar to Dual specificity mitogen-	100.0%	7.3	1	2	2	3	610,455	592,349	631,862	661,033	45,805	23,022	32,099	19,777	16.8	8.7	11.4	6.7	-1.0	0.7	1.0	0.7	1.1	0.3	1.1	0.3	1.1	0.05	1.0	0.5
				LCDFGVSGQLIDSMANSFVGTR	2	100.0%	1																									
				LCDFGVSGQLIDSMANSFVGTR	3	99.6%	1																									
IPI00219616	PRPS1	Ribose-phosphate pyrophosphokinase 1	99.4%	10.1	2	2	2	6	491,418	502,334	499,697	506,687	52,853	31,492	29,137	32,619	24.1	14.0	13.0	14.4	1.0	0.9	1.0	0.9	1.0	0.8	-1.0	1	1.0	0.9	1.0	0.9
IPI00552495	PRPS1	Ribose-phosphate pyrophosphokinase	99.4%	14.7	2	2	2	6	491,418	502,334	499,697	506,687	52,853	31,492	29,137	32,619	24.1	14.0	13.0	14.4	1.0	0.9	1.0	0.9	1.0	0.8	-1.0	1	1.0	0.9	1.0	0.9
IPI00219617	PRPS2	isoform 1 of Ribose-phosphate pyrophosphokinase 2	99.4%	10.1	2	2	2	6	491,418	502,334	499,697	506,687	52,853	31,492	29,137	32,619	24.1	14.0	13.0	14.4	1.0	0.9	1.0	0.9	1.0	0.8	-1.0	1	1.0	0.9	1.0	0.9
IPI00718888	PRPS2	isoform 2 of Ribose-phosphate pyrophosphokinase 2	99.4%	10.0	2	2	2	6	491,418	502,334	499,697	506,687	52,853	31,492	29,137	32,619	24.1	14.0	13.0	14.4	1.0	0.9	1.0	0.9	1.0	0.8	-1.0	1	1.0	0.9	1.0	0.9
IPI00947377	PRPS2	19 kDa protein	99.4%	18.5	2	2	2	6	491,418	502,334	499,697	506,687	52,853	31,492	29,137	32,619	24.1	14.0	13.0	14.4	1.0	0.9	1.0	0.9	1.0	0.8	-1.0	1	1.0	0.9	1.0	0.9
IPI00947401	PRPS2	16 kDa protein	99.4%	21.3	2	2	2	6	491,418	502,334	499,697	506,687	52,853	31,492	29,137	32,619	24.1	14.0	13.0	14.4	1.0	0.9	1.0	0.9	1.0	0.8	-1.0	1	1.0	0.9	1.0	0.9
				IQVIDISMILAEAIR	2	99.4%	1																									
				VYAILTHGIFSGPAISR	2	98.1%	1																									
IPI00219622	PSMA2	Proteasome subunit alpha type-2	100.0%	27.8	4	5	5	1	22,889,657	25,714,738	24,350,851	30,530,099	2,596,544	1,561,908	1,558,032	1,817,004	25.4	13.6	14.3	13.3	1.1	0.4	1.1	0.6	1.3	0.04	-1.1	0.6	1.2	0.08	1.3	0.03
				AANGVVLATEK	2	100.0%	1																									
				GYSFSLTTFSPSGK	2	100.0%	1																									
				LVQIEYALAAVAGGAPSVGIK	2	99.9%	1																									
				LVQIEYALAAVAGGAPSVGIK	3	100.0%	1																									
				YNEDLELEDAIHTAILTLK	3	99.5%	1																									
IPI00219673	GSTK1	isoform 1 of Glutathione S-transferase kappa 1	100.0%	22.6	4	4	5	1	21,118,590	23,550,105	22,605,780	26,489,755	1,756,102	869,242	1,828,505	580,090	18.6	8.3	18.1	4.9	1.1	0.2	1.1	0.6	1.3	0.03	-1.0	0.7	1.1	0.02	1.2	0.1
				AGMSAEQAQGLLEK	2	100.0%	1																									
				KGLYMANDLK	2	96.1%	1																									
				MELLAHLLGEK	2	99.6%	1																									
				NEDITEPQSILAAAEK	2	100.0%	2																									
IPI00219678	EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	100.0%	30.8	7	7	8	1	42,532,084	43,074,712	43,387,102	49,220,550	2,810,227	1,868,117	2,226,691	1,829,066	14.8	9.7	11.5	8.3	1.0	0.9	1.0	0.8	1.2	0.08	1.0	0.9	1.1	0.05	1.1	0.08
				FPEVEDVVMVNVR	2	98.9%	1																									
				GVFNVQMEPK	2	95.4%	1																									
				HAVSDPSILDSLDLNEDER	3	86.6%	1																									
				HVAEVLEYTKDEQLESLFQR	3	100.0%	1																									
				INLIAPPR	2	99.3%	1																									
				TEGLSVLSQAMAVIK	2	100.0%	1																									
				VVTDTDETELAR	2	100.0%	2																									
IPI00219740	MCM7	isoform 2 of DNA replication licensing factor MCM7	98.9%	3.6	1	1	1	2	1,623,765	1,561,260	1,517,130	1,804,820	180,825	98,416	133,032	121,826	24.9	14.1	19.6	15.1	-1.0	0.8	-1.1	0.6	1.1	0.4	-1.0	0.8	1.2	0.2	1.2	0.1
IPI00299904	MCM7	isoform 1 of DNA replication licensing factor MCM7	98.9%	2.0	1	1	1	2	1,623,765	1,561,260	1,517,130	1,804,820	180,825	98,416	133,032	121,826	24.9	14.1	19.6	15.1	-1.0	0.8	-1.1	0.6	1.1	0.4	-1.0	0.8	1.2	0.2	1.2	0.1
				LFADAVQELLPQYK	2	98.9%	1																									
IPI00219743	CTNND1	isoform 4ABC of Catenin delta-1	100.0%	17.7	9	10	11	4	1,481,327	1,588,995	1,485,042	1,733,078	109,583	63,067	148,161	37,028	16.5	8.9	22.3	4.8	1.1	0.4	1.0	1	1.2	0.08	-1.1	0.5	1.1	0.08	1.2	0.2
IPI00219744	CTNND1	isoform 4AB of Catenin delta-1	100.0%	17.8	9	10	11	4	1,481,327	1,588,995	1,485,042	1,733,078	109,583	63,067	148,161	37,028	16.5	8.9	22.3	4.8	1.1	0.4	1.0	1	1.2	0.08	-1.1	0.5	1.1	0.08	1.2	0.2
IPI00219745	CTNND1	isoform 4AC of Catenin delta-1	100.0%	18.5	9	10	11	4	1,481,327	1,588,995	1,485,042	1,733,078	109,583	63,067	148,161	37,028	16.5	8.9	22.3	4.8	1.1	0.4	1.0	1	1.2	0.08	-1.1	0.5	1.1	0.08	1.2	0.2
IPI00219747	CTNND1	isoform 4A of Catenin delta-1	100.0%	18.7	9	10	11	4	1,481,327	1,588,995	1,485,042	1,733,078	109,583	63,067	148,161	37,028	16.5	8.9	22.3	4.8	1.1	0.4	1.0	1	1.2	0.08	-1.1	0.5	1.1	0.08	1.2	0.2
				AAALVLQTIWGYK	2	100.0%	2																									
				GYELLFQPEVVR	2	100.0%	1																									
				HAIPNLVK	2	100.0%	1																									
				NLAVDAR	1	83.0%	1																									
				QPELPEVIAMLGFR	2	99.9%	1																									
				SDFQVNLNNASR	2	99.9%	1																									
				SLDNNYSTPNER	2	99.7%	1																									
				SQSSHSYDDSTLPLIDR	2	94.8%	1																									
				SQSSHSYDDSTLPLIDR	3	99.4%	1																									
				TPAILEASAGAIQNLCAGR	3	98.3%	1																									
IPI00219746	CTNND1	isoform 4BC of Catenin delta-1	100.0%	16.3	8	9	10	5	1,335,466	1,400,758	1,327,457	1,535,403	100,154	62,992	139,929	42,685	16.8	10.1	23.6	6.2	1.0	0.6	-1.0	1	1.1	0.1	-1.1	0.6	1.1	0.1	1.2	0.2
IPI00219748	CTNND1	isoform 4B of Catenin delta-1	100.0%	16.5	8	9	10	5	1,335,466	1,400,758	1,327,457	1,535,403	100,154	62,992	139,929	42,685	16.8	10.1	23.6	6.2	1.0	0.6	-1.0	1	1.1	0.1	-1.1	0.6	1.1	0.1	1.2	0.2
IPI00219749	CTNND1	isoform 4C of Catenin delta-1	100.0%	17.1	8	9	10	5	1,335,466	1,400,758	1,327,457	1,535,403	100,154	62,992	139,929	42,685	16.8	10.1	23.6	6.2	1.0	0.6	-1.0	1	1.1	0.1	-1.1	0.6	1.1	0.1	1.2	0.2
IPI00219750	CTNND1	isoform 4 of Catenin delta-1	100.0%	17.3	8	9	10	5	1,335,466	1,400,758	1,327,457	1,535,403	100,154	62,992	139,929	42,685	16.8	10.1	23.6	6.2	1.0	0.6	-1.0	1	1.1	0.1	-1.1	0.6	1.1	0.1	1.2	0.2
IPI00981242	CTNND1	69 kDa protein	100.0%	16.5	8	9	10	5	1,335,466	1,400,758	1,327,457	1,535,403	100,154	62,992	139,929	42,685	16.8	10.1	23.6	6.2	1.0	0.6	-1.0	1	1.1	0.1	-1.1	0.6	1.1	0.1	1.2	0.2
				AAALVLQTIWGYK	2	100.0%	2																									
				GYELLFQPEVVR	2	100.0%	1																									
				HAIPNLVK	2	100.0%	1																									
				NLAVDAR	1	83.0%	1																									
				QPELPEVIAMLGFR	2	99.9%	1																									
				SDFQVNLNNASR	2	99.9%	1																									
				SQSSHSYDDSTLPLIDR	2	94.8%	1																									
				SQSSHSYDDSTLPLIDR	3	99.4%	1																									
				TPAILEASAGAIQNLCAGR	3	98.3%	1																									
IPI00219757	GSTP1	Glutathione S-transferase P	100.0%	70.0	11	16	27	1	165,553,850	169,426,890	164,861,110	192,017,965	########	7,247,941	########	7,039,022	26.4	9.6	18.7	8.2	1.0	0.9	-1.0	1	1.2	0.3	-1.0	0.8	1.1	0.06	1.2	0.1
				AFLASPEYVNLPINGNGK	2	100.0%	3																									
				AFLASPEYVNLPINGNGK	3	100.0%	1																									
				AFLASPEYVNLPINGNGKQ	2	100.0%	3																									
				AFLASPEYVNLPINGNGKQ	3	99.9%	1																									
				ALPGQLKPFETLLSQNQGGK	2	100.0%	1																									
				ALPGQLKPFETLLSQNQGGK	3	100.0%	1																									
				ASCLYGQLPK	2	100.0%	2																									
				DQQEAALVDMVNDGVEDLR	2	100.0%	2																									
				DQQEAALVDMVNDGVEDLR	3	100.0%	1																									
				EEVVTVETWQEGSLK	2	100.0%	1																									
				FQDGDLTLYQSNTILR	2	100.0%	3																									
				MLLADQGQSWK	2	100.0%	2																									
				MPPYTVVYFPVR	2	100.0%	2																									
				TLGLYGK	1	97.4%	1																									
				YISLIYTNYEAGKDDYVK	2	100.0%	2																									
				YISLIYTNYEAGKDDYVK	3	99.5%	1																									
IPI00219762	CSE1L	Cellular apoptosis susceptibility protein variant 2	100.0%	17.3	10	12	16	1	10,779,712	11,317,607	10,486,607	12,681,297	877,134	546,695	914,217	486,121	18.2	10.8	19.5	8.6	1.0	0.6	-1.0	0.8	1.2	0.09	-1.1	0.5	1.1	0.1	1.2	0.07
				AADEEAFEDNSEEYIRR	3	98.5%	1																									
				ALTLPGSSENEYIMK	2	99.9%	1																									
				FFEGPVTGIFSGYVNSMLQEYAK	2	100.0%	2																									
				FFEGPVTGIFSGYVNSMLQEYAK	3	100.0%	1																									
				FLESVEGNQNYPLLLLTLLEK	2	100.0%	2																									
				FLESVEGNQNYPLLLLTLLEK	3	100.0%	2																									
				GSNTIASAAADKIPGLLGVFQK	3	100.0%	1																									
				LVLDAFALPLTNLFK	2	100.0%	2																									
				SANVNEFPVLK	2	96.6%	1																									
				TLDPDPAIR	2	98.9%	1																									
				VIVPNMEFR	2	99.6%	1																									
				YGALALQEIFDGIQPK	2	96.9%	1																									
IPI00219817	MAPK8IP3	isoform 2 of C-Jun-amino-terminal kinase-interacting protein 3	92.0%	0.7	1	1	1	2	665,254	725,767	626,421	741,361	91,899	68,864	79,918	39,980	30.9	21.2	28.5	12.1	1.1	0.6	-1.1	0.8	1.1	0.5	-1.2	0.4	1.0	0.8	1.2	0.2
IPI00398504	MAPK8IP3	isoform 1 of C-Jun-amino-terminal kinase-interacting protein 3	92.0%	0.7	1	1	1	2	665,254	725,767	626,421	741,361	91,899	68,864	79,918	39,980	30.9	21.2	28.5	12.1	1.1	0.6	-1.1	0.8	1.1	0.5	-1.2	0.4	1.0	0.8	1.2	0.2
				LMELQEAVR	2	92.1%	1																									
IPI00219861	ACP1	isoform 1 of Low molecular weight phosphotyrosine protein phosphatase	100.0%	38.0	5	5	6	1	21,236,765	23,111,891	20,205,606	25,182,352	3,228,584	870,545	1,413,271	662,404	34.0	8.4	15.6	5.9	1.1	0.6	-1.1	0.8	1.2	0.3	-1.1	0.1	1.1	0.1	1.2	0.01
				HGIPMSHVAR	3	99.8%	1																									
				IELLGSYDPQK	2	99.9%	2																									
				LVTDQNISENWR	2	100.0%	1																									
				SPIAEAVFR	2	99.9%	1																									
				VDSAATSGYEIGNPPDYR	2	100.0%	1																									
IPI00219871	NAA38	N-alpha-acetyltransferase 38, NatC auxiliary subunit	100.0%	16.7	1	2	2	4	1,325,678	1,387,770	1,467,158	1,506,750	104,114	77,266	120,255	50,325	17.6	12.5	18.3	7.5	1.0	0.6	1.1	0.4	1.1	0.2	1.1	0.6	1.1	0.2	1.0	0.8
IPI00924467	NAA38	Uncharacterized protein	100.0%	20.5	1	2	2	4	1,325,678	1,387,770	1,467,158	1,506,750	104,114	77,266	120,255	50,325	17.6	12.5	18.3	7.5	1.0	0.6	1.1	0.4	1.1	0.2	1.1	0.6	1.1	0.2	1.0	0.8
IPI00924695	NAA38	Uncharacterized protein	100.0%	21.3	1	2	2	4	1,325,678	1,387,770	1,467,158	1,506,750	104,114	77,266	120,255	50,325	17.6	12.5	18.3	7.5	1.0	0.6	1.1	0.4	1.1	0.2	1.1	0.6	1.1	0.2	1.0	0.8
IPI00924875	NAA38	7 kDa protein	100.0%	23.9	1	2	2	4	1,325,678	1,387,770	1,467,158	1,506,750	104,114	77,266	120,255	50,325	17.6	12.5	18.3	7.5	1.0	0.6	1.1	0.4	1.1	0.2	1.1	0.6	1.1	0.2	1.0	0.8
				GFDQTINLILDESHER	2	100.0%	1																									
				GFDQTINLILDESHER	3	100.0%	1																									
IPI00302740	RPS4Y1	40S ribosomal protein S4, Y isoform 1	100.0%	3.8	1	1	1	3	972,173	881,933	1,061,285	882,473	100,302	50,569	29,710	129,656	23.1	12.8	6.3	32.9	-1.1	0.4	1.1	0.4	-1.1	0.6	1.2	0.02	1.0	1	-1.2	0.2
IPI00643830	RPS4Y1	Uncharacterized protein	100.0%	3.8	1	1	1	3	972,173	881,933	1,061,285	882,473	100,302	50,569	29,710	129,656	23.1	12.8	6.3	32.9	-1.1	0.4	1.1	0.4	-1.1	0.6	1.2	0.02	1.0	1	-1.2	0.2
IPI00219894	RPS4Y2	40S ribosomal protein S4, Y isoform 2	100.0%	3.8	1	1	1	3	972,173	881,933	1,061,285	882,473	100,302	50,569	29,710	129,656	23.1	12.8	6.3	32.9	-1.1	0.4	1.1	0.4	-1.1	0.6	1.2	0.02	1.0	1	-1.2	0.2
				DANGNSFATR	2	99.4%	1																									
IPI00219910	-	22 kDa protein	100.0%	33.8	5	6	8	2	17,609,115	17,367,715	16,703,630	18,542,090	691,906	634,896	677,959	648,597	8.8	8.2	9.1	7.8	-1.0	0.8	-1.1	0.4	1.1	0.4	-1.0	0.5	1.1	0.2	1.1	0.09
IPI00783862	BLVRB	Flavin reductase	100.0%	34.0	5	6	8	2	17,609,115	17,367,715	16,703,630	18,542,090	691,906	634,896	677,959	648,597	8.8	8.2	9.1	7.8	-1.0	0.8	-1.1	0.4	1.1	0.4	-1.0	0.5	1.1	0.2	1.1	0.09
				HDLGHFMLR	3	100.0%	1																									
				LPSEGPRPAHVVVGDVLQAADVDK	3	99.3%	1																									
				LQAVTDDHIR	2	100.0%	2																									
				LQAVTDDHIR	3	99.9%	1																									
				NDLSPTTVMSEGAR	2	100.0%	2																									
				NDLSPTTVMSEGARNIVAAMKAHGVDK	3	92.3%	1																									
IPI00219913	USP14	Ubiquitin carboxyl-terminal hydrolase 14	100.0%	32.6	11	11	12	1	19,366,622	21,970,195	21,084,023	25,093,775	2,536,252	1,335,894	2,085,643	601,432	29.3	13.6	22.1	5.4	1.1	0.4	1.1	0.6	1.3	0.09	-1.0	0.7	1.1	0.07	1.2	0.1
				AQLFALTGVQPAR	2	99.9%	1																									
				ASGEMASAQYITAALR	2	100.0%	1																									
				EKFEGVELNTDEPPMVFK	3	99.9%	1																									
				FEGVELNTDEPPMVFK	2	100.0%	1																									
				FPLMLDMYELCTPELQEK	2	99.7%	1																									
				GGTLKDDDWGNIK	2	98.6%	1																									
				LEAIEDDSVKETDSSSASAATPSK	3	100.0%	1																									
				LPAYLTIQMVR	2	100.0%	2																									
				NGMTLLMMGSADALPEEPSAK	2	98.3%	1																									
				RVEIMEEESEQ	2	100.0%	1																									
				SLIDQFFGVEFETTMK	2	100.0%	1																									
IPI00219930	CRABP1	Cellular retinoic acid-binding protein 1	100.0%	31.4	4	4	5	1	34,956,178	36,131,867	35,825,932	42,130,330	3,305,164	1,398,686	2,469,054	1,931,215	21.1	8.7	15.4	10.3	1.0	0.8	1.0	0.8	1.2	0.1	-1.0	0.9	1.2	0.04	1.2	0.08
				ALGVNAMLR	2	99.9%	1																									
				IHCTQTLLEGDGPK	2	99.9%	1																									
				SLATWENENK	2	98.9%	1																									
				SSENFDELLK	2	99.8%	2																									
IPI00219953	CMPK1	UMP-CMP kinase isoform a	100.0%	40.8	9	11	16	1	24,717,102	25,565,863	25,122,677	29,408,444	3,046,405	1,057,892	1,905,412	712,893	27.6	9.3	17.0	5.4	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.8	1.2	0.02	1.2	0.09
				FLIDGFPR	2	92.4%	1																									
				IQTYLQSTKPIIDLYEEMGK	3	100.0%	2																									
				IVPVEITISLLK	2	100.0%	1																									
				KNPDSQYGELIEK	2	100.0%	1																									
				NPDSQYGELIEK	2	98.9%	1																									
				NQDNLQGWNK	2	100.0%	2																									
				SVDEVFDEVVQIFDK	2	100.0%	2																									
				SVDEVFDEVVQIFDKEG	2	100.0%	2																									
				SVDEVFDEVVQIFDKEG	3	100.0%	1																									
				YGYTHLSAGELLR	2	100.0%	2																									
				YGYTHLSAGELLR	3	100.0%	1																									

IPI00219973	EYA4	isoform 2 of Eyes absent homolog 4	99.8%	1.8	1	1	1	8	587,393	577,703	567,116	662,994	60,318	37,777	53,748	29,537	23.0	14.6	21.2	10.0	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.1	1.2	0.2
IPI00300775	EYA4	cDNA FLJ61361, highly similar to Eyes absent homolog 4	99.8%	1.7	1	1	1	8	587,393	577,703	567,116	662,994	60,318	37,777	53,748	29,537	23.0	14.6	21.2	10.0	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.1	1.2	0.2
IPI00300776	EYA4	isoform 4 of Eyes absent homolog 4	99.8%	1.7	1	1	1	8	587,393	577,703	567,116	662,994	60,318	37,777	53,748	29,537	23.0	14.6	21.2	10.0	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.1	1.2	0.2
IPI00377184	EYA4	isoform 3 of Eyes absent homolog 4	99.8%	2.4	1	1	1	8	587,393	577,703	567,116	662,994	60,318	37,777	53,748	29,537	23.0	14.6	21.2	10.0	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.1	1.2	0.2
IPI00908921	EYA4	cDNA FLJ55557, highly similar to Eyes absent homolog 4	99.8%	1.9	1	1	1	8	587,393	577,703	567,116	662,994	60,318	37,777	53,748	29,537	23.0	14.6	21.2	10.0	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.1	1.2	0.2
IPI00974164	EYA4	cDNA FLJ61280, highly similar to Eyes absent homolog 4	99.8%	1.9	1	1	1	8	587,393	577,703	567,116	662,994	60,318	37,777	53,748	29,537	23.0	14.6	21.2	10.0	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.1	1.2	0.2
IPI00980015	EYA4	Uncharacterized protein	99.8%	1.8	1	1	1	8	587,393	577,703	567,116	662,994	60,318	37,777	53,748	29,537	23.0	14.6	21.2	10.0	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.1	1.2	0.2
IPI00980204	EYA4	isoform 1 of Eyes absent homolog 4	99.8%	1.7	1	1	1	8	587,393	577,703	567,116	662,994	60,318	37,777	53,748	29,537	23.0	14.6	21.2	10.0	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.1	1.2	0.2
				DPPMAVTLGLR	2	99.1%	1																									
IPI00220014	IDI1	isoform 2 of Isopentenyl-diphosphate Delta-isomerase 1	100.0%	29.9	6	6	7	2	8,065,558	8,172,833	8,673,595	9,258,635	614,853	256,631	469,525	390,190	17.1	7.0	12.1	9.4	1.0	0.9	1.1	0.5	1.1	0.1	1.1	0.4	1.1	0.05	1.1	0.4
IPI00645307	IDI1	isoform 1 of Isopentenyl-diphosphate Delta-isomerase 1	100.0%	37.4	6	6	7	2	8,065,558	8,172,833	8,673,595	9,258,635	614,853	256,631	469,525	390,190	17.1	7.0	12.1	9.4	1.0	0.9	1.1	0.5	1.1	0.1	1.1	0.4	1.1	0.05	1.1	0.4
				AELGIPLEEVPPEEINYLTR	2	100.0%	1																									
				AQSDGIWGEHEIDYILLVR	3	100.0%	1																									
				ITFPGCFTNTCCSHPLSNPAELEESDALGVR	3	100.0%	1																									
				KNVTLNPDPNEIK	2	92.8%	1																									
				LKAELGIPLEEVPPEEINYLTR	3	84.7%	1																									
				NVTLNPDPNEIK	2	100.0%	2																									
IPI00220030	PXN	isoform Alpha of Paxillin	90.2%	2.3	1	1	1	7	1,010,463	1,055,850	1,354,856	1,106,377	96,213	153,055	114,587	48,726	21.3	32.4	18.9	9.9	1.0	0.8	1.3	0.05	1.1	0.4	1.3	0.2	1.0	0.8	-1.2	0.08
IPI00220031	PXN	isoform Gamma of Paxillin	90.2%	2.2	1	1	1	7	1,010,463	1,055,850	1,354,856	1,106,377	96,213	153,055	114,587	48,726	21.3	32.4	18.9	9.9	1.0	0.8	1.3	0.05	1.1	0.4	1.3	0.2	1.0	0.8	-1.2	0.08
IPI00335634	PXN	isoform Beta of Paxillin	90.2%	2.2	1	1	1	7	1,010,463	1,055,850	1,354,856	1,106,377	96,213	153,055	114,587	48,726	21.3	32.4	18.9	9.9	1.0	0.8	1.3	0.05	1.1	0.4	1.3	0.2	1.0	0.8	-1.2	0.08
IPI00555917	PXN	Paxillin variant (Fragment)	90.2%	1.8	1	1	1	7	1,010,463	1,055,850	1,354,856	1,106,377	96,213	153,055	114,587	48,726	21.3	32.4	18.9	9.9	1.0	0.8	1.3	0.05	1.1	0.4	1.3	0.2	1.0	0.8	-1.2	0.08
IPI00890738	PXN	isoform 4 of Paxillin	90.2%	3.1	1	1	1	7	1,010,463	1,055,850	1,354,856	1,106,377	96,213	153,055	114,587	48,726	21.3	32.4	18.9	9.9	1.0	0.8	1.3	0.05	1.1	0.4	1.3	0.2	1.0	0.8	-1.2	0.08
IPI01013237	PXN	35 kDa protein	90.2%	4.1	1	1	1	7	1,010,463	1,055,850	1,354,856	1,106,377	96,213	153,055	114,587	48,726	21.3	32.4	18.9	9.9	1.0	0.8	1.3	0.05	1.1	0.4	1.3	0.2	1.0	0.8	-1.2	0.08
IPI01015055	PXN	cDNA FLJ16691 fis, clone TRACH3000692, highly similar to Paxillin	90.2%	2.2	1	1	1	7	1,010,463	1,055,850	1,354,856	1,106,377	96,213	153,055	114,587	48,726	21.3	32.4	18.9	9.9	1.0	0.8	1.3	0.05	1.1	0.4	1.3	0.2	1.0	0.8	-1.2	0.08
				ELDELMASLSDFK	2	85.9%	1																									
IPI00220038	SRRT	isoform 2 of Serrate RNA effector molecule homolog	100.0%	6.7	4	4	4	6	2,710,468	2,820,437	2,691,897	3,001,616	246,806	151,430	121,435	163,448	20.4	12.0	10.1	12.2	1.0	0.7	-1.0	0.9	1.1	0.4	-1.0	0.5	1.1	0.4	1.1	0.2
IPI00375144	SRRT	isoform 1 of Serrate RNA effector molecule homolog	100.0%	6.6	4	4	4	6	2,710,468	2,820,437	2,691,897	3,001,616	246,806	151,430	121,435	163,448	20.4	12.0	10.1	12.2	1.0	0.7	-1.0	0.9	1.1	0.4	-1.0	0.5	1.1	0.4	1.1	0.2
IPI00888085	SRRT	isoform 4 of Serrate RNA effector molecule homolog	100.0%	6.7	4	4	4	6	2,710,468	2,820,437	2,691,897	3,001,616	246,806	151,430	121,435	163,448	20.4	12.0	10.1	12.2	1.0	0.7	-1.0	0.9	1.1	0.4	-1.0	0.5	1.1	0.4	1.1	0.2
IPI00888510	SRRT	isoform 3 of Serrate RNA effector molecule homolog	100.0%	6.6	4	4	4	6	2,710,468	2,820,437	2,691,897	3,001,616	246,806	151,430	121,435	163,448	20.4	12.0	10.1	12.2	1.0	0.7	-1.0	0.9	1.1	0.4	-1.0	0.5	1.1	0.4	1.1	0.2
IPI00927582	SRRT	isoform 5 of Serrate RNA effector molecule homolog	100.0%	6.9	4	4	4	6	2,710,468	2,820,437	2,691,897	3,001,616	246,806	151,430	121,435	163,448	20.4	12.0	10.1	12.2	1.0	0.7	-1.0	0.9	1.1	0.4	-1.0	0.5	1.1	0.4	1.1	0.2
IPI00925539	SRRT	57 kDa protein	100.0%	11.6	4	4	4	6	2,710,468	2,820,437	2,691,897	3,001,616	246,806	151,430	121,435	163,448	20.4	12.0	10.1	12.2	1.0	0.7	-1.0	0.9	1.1	0.4	-1.0	0.5	1.1	0.4	1.1	0.2
				ECELSPGVNR	2	84.9%	1																									
				EVAFFNNFLTDAK	2	100.0%	1																									
				FVTSNTQELGKDK	2	99.2%	1																									
				IVHSLDYYNTCEYPNEDEMPNR	3	99.3%	1																									
IPI00220099	STX3	isoform B of Syntaxin-3	98.7%	3.6	1	1	1	5	862,942	813,032	868,636	911,204	65,306	28,357	28,224	31,418	16.9	7.8	7.3	7.7	-1.1	0.5	1.0	0.9	1.1	0.5	1.1	0.2	1.1	0.05	1.0	0.3
IPI00395768	STX3	isoform A of Syntaxin-3	98.7%	3.1	1	1	1	5	862,942	813,032	868,636	911,204	65,306	28,357	28,224	31,418	16.9	7.8	7.3	7.7	-1.1	0.5	1.0	0.9	1.1	0.5	1.1	0.2	1.1	0.05	1.0	0.3
IPI00909631	STX3	cDNA FLJ52253, highly similar to Mus musculus syntaxin 3 (Stx3), transcript variant	98.7%	5.0	1	1	1	5	862,942	813,032	868,636	911,204	65,306	28,357	28,224	31,418	16.9	7.8	7.3	7.7	-1.1	0.5	1.0	0.9	1.1	0.5	1.1	0.2	1.1	0.05	1.0	0.3
IPI00964617	STX3	syntaxin-3 isoform 2	98.7%	3.3	1	1	1	5	862,942	813,032	868,636	911,204	65,306	28,357	28,224	31,418	16.9	7.8	7.3	7.7	-1.1	0.5	1.0	0.9	1.1	0.5	1.1	0.2	1.1	0.05	1.0	0.3
IPI00982270	STX3	Uncharacterized protein	98.7%	3.5	1	1	1	5	862,942	813,032	868,636	911,204	65,306	28,357	28,224	31,418	16.9	7.8	7.3	7.7	-1.1	0.5	1.0	0.9	1.1	0.5	1.1	0.2	1.1	0.05	1.0	0.3
				YNEAQVDFR	2	98.7%	1																									
IPI00220113	MAP4	isoform 2 of Microtubule-associated protein 4	100.0%	15.9	11	13	14	1	7,666,591	7,864,648	7,697,423	8,712,366	774,718	246,633	414,828	394,978	22.6	7.0	12.1	10.1	1.0	0.8	1.0	1	1.1	0.3	-1.0	0.7	1.1	0.1	1.1	0.1
				DFIATLEAEAFDDVVGETVGK	2	100.0%	2																									
				DFIATLEAEAFDDVVGETVGK	3	100.0%	1																									
				DMQPSMESDMALVK	2	99.5%	1																									
				DMSPLSETEMALGK	2	99.4%	1																									
				EAQTLDSQIQETSI	2	95.4%	1																									
				SVPADLSRPK	2	86.6%	1																									
				TAGPIASAQK	2	99.8%	1																									
				TTTAAAVASTGPSSR	2	99.6%	1																									
				TTTLSGTAPAAGVVPSR	2	100.0%	1																									
				VALSSETEVALAR	2	98.0%	1																									
				VGSLDNVGHLPAGGAVK	2	99.7%	1																									
				VGSLDNVGHLPAGGAVK	3	100.0%	1																									
				WPTETDVSSAK	2	99.7%	1																									
IPI00220194	SLC2A1	Solute carrier family 2, facilitated glucose transporter member 1	100.0%	12.0	5	5	8	2	11,204,403	11,280,753	11,301,473	12,873,475	1,093,604	411,034	740,623	415,668	21.8	8.2	14.7	7.2	1.0	1	1.0	0.9	1.1	0.2	1.0	1	1.1	0.03	1.1	0.1
IPI00909237	SLC2A1	cDNA FLJ55703, highly similar to Solute carrier family 2, facilitated glucose transpor	100.0%	13.6	5	5	8	2	11,204,403	11,280,753	11,301,473	12,873,475	1,093,604	411,034	740,623	415,668	21.8	8.2	14.7	7.2	1.0	1	1.0	0.9	1.1	0.2	1.0	1	1.1	0.03	1.1	0.1
				GTADVTHDLQEMKEESR	3	100.0%	2																									
				QGGASQSDKTPEELFHPLGADSQV	3	99.9%	1																									
				TFDEIASGFR	2	100.0%	2																									
				TPEELFHPLGADSQV	2	99.9%	1																									
				VTILELFR	2	100.0%	2																									
IPI00220218	SDCBP2	isoform 3 of Syntenin-2	100.0%	5.3	1	1	1	1	1,731,125	1,873,305	1,669,260	2,066,540	195,733	88,843	98,186	152,109	25.3	10.6	13.2	16.5	1.1	0.5	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.3	1.2	0.06
				FGDQLLQIDGR	2	100.0%	1																									
IPI00220219	COPB2	Coatomer subunit beta'	100.0%	15.7	10	10	11	2	29,659,597	30,155,138	28,249,081	31,838,693	1,649,864	1,094,675	1,889,053	916,822	12.4	8.1	15.0	6.4	1.0	0.8	-1.0	0.6	1.1	0.3	-1.1	0.4	1.1	0.3	1.1	0.1
IPI00789674	COPB2	cDNA FLJ56271, highly similar to Coatomer subunit beta	100.0%	16.2	10	10	11	2	29,659,597	30,155,138	28,249,081	31,838,693	1,649,864	1,094,675	1,889,053	916,822	12.4	8.1	15.0	6.4	1.0	0.8	-1.0	0.6	1.1	0.3	-1.1	0.4	1.1	0.3	1.1	0.1
				AAESLADPTEYENLFPGLK	2	100.0%	1																									
				DMGSCEIYPQTIQHNPNGR	3	100.0%	1																									
				DNNQFASASLDR	2	99.9%	2																									
				FELALQLGELK	2	100.0%	1																									
				GSNNVALGYDEGSIIVK	2	100.0%	1																									
				QYPLVTPNEER	2	88.3%	1																									
				SVNGLAFYDWDNTELIR	2	100.0%	1																									
				TYLPSQVSR	2	88.8%	1																									
				VFNYNTLER	2	99.6%	1																									
				VWQLGSSSPNFTLEGHEK	3	98.0%	1																									
IPI00220267	ASL	Argininosuccinate lyase	100.0%	18.3	7	8	8	2	11,411,117	11,563,721	10,363,170	14,206,377	1,399,477	727,236	993,023	850,814	27.4	14.1	21.4	13.4	1.0	0.9	-1.1	0.6	1.2	0.1	-1.1	0.4	1.2	0.05	1.4	0.02
IPI00607562	ASL	argininosuccinate lyase isoform 2	100.0%	19.1	7	8	8	2	11,411,117	11,563,721	10,363,170	14,206,377	1,399,477	727,236	993,023	850,814	27.4	14.1	21.4	13.4	1.0	0.9	-1.1	0.6	1.2	0.1	-1.1	0.4	1.2	0.05	1.4	0.02
				FVGAVDPIMEK	2	97.3%	1																									
				HLWEVDVQGSK	2	99.9%	1																									
				INVLPLGSGAIAGNPLGVDR	2	99.3%	1																									
				INVLPLGSGAIAGNPLGVDR	3	82.0%	1																									
				NPDSLELIR	2	93.8%	1																									
				QTCSTLSGLLWELIR	2	99.9%	1																									
				SRNDQVVTDLR	2	87.9%	1																									
				SSVDWQIR	2	96.9%	1																									
IPI00220271	AKR1A1	Alcohol dehydrogenase [NADP+]	100.0%	26.8	7	7	8	1	37,584,820	40,167,300	39,247,100	44,601,770	3,214,590	1,767,361	1,837,079	2,090,325	19.1	9.8	10.5	10.5	1.1	0.5	1.0	0.7	1.2	0.1	-1.0	0.7	1.1	0.1	1.1	0.09
				AWRDPDEPVLLEEPVVLALAEK	3	100.0%	1																									
				GLEVTAYSPLGSSDR	2	100.0%	2																									
				HHPEDVEPALR	3	93.4%	1																									
				SPAQILLR	2	84.9%	1																									
				VFDFTFSPEEMK	2	100.0%	1																									
				YALSVGYR	2	97.6%	1																									
				YIVPMLTVDGK	2	89.6%	1																									
IPI00220301	PRDX6	Peroxiredoxin-6	100.0%	60.3	13	15	18	1	121,853,857	122,700,540	127,073,940	139,135,340	8,655,683	3,396,222	8,311,509	5,115,449	15.9	6.2	14.6	8.2	1.0	0.9	1.0	0.7	1.1	0.1	1.0	0.6	1.1	0.03	1.1	0.3
				DFTPVCTTELGR	2	100.0%	2																									
				DINAYNCEEPTEKLPFPIIDDR	3	99.9%	1																									
				ELAILLGMLDPAEKDEK	2	100.0%	1																									
				ELAILLGMLDPAEKDEK	3	99.4%	1																									
				LIALSIDSVEDHLAWSK	2	100.0%	1																									
				LPFPIIDDR	2	100.0%	2																									
				LSILYPATTGR	2	99.9%	1																									
				NFDEILR	2	99.1%	1																									
				NRELAILLGMLDPAEKDEK	3	99.9%	1																									
				VATPVDWKDGDSVMVLPTIPEEEAK	3	95.5%	1																									
				VVFVFGPDK	2	93.8%	1																									
				VVFVFGPDKK	2	100.0%	2																									
				VVFVFGPDKK	3	100.0%	1																									
				VVISLQLTAEK	2	100.0%	1																									
				VVISLQLTAEKR	2	99.7%	1																									
IPI00220317	POLA1	DNA polymerase alpha catalytic subunit	99.3%	2.5	2	2	2	2	2,549,971	2,544,965	2,683,877	2,862,830	444,120	164,934	261,615	258,374	38.9	14.5	21.8	20.2	-1.0	1	1.1	0.8	1.1	0.6	1.1	0.7	1.1	0.3	1.1	0.6
IPI00647655	POLA1	DNA polymerase	99.3%	2.5	2	2	2	2	2,549,971	2,544,965	2,683,877	2,862,830	444,120	164,934	261,615	258,374	38.9	14.5	21.8	20.2	-1.0	1	1.1	0.8	1.1	0.6	1.1	0.7	1.1	0.3	1.1	0.6
				KAAYAGGLVLDPK	2	92.5%	1																									
				RLIEIGENVLNGSVPVSQFEINK	3	91.1%	1																									
IPI00220327	KRT1	Keratin, type II cytoskeletal 1	100.0%	26.9	16	16	24	1	106,258,714	111,376,807	104,426,611	118,795,810	6,034,310	4,515,118	5,702,077	4,576,031	12.7	9.1	12.2	8.6	1.0	0.5	-1.0	0.8	1.1	0.1	-1.1	0.4	1.1	0.3	1.1	0.08
				AQYEDIAQK	2	99.9%	1																									
				FLEQQNQVLQTK	2	99.3%	2																									
				FSSCGGGGGSFGAGGGFGSR	2	100.0%	1																									
				LALDLEIATYR	2	97.7%	2																									
				LLEGEESR	2	100.0%	1																									
				NKLNDLEDALQQAK	2	99.9%	1																									
				NKLNDLEDALQQAKEDLAR	3	100.0%	1																									
				NKYEDEINKR	2	99.9%	2																									
				NMQDMVEDYR	2	100.0%	2																									
				SKAEAESLYQSK	2	100.0%	1																									
				SLDLDSIIAEVK	2	100.0%	2																									
				SLNNQFASFIDK	2	100.0%	2																									
				THNLEPYFESFINNLR	3	100.0%	2																									
				TNAENEFVTIK	2	97.0%	1																									
				TNAENEFVTIKK	2	99.9%	1																									
				YEELQITAGR	2	100.0%	2																									
IPI00220342	DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	100.0%	28.8	5	6	6	4	10,837,758	11,616,805	10,446,840	12,434,683	884,695	459,929	720,691	489,231	18.3	8.9	15.4	8.8	1.1	0.5	-1.0	0.7	1.1	0.2	-1.1	0.2	1.1	0.3	1.2	0.05
IPI00910124	DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 isoform 2	100.0%	45.1	5	6	6	4	10,837,758	11,616,805	10,446,840	12,434,683	884,695	459,929	720,691	489,231	18.3	8.9	15.4	8.8	1.1	0.5	-1.0	0.7	1.1	0.2	-1.1	0.2	1.1	0.3	1.2	0.05
IPI01011679	DDAH1	cDNA FLJ54083, highly similar to NG,NG-dimethylarginine dimethylaminohydrolase	100.0%	42.7	5	6	6	4	10,837,758	11,616,805	10,446,840	12,434,683	884,695	459,929	720,691	489,231	18.3	8.9	15.4	8.8	1.1	0.5	-1.0	0.7	1.1	0.2	-1.1	0.2	1.1	0.3	1.2	0.05
IPI01015224	DDAH1	cDNA FLJ54119, highly similar to NG,NG-dimethylarginine dimethylaminohydrolase	100.0%	44.3	5	6	6	4	10,837,758	11,616,805	10,446,840	12,434,683	884,695	459,929	720,691	489,231	18.3	8.9	15.4	8.8	1.1	0.5	-1.0	0.7	1.1	0.2	-1.1	0.2	1.1	0.3	1.2	0.05
				DYAVSTVPVADGLHLK	2	99.7%	1																									
				GAEILADTFKDYAVSTVPVADGLHLK	3	97.0%	1																									
				LKDHMLIPVSMSELEK	3	90.2%	1																									
				LTVPDDIAANCIYLNIPNK	2	100.0%	1																									
				LTVPDDIAANCIYLNIPNK	3	98.5%	1																									
				SFCSMAGPNLIAIGSSESAQK	2	100.0%	1																									
IPI00220362	HSPE1	10 kDa heat shock protein, mitochondrial	100.0%	40.2	4	5	9	1	25,718,936	26,380,110	25,287,776	28,579,154	2,819,224	1,185,340	2,159,390	962,491	24.5	10.1	19.1	7.5	1.0	0.8	-1.0	0.9	1.1	0.4	-1.0	0.7	1.1	0.2	1.1	0.2
				DGDILGK	1	98.5%	2																									
				DGDILGK	2	99.6%	2																									
				KFLPLFDR	2	99.1%	1																									
				VLQATVVAVGSGSK	2	100.0%	2																									
				VVLDDKDYFLFR	3	100.0%	2																									

IPI00220373	IDE	Insulin-degrading enzyme	95.0%	1.5	1	1	1	2	931,600	1,092,300	1,046,680	1,187,805	89,433	158,307	94,751	127,275	21.5	32.4	20.2	24.0	1.2	0.4	1.1	0.4	1.3	0.1	-1.0	0.8	1.1	0.7	1.1	0.4
IPI00514444	IDE	Insulin-degrading enzyme	95.0%	5.8	1	1	1	2	931,600	1,092,300	1,046,680	1,187,805	89,433	158,307	94,751	127,275	21.5	32.4	20.2	24.0	1.2	0.4	1.1	0.4	1.3	0.1	-1.0	0.8	1.1	0.7	1.1	0.4
				FAQFFLCPLFDESCK	2	95.0%	1																									
IPI00220416	UQCRB	Cytochrome b-c1 complex subunit 7	99.5%	11.7	1	1	2	2	3,595,025	4,011,820	3,766,380	4,735,895	551,807	243,062	439,256	183,504	34.3	13.6	26.1	8.7	1.1	0.5	1.0	0.8	1.3	0.1	-1.1	0.6	1.2	0.04	1.3	0.08
IPI00976562	UQCRB	cytochrome b-c1 complex subunit 7 isoform 2	99.5%	16.5	1	1	2	2	3,595,025	4,011,820	3,766,380	4,735,895	551,807	243,062	439,256	183,504	34.3	13.6	26.1	8.7	1.1	0.5	1.0	0.8	1.3	0.1	-1.1	0.6	1.2	0.04	1.3	0.08
				YEEENFYLEPYLK	2	99.5%	2																									
IPI00220445	COL20A1	isoform 1 of Collagen alpha-1(XX) chain	96.6%	1.6	1	1	1	3	2,322,507	2,315,417	2,320,433	2,508,623	129,211	157,184	133,923	106,499	12.4	15.2	12.9	9.5	-1.0	1	-1.0	1	1.1	0.3	1.0	1	1.1	0.3	1.1	0.3
IPI00414102	COL20A1	isoform 2 of Collagen alpha-1(XX) chain	96.6%	1.5	1	1	1	3	2,322,507	2,315,417	2,320,433	2,508,623	129,211	157,184	133,923	106,499	12.4	15.2	12.9	9.5	-1.0	1	-1.0	1	1.1	0.3	1.0	1	1.1	0.3	1.1	0.3
IPI00414583	COL20A1	isoform 3 of Collagen alpha-1(XX) chain	96.6%	1.5	1	1	1	3	2,322,507	2,315,417	2,320,433	2,508,623	129,211	157,184	133,923	106,499	12.4	15.2	12.9	9.5	-1.0	1	-1.0	1	1.1	0.3	1.0	1	1.1	0.3	1.1	0.3
				VTCLYPGGGSSTLTGRVTTK	2	96.6%	1																									
IPI00220466	LIMA1	isoform 3 of LIM domain and actin-binding protein 1	100.0%	18.4	5	5	7	1	7,266,418	7,852,593	8,469,073	8,523,935	302,588	279,514	698,208	379,695	9.3	8.0	18.4	10.0	1.1	0.2	1.2	0.2	1.2	0.03	1.1	0.4	1.1	0.2	1.0	0.9
				IAWPPPTELGSSGSALEEGIK	2	99.9%	1																									
				ISANENSLAVR	2	100.0%	2																									
				NENEEILERPAQLANAR	3	100.0%	1																									
				SLNWSSFVDNTFAEEFTTQNQK	3	100.0%	1																									
				SQDVELWEGEVVK	2	100.0%	2																									
IPI00220487	ATP5H	isoform 1 of ATP synthase subunit d, mitochondrial	100.0%	38.5	5	5	6	2	12,915,772	13,857,745	13,873,581	15,292,405	1,067,419	573,789	1,177,249	544,159	18.5	9.3	19.0	8.0	1.1	0.5	1.1	0.6	1.2	0.08	1.0	1	1.1	0.1	1.1	0.3
IPI00456049	ATP5H	isoform 2 of ATP synthase subunit d, mitochondrial	100.0%	45.3	5	5	6	2	12,915,772	13,857,745	13,873,581	15,292,405	1,067,419	573,789	1,177,249	544,159	18.5	9.3	19.0	8.0	1.1	0.5	1.1	0.6	1.2	0.08	1.0	1	1.1	0.1	1.1	0.3
				AGLVDDFEKK	3	98.7%	1																									
				NLIPFDQMTIEDLNEAFPETK	2	100.0%	2																									
				SCAEWVSLSK	2	98.6%	1																									
				SWNETLTSR	2	99.1%	1																									
				YPYWPHQPIENL	2	92.0%	1																									
IPI00220493	LSM5	isoform 1 of U6 snRNA-associated Sm-like protein LSm5	96.3%	25.3	1	1	1	2	2,647,305	3,123,950	3,114,205	3,445,695	671,934	394,442	495,168	284,332	56.8	28.2	35.6	18.5	1.2	0.6	1.2	0.6	1.3	0.3	-1.0	1	1.1	0.5	1.1	0.6
IPI00908769	LSM5	isoform 2 of U6 snRNA-associated Sm-like protein LSm5	96.3%	37.1	1	1	1	2	2,647,305	3,123,950	3,114,205	3,445,695	671,934	394,442	495,168	284,332	56.8	28.2	35.6	18.5	1.2	0.6	1.2	0.6	1.3	0.3	-1.0	1	1.1	0.5	1.1	0.6
				LDQILLNGNNITMLVPGGEGPEV	2	96.3%	1																									
IPI00220503	DCTN2	isoform 2 of Dynactin subunit 2	100.0%	19.5	6	6	8	4	6,829,371	6,860,347	6,839,220	7,651,207	371,972	197,823	457,312	207,886	12.2	6.5	15.0	6.1	1.0	0.9	1.0	1	1.1	0.09	-1.0	1	1.1	0.02	1.1	0.1
IPI00973457	DCTN2	isoform 1 of Dynactin subunit 2	100.0%	19.7	6	6	8	4	6,829,371	6,860,347	6,839,220	7,651,207	371,972	197,823	457,312	207,886	12.2	6.5	15.0	6.1	1.0	0.9	1.0	1	1.1	0.09	-1.0	1	1.1	0.02	1.1	0.1
IPI00973500	DCTN2	isoform 3 of Dynactin subunit 2	100.0%	19.6	6	6	8	4	6,829,371	6,860,347	6,839,220	7,651,207	371,972	197,823	457,312	207,886	12.2	6.5	15.0	6.1	1.0	0.9	1.0	1	1.1	0.09	-1.0	1	1.1	0.02	1.1	0.1
IPI01015908	DCTN2	45 kDa protein	100.0%	19.5	6	6	8	4	6,829,371	6,860,347	6,839,220	7,651,207	371,972	197,823	457,312	207,886	12.2	6.5	15.0	6.1	1.0	0.9	1.0	1	1.1	0.09	-1.0	1	1.1	0.02	1.1	0.1
				DNTTLLTQVQTTMR	2	99.9%	1																									
				LLLQLEATK	2	99.7%	2																									
				LTELETAVR	2	98.9%	1																									
				TGYESGEYEMLGEGLGVK	2	100.0%	1																									
				VSALDLAVLDQVEAR	2	100.0%	2																									
				WSPIASTLPELVQR	2	100.0%	1																									
IPI00220528	SNRPF	Small nuclear ribonucleoprotein F	98.8%	16.3	2	2	2	1	13,250,150	12,511,260	13,335,510	14,204,020	1,875,578	933,173	1,431,497	650,930	31.7	16.7	24.0	10.3	-1.1	0.7	1.0	1	1.1	0.7	1.1	0.6	1.1	0.2	1.1	0.6
				CNNVLYIR	2	92.4%	1																									
				WGMEYK	2	84.3%	1																									
IPI00220602	FERMT1	FERMT1 protein	94.3%	4.5	1	1	1	3	225,702	231,097	208,084	266,400	33,757	23,826	28,458	17,233	33.4	23.1	30.6	14.5	1.0	0.9	-1.1	0.7	1.2	0.3	-1.1	0.6	1.2	0.3	1.3	0.1
IPI00304754	FERMT1	isoform 1 of Fermitin family homolog 1	94.3%	2.8	1	1	1	3	225,702	231,097	208,084	266,400	33,757	23,826	28,458	17,233	33.4	23.1	30.6	14.5	1.0	0.9	-1.1	0.7	1.2	0.3	-1.1	0.6	1.2	0.3	1.3	0.1
IPI00643475	FERMT1	Uncharacterized protein	94.3%	3.4	1	1	1	3	225,702	231,097	208,084	266,400	33,757	23,826	28,458	17,233	33.4	23.1	30.6	14.5	1.0	0.9	-1.1	0.7	1.2	0.3	-1.1	0.6	1.2	0.3	1.3	0.1
				TMADSSYQPEVLNILSFLR	2	94.3%	1																									
IPI00220637	SARS	Seryl-tRNA synthetase, cytoplasmic	99.6%	10.9	4	4	4	2	6,024,308	5,753,677	6,274,176	7,060,055	540,553	248,643	602,435	223,035	20.1	9.7	21.5	7.1	-1.0	0.7	1.0	0.8	1.2	0.1	1.1	0.4	1.2	0.004	1.1	0.3
IPI00514587	SARS	Seryl-tRNA synthetase	99.6%	10.5	4	4	4	2	6,024,308	5,753,677	6,274,176	7,060,055	540,553	248,643	602,435	223,035	20.1	9.7	21.5	7.1	-1.0	0.7	1.0	0.8	1.2	0.1	1.1	0.4	1.2	0.004	1.1	0.3
				ELVSCSNCTDYQAR	2	99.5%	1																									
				EVMQEVAQLSQFDEELYK	2	99.6%	1																									
				KLDLEAWFPGSGAFR	2	81.0%	1																									
				YAGLSTCFR	2	99.2%	1																									
IPI00220642	YWHAG	14-3-3 protein gamma	100.0%	47.0	8	10	12	1	25,170,808	26,111,597	25,014,089	28,903,249	2,159,392	1,333,841	1,939,822	1,017,500	19.2	11.4	17.3	7.9	1.0	0.7	-1.0	1	1.1	0.2	-1.0	0.7	1.1	0.1	1.2	0.1
				DNLTLWTSDQQDDDGGEGNN	2	100.0%	2																									
				EHMQPTHPIR	3	99.1%	1																									
				LAEQAERYDDMAAAMK	3	99.6%	1																									
				LGLALNYSVFYYEIQNAPEQACHLAK	3	100.0%	1																									
				NVTELNEPLSNEER	2	100.0%	2																									
				TAFDDAIAELDTLNEDSYK	2	100.0%	1																									
				TAFDDAIAELDTLNEDSYK	3	100.0%	1																									
				YDDMAAAMK	2	100.0%	1																									
				YLAEVATGEKR	2	100.0%	1																									
				YLAEVATGEKR	3	100.0%	1																									
IPI00220648	PMVK	Phosphomevalonate kinase	99.5%	6.8	1	1	1	2	983,535	1,015,810	1,331,470	1,005,440	54,945	93,068	140,244	63,976	12.5	20.5	23.6	14.2	1.0	0.8	1.4	0.07	1.0	0.8	1.3	0.1	-1.0	0.9	-1.3	0.07
IPI00977942	PMVK	Conserved hypothetical protein	99.5%	17.6	1	1	1	2	983,535	1,015,810	1,331,470	1,005,440	54,945	93,068	140,244	63,976	12.5	20.5	23.6	14.2	1.0	0.8	1.4	0.07	1.0	0.8	1.3	0.1	-1.0	0.9	-1.3	0.07
				LEEQLENLIEFIR	2	99.5%	1																									
IPI00220669	SHMT1	isoform 3 of Serine hydroxymethyltransferase, cytosolic	95.9%	4.2	1	1	1	1	470,163	498,545	507,325	473,925	32,422	26,401	29,383	27,264	15.4	11.8	13.0	12.9	1.1	0.5	1.1	0.4	1.0	0.9	1.0	0.8	-1.1	0.5	-1.1	0.4
				YYGGTEFIDELETLCQK	2	96.4%	1																									
IPI00220683	HNRNPD	isoform 2 of Heterogeneous nuclear ribonucleoprotein D0	100.0%	29.8	10	12	18	4	7,352,843	7,760,636	7,219,494	8,331,653	701,365	214,195	463,863	291,700	21.3	6.2	14.4	7.8	1.1	0.6	-1.0	0.9	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.08
IPI00220685	HNRNPD	isoform 4 of Heterogeneous nuclear ribonucleoprotein D0	100.0%	34.8	10	12	18	4	7,352,843	7,760,636	7,219,494	8,331,653	701,365	214,195	463,863	291,700	21.3	6.2	14.4	7.8	1.1	0.6	-1.0	0.9	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.08
IPI00903278	HNRNPD	P37 AUF1	100.0%	35.0	10	12	18	4	7,352,843	7,760,636	7,219,494	8,331,653	701,365	214,195	463,863	291,700	21.3	6.2	14.4	7.8	1.1	0.6	-1.0	0.9	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.08
IPI01014602	HNRNPD	cDNA FLJ54150, highly similar to Heterogeneous nuclear ribonucleoprotein D0	100.0%	33.0	10	12	18	4	7,352,843	7,760,636	7,219,494	8,331,653	701,365	214,195	463,863	291,700	21.3	6.2	14.4	7.8	1.1	0.6	-1.0	0.9	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.08
				ESESVDKVMDQK	2	99.9%	2																									
				EYFGGFGEVESIELPMDNK	2	100.0%	1																									
				FGEVVDCTLK	2	95.0%	2																									
				FGEVVDCTLKLDPITGR	3	99.9%	1																									
				GFCFITFKEEEPVKK	3	83.5%	1																									
				GFGFVLFK	2	100.0%	2																									
				IFVGGLSPDTPEEK	2	100.0%	2																									
				IREYFGGFGEVESIELPMDNK	2	99.9%	1																									
				IREYFGGFGEVESIELPMDNK	3	100.0%	1																									
				MFIGGLSWDTTK	2	100.0%	2																									
				MFIGGLSWDTTKK	2	100.0%	2																									
				MFIGGLSWDTTKK	3	100.0%	1																									
IPI00982925	-	Truncated beta-globin	99.9%	15.9	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI01008981	-	Mutant beta-globin	99.9%	7.2	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00654755	HBB	Hemoglobin subunit beta	99.9%	6.8	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00796636	HBB	Uncharacterized protein	99.9%	11.1	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00815947	HBB	Truncated beta-globin (Fragment)	99.9%	25.0	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00976282	HBB	Mutant beta-globin	99.9%	11.2	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00473011	HBD	Hemoglobin subunit delta	99.9%	6.8	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00657660	HBD	Uncharacterized protein	99.9%	7.1	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00791558	HBD	Uncharacterized protein	99.9%	9.6	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00829896	HBD	Hemoglobin Lepore-Baltimore (Fragment)	99.9%	9.5	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00930351	HBD	Hbbm fused globin protein (Fragment)	99.9%	9.9	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00853641	HBE1	Uncharacterized protein	99.9%	11.5	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00220706	HBG1	Hemoglobin subunit gamma-1	99.9%	6.8	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00744503	HBG1	17 kDa protein	99.9%	6.3	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00554676	HBG2	Hemoglobin subunit gamma-2	99.9%	6.8	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00657911	HBG2	Uncharacterized protein	99.9%	7.3	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00749035	HBG2	Uncharacterized protein	99.9%	6.3	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00939160	HBG2	G-gamma globin Paulinia variant	99.9%	6.8	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
IPI00939544	HBG2	A-gamma globin Osilo variant	99.9%	6.8	1	1	2	19	408,135	426,499	385,994	438,256	16,507	15,129	14,856	15,730	9.0	7.9	8.6	8.0	1.0	0.4	-1.1	0.3	1.1	0.2	-1.1	0.09	1.0	0.6	1.1	0.04
				LLVVYPWTQR	2	99.8%	2																									
IPI00220709	TPM2	isoform 2 of Tropomyosin beta chain	100.0%	14.8	5	5	8	2	2,059,220	2,021,194	2,347,380	2,377,877	224,479	25,771	187,416	125,952	24.4	2.9	17.9	11.8	-1.0	0.9	1.1	0.4	1.2	0.3	1.2	0.2	1.2	0.05	1.0	0.9
IPI00646748	TPM2	Tropomyosin 2	100.0%	14.8	5	5	8	2	2,059,220	2,021,194	2,347,380	2,377,877	224,479	25,771	187,416	125,952	24.4	2.9	17.9	11.8	-1.0	0.9	1.1	0.4	1.2	0.3	1.2	0.2	1.2	0.05	1.0	0.9
				IQLVEEELDR	2	100.0%	2																									
				LATALQK	1	96.5%	2																									
				LEEAEKAADESER	2	98.5%	1																									
				QLEEEQQALQK	2	99.7%	1																									
				RIQLVEEELDR	2	100.0%	2																									
IPI00220740	NPM1	isoform 2 of Nucleophosmin	100.0%	43.0	12	16	25	2	95,974,903	97,460,164	98,352,277	110,485,668	6,781,252	4,031,921	5,045,567	3,188,305	15.8	9.3	11.5	6.5	1.0	0.9	1.0	0.8	1.2	0.09	1.0	0.9	1.1	0.04	1.1	0.08
IPI00549248	NPM1	isoform 1 of Nucleophosmin	100.0%	38.8	12	16	25	2	95,974,903	97,460,164	98,352,277	110,485,668	6,781,252	4,031,921	5,045,567	3,188,305	15.8	9.3	11.5	6.5	1.0	0.9	1.0	0.8	1.2	0.09	1.0	0.9	1.1	0.04	1.1	0.08
				ADKDYHFKVDNDENEHQLSLR	3	100.0%	1																									
				DELHIVEAEAMNYEGSPIK	3	100.0%	2																									
				FINYVK	1	96.2%	1																									
				GPSSVEDIK	1	100.0%	1																									
				GPSSVEDIK	2	100.0%	3																									
				LLSISGK	1	97.9%	1																									
				LLSISGKR	2	96.9%	1																									
				MQASIEK	1	99.3%	2																									
				MSVQPTVSLGGFEITPPVVLR	2	100.0%	3																									
				MSVQPTVSLGGFEITPPVVLR	3	100.0%	1																									
				MTDQEAIQDLWQWR	3	100.0%	2																									
				TVSLGAGAK	1	85.7%	1																									
				TVSLGAGAKDELHIVEAEAMNYEGSPIK	2	100.0%	1																									
				TVSLGAGAKDELHIVEAEAMNYEGSPIK	3	100.0%	2																									
				VDNDENEHQLSLR	2	100.0%	2																									
				VDNDENEHQLSLR	3	99.9%	1																									
IPI00220766	GLO1	Lactoylglutathione lyase	100.0%	42.9	7	8	11	1	72,925,950	71,680,790	69,450,900	80,219,880	6,703,590	2,994,217	4,974,108	2,351,547	20.6	9.3	16.0	6.6	-1.0	0.9	-1.1	0.7	1.1	0.4	-1.0	0.7	1.1	0.06	1.2	0.09
				DFLLQQTMLR	2	100.0%	2																									
				GFGHIGIAVPDVYSACK	3	96.2%	1																									
				GLAFIQDPDGYWIEILNPNK	2	100.0%	2																									
				GLAFIQDPDGYWIEILNPNK	3	100.0%	1																									
				IAWALSR	2	99.8%	2																									
				KSLDFYTR	2	98.4%	1																									
				RFEELGVK	2	100.0%	1																									
				VLGMTLIQK	2	92.4%	1																									
IPI00220797	ENSA	isoform 2 of Alpha-endosulfine	100.0%	17.1	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
IPI00383552	ENSA	isoform 1 of Alpha-endosulfine	100.0%	16.5	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
IPI00410177	ENSA	Endosulfine alpha	100.0%	10.7	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
IPI00410178	ENSA	alpha-endosulfine isoform 2	100.0%	15.0	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
IPI00410179	ENSA	isoform 7 of Alpha-endosulfine	100.0%	15.0	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
IPI00410180	ENSA	isoform 5 of Alpha-endosulfine	100.0%	17.1	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
IPI00410181	ENSA	isoform 6 of Alpha-endosulfine	100.0%	17.7	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
IPI00470835	ENSA	Uncharacterized protein	100.0%	13.9	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
IPI00644717	ENSA	isoform 3 of Alpha-endosulfine	100.0%	14.6	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
IPI00929648	ENSA	isoform 4 of Alpha-endosulfine	100.0%	14.3	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
IPI00967420	ENSA	Uncharacterized protein	100.0%	16.5	2	2	2	11	3,165,176	3,031,382	3,751,350	3,323,602	165,209	230,357	123,501	168,908	11.7	17.0	7.4	11.4	-1.0	0.6	1.2	0.02	1.1	0.5	1.2	0.02	1.1	0.3	-1.1	0.08
				PGGSDFLMK	2	99.9%	1																									

				YFDSGDYNMAK	2	100.0%	1																									
IPI00220827	TMSB10	Thymosin beta-10	100.0%	31.8	2	3	4	1	31,457,700	34,606,480	29,820,200	37,899,737	2,745,941	2,722,792	2,546,178	1,974,335	19.5	17.6	19.1	11.7	1.1	0.4	-1.1	0.7	1.2	0.09	-1.2	0.2	1.1	0.4	1.3	0.04
				NTLPTKETIEQEK	2	99.7%	1																									
				NTLPTKETIEQEKR	2	100.0%	2																									
				NTLPTKETIEQEKR	3	99.9%	1																									
IPI00220834	XRCC5	X-ray repair cross-complementing protein 5	100.0%	22.3	12	14	17	1	63,648,332	67,255,423	69,212,188	79,414,320	6,812,232	3,831,672	5,657,499	1,734,087	23.9	12.7	18.3	4.9	1.1	0.7	1.1	0.5	1.2	0.08	1.0	0.8	1.2	0.02	1.1	0.1
				DKPSGDTAAVFEEGGDVDDLLDMI	2	100.0%	2																									
				DQVTAQEIFQDNHEDGPTAK	3	99.5%	1																									
				EPLPPIQQHIWNMLNPPAEVTTK	3	99.5%	1																									
				HIEIFTDLSSR	2	100.0%	2																									
				HLMLPDFDLLEDIESK	2	100.0%	1																									
				KYAPTEAQLNAVDALIDSMSLAK	3	100.0%	1																									
				LFQCLLHR	3	99.7%	1																									
				LGGHGPSFPLK	2	99.9%	1																									
				LGGHGPSFPLK	3	97.4%	1																									
				LTIGSNLSIR	2	99.6%	1																									
				QYMFSSLK	2	98.8%	1																									
				TLFPLIEAK	2	95.8%	1																									
				YAPTEAQLNAVDALIDSMSLAK	2	100.0%	2																									
				YAPTEAQLNAVDALIDSMSLAK	3	100.0%	1																									
IPI00220846	ITGB4	isoform Beta-4B of Integrin beta-4	100.0%	3.2	4	4	5	1	9,655,796	9,192,340	9,000,644	10,102,673	571,119	484,200	620,935	358,255	13.2	11.8	15.4	7.9	-1.1	0.6	-1.1	0.5	1.0	0.5	-1.0	0.8	1.1	0.2	1.1	0.2
				DSIILAGRPAAPSWGPDSR	3	95.7%	1																									
				DYIPVEGELLFQPGEAWK	2	100.0%	1																									
				HVTQEFVSR	2	99.8%	2																									
				QEVEENLNEVYR	2	99.9%	1																									
IPI00909605	-	Integrin beta	100.0%	2.1	1	1	1	2	1,426,883	1,170,708	1,393,578	1,256,787	66,765	77,553	64,888	51,923	10.5	14.8	10.4	9.2	-1.2	0.04	-1.0	0.7	-1.1	0.08	1.2	0.06	1.1	0.4	-1.1	0.1
IPI00220848	ITGB4	isoform Beta-4E of Integrin beta-4	100.0%	1.4	1	1	1	2	1,426,883	1,170,708	1,393,578	1,256,787	66,765	77,553	64,888	51,923	10.5	14.8	10.4	9.2	-1.2	0.04	-1.0	0.7	-1.1	0.08	1.2	0.06	1.1	0.4	-1.1	0.1
				NVISLTEDVDEFR	2	100.0%	1																									
IPI00220857	CAST	isoform 2 of Calpastatin	100.0%	10.1	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00305750	CAST	isoform 1 of Calpastatin	100.0%	9.9	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00413492	CAST	calpastatin isoform b	100.0%	10.2	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00760715	CAST	isoform 5 of Calpastatin	100.0%	9.3	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00760909	CAST	Uncharacterized protein	100.0%	16.6	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00761035	CAST	isoform 7 of Calpastatin	100.0%	9.1	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00761069	CAST	calpastatin isoform f	100.0%	9.3	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00761160	CAST	isoform 6 of Calpastatin	100.0%	8.9	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00939354	CAST	Uncharacterized protein	100.0%	16.2	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00964032	CAST	cDNA FLJ56123, highly similar to Calpastatin	100.0%	10.1	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00964761	CAST	Uncharacterized protein	100.0%	10.1	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00965413	CAST	Calpastatin	100.0%	16.1	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00966074	CAST	cDNA FLJ50632, highly similar to Calpastatin	100.0%	10.8	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00967304	CAST	cDNA FLJ50686, highly similar to Calpastatin	100.0%	11.0	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00968085	CAST	cDNA FLJ56102, highly similar to Homo sapiens calpastatin (CAST), transcript varia	100.0%	9.3	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
IPI00979393	CAST	isoform 3 of Calpastatin	100.0%	11.9	3	4	4	16	1,022,413	1,067,557	981,276	1,179,860	65,171	45,009	51,366	49,464	14.3	9.4	11.7	9.4	1.0	0.6	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.1	1.2	0.02
				EQLPPMSEDFLLDALSEDFSGPQNASSLK	3	99.8%	1																									
				GTVPDDAVEALADSLGK	2	99.8%	1																									
				LAAAISEVVSQTPASTTQAGAPPR	2	99.9%	1																									
				LAAAISEVVSQTPASTTQAGAPPR	3	99.3%	1																									
IPI00220967	RRBP1	isoform 1 of Ribosome-binding protein 1	100.0%	30.3	32	33	38	1	41,127,823	43,964,040	42,063,335	48,344,417	3,439,968	1,903,256	3,120,939	1,593,590	18.7	9.7	16.6	7.4	1.1	0.5	1.0	0.8	1.2	0.09	-1.0	0.6	1.1	0.1	1.1	0.1
				AAILETAPK	2	89.4%	1																									
				AGIIQDTWHK	3	96.7%	1																									
				AQEQQQQMAELHSK	3	100.0%	2																									
				EHTSHLEAELEK	2	99.9%	1																									
				EQEITAVQAR	2	100.0%	1																									
				EVPMVVVPPVGAK	2	99.4%	1																									
				HLEEIVEK	2	100.0%	2																									
				HPPAPAEPSSDLASK	2	100.0%	1																									
				KLTSDLGR	2	81.1%	1																									
				LKELESQVSGLEK	2	99.9%	1																									
				LKGELESSDQVR	3	99.9%	1																									
				LLATEQEDAAVAK	2	100.0%	2																									
				LQQENSILR	2	98.0%	1																									
				LQSSEAEVR	2	89.3%	1																									
				LREAEETQSTLQAECDQYR	3	98.3%	1																									
				LTAEFEEAQTSACR	2	99.9%	1																									
				NTDVAQSPEAPKQEAPAK	3	91.3%	1																									
				QLLLESQSQLDAAK	2	100.0%	2																									
				QSDELALVR	2	88.6%	1																									
				QVLQLQASHR	2	88.0%	1																									
				SHVEDGDIAGAPASSPEAPPAEQDPVQLK	3	100.0%	1																									
				SIEALLEAGQAR	2	99.9%	1																									
				SILAETEGMLR	2	100.0%	2																									
				SKCEELSGLHGQLQEAR	3	80.4%	1																									
				SVEEEEQVWR	2	100.0%	1																									
				TAGPLESSETEEASQLKER	3	98.7%	1																									
				TLQEQLENGPNTQLAR	2	100.0%	1																									
				TLVSTVGSMVFNEGEAQR	2	100.0%	1																									
				TQLEWTEAILEDEQTQR	3	100.0%	1																									
				VDTTPNQGKK	2	89.4%	1																									
				VEPAVSSVVNSIQVLTSK	2	99.9%	1																									
				VEPAVSSVVNSIQVLTSK	3	100.0%	1																									
				VGAAEEELQK	2	98.3%	1																									
IPI00220970	COLQ	isoform II of Acetylcholinesterase collagenic tail peptide	97.7%	7.4	1	1	1	2	698,618	757,282	648,320	920,700	119,201	134,091	76,679	144,280	38.2	39.6	26.5	35.0	1.1	0.8	-1.1	0.7	1.3	0.3	-1.2	0.5	1.2	0.4	1.4	0.1
IPI01011001	COLQ	47 kDa protein	97.7%	7.4	1	1	1	2	698,618	757,282	648,320	920,700	119,201	134,091	76,679	144,280	38.2	39.6	26.5	35.0	1.1	0.8	-1.1	0.7	1.3	0.3	-1.2	0.5	1.2	0.4	1.4	0.1
				MTGSSFSLAHLLIISGLLCYSAGCLALPSLDQK	3	97.7%	1																									
IPI00220994	H2AFY2	Core histone macro-H2A.2	100.0%	4.6	1	1	1	2	1,008,190	1,023,504	1,051,916	1,222,026	42,809	92,279	65,051	101,203	9.5	20.2	13.8	18.5	1.0	0.9	1.0	0.6	1.2	0.09	1.0	0.8	1.2	0.2	1.2	0.2
IPI00966623	H2AFY	Histone H2A	100.0%	10.3	1	1	1	2	1,008,190	1,023,504	1,051,916	1,222,026	42,809	92,279	65,051	101,203	9.5	20.2	13.8	18.5	1.0	0.9	1.0	0.6	1.2	0.09	1.0	0.8	1.2	0.2	1.2	0.2
				HILLAVANDEELNQLLK	3	99.9%	1																									
IPI00221035	BTF3	isoform 1 of Transcription factor BTF3	100.0%	27.7	3	4	5	2	13,129,907	13,144,474	12,505,818	14,736,800	708,949	692,548	786,014	612,204	12.1	11.8	14.1	9.3	1.0	1	-1.0	0.6	1.1	0.1	-1.1	0.6	1.1	0.1	1.2	0.06
IPI00419473	BTF3	isoform 2 of Transcription factor BTF3	100.0%	35.2	3	4	5	2	13,129,907	13,144,474	12,505,818	14,736,800	708,949	692,548	786,014	612,204	12.1	11.8	14.1	9.3	1.0	1	-1.0	0.6	1.1	0.1	-1.1	0.6	1.1	0.1	1.2	0.06
				LAEALPK	2	85.4%	1																									
				LGVNNISGIEEVNMFTNQGTVIHFNNPK	3	100.0%	1																									
				QLTEMLPSILNQLGADSLTSLR	2	100.0%	2																									
				QLTEMLPSILNQLGADSLTSLR	3	100.0%	1																									
IPI00221088	RPS9	40S ribosomal protein S9	95.0%	4.6	1	1	1	4	813,310	868,623	794,708	889,255	74,275	57,569	94,801	38,657	20.4	14.8	26.7	9.7	1.1	0.6	-1.0	0.9	1.1	0.4	-1.1	0.5	1.0	0.8	1.1	0.4
IPI00847192	RPS9	RPS9 protein (Fragment)	95.0%	8.0	1	1	1	4	813,310	868,623	794,708	889,255	74,275	57,569	94,801	38,657	20.4	14.8	26.7	9.7	1.1	0.6	-1.0	0.9	1.1	0.4	-1.1	0.5	1.0	0.8	1.1	0.4
IPI00879238	RPS9	cDNA FLJ61636, highly similar to 40S ribosomal protein S9	95.0%	6.5	1	1	1	4	813,310	868,623	794,708	889,255	74,275	57,569	94,801	38,657	20.4	14.8	26.7	9.7	1.1	0.6	-1.0	0.9	1.1	0.4	-1.1	0.5	1.0	0.8	1.1	0.4
IPI00925580	RPS9	Uncharacterized protein	95.0%	5.8	1	1	1	4	813,310	868,623	794,708	889,255	74,275	57,569	94,801	38,657	20.4	14.8	26.7	9.7	1.1	0.6	-1.0	0.9	1.1	0.4	-1.1	0.5	1.0	0.8	1.1	0.4
				LFEGNALLR	2	95.0%	1																									
IPI00221090	-	152 kDa protein	95.5%	1.1	1	1	1	4	1,809,278	1,876,268	1,688,068	1,846,083	113,840	104,785	83,726	104,233	14.1	12.5	11.1	12.6	1.0	0.7	-1.1	0.4	1.0	0.8	-1.1	0.2	-1.0	0.8	1.1	0.3
IPI00983249	LOC100505868	zinc finger homeobox protein 2-like	95.5%	0.6	1	1	1	4	1,809,278	1,876,268	1,688,068	1,846,083	113,840	104,785	83,726	104,233	14.1	12.5	11.1	12.6	1.0	0.7	-1.1	0.4	1.0	0.8	-1.1	0.2	-1.0	0.8	1.1	0.3
IPI00985261	LOC100505868	zinc finger homeobox protein 2-like	95.5%	0.6	1	1	1	4	1,809,278	1,876,268	1,688,068	1,846,083	113,840	104,785	83,726	104,233	14.1	12.5	11.1	12.6	1.0	0.7	-1.1	0.4	1.0	0.8	-1.1	0.2	-1.0	0.8	1.1	0.3
IPI00926149	ZFHX2	isoform 1 of Zinc finger homeobox protein 2	95.5%	0.6	1	1	1	4	1,809,278	1,876,268	1,688,068	1,846,083	113,840	104,785	83,726	104,233	14.1	12.5	11.1	12.6	1.0	0.7	-1.1	0.4	1.0	0.8	-1.1	0.2	-1.0	0.8	1.1	0.3
				KPVAGPTSSSNDALK	3	95.5%	1																									
IPI00221091	RPS15A	40S ribosomal protein S15a	99.4%	6.9	1	1	1	1	6,095,110	5,481,070	4,433,170	6,335,520	765,687	653,871	584,967	314,458	28.1	26.7	29.5	11.1	-1.1	0.6	-1.4	0.1	1.0	0.8	-1.2	0.3	1.2	0.3	1.4	0.02
				WQNNLLPSR	2	99.4%	1																									
IPI00397701	-	cDNA FLJ56786, moderately similar to 40S ribosomal protein S16	99.1%	7.5	1	1	1	3	3,571,653	3,308,710	3,672,260	3,956,140	478,378	188,828	288,123	266,171	30.0	12.8	17.5	15.0	-1.1	0.6	1.0	0.9	1.1	0.5	1.1	0.3	1.2	0.08	1.1	0.5
IPI00221092	RPS16	40S ribosomal protein S16	99.1%	7.5	1	1	1	3	3,571,653	3,308,710	3,672,260	3,956,140	478,378	188,828	288,123	266,171	30.0	12.8	17.5	15.0	-1.1	0.6	1.0	0.9	1.1	0.5	1.1	0.3	1.2	0.08	1.1	0.5
IPI00450975	RPS16	RPS16 protein	99.1%	7.2	1	1	1	3	3,571,653	3,308,710	3,672,260	3,956,140	478,378	188,828	288,123	266,171	30.0	12.8	17.5	15.0	-1.1	0.6	1.0	0.9	1.1	0.5	1.1	0.3	1.2	0.08	1.1	0.5
				GPLQSVQVFGR	2	99.1%	1																									
IPI00221093	RPS17	40S ribosomal protein S17	100.0%	52.6	4	6	7	1	29,342,770	31,737,185	31,365,725	34,368,575	2,533,373	1,297,587	2,306,960	1,143,231	19.3	9.1	16.5	7.4	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.9	1.1	0.2	1.1	0.3
				IAGYVTHLMK	2	100.0%	2																									
				IAGYVTHLMK	3	99.4%	1																									
				LLDFGSLSNLQVTQPTVGMNFK	3	100.0%	1																									
				RDNYVPEVSALDQEIIEVDPDTKEMLK	3	97.9%	1																									
				VCEEIAIIPSKK	2	99.0%	1																									
				VCEEIAIIPSKK	3	99.8%	1																									
IPI00221101	SI	Sucrase-isomaltase, intestinal	95.4%	0.7	1	1	1	1	9,585,500	10,595,890	10,943,920	11,428,430	401,161	642,207	958,541	697,035	9.4	13.6	19.6	13.6	1.1	0.2	1.1	0.2	1.2	0.05	1.0	0.8	1.1	0.4	1.0	0.7
				TLTEDEAVNASR	2	95.4%	1																									
IPI00221106	SF3B2	Splicing factor 3B subunit 2	100.0%	15.3	9	9	11	3	18,312,855	18,991,007	18,984,320	22,297,123	1,327,603	987,876	1,487,858	623,891	16.2	11.6	17.5	6.3	1.0	0.7	1.0	0.7	1.2	0.03	-1.0	1	1.2	0.02	1.2	0.07
IPI00477803	SF3B2	Putative uncharacterized protein DKFZp781L0540 (Fragment)	100.0%	17.2	9	9	11	3	18,312,855	18,991,007	18,984,320	22,297,123	1,327,603	987,876	1,487,858	623,891	16.2	11.6	17.5	6.3	1.0	0.7	1.0	0.7	1.2	0.03	-1.0	1	1.2	0.02	1.2	0.07
IPI00978402	SF3B2	Uncharacterized protein	100.0%	15.6	9	9	11	3	18,312,855	18,991,007	18,984,320	22,297,123	1,327,603	987,876	1,487,858	623,891	16.2	11.6	17.5	6.3	1.0	0.7	1.0	0.7	1.2	0.03	-1.0	1	1.2	0.02	1.2	0.07
				AAVLLEQER	2	98.9%	1																									
				KGPAPELQGVEVALAPEELELDPMAMTQK	3	99.9%	1																									
				KPGDLSDELR	2	99.9%	1																									
				LAQQQAALLMQQEER	2	100.0%	1																									
				QLVARPDVVEMHDVTAQDPK	3	100.0%	1																									
				SSLGQSASETEEDTVSVSKK	3	99.8%	1																									
				VGEPVALSEEER	2	100.0%	2																									
				VPPPWLIAMQR	2	99.8%	2																									
				YGPPPSYPNLK	2	98.3%	1																									
IPI00221117	ACYP1	Acylphosphatase-1	99.3%	13.1	1	1	1	1	5,360,260	5,586,450	5,150,800	6,256,240	572,021	372,549	325,750	365,612	23.9	14.9	14.1	13.1	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.4	1.1	0.2	1.2	0.05
				GTVQGQLQGPISK	2	99.3%	1																									
IPI00221142	MAPK14	isoform Mxi2 of Mitogen-activated protein kinase 14	94.2%	8.1	1	1	1	3	91,873	91,797	102,560	120,280	6,414	10,162	7,224	8,927	15.6	24.8	15.8	16.6	-1.0	1	1.1	0.3	1.3	0.03	1.1	0.4	1.3	0.07	1.2	0.2
IPI00221143	MAPK14	isoform Exip of Mitogen-activated protein kinase 14	94.2%	7.8	1	1	1	3	91,873	91,797	102,560	120,280	6,414	10,162	7,224	8,927	15.6	24.8	15.8	16.6	-1.0	1	1.1	0.3	1.3	0.03	1.1	0.4	1.3	0.07	1.2	0.2
IPI00984307	MAPK14	Uncharacterized protein	94.2%	18.1	1	1	1	3	91,873	91,797	102,560	120,280	6,414	10,162	7,224	8,927	15.6	24.8	15.8	16.6	-1.0	1	1.1	0.3	1.3	0.03	1.1	0.4	1.3	0.07	1.2	0.2
				SLEEFNDVYLVTHLMGADLNNIVK	3	94.2%	1																									
IPI00221178	TPD52L2	isoform 2 of Tumor protein D54	100.0%	53.2	6	6	8	3	6,039,016	5,675,533	5,755,123	6,977,222	464,620	381,385	383,445	377,317	17.2	15.0	14.9	12.1	-1.1	0.6	-1.0	0.7	1.2	0.2	1.0	0.9	1.2	0.04	1.2	0.05
IPI00399266	TPD52L2	isoform 3 of Tumor protein D54	100.0%	47.4	6	6	8	3	6,039,016	5,675,533	5,755,123	6,977,222	464,620	381,385	383,445	377,317	17.2	15.0	14.9	12.1	-1.1	0.6	-1.0	0.7	1.2	0.2	1.0	0.9	1.2	0.04	1.2	0.05
IPI00399268	TPD52L2	isoform 4 of Tumor protein D54	100.0%	49.5	6	6	8	3	6,039,016	5,675,533	5,755,123	6,977,222	464,620	381,385	383,445	377,317	17.2	15.0	14.9	12.1	-1.1	0.6	-1.0	0.7	1.2	0.2	1.0	0.9	1.2	0.04	1.2	0.05
				GLLSDSMTDVPVDTGVAAR	2	100.0%	2																									
				LGLSTLGELK	2	100.0%	2																									
				TPAVEGLTEAEEEELRAELTK	3	97.6%	1																									
				TPAVEGLTEAEEEELRAELTKVEEEIVTLR	3	100.0%	1																									
				TQETLSQAGQK	2	100.0%	1																									
				VVGDRENGSDNLPSSAGSGDKPLSDPAPF	3	100.0%	1																									
IPI00221222	SUB1	Activated RNA polymerase II transcriptional coactivator p15	100.0%	31.5	6	6	9	1	27,783,955	26,340,800	27,858,150	30,689,495	2,076,846	589,384	1,222,610	951,460	16.7	5.0	9.8	6.9	-1.1	0.5	1.0	1	1.1	0.2	1.1	0.3	1.2	0.005	1.1	0.1

				DDNMFQIGK	2	100.0%	2																									
				EQISDIDDAVR	2	100.0%	2																									
				GISLNPEQWSQLK	2	100.0%	2																									
				GISLNPEQWSQLKEQISDIDDAVR	3	100.0%	1																									
				KGISLNPEQWSQLK	2	87.4%	1																									
				VLIDIR	2	81.7%	1																									
IPI00221224	ANPEP	Aminopeptidase N	96.4%	1.8	1	1	1	2	2,096,455	2,092,465	2,197,345	2,352,575	246,191	111,718	170,459	102,051	26.3	11.9	17.4	9.7	-1.0	1	1.0	0.7	1.1	0.4	1.1	0.6	1.1	0.1	1.1	0.5
IPI01010673	ANPEP	cDNA FLJ51269, highly similar to Aminopeptidase N	96.4%	3.5	1	1	1	2	2,096,455	2,092,465	2,197,345	2,352,575	246,191	111,718	170,459	102,051	26.3	11.9	17.4	9.7	-1.0	1	1.0	0.7	1.1	0.4	1.1	0.6	1.1	0.1	1.1	0.5
				VPVTLALNNTLFLIEER	3	82.1%	1																									
IPI00221232	GNG12	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	99.6%	37.5	2	2	2	1	6,657,660	6,314,640	7,015,280	6,942,470	534,303	338,692	626,355	156,331	18.0	12.0	20.0	5.0	-1.1	0.6	1.1	0.7	1.0	0.6	1.1	0.4	1.1	0.1	-1.0	0.9
				SDPLLIGIPTSENPFK	2	99.6%	1																									
				TASTNNIAQAR	2	97.3%	1																									
IPI00221234	ALDH7A1	isoform 1 of Alpha-aminoadipic semialdehyde dehydrogenase	100.0%	24.1	9	9	11	2	23,012,951	24,083,618	22,441,915	27,046,509	2,504,487	1,342,919	1,894,258	774,994	24.3	12.5	18.9	6.4	1.0	0.7	-1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.09	1.2	0.05
IPI00936002	ALDH7A1	isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase	100.0%	25.4	9	9	11	2	23,012,951	24,083,618	22,441,915	27,046,509	2,504,487	1,342,919	1,894,258	774,994	24.3	12.5	18.9	6.4	1.0	0.7	-1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.09	1.2	0.05
				EGGTVVYGGK	2	89.1%	1																									
				ELGLREENEGVYNGSWGGR	3	100.0%	1																									
				GAPTTSLISVAVTK	2	100.0%	2																									
				GEVITTYCPANNEPIAR	2	100.0%	1																									
				IQVLGSLVSLEMGK	2	100.0%	1																									
				QAVSMFLGAVEEAKK	2	86.5%	1																									
				QGLSSSIFTK	2	99.9%	1																									
				VGNPWDPNVLYGPLHTK	3	97.0%	1																									
				VNLLSFTGSTQVGK	2	100.0%	2																									
IPI00221300	EIF2B1	Translation initiation factor eIF-2B subunit alpha	96.3%	4.6	1	1	1	5	1,536,290	1,470,512	1,505,844	1,648,614	101,630	46,843	93,241	51,128	14.8	7.1	13.9	6.9	-1.0	0.6	-1.0	0.8	1.1	0.4	1.0	0.7	1.1	0.03	1.1	0.2
IPI00910969	EIF2B1	cDNA FLJ60506, highly similar to Translation initiation factor eIF-2B subunit alpha	96.3%	6.3	1	1	1	5	1,536,290	1,470,512	1,505,844	1,648,614	101,630	46,843	93,241	51,128	14.8	7.1	13.9	6.9	-1.0	0.6	-1.0	0.8	1.1	0.4	1.0	0.7	1.1	0.03	1.1	0.2
IPI01013010	EIF2B1	22 kDa protein	96.3%	6.9	1	1	1	5	1,536,290	1,470,512	1,505,844	1,648,614	101,630	46,843	93,241	51,128	14.8	7.1	13.9	6.9	-1.0	0.6	-1.0	0.8	1.1	0.4	1.0	0.7	1.1	0.03	1.1	0.2
IPI01014305	EIF2B1	Protein	96.3%	9.2	1	1	1	5	1,536,290	1,470,512	1,505,844	1,648,614	101,630	46,843	93,241	51,128	14.8	7.1	13.9	6.9	-1.0	0.6	-1.0	0.8	1.1	0.4	1.0	0.7	1.1	0.03	1.1	0.2
IPI01015264	EIF2B1	34 kDa protein	96.3%	4.6	1	1	1	5	1,536,290	1,470,512	1,505,844	1,648,614	101,630	46,843	93,241	51,128	14.8	7.1	13.9	6.9	-1.0	0.6	-1.0	0.8	1.1	0.4	1.0	0.7	1.1	0.03	1.1	0.2
				FISLASLEYSDYSK	2	96.3%	1																									
IPI00221325	RANBP2	E3 SUMO-protein ligase RanBP2	100.0%	2.5	6	6	6	1	36,775,688	41,036,602	36,029,328	43,185,837	3,944,073	1,304,295	3,019,845	727,839	24.0	7.1	18.7	3.8	1.1	0.4	-1.0	0.9	1.2	0.2	-1.1	0.2	1.1	0.2	1.2	0.08
				AWMWLASDFSDGDAK	2	100.0%	1																									
				EQLLDCEGEDGWNK	3	99.4%	1																									
				FGHVDQENSPSFMFQGSSNTEFK	3	99.9%	1																									
				FGNTEQGFK	2	83.4%	1																									
				FVFGSESVK	2	96.6%	1																									
				IAVAVLEETTR	2	97.8%	1																									
IPI00221332	DNM3	isoform 1 of Dynamin-3	100.0%	3.3	2	2	2	6	578,294	585,981	577,931	671,669	36,268	21,419	67,836	19,402	14.0	8.2	26.3	6.5	1.0	0.9	-1.0	1	1.2	0.05	-1.0	0.9	1.1	0.02	1.2	0.2
IPI00480085	DNM3	isoform 2 of Dynamin-3	100.0%	3.4	2	2	2	6	578,294	585,981	577,931	671,669	36,268	21,419	67,836	19,402	14.0	8.2	26.3	6.5	1.0	0.9	-1.0	1	1.2	0.05	-1.0	0.9	1.1	0.02	1.2	0.2
IPI00641436	DNM3	Uncharacterized protein	100.0%	3.3	2	2	2	6	578,294	585,981	577,931	671,669	36,268	21,419	67,836	19,402	14.0	8.2	26.3	6.5	1.0	0.9	-1.0	1	1.2	0.05	-1.0	0.9	1.1	0.02	1.2	0.2
IPI00895844	DNM3	isoform 4 of Dynamin-3	100.0%	3.3	2	2	2	6	578,294	585,981	577,931	671,669	36,268	21,419	67,836	19,402	14.0	8.2	26.3	6.5	1.0	0.9	-1.0	1	1.2	0.05	-1.0	0.9	1.1	0.02	1.2	0.2
IPI00914615	DNM3	Dynamin 3, isoform CRA_d	100.0%	5.2	2	2	2	6	578,294	585,981	577,931	671,669	36,268	21,419	67,836	19,402	14.0	8.2	26.3	6.5	1.0	0.9	-1.0	1	1.2	0.05	-1.0	0.9	1.1	0.02	1.2	0.2
IPI00977141	DNM3	isoform 3 of Dynamin-3	100.0%	3.4	2	2	2	6	578,294	585,981	577,931	671,669	36,268	21,419	67,836	19,402	14.0	8.2	26.3	6.5	1.0	0.9	-1.0	1	1.2	0.05	-1.0	0.9	1.1	0.02	1.2	0.2
				SSVLENFVGR	2	99.9%	1																									
				VYSPHVLNLTLIDLPGITK	3	100.0%	1																									
IPI00428056	-	BBF2H7/FUS protein (Fragment)	100.0%	15.9	2	2	2	6	1,945,966	1,819,784	2,005,364	2,210,493	144,582	122,388	90,149	125,578	16.6	15.0	10.1	12.7	-1.1	0.5	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.06	1.1	0.2
IPI00221354	FUS	isoform Short of RNA-binding protein FUS	100.0%	4.8	2	2	2	6	1,945,966	1,819,784	2,005,364	2,210,493	144,582	122,388	90,149	125,578	16.6	15.0	10.1	12.7	-1.1	0.5	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.06	1.1	0.2
IPI00260715	FUS	Fus-like protein (Fragment)	100.0%	4.7	2	2	2	6	1,945,966	1,819,784	2,005,364	2,210,493	144,582	122,388	90,149	125,578	16.6	15.0	10.1	12.7	-1.1	0.5	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.06	1.1	0.2
IPI00645208	FUS	RNA-binding protein FUS isoform 3	100.0%	4.8	2	2	2	6	1,945,966	1,819,784	2,005,364	2,210,493	144,582	122,388	90,149	125,578	16.6	15.0	10.1	12.7	-1.1	0.5	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.06	1.1	0.2
IPI00854677	FUS	Uncharacterized protein	100.0%	16.6	2	2	2	6	1,945,966	1,819,784	2,005,364	2,210,493	144,582	122,388	90,149	125,578	16.6	15.0	10.1	12.7	-1.1	0.5	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.06	1.1	0.2
IPI00909890	FUS	cDNA FLJ58049, highly similar to RNA-binding protein FUS	100.0%	5.8	2	2	2	6	1,945,966	1,819,784	2,005,364	2,210,493	144,582	122,388	90,149	125,578	16.6	15.0	10.1	12.7	-1.1	0.5	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.06	1.1	0.2
				AAIDWFDGK	2	98.2%	1																									
				LKGEATVSFDDPPSAK	3	100.0%	1																									
IPI00234252	SMARCC1	SWI/SNF complex subunit SMARCC1	99.4%	1.1	1	1	1	1	610,418	651,025	730,415	706,313	72,427	51,024	66,657	58,017	26.5	17.5	20.4	18.4	1.1	0.7	1.2	0.3	1.2	0.3	1.1	0.4	1.1	0.5	-1.0	0.8
				SLVALLVETQMK	2	99.0%	1																									
IPI00234368	ADK	isoform Short of Adenosine kinase	99.1%	4.6	1	1	1	3	606,107	573,149	697,430	610,337	114,045	85,071	60,077	101,337	42.1	33.2	19.3	37.1	-1.1	0.8	1.2	0.5	1.0	1	1.2	0.3	1.1	0.8	-1.1	0.5
IPI00290279	ADK	isoform Long of Adenosine kinase	99.1%	4.4	1	1	1	3	606,107	573,149	697,430	610,337	114,045	85,071	60,077	101,337	42.1	33.2	19.3	37.1	-1.1	0.8	1.2	0.5	1.0	1	1.2	0.3	1.1	0.8	-1.1	0.5
IPI00976200	ADK	adenosine kinase isoform c	99.1%	4.9	1	1	1	3	606,107	573,149	697,430	610,337	114,045	85,071	60,077	101,337	42.1	33.2	19.3	37.1	-1.1	0.8	1.2	0.5	1.0	1	1.2	0.3	1.1	0.8	-1.1	0.5
				IFTLNLSAPFISQFYK	2	99.1%	1																									
IPI00235412	DNM1L	64 kDa protein	100.0%	7.8	3	3	3	1	1,420,139	1,383,083	1,445,651	1,702,694	56,536	49,609	104,705	70,805	8.9	8.0	16.2	9.3	-1.0	0.6	1.0	0.8	1.2	0.01	1.0	0.6	1.2	0.006	1.2	0.08
				IFSPNVVNLTLVDLPGMTK	2	99.4%	1																									
				LDLMDAGTDAMDVLMGR	2	99.4%	1																									
				LGIIGVVNR	2	92.5%	1																									
IPI00239077	HINT1	Histidine triad nucleotide-binding protein 1	100.0%	45.2	5	5	5	1	21,259,138	22,673,038	21,298,494	23,944,582	2,293,817	862,182	1,165,272	1,001,131	24.1	8.5	12.2	9.4	1.1	0.6	1.0	1	1.1	0.3	-1.1	0.4	1.1	0.4	1.1	0.1
				AQVARPGGDTIFGK	2	100.0%	1																									
				CAADLGLNK	2	100.0%	1																									
				CLAFHDISPQAPTHFLVIPK	3	99.3%	1																									
				IIFEDDR	2	97.9%	1																									
				QMHWPPG	2	92.7%	1																									
IPI00239405	SYNE2	isoform 1 of Nesprin-2	100.0%	1.3	5	5	5	2	4,755,270	4,683,188	5,072,565	5,685,353	255,902	138,136	375,855	332,746	12.0	6.6	16.6	13.1	-1.0	0.8	1.1	0.5	1.2	0.06	1.1	0.4	1.2	0.02	1.1	0.3
IPI00239406	SYNE2	isoform 2 of Nesprin-2	100.0%	1.3	5	5	5	2	4,755,270	4,683,188	5,072,565	5,685,353	255,902	138,136	375,855	332,746	12.0	6.6	16.6	13.1	-1.0	0.8	1.1	0.5	1.2	0.06	1.1	0.4	1.2	0.02	1.1	0.3
				AQQLLGQRESPGELISKHK	2	97.6%	1																									
				ELHPFDLHAMQNIILKYKTQFEGMNHR	3	99.8%	1																									
				FIASIEK	1	100.0%	1																									
				HLLSYNRDSDQLTKWLESSQHTLNYWK	3	98.5%	1																									
				KNLEDGINNLK	3	93.6%	1																									
IPI00239415	SYNE2	Polytrophin	100.0%	0.8	3	3	3	1	1,308,936	1,344,200	1,551,803	1,566,650	82,103	75,891	92,715	50,906	14.0	12.6	13.4	7.3	1.0	0.8	1.2	0.09	1.2	0.03	1.2	0.1	1.2	0.04	1.0	0.9
				AQQLLGQRESPGELISKHK	2	97.6%	1																									
				ELHPFDLHAMQNIILKYKTQFEGMNHR	3	99.8%	1																									
				FIASIEK	1	100.0%	1																									
IPI00240059	TMCC3	Transmembrane and coiled-coil domains protein 3	99.3%	5.2	2	2	2	1	13,549,280	13,730,230	13,190,366	14,975,400	680,069	771,410	860,786	1,108,248	11.2	12.6	14.6	16.6	1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
				DTQAQLAEDIEALK	2	96.2%	1																									
				SAHSIAQLQKK	2	82.3%	1																									
IPI00240675	PDCD4	programmed cell death protein 4 isoform 2	100.0%	12.0	3	3	3	3	4,212,767	4,596,077	4,407,273	5,105,880	465,124	411,382	510,851	166,649	24.7	20.0	25.9	7.3	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.8	1.1	0.3	1.2	0.3
IPI00290110	PDCD4	Programmed cell death protein 4	100.0%	11.7	3	3	3	3	4,212,767	4,596,077	4,407,273	5,105,880	465,124	411,382	510,851	166,649	24.7	20.0	25.9	7.3	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.8	1.1	0.3	1.2	0.3
IPI00647084	PDCD4	programmed cell death protein 4 isoform 3	100.0%	12.1	3	3	3	3	4,212,767	4,596,077	4,407,273	5,105,880	465,124	411,382	510,851	166,649	24.7	20.0	25.9	7.3	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.8	1.1	0.3	1.2	0.3
				LLSDLCGTVMSTTDVEK	2	98.4%	1																									
				SGVPVLAVSLALEGK	2	99.7%	1																									
				TLTPIIQEYFEHGDTNEVAEMLR	3	97.3%	1																									
IPI00242956	FCGBP	IgGFc-binding protein	100.0%	7.2	26	26	31	1	46,348,173	49,416,795	46,370,937	53,651,790	3,908,114	1,876,754	2,996,213	1,528,053	18.9	8.5	14.5	6.4	1.1	0.5	1.0	1	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.06
				AGCVAESTAVCR	2	100.0%	2																									
				AIGYATAADCGR	2	100.0%	1																									
				AISGLTIDGHAVGAK	2	100.0%	1																									
				APGWDPLCWDECR	2	100.0%	1																									
				ASQHGSDVVIETDFGLR	3	100.0%	1																									
				CLANGGIHYITLDGR	2	99.0%	1																									
				CPGLQNTIPWYR	2	100.0%	1																									
				EGCVCDAGFVLSGDTCVPVGQCGCLHDGR	3	92.9%	1																									
				GATTSPGVYELSSR	2	100.0%	1																									
				GEVGFVLVDNQR	2	100.0%	2																									
				GNPAVSYVR	2	93.2%	1																									
				LPVSLSEGR	2	95.8%	1																									
				LPVVLANGQIR	2	100.0%	2																									
				LRVPAAYAGSLCGLCGNYNQDPADDLK	3	100.0%	1																									
				NPQGPFATCQAVLSPSEYFR	2	100.0%	1																									
				SPANCPLSCPANSR	2	99.8%	1																									
				SVPGCEGVALVVAQTK	2	100.0%	1																									
				TPDGSLLVR	2	99.9%	1																									
				TVLSPVEPSCEGMQCAAGQR	3	98.8%	1																									
				VAVIVSNDHAGK	2	99.4%	1																									
				VAYDLVYYVR	2	100.0%	1																									
				VNGVLTALPVSVADGR	2	100.0%	2																									
				VTLQPYNVAQLQSSVDLSGSK	3	99.9%	1																									
				VTVNGVDMK	2	100.0%	2																									
				YDLAFVVASQATK	2	100.0%	1																									
				YQKEEFCGLLSSPTGPLSSCHK	3	99.8%	1																									
IPI00244391	XDH	Xanthine dehydrogenase/oxidase	98.3%	3.4	2	2	2	1	5,812,340	6,757,190	5,043,890	7,634,350	984,525	642,343	508,744	433,480	37.9	21.3	22.6	12.7	1.2	0.4	-1.2	0.5	1.3	0.1	-1.3	0.07	1.1	0.3	1.5	0.005
				GFGGPQGMLIAECWMSEVAVTCGMPAEEVRR	3	90.3%	1																									
				LDPTFASATLLFQK	2	97.5%	1																									
IPI00246058	PDCD6IP	Programmed cell death 6-interacting protein	100.0%	16.7	11	14	16	2	35,700,263	35,217,291	35,828,935	39,988,719	1,846,750	1,502,974	1,784,379	1,086,624	11.6	9.5	11.1	6.1	-1.0	0.8	1.0	1	1.1	0.08	1.0	0.8	1.1	0.03	1.1	0.08
IPI00938079	PDCD6IP	programmed cell death 6-interacting protein isoform 2	100.0%	16.6	11	14	16	2	35,700,263	35,217,291	35,828,935	39,988,719	1,846,750	1,502,974	1,784,379	1,086,624	11.6	9.5	11.1	6.1	-1.0	0.8	1.0	1	1.1	0.08	1.0	0.8	1.1	0.03	1.1	0.08
				FLTALAQDGVINEEALSVTELDR	2	100.0%	1																									
				FTDLFEK	2	90.3%	1																									
				FYNELTEILVR	2	100.0%	1																									
				LALASLGYEK	2	99.5%	1																									
				LANQAADYFGDAFK	2	100.0%	2																									
				LLDEEEATDNDLR	2	100.0%	1																									
				MVPVSVQQSLAAYNQR	2	100.0%	1																									
				MVPVSVQQSLAAYNQR	3	86.1%	1																									
				NLATAYDNFVELVANLK	2	100.0%	2																									
				NLATAYDNFVELVANLK	3	100.0%	1																									
				SLLSNLDEVKK	2	86.5%	1																									
				TPSNELYKPLR	2	99.9%	1																									
				TSEVDLAKPLVK	2	99.5%	1																									
				TSEVDLAKPLVK	3	82.1%	1																									
IPI00247295	SYNE1	isoform 4 of Nesprin-1	97.0%	0.2	1	1	1	5	2,052,758	2,098,814	1,892,306	2,248,214	274,788	123,624	192,733	179,884	29.9	13.2	22.8	17.9	1.0	0.9	-1.1	0.6	1.1	0.6	-1.1	0.4	1.1	0.5	1.2	0.2
IPI00386444	SYNE1	isoform 1 of Nesprin-1	97.0%	0.2	1	1	1	5	2,052,758	2,098,814	1,892,306	2,248,214	274,788	123,624	192,733	179,884	29.9	13.2	22.8	17.9	1.0	0.9	-1.1	0.6	1.1	0.6	-1.1	0.4	1.1	0.5	1.2	0.2
IPI00396977	SYNE1	isoform 7 of Nesprin-1	97.0%	0.3	1	1	1	5	2,052,758	2,098,814	1,892,306	2,248,214	274,788	123,624	192,733	179,884	29.9	13.2	22.8	17.9	1.0	0.9	-1.1	0.6	1.1	0.6	-1.1	0.4	1.1	0.5	1.2	0.2
IPI00647370	SYNE1	Uncharacterized protein	97.0%	0.2	1	1	1	5	2,052,758	2,098,814	1,892,306	2,248,214	274,788	123,624	192,733	179,884	29.9	13.2	22.8	17.9	1.0	0.9	-1.1	0.6	1.1	0.6	-1.1	0.4	1.1	0.5	1.2	0.2
IPI00748856	SYNE1	Uncharacterized protein	97.0%	0.2	1	1	1	5	2,052,758	2,098,814	1,892,306	2,248,214	274,788	123,624	192,733	179,884	29.9	13.2	22.8	17.9	1.0	0.9	-1.1	0.6	1.1	0.6	-1.1	0.4	1.1	0.5	1.2	0.2
				NLETPPDLQFIEADLMQK	2	88.7%	1																									
IPI00247583	RPL21	60S ribosomal protein L21	98.9%	11.3	1	1	1	2	1,294,995	1,236,010	1,295,060	1,379,440	177,798	64,513	133,520	87,739	30.7	11.7	23.1	14.2	-1.0	0.8	1.0	1	1.1	0.7	1.0	0.7	1.1	0.2	1.1	0.6
IPI00845507	RPL21	Similar to 60S ribosomal protein L21	98.9%	11.3	1	1	1	2	1,294,995	1,236,010	1,295,060	1,379,440	177,798	64,513	133,520	87,739	30.7	11.7	23.1	14.2	-1.0	0.8	1.0	1	1.1	0.7	1.0	0.7	1.1	0.2	1.1	0.6
				TNGKEPELLEPIPYEFMA	2	98.9%	1																									
IPI00247871	TCERG1	isoform 1 of Transcription elongation regulator 1	99.9%	2.6	2	2	2	2	8,400,805	8,962,535	8,765,355	9,545,970	693,080	250,950	625,601	532,345	18.5	6.3	16.0	12.5	1.1	0.5	1.0	0.7	1.1	0.2	-1.0	0.8	1.1	0.4	1.1	0.4
IPI00744062	TCERG1	isoform 2 of Transcription elongation regulator 1	99.9%	2.6	2	2	2	2	8,400,805	8,962,535	8,765,355	9,545,970	693,080	250,950	625,601	532,345	18.5	6.3	16.0	12.5	1.1	0.5	1.0	0.7	1.1	0.2	-1.0	0.8	1.1	0.4	1.1	0.4
				EALFNEFVAAAR	2	99.7%	1																									
				QLLDETSAITLTSTWK	2	98.4%	1																									

IPI00249080	ASMTL	isoform 2 of N-acetylserotonin O-methyltransferase-like protein	100.0%	3.5	1	1	1	5	957,422	1,017,512	1,038,870	1,185,524	97,320	68,019	84,915	21,003	22.7	15.0	18.3	4.0	1.1	0.6	1.1	0.5	1.2	0.08	1.0	0.8	1.2	0.07	1.1	0.2
IPI00479385	ASMTL	isoform 1 of N-acetylserotonin O-methyltransferase-like protein	100.0%	3.4	1	1	1	5	957,422	1,017,512	1,038,870	1,185,524	97,320	68,019	84,915	21,003	22.7	15.0	18.3	4.0	1.1	0.6	1.1	0.5	1.2	0.08	1.0	0.8	1.2	0.07	1.1	0.2
IPI00909010	ASMTL	cDNA FLJ59356, highly similar to N-acetylserotonin O-methyltransferase-like protei	100.0%	3.9	1	1	1	5	957,422	1,017,512	1,038,870	1,185,524	97,320	68,019	84,915	21,003	22.7	15.0	18.3	4.0	1.1	0.6	1.1	0.5	1.2	0.08	1.0	0.8	1.2	0.07	1.1	0.2
IPI00956483	ASMTL	N-acetylserotonin O-methyltransferase-like protein isoform 2	100.0%	3.7	1	1	1	5	957,422	1,017,512	1,038,870	1,185,524	97,320	68,019	84,915	21,003	22.7	15.0	18.3	4.0	1.1	0.6	1.1	0.5	1.2	0.08	1.0	0.8	1.2	0.07	1.1	0.2
IPI00888266	LOC100133578	n-acetylserotonin O-methyltransferase-like protein-like	100.0%	5.8	1	1	1	5	957,422	1,017,512	1,038,870	1,185,524	97,320	68,019	84,915	21,003	22.7	15.0	18.3	4.0	1.1	0.6	1.1	0.5	1.2	0.08	1.0	0.8	1.2	0.07	1.1	0.2
				FSELSEELLWEYVHSGEPMDK	3	99.5%	1																									
IPI00250153	YBX2	Y-box-binding protein 2	100.0%	4.7	1	1	2	2	319,882	344,752	321,805	333,941	25,013	19,201	27,160	12,036	17.5	12.5	18.9	8.1	1.1	0.5	1.0	1	1.0	0.6	-1.1	0.5	-1.0	0.6	1.0	0.7
IPI00556023	YBX2	Germ cell specific Y-box binding protein variant (Fragment)	100.0%	6.3	1	1	2	2	319,882	344,752	321,805	333,941	25,013	19,201	27,160	12,036	17.5	12.5	18.9	8.1	1.1	0.5	1.0	1	1.0	0.6	-1.1	0.5	-1.0	0.6	1.0	0.7
				SVGDGETVEFDVVEGEK	2	100.0%	2																									
IPI00251161	KIAA1109	isoform 6 of Uncharacterized protein KIAA1109	98.3%	0.4	1	1	1	5	562,284	545,600	567,628	563,230	60,794	31,242	37,572	24,809	24.2	12.8	14.8	9.9	-1.0	0.8	1.0	0.9	1.0	1	1.0	0.7	1.0	0.7	-1.0	0.9
IPI00398012	KIAA1109	isoform 2 of Uncharacterized protein KIAA1109	98.3%	0.5	1	1	1	5	562,284	545,600	567,628	563,230	60,794	31,242	37,572	24,809	24.2	12.8	14.8	9.9	-1.0	0.8	1.0	0.9	1.0	1	1.0	0.7	1.0	0.7	-1.0	0.9
IPI00852643	KIAA1109	isoform 1 of Uncharacterized protein KIAA1109	98.3%	0.3	1	1	1	5	562,284	545,600	567,628	563,230	60,794	31,242	37,572	24,809	24.2	12.8	14.8	9.9	-1.0	0.8	1.0	0.9	1.0	1	1.0	0.7	1.0	0.7	-1.0	0.9
IPI00853372	KIAA1109	isoform 7 of Uncharacterized protein KIAA1109	98.3%	0.4	1	1	1	5	562,284	545,600	567,628	563,230	60,794	31,242	37,572	24,809	24.2	12.8	14.8	9.9	-1.0	0.8	1.0	0.9	1.0	1	1.0	0.7	1.0	0.7	-1.0	0.9
IPI00885111	KIAA1109	isoform 4 of Uncharacterized protein KIAA1109	98.3%	0.3	1	1	1	5	562,284	545,600	567,628	563,230	60,794	31,242	37,572	24,809	24.2	12.8	14.8	9.9	-1.0	0.8	1.0	0.9	1.0	1	1.0	0.7	1.0	0.7	-1.0	0.9
				QSGAVLYNSFGIMGK	2	93.2%	1																									
IPI00556571	HD1-EIF4EBP3;ANK	isoform 2 of Ankyrin repeat and KH domain-containing protein 1	98.8%	1.9	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00797397	HD1-EIF4EBP3;ANK	isoform 1 of Ankyrin repeat and KH domain-containing protein 1	98.8%	0.5	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00798060	HD1-EIF4EBP3;ANK	Uncharacterized protein	98.8%	0.8	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00815707	HD1-EIF4EBP3;ANK	Uncharacterized protein	98.8%	0.5	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00871927	HD1-EIF4EBP3;ANK	isoform 5 of Ankyrin repeat and KH domain-containing protein 1	98.8%	2.1	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI01013084	HD1-EIF4EBP3;ANK	isoform 4 of Ankyrin repeat and KH domain-containing protein 1	98.8%	0.5	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI01013411	HD1-EIF4EBP3;ANK	ANKHD1-EIF4EBP3 protein	98.8%	0.5	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00251783	ANKRD17	isoform 3 of Ankyrin repeat domain-containing protein 17	98.8%	1.0	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00783186	ANKRD17	isoform 2 of Ankyrin repeat domain-containing protein 17	98.8%	0.5	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00784020	ANKRD17	isoform 1 of Ankyrin repeat domain-containing protein 17	98.8%	0.5	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00868922	ANKRD17	isoform 4 of Ankyrin repeat domain-containing protein 17	98.8%	0.6	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00909867	ANKRD17	cDNA FLJ57343, highly similar to Homo sapiens ankyrin repeat domain 17 (ANKRD	98.8%	0.9	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00953250	ANKRD17	Uncharacterized protein	98.8%	1.0	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00966022	ANKRD17	Uncharacterized protein	98.8%	0.5	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
IPI00976634	ANKRD17	Uncharacterized protein	98.8%	0.6	1	1	1	15	1,153,675	1,445,813	1,311,333	1,481,987	243,363	88,753	62,943	41,379	47.2	13.7	10.7	6.2	1.3	0.3	1.1	0.6	1.3	0.3	-1.1	0.3	1.0	0.7	1.1	0.05
				LEALLEAAGIGK	2	98.8%	1																									
IPI00253279	ADD1	Adducin 1	100.0%	8.6	4	4	5	1	4,227,746	4,751,019	3,986,126	4,537,429	395,862	209,301	225,429	205,797	20.9	9.9	12.7	10.1	1.1	0.3	-1.1	0.6	1.1	0.5	-1.2	0.04	-1.0	0.5	1.1	0.1
				INLQGDIVDR	2	99.9%	1																									
				TAGPQSQVLCGVVMDR	2	99.9%	1																									
				TLASAGGPDNLVLLNPEK	2	100.0%	1																									
				WQIGEQEFEALMR	2	100.0%	2																									
IPI00253281	EPS8L1	isoform 2 of Epidermal growth factor receptor kinase substrate 8-like protein 1	100.0%	12.3	5	5	5	2	2,495,986	2,264,089	2,481,139	2,747,887	322,280	95,837	149,925	180,835	28.9	9.5	13.5	14.7	-1.1	0.5	-1.0	1	1.1	0.5	1.1	0.3	1.2	0.05	1.1	0.3
IPI00759466	EPS8L1	cDNA FLJ60362, highly similar to Epidermal growth factor receptor kinase substrate	100.0%	9.1	5	5	5	2	2,495,986	2,264,089	2,481,139	2,747,887	322,280	95,837	149,925	180,835	28.9	9.5	13.5	14.7	-1.1	0.5	-1.0	1	1.1	0.5	1.1	0.3	1.2	0.05	1.1	0.3
				APEPQLSPGSDASEVR	2	99.5%	1																									
				DLEPESEPQLESETAGK	2	100.0%	1																									
				EVDILNHVFDDVESFVSR	3	99.9%	1																									
				GPDLAVLQAER	2	99.8%	1																									
				WVLCNYDFQAR	2	99.9%	1																									
IPI00256684	AP2A1	isoform B of AP-2 complex subunit alpha-1	99.9%	4.6	3	3	3	2	10,390,273	9,485,233	9,931,102	11,220,403	665,592	445,191	395,902	285,281	14.3	10.5	8.9	5.7	-1.1	0.3	-1.0	0.6	1.1	0.3	1.0	0.5	1.2	0.01	1.1	0.03
IPI00304577	AP2A1	isoform A of AP-2 complex subunit alpha-1	99.9%	4.5	3	3	3	2	10,390,273	9,485,233	9,931,102	11,220,403	665,592	445,191	395,902	285,281	14.3	10.5	8.9	5.7	-1.1	0.3	-1.0	0.6	1.1	0.3	1.0	0.5	1.2	0.01	1.1	0.03
				FFQPTEMAAQDFFQR	2	98.0%	1																									
				LVECLETVLNK	2	94.1%	1																									
				VGGYILGEFGNLIAGDPR	2	100.0%	1																									
IPI00257508	DPYSL2	Dihydropyrimidinase-related protein 2	100.0%	38.6	13	14	20	1	15,613,953	16,440,508	16,358,514	18,019,547	1,355,835	615,167	1,398,002	508,307	19.4	8.4	19.1	6.3	1.1	0.6	1.0	0.7	1.2	0.2	-1.0	1	1.1	0.08	1.1	0.3
				AITIANQTNCPLYITK	2	100.0%	1																									
				DIGAIAQVHAENGDIIAEEQQR	3	100.0%	2																									
				DNFTLIPEGTNGTEER	2	88.3%	1																									
				FQLTDCQIYEVLSVIR	2	96.3%	1																									
				FQLTDCQIYEVLSVIR	3	97.5%	1																									
				FQMPDQGMTSADDFFQGTK	2	100.0%	2																									
				GIQEEMEALVK	2	100.0%	2																									
				GLYDGPVCEVSVTPK	2	100.0%	2																									
				ILDLGITGPEGHVLSRPEEVEAEAVNR	3	100.0%	1																									
				IVNDDQSFYADIYMEDGLIK	2	100.0%	1																									
				MDENQFVAVTSTNAAK	2	98.9%	1																									
				NLHQSGFSLSGAQIDDNIPR	3	100.0%	1																									
				QIGENLIVPGGVK	2	99.9%	2																									
				SSAEVIAQAR	2	99.4%	2																									
IPI00257882	PEPD	Xaa-Pro dipeptidase	100.0%	4.1	2	2	2	1	25,924,510	25,963,880	23,502,920	29,655,220	2,179,750	1,752,611	2,239,426	2,227,485	18.8	15.1	21.3	16.8	1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.4	1.1	0.2	1.3	0.09
				LPASHATWMGK	3	99.7%	1																									
				TDMELEVLR	2	99.7%	1																									
IPI00288965	ROS1	Proto-oncogene tyrosine-protein kinase ROS	91.3%	0.8	1	1	1	2	441,394	429,250	559,385	479,047	32,743	29,934	81,060	33,412	16.6	15.6	32.4	15.6	-1.0	0.8	1.3	0.2	1.1	0.4	1.3	0.2	1.1	0.3	-1.2	0.4
IPI00647703	ROS1	Tyrosine-protein kinase receptor	91.3%	0.8	1	1	1	2	441,394	429,250	559,385	479,047	32,743	29,934	81,060	33,412	16.6	15.6	32.4	15.6	-1.0	0.8	1.3	0.2	1.1	0.4	1.3	0.2	1.1	0.3	-1.2	0.4
				GSTDQEKIEFLKEAHLMSK	3	91.3%	1																									
IPI00289061	FASTKD1	isoform 2 of FAST kinase domain-containing protein 1	92.8%	1.9	1	1	1	4	664,990	788,520	835,005	717,595	65,339	88,213	120,513	31,432	22.0	25.0	32.3	9.8	1.2	0.3	1.3	0.3	1.1	0.5	1.1	0.8	-1.1	0.5	-1.2	0.4
IPI00300186	FASTKD1	isoform 1 of FAST kinase domain-containing protein 1	92.8%	1.8	1	1	1	4	664,990	788,520	835,005	717,595	65,339	88,213	120,513	31,432	22.0	25.0	32.3	9.8	1.2	0.3	1.3	0.3	1.1	0.5	1.1	0.8	-1.1	0.5	-1.2	0.4
IPI00807371	FASTKD1	Putative uncharacterized protein FLJ21901	92.8%	1.8	1	1	1	4	664,990	788,520	835,005	717,595	65,339	88,213	120,513	31,432	22.0	25.0	32.3	9.8	1.2	0.3	1.3	0.3	1.1	0.5	1.1	0.8	-1.1	0.5	-1.2	0.4
IPI00925009	FASTKD1	Uncharacterized protein	92.8%	5.4	1	1	1	4	664,990	788,520	835,005	717,595	65,339	88,213	120,513	31,432	22.0	25.0	32.3	9.8	1.2	0.3	1.3	0.3	1.1	0.5	1.1	0.8	-1.1	0.5	-1.2	0.4
				DHPQFLTLHNLATNK	2	92.8%	1																									
IPI00289329	EPHB3	Ephrin type-B receptor 3	99.9%	4.9	2	2	2	1	5,684,610	5,539,000	5,706,200	5,828,800	294,376	288,531	493,262	247,295	11.6	11.7	19.3	9.5	-1.0	0.7	1.0	1	1.0	0.7	1.0	0.8	1.1	0.5	1.0	0.8
				ARPPPPPSPPPGLLPLLPPLLLLPLLLLPAGCR	3	98.8%	1																									
				VYIDPFTYEDPNEAVR	2	92.1%	1																									
IPI00289334	FLNB	isoform 1 of Filamin-B	100.0%	29.6	53	58	70	4	56,545,198	58,464,035	55,855,177	64,754,572	4,922,752	2,368,706	3,319,936	1,364,591	19.5	9.1	13.3	4.7	1.0	0.7	-1.0	0.9	1.1	0.2	-1.0	0.5	1.1	0.05	1.2	0.04
IPI00477536	FLNB	filamin-B isoform 3	100.0%	29.7	53	58	70	4	56,545,198	58,464,035	55,855,177	64,754,572	4,922,752	2,368,706	3,319,936	1,364,591	19.5	9.1	13.3	4.7	1.0	0.7	-1.0	0.9	1.1	0.2	-1.0	0.5	1.1	0.05	1.2	0.04
IPI00900293	FLNB	filamin-B isoform 1	100.0%	29.2	53	58	70	4	56,545,198	58,464,035	55,855,177	64,754,572	4,922,752	2,368,706	3,319,936	1,364,591	19.5	9.1	13.3	4.7	1.0	0.7	-1.0	0.9	1.1	0.2	-1.0	0.5	1.1	0.05	1.2	0.04
IPI00943563	FLNB	isoform 2 of Filamin-B	100.0%	29.9	53	58	70	4	56,545,198	58,464,035	55,855,177	64,754,572	4,922,752	2,368,706	3,319,936	1,364,591	19.5	9.1	13.3	4.7	1.0	0.7	-1.0	0.9	1.1	0.2	-1.0	0.5	1.1	0.05	1.2	0.04
				AAGSGELGVTMK	2	100.0%	1																									
				ADIEMPFDPSK	2	97.7%	1																									
				AGLAPLEVR	2	99.9%	1																									
				AGPGTLSVTIEGPSK	2	100.0%	2																									
				ALGALVDSCAPGLCPDWESWDPQKPVDNAR	3	98.9%	1																									
				APSVATVGSICDLNLK	2	100.0%	1																									
				AWGPGLHGGIVGR	2	99.9%	1																									
				CLATGPGIASTVK	2	99.9%	1																									
				DAGEGLLAVQITDQEGKPK	3	100.0%	1																									
				DAGYGGISLAVEGPSK	2	100.0%	2																									
				DGTYAVTYIPDK	2	99.5%	1																									
				DLDIIDNYDYSHTVK	3	99.8%	1																									
				EAGAGGLSIAVEGPSK	2	100.0%	2																									
				EATTDFTVDSR	2	94.6%	1																									
				EATTDFTVDSRPLTQVGGDHIK	3	100.0%	1																									
				FNGSHVVGSPFK	2	97.1%	1																									
				FNGSHVVGSPFK	3	96.8%	1																									
				GAGIGGLGITVEGPSESK	2	100.0%	2																									
				GAGTGGLGLTVEGPCEAK	2	100.0%	1																									
				GLHVVEVTYDDVPIPNSPFK	3	99.8%	1																									
				IFFAGDTIPK	2	98.6%	1																									
				IGNLQTDLSDGLR	2	100.0%	2																									
				IKVFGPGIEGK	3	99.8%	1																									
				IPYLPITNFNQNWQDGK	2	100.0%	2																									
				IPYLPITNFNQNWQDGK	3	100.0%	1																									
				LIALLEVLSQK	2	100.0%	2																									
				LLGWIQNK	2	98.6%	1																									
				LTVMSLQESGLK	2	100.0%	2																									
				LVSPGSANETSSILVESVTR	2	100.0%	2																									
				MDGTYACSYTPVK	2	100.0%	1																									
				NGNHVANSPVSIMVVQSEIGDARRAK	3	99.0%	1																									
				NTVELLVEDKGNQVYR	3	99.9%	1																									
				QKDFLDGVYAFEYYPSTPGR	3	95.3%	1																									
				QMQLENVSVALEFLDRESIK	3	99.2%	1																									
				SGCIVNNLAEFTVDPK	2	100.0%	1																									
				SPFEVQVGPEAGMQK	2	100.0%	2																									
				SPFEVSVDK	2	99.9%	1																									
				TFEMSDFIVDTR	2	100.0%	1																									
				TGEEVGFVVDAK	2	100.0%	1																									
				VAVTEGCQPSR	2	100.0%	1																									
				VDIQTEDLEDGTCK	2	99.0%	1																									
				VEVGKDQEFTVDTR	2	99.5%	1																									
				VEVGKDQEFTVDTR	3	99.8%	1																									
				VLFASQEIPASPFR	2	100.0%	1																									
				VLQSFTVDSSK	2	99.9%	1																									
				VLSEDEEDVDFDIIHNANDTFTVK	3	99.7%	1																									
				VNQPASFAIR	2	91.6%	1																									
				VPVKDVVDPSK	3	89.9%	1																									
				VQAQGPGLK	1	97.7%	1																									
				VTASGPGLSSYGVPASLPVDFAIDAR	2	100.0%	2																									
				VTEAEIVPMGK	2	100.0%	1																									
				VTVLFAGQHISK	2	95.5%	1																									
				VTVLFAGQHISK	3	97.6%	1																									
				VVASGPGLEHGK	2	99.9%	1																									
				YGGELVPHFPAR	2	100.0%	1																									
				YGGELVPHFPAR	3	100.0%	1																									
				YGGPNHIVGSPFK	2	100.0%	2																									
				YMIGVTYGGDDIPLSPYR	2	100.0%	1																									
IPI00289357	ULK1	Serine/threonine-protein kinase ULK1	91.8%	0.7	1	1	1	2	2,837,440	2,815,545	2,319,070	3,053,560	84,714	155,586	196,411	139,169	6.7	12.4	18.9	10.2	-1.0	0.9	-1.2	0.04	1.1	0.2	-1.2	0.08	1.1	0.3	1.3	0.02
IPI01015003	ULK1	32 kDa protein	91.8%	2.4	1	1	1	2	2,837,440	2,815,545	2,319,070	3,053,560	84,714	155,586	196,411	139,169	6.7	12.4	18.9	10.2	-1.0	0.9	-1.2	0.04	1.1	0.2	-1.2	0.08	1.1	0.3	1.3	0.02
				RLNELYK	2	91.8%	1																									
IPI00289499	ATIC	Bifunctional purine biosynthesis protein PURH	100.0%	44.4	18	20	23	2	47,943,965	50,043,545	51,019,828	56,810,445	4,337,746	1,716,024	3,678,130	1,917,337	20.2	7.7	16.1	7.6	1.0	0.7	1.1	0.6	1.2	0.1	1.0	0.8	1.1	0.03	1.1	0.2
IPI00925601	ATIC	Uncharacterized protein	100.0%	44.5	18	20	23	2	47,943,965	50,043,545	51,019,828	56,810,445	4,337,746	1,716,024	3,678,130	1,917,337	20.2	7.7	16.1	7.6	1.0	0.7	1.1	0.6	1.2	0.1	1.0	0.8	1.1	0.03	1.1	0.2
				AEISNAIDQYVTGTIGEDEDLIK	2	100.0%	1																									
				AFTHTAQYDEAISDYFR	3	98.3%	1																									
				ALFEEVPELLTEAEK	2	99.8%	1																									

				ALFEEVPELLTEAEKK	2	86.4%	1																									
				ALFEEVPELLTEAEKK	3	91.4%	1																									
				DVSELTGFPEMLGGR	2	100.0%	2																									
				EVSDGIIAPGYEEEALTILSK	2	100.0%	2																									
				EVSDGIIAPGYEEEALTILSK	3	100.0%	1																									
				HVSPAGAAVGIPLSEDEAK	3	96.9%	1																									
				LDFNLIR	2	97.2%	1																									
				LTEVSISSDAFFPFRDNVDR	3	99.4%	1																									
				MSSFGDFVALSDVCDVPTAK	2	100.0%	1																									
				NGNYCVLQMDQSYKPDENEVR	3	100.0%	1																									
				NGQVIGIGAGQQSR	2	100.0%	2																									
				NLTALGLNLVASGGTAK	2	100.0%	1																									
				TGLVEFAR	2	99.6%	1																									
				TLFGLHLSQK	2	96.9%	1																									
				TLHPAVHAGILAR	3	99.9%	1																									
				VVACNLYPFVK	2	99.9%	1																									
				YTQSNSVCYAK	2	100.0%	1																									
IPI00289601	HDAC2	Histone deacetylase 2	99.8%	5.0	2	2	2	2	2,617,441	2,767,813	2,698,981	2,838,202	273,243	253,304	221,921	52,584	23.3	20.5	18.4	4.1	1.1	0.7	1.0	0.8	1.1	0.5	-1.0	0.8	1.0	0.8	1.1	0.6
IPI00972999	HDAC2	Histone deacetylase	99.8%	6.3	2	2	2	2	2,617,441	2,767,813	2,698,981	2,838,202	273,243	253,304	221,921	52,584	23.3	20.5	18.4	4.1	1.1	0.7	1.0	0.8	1.1	0.5	-1.0	0.8	1.0	0.8	1.1	0.6
				TFNLPLLMLGGGGYTIR	2	99.6%	1																									
				YGEYFPGTGDLR	2	81.5%	1																									
IPI00289608	AP3D1	isoform 2 of AP-3 complex subunit delta-1	90.0%	1.2	1	1	1	6	633,963	614,058	686,483	779,852	59,271	71,283	26,563	30,130	20.9	26.0	8.7	8.6	-1.0	0.8	1.1	0.4	1.2	0.06	1.1	0.4	1.3	0.06	1.1	0.05
IPI00411453	AP3D1	isoform 1 of AP-3 complex subunit delta-1	90.0%	1.1	1	1	1	6	633,963	614,058	686,483	779,852	59,271	71,283	26,563	30,130	20.9	26.0	8.7	8.6	-1.0	0.8	1.1	0.4	1.2	0.06	1.1	0.4	1.3	0.06	1.1	0.05
IPI00411677	AP3D1	isoform 4 of AP-3 complex subunit delta-1	90.0%	1.3	1	1	1	6	633,963	614,058	686,483	779,852	59,271	71,283	26,563	30,130	20.9	26.0	8.7	8.6	-1.0	0.8	1.1	0.4	1.2	0.06	1.1	0.4	1.3	0.06	1.1	0.05
IPI00413686	AP3D1	isoform 3 of AP-3 complex subunit delta-1	90.0%	1.3	1	1	1	6	633,963	614,058	686,483	779,852	59,271	71,283	26,563	30,130	20.9	26.0	8.7	8.6	-1.0	0.8	1.1	0.4	1.2	0.06	1.1	0.4	1.3	0.06	1.1	0.05
IPI00719680	AP3D1	isoform 5 of AP-3 complex subunit delta-1	90.0%	1.1	1	1	1	6	633,963	614,058	686,483	779,852	59,271	71,283	26,563	30,130	20.9	26.0	8.7	8.6	-1.0	0.8	1.1	0.4	1.2	0.06	1.1	0.4	1.3	0.06	1.1	0.05
IPI00981882	AP3D1	Uncharacterized protein	90.0%	1.3	1	1	1	6	633,963	614,058	686,483	779,852	59,271	71,283	26,563	30,130	20.9	26.0	8.7	8.6	-1.0	0.8	1.1	0.4	1.2	0.06	1.1	0.4	1.3	0.06	1.1	0.05
				HRPSEADEEELAR	3	90.1%	1																									
IPI00289746	PAK1	isoform 2 of Serine/threonine-protein kinase PAK 1	100.0%	19.2	8	8	8	3	6,593,510	7,163,030	6,834,643	7,784,773	384,706	352,323	384,593	186,339	13.1	11.0	12.6	5.4	1.1	0.3	1.0	0.7	1.2	0.02	-1.0	0.5	1.1	0.2	1.1	0.06
IPI00656138	PAK1	isoform 1 of Serine/threonine-protein kinase PAK 1	100.0%	19.5	8	8	8	3	6,593,510	7,163,030	6,834,643	7,784,773	384,706	352,323	384,593	186,339	13.1	11.0	12.6	5.4	1.1	0.3	1.0	0.7	1.2	0.02	-1.0	0.5	1.1	0.2	1.1	0.06
IPI00980126	PAK1	cDNA FLJ30666 fis, clone FCBBF1000627, highly similar to Serine/threonine-protei	100.0%	20.3	8	8	8	3	6,593,510	7,163,030	6,834,643	7,784,773	384,706	352,323	384,593	186,339	13.1	11.0	12.6	5.4	1.1	0.3	1.0	0.7	1.2	0.02	-1.0	0.5	1.1	0.2	1.1	0.06
				DAGTLNHGSKPLPPNPEEK	3	85.8%	1																									
				LLQTSNITK	2	90.3%	1																									
				LTDFGFCAQITPEQSK	2	100.0%	1																									
				MSDEEILEK	2	97.2%	1																									
				QMNLQQQPK	2	93.9%	1																									
				SAEDYNSSNALNVK	2	99.9%	1																									
				SDNILLGMDGSVK	2	99.8%	1																									
				STMVGTPYWMAPEVVTR	2	97.1%	1																									
IPI00289758	CAPN2	Calpain-2 catalytic subunit	100.0%	22.7	10	12	13	1	16,572,546	16,347,526	16,945,930	18,237,881	1,199,918	442,826	656,720	860,943	16.2	6.1	8.7	10.6	-1.0	0.9	1.0	0.8	1.1	0.3	1.0	0.5	1.1	0.09	1.1	0.3
				DGELLFVHSAEGSEFWSALLEK	3	100.0%	1																									
				FADDQLIIDFDNFVR	2	100.0%	1																									
				FADDQLIIDFDNFVR	3	95.2%	1																									
				GHAYSVTGAEEVESNGSLQK	3	82.0%	1																									
				LEICNLTPDTLTSDTYKK	3	99.9%	1																									
				LFAQLAGEDAEISAFELQTILR	2	100.0%	1																									
				LFAQLAGEDAEISAFELQTILR	3	100.0%	1																									
				NPWGEVEWTGR	2	100.0%	1																									
				NYPNTFWMNPQYLIK	2	100.0%	2																									
				RPTEICADPQFIIGGATR	3	86.0%	1																									
				SDTFINLR	2	89.4%	1																									
				YLNQDYEALR	2	99.8%	1																									
IPI00289802	CSMD2	isoform 1 of CUB and sushi domain-containing protein 2	91.4%	0.4	1	1	1	2	4,830,245	4,719,065	4,743,195	5,192,465	539,765	362,644	539,774	115,472	25.0	17.2	25.5	5.0	-1.0	0.9	-1.0	0.9	1.1	0.5	1.0	1	1.1	0.3	1.1	0.5
IPI00394770	CSMD2	CSMD2 protein	91.4%	0.4	1	1	1	2	4,830,245	4,719,065	4,743,195	5,192,465	539,765	362,644	539,774	115,472	25.0	17.2	25.5	5.0	-1.0	0.9	-1.0	0.9	1.1	0.5	1.0	1	1.1	0.3	1.1	0.5
				IISCGELPIPPNGHR	3	91.4%	1																									
IPI00289862	SCRN1	Secernin-1	100.0%	7.0	2	3	3	3	12,940,650	13,031,770	11,831,091	14,303,795	765,789	627,190	812,455	590,464	13.2	10.8	15.4	9.2	1.0	0.9	-1.1	0.3	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.04
IPI00917645	SCRN1	secernin-1 isoform b	100.0%	6.7	2	3	3	3	12,940,650	13,031,770	11,831,091	14,303,795	765,789	627,190	812,455	590,464	13.2	10.8	15.4	9.2	1.0	0.9	-1.1	0.3	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.04
IPI00917523	SCRN1	Uncharacterized protein	100.0%	11.8	2	3	3	3	12,940,650	13,031,770	11,831,091	14,303,795	765,789	627,190	812,455	590,464	13.2	10.8	15.4	9.2	1.0	0.9	-1.1	0.3	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.04
				EPAAEIEALLGMDLVR	2	99.7%	1																									
				EPAAEIEALLGMDLVR	3	100.0%	1																									
				VECTYISIDQVPR	2	95.8%	1																									
IPI00289876	STX7	isoform 1 of Syntaxin-7	100.0%	5.4	1	1	2	2	2,979,825	3,270,335	3,186,350	3,624,375	336,205	196,911	230,132	115,384	25.2	13.5	16.2	7.1	1.1	0.5	1.1	0.6	1.2	0.1	-1.0	0.8	1.1	0.2	1.1	0.1
IPI00552913	STX7	isoform 2 of Syntaxin-7	100.0%	5.9	1	1	2	2	2,979,825	3,270,335	3,186,350	3,624,375	336,205	196,911	230,132	115,384	25.2	13.5	16.2	7.1	1.1	0.5	1.1	0.6	1.2	0.1	-1.0	0.8	1.1	0.2	1.1	0.1
				LVAEFTTSLTNFQK	2	99.9%	2																									
IPI00290085	CDH2	Cadherin-2	99.0%	3.5	1	1	1	2	2,913,540	2,698,565	2,997,730	2,522,150	122,220	190,065	106,598	102,280	9.4	15.8	8.0	9.1	-1.1	0.4	1.0	0.6	-1.2	0.04	1.1	0.2	-1.1	0.4	-1.2	0.01
IPI00658202	CDH2	cDNA FLJ53252, highly similar to Cadherin-2	99.0%	3.7	1	1	1	2	2,913,540	2,698,565	2,997,730	2,522,150	122,220	190,065	106,598	102,280	9.4	15.8	8.0	9.1	-1.1	0.4	1.0	0.6	-1.2	0.04	1.1	0.2	-1.1	0.4	-1.2	0.01
				IVSQAPSTPSPNMFTINNETGDIITVAAGLDR	3	99.0%	1																									
IPI00290089	CDH17	Cadherin-17	100.0%	22.4	11	11	11	1	81,266,266	101,512,621	80,057,745	102,970,471	9,918,300	6,981,116	8,144,295	3,846,823	27.3	15.4	22.8	8.4	1.2	0.1	-1.0	0.9	1.3	0.09	-1.3	0.08	1.0	0.9	1.3	0.03
				AENPEPLVFGVK	2	99.9%	1																									
				DEYGKPLSYPLEIHVK	3	99.3%	1																									
				DINDNRPTFLQSK	2	99.9%	1																									
				FPFSIDQEGDIYVTQPLDREEK	3	100.0%	1																									
				KPLDFETAAVSNIVFK	2	100.0%	1																									
				LGNSIGTLTAHDRDEENTANSFLNYR	3	100.0%	1																									
				LGVDTDPHTNTGYVIIK	3	94.9%	1																									
				TGAISLTR	2	95.4%	1																									
				TLCFVQINVIDINDQIPIFEK	2	99.2%	1																									
				VKDINDNPPTCPSPVTVFEVQENER	3	100.0%	1																									
				VSEDVAIGTK	2	99.9%	1																									
IPI00290337	EPS8	Epidermal growth factor receptor kinase substrate 8	96.8%	4.9	2	2	2	2	2,849,957	3,119,438	2,420,242	3,347,790	362,226	135,728	283,276	275,615	28.4	9.7	26.2	18.4	1.1	0.5	-1.2	0.4	1.2	0.3	-1.3	0.06	1.1	0.5	1.4	0.05
IPI00794000	EPS8	cDNA, FLJ79138, highly similar to Epidermal growth factor receptor kinase substrate	96.8%	7.1	2	2	2	2	2,849,957	3,119,438	2,420,242	3,347,790	362,226	135,728	283,276	275,615	28.4	9.7	26.2	18.4	1.1	0.5	-1.2	0.4	1.2	0.3	-1.3	0.06	1.1	0.5	1.4	0.05
				KSQMEEVQDELIHR	2	90.1%	1																									
				NASGDSGFVPNNILDIVRPPESGLGR	3	80.8%	1																									
IPI00290350	PCDH19	isoform 2 of Protocadherin-19	97.0%	2.5	1	1	1	3	394,966	398,976	361,344	401,280	42,711	39,905	32,499	52,563	24.2	22.4	20.1	29.3	1.0	0.9	-1.1	0.5	1.0	0.9	-1.1	0.5	1.0	1	1.1	0.5
IPI00552819	PCDH19	isoform 1 of Protocadherin-19	97.0%	2.4	1	1	1	3	394,966	398,976	361,344	401,280	42,711	39,905	32,499	52,563	24.2	22.4	20.1	29.3	1.0	0.9	-1.1	0.5	1.0	0.9	-1.1	0.5	1.0	1	1.1	0.5
IPI00867653	PCDH19	protocadherin-19 isoform b precursor	97.0%	2.6	1	1	1	3	394,966	398,976	361,344	401,280	42,711	39,905	32,499	52,563	24.2	22.4	20.1	29.3	1.0	0.9	-1.1	0.5	1.0	0.9	-1.1	0.5	1.0	1	1.1	0.5
				MNVVSCSSLTSSLNYFDYHQQTLPLGCR	3	97.0%	1																									
IPI00290416	OLA1	isoform 1 of Obg-like ATPase 1	100.0%	13.6	4	4	5	2	4,690,674	5,089,561	4,357,843	5,474,377	620,504	285,042	357,090	390,105	29.6	12.5	18.3	15.9	1.1	0.6	-1.1	0.7	1.2	0.3	-1.2	0.1	1.1	0.4	1.3	0.07
IPI00916847	OLA1	47 kDa protein	100.0%	13.0	4	4	5	2	4,690,674	5,089,561	4,357,843	5,474,377	620,504	285,042	357,090	390,105	29.6	12.5	18.3	15.9	1.1	0.6	-1.1	0.7	1.2	0.3	-1.2	0.1	1.1	0.4	1.3	0.07
				FYHDWNDKEIEVLNK	3	96.4%	1																									
				IGIVGLPNVGK	2	99.9%	1																									
				IPAFLNVVDIAGLVK	2	100.0%	2																									
				YLEANMTQSALPK	2	98.4%	1																									
IPI00290452	TMBIM1	Transmembrane BAX inhibitor motif-containing protein 1	98.9%	4.5	1	1	1	10	155,721	215,718	148,103	181,346	18,235	21,952	23,501	9,351	26.2	22.8	35.5	11.5	1.4	0.07	-1.1	0.8	1.2	0.2	-1.5	0.07	-1.2	0.2	1.2	0.2
IPI00909106	TMBIM1	cDNA FLJ53658, highly similar to Transmembrane BAX inhibitor motif-containing pr	98.9%	6.5	1	1	1	10	155,721	215,718	148,103	181,346	18,235	21,952	23,501	9,351	26.2	22.8	35.5	11.5	1.4	0.07	-1.1	0.8	1.2	0.2	-1.5	0.07	-1.2	0.2	1.2	0.2
IPI00924650	TMBIM1	Uncharacterized protein	98.9%	8.2	1	1	1	10	155,721	215,718	148,103	181,346	18,235	21,952	23,501	9,351	26.2	22.8	35.5	11.5	1.4	0.07	-1.1	0.8	1.2	0.2	-1.5	0.07	-1.2	0.2	1.2	0.2
IPI00925342	TMBIM1	Uncharacterized protein	98.9%	15.2	1	1	1	10	155,721	215,718	148,103	181,346	18,235	21,952	23,501	9,351	26.2	22.8	35.5	11.5	1.4	0.07	-1.1	0.8	1.2	0.2	-1.5	0.07	-1.2	0.2	1.2	0.2
IPI00925438	TMBIM1	Uncharacterized protein	98.9%	13.1	1	1	1	10	155,721	215,718	148,103	181,346	18,235	21,952	23,501	9,351	26.2	22.8	35.5	11.5	1.4	0.07	-1.1	0.8	1.2	0.2	-1.5	0.07	-1.2	0.2	1.2	0.2
IPI00925684	TMBIM1	cDNA FLJ53633, highly similar to Transmembrane BAX inhibitor motif-containing pr	98.9%	5.6	1	1	1	10	155,721	215,718	148,103	181,346	18,235	21,952	23,501	9,351	26.2	22.8	35.5	11.5	1.4	0.07	-1.1	0.8	1.2	0.2	-1.5	0.07	-1.2	0.2	1.2	0.2
IPI00925781	TMBIM1	Uncharacterized protein	98.9%	8.4	1	1	1	10	155,721	215,718	148,103	181,346	18,235	21,952	23,501	9,351	26.2	22.8	35.5	11.5	1.4	0.07	-1.1	0.8	1.2	0.2	-1.5	0.07	-1.2	0.2	1.2	0.2
IPI00926037	TMBIM1	15 kDa protein	98.9%	10.0	1	1	1	10	155,721	215,718	148,103	181,346	18,235	21,952	23,501	9,351	26.2	22.8	35.5	11.5	1.4	0.07	-1.1	0.8	1.2	0.2	-1.5	0.07	-1.2	0.2	1.2	0.2
IPI00926582	TMBIM1	Uncharacterized protein	98.9%	13.2	1	1	1	10	155,721	215,718	148,103	181,346	18,235	21,952	23,501	9,351	26.2	22.8	35.5	11.5	1.4	0.07	-1.1	0.8	1.2	0.2	-1.5	0.07	-1.2	0.2	1.2	0.2
IPI00927460	TMBIM1	Uncharacterized protein	98.9%	9.3	1	1	1	10	155,721	215,718	148,103	181,346	18,235	21,952	23,501	9,351	26.2	22.8	35.5	11.5	1.4	0.07	-1.1	0.8	1.2	0.2	-1.5	0.07	-1.2	0.2	1.2	0.2
				AVSDSFGPGEWDDR	2	98.9%	1																									
IPI00290459	DCLRE1C	isoform 1 of Protein artemis	95.0%	3.2	1	1	1	6	399,942	358,769	360,114	328,043	36,572	50,596	55,600	52,522	20.5	31.5	34.5	35.8	-1.1	0.5	-1.1	0.6	-1.2	0.3	1.0	1	-1.1	0.7	-1.1	0.7
IPI00290918	DCLRE1C	isoform 4 of Protein artemis	95.0%	5.1	1	1	1	6	399,942	358,769	360,114	328,043	36,572	50,596	55,600	52,522	20.5	31.5	34.5	35.8	-1.1	0.5	-1.1	0.6	-1.2	0.3	1.0	1	-1.1	0.7	-1.1	0.7
IPI00396624	DCLRE1C	isoform 3 of Protein artemis	95.0%	3.8	1	1	1	6	399,942	358,769	360,114	328,043	36,572	50,596	55,600	52,522	20.5	31.5	34.5	35.8	-1.1	0.5	-1.1	0.6	-1.2	0.3	1.0	1	-1.1	0.7	-1.1	0.7
IPI00607742	DCLRE1C	isoform 2 of Protein artemis	95.0%	3.9	1	1	1	6	399,942	358,769	360,114	328,043	36,572	50,596	55,600	52,522	20.5	31.5	34.5	35.8	-1.1	0.5	-1.1	0.6	-1.2	0.3	1.0	1	-1.1	0.7	-1.1	0.7
IPI00645024	DCLRE1C	14 kDa protein	95.0%	18.8	1	1	1	6	399,942	358,769	360,114	328,043	36,572	50,596	55,600	52,522	20.5	31.5	34.5	35.8	-1.1	0.5	-1.1	0.6	-1.2	0.3	1.0	1	-1.1	0.7	-1.1	0.7
IPI00646355	DCLRE1C	10 kDa protein	95.0%	26.2	1	1	1	6	399,942	358,769	360,114	328,043	36,572	50,596	55,600	52,522	20.5	31.5	34.5	35.8	-1.1	0.5	-1.1	0.6	-1.2	0.3	1.0	1	-1.1	0.7	-1.1	0.7
				DIQSVYLDTTFCDPRFYQIPSR	3	95.0%	1																									
IPI00290460	EIF3G	Eukaryotic translation initiation factor 3 subunit G	99.8%	4.4	1	1	1	1	1,188,489	1,143,822	1,045,896	1,374,021	142,576	99,148	114,188	131,246	26.8	19.4	24.4	21.4	-1.0	0.8	-1.1	0.5	1.2	0.4	-1.1	0.5	1.2	0.2	1.3	0.1
				LPGELEPVQATQNK	2	99.8%	1																									
IPI00290461	EIF3J	Eukaryotic translation initiation factor 3 subunit J	99.9%	8.5	2	2	2	3	6,207,969	6,598,467	5,807,168	6,464,129	742,676	614,053	595,945	394,139	26.8	20.8	23.0	13.6	1.1	0.7	-1.1	0.7	1.0	0.8	-1.1	0.4	-1.0	0.9	1.1	0.4
IPI00910728	EIF3J	cDNA FLJ57599, moderately similar to Eukaryotic translation initiation factor 3 subu	99.9%	10.8	2	2	2	3	6,207,969	6,598,467	5,807,168	6,464,129	742,676	614,053	595,945	394,139	26.8	20.8	23.0	13.6	1.1	0.7	-1.1	0.7	1.0	0.8	-1.1	0.4	-1.0	0.9	1.1	0.4
IPI01014572	EIF3J	23 kDa protein	99.9%	10.5	2	2	2	3	6,207,969	6,598,467	5,807,168	6,464,129	742,676	614,053	595,945	394,139	26.8	20.8	23.0	13.6	1.1	0.7	-1.1	0.7	1.0	0.8	-1.1	0.4	-1.0	0.9	1.1	0.4
				ITNSLTVLCSEK	2	100.0%	1																									
				KGVVPGGGLK	2	86.6%	1																									
IPI00290462	CBR3	Carbonyl reductase [NADPH] 3	100.0%	5.8	1	1	2	1	657,474	705,856	725,002	746,900	31,557	43,083	67,154	30,774	10.7	13.7	20.7	9.2	1.1	0.4	1.1	0.4	1.1	0.08	1.0	0.8	1.1	0.5	1.0	0.8
				GQAAVQQLQAEGLSPR	2	100.0%	2																									
IPI00290542	STAM2	isoform 1 of Signal transducing adapter molecule 2	98.3%	3.1	1	1	1	2	1,239,285	1,226,115	1,384,305	1,206,970	161,465	93,906	70,122	158,722	29.1	17.1	11.3	29.4	-1.0	0.9	1.1	0.4	-1.0	0.9	1.1	0.2	-1.0	0.9	-1.1	0.3
IPI00607771	STAM2	isoform 2 of Signal transducing adapter molecule 2	98.3%	4.7	1	1	1	2	1,239,285	1,226,115	1,384,305	1,206,970	161,465	93,906	70,122	158,722	29.1	17.1	11.3	29.4	-1.0	0.9	1.1	0.4	-1.0	0.9	1.1	0.2	-1.0	0.9	-1.1	0.3
				ALYDFEAVEDNELTFK	2	98.3%	1																									
IPI00290566	TCP1	T-complex protein 1 subunit alpha	100.0%	50.4	19	23	30	1	131,851,903	138,629,943	132,482,105	151,758,454	9,036,941	4,123,983	7,958,210	5,310,133	15.3	6.7	13.4	7.8	1.1	0.5	1.0	1	1.2	0.09	-1.0	0.5	1.1	0.09	1.1	0.08
				AFHNEAQVNPER	3	85.5%	1																									
				AFHNEAQVNPERK	3	98.3%	1																									
				DDKHGSYEDAVHSGALND	3	100.0%	1																									
				FATEAAITILR	2	99.9%	1																									
				GANDFMCDEMER	2	100.0%	2																									
				IACLDFSLQK	2	100.0%	2																									
				ILATGANVILTTGGIDDMCLK	2	100.0%	2																									
				LGVQVVITDPEKLDQIR	3	100.0%	1																									
				LLEVEHPAAK	2	99.9%	1																									
				LLEVEHPAAK	3	99.9%	1																									
				MLVDDIGDVTITNDGATILK	2	100.0%	2																									
				MLVDDIGDVTITNDGATILK	3	100.0%	1																									
				QAGVFEPTIVK	2	99.8%	2																									
				SLLVIPNTLAVNAAQDSTDLVAK	2	100.0%	1																									
				SLLVIPNTLAVNAAQDSTDLVAK	3	100.0%	1																									
				SQNVMAAASIANIVK	2	100.0%	2																									
				SSLGPVGLDK	2	99.1%	1																									
				SVVPGGGAVEAALSIYLENYATSMGSR	2	100.0%	2																									
				SVVPGGGAVEAALSIYLENYATSMGSR	3	100.0%	1																									
				VLCELADLQDKEVGDGTTSVVIIAAELLK	3	99.9%	1																									
				WIGLDLSNGKPR	2	99.3%	1																									
				YFVEAGAMAVR	2	99.8%	1																									
				YPVNSVNILK	2	99.3%	1																									

IPI00290652	RSF1	isoform 1 of Remodeling and spacing factor 1	96.5%	1.8	1	1	1	4	810,868	869,670	758,190	873,408	119,498	120,964	61,723	58,850	33.0	31.1	18.2	15.1	1.1	0.7	-1.1	0.7	1.1	0.7	-1.1	0.4	1.0	1	1.2	0.2
IPI00514411	RSF1	isoform 2 of Remodeling and spacing factor 1	96.5%	1.8	1	1	1	4	810,868	869,670	758,190	873,408	119,498	120,964	61,723	58,850	33.0	31.1	18.2	15.1	1.1	0.7	-1.1	0.7	1.1	0.7	-1.1	0.4	1.0	1	1.2	0.2
IPI00977965	RSF1	32 kDa protein	96.5%	9.4	1	1	1	4	810,868	869,670	758,190	873,408	119,498	120,964	61,723	58,850	33.0	31.1	18.2	15.1	1.1	0.7	-1.1	0.7	1.1	0.7	-1.1	0.4	1.0	1	1.2	0.2
IPI00982445	RSF1	isoform 3 of Remodeling and spacing factor 1	96.5%	2.2	1	1	1	4	810,868	869,670	758,190	873,408	119,498	120,964	61,723	58,850	33.0	31.1	18.2	15.1	1.1	0.7	-1.1	0.7	1.1	0.7	-1.1	0.4	1.0	1	1.2	0.2
				FDEFDEAIDEAIEDDIKEADGGGVGR	3	96.5%	1																									
IPI00290684	PNKP	Bifunctional polynucleotide phosphatase/kinase	93.4%	5.0	1	1	1	1	1,278,423	1,498,606	1,283,786	1,442,836	322,710	279,001	176,538	209,386	56.4	41.6	30.8	32.5	1.2	0.6	1.0	1	1.1	0.7	-1.2	0.5	-1.0	0.9	1.1	0.6
				LWLESPPGGAPPIFLPSDGQALVLGR	3	93.4%	1																									
IPI00291006	MDH2	Malate dehydrogenase, mitochondrial	100.0%	53.0	14	16	25	1	69,098,066	70,477,167	67,321,780	74,370,927	6,168,653	1,474,468	4,031,632	2,204,559	20.0	4.7	13.4	6.6	1.0	0.8	-1.0	0.8	1.1	0.5	-1.0	0.5	1.1	0.2	1.1	0.2
				ANTFVAELK	2	100.0%	2																									
				EGVVECSFVK	2	100.0%	1																									
				GCDVVVIPAGVPR	2	100.0%	2																									
				GYLGPEQLPDCLK	2	100.0%	2																									
				IFGVTTLDIVR	2	100.0%	2																									
				IQEAGTEVVK	2	100.0%	2																									
				LTLYDIAHTPGVAADLSHIETK	3	100.0%	1																									
				MISDAIPELK	2	99.8%	1																									
				NSPLVSR	1	96.4%	1																									
				SQETECTYFSTPLLLGK	2	100.0%	1																									
				TIIPLISQCTPK	2	100.0%	2																									
				VAVLGASGGIGQPLSLLLK	2	100.0%	2																									
				VAVLGASGGIGQPLSLLLK	3	100.0%	1																									
				VDFPQDQLTALTGR	2	100.0%	3																									
				VNVPVIGGHAGK	2	100.0%	1																									
				VNVPVIGGHAGK	3	100.0%	1																									
IPI00291093	POLR2E	DNA-directed RNA polymerases I, II, and III subunit RPABC1	99.6%	8.1	1	1	1	1	1,991,980	2,059,560	2,292,830	2,283,240	70,206	186,129	244,647	171,702	7.9	20.2	23.9	16.8	1.0	0.7	1.2	0.3	1.1	0.2	1.1	0.5	1.1	0.4	-1.0	1
				GYLVTQDELDQTLEEFK	2	99.6%	1																									
IPI00291131	THOC7	THO complex subunit 7 homolog	94.5%	4.9	1	1	1	1	4,486,840	5,230,280	5,616,370	4,918,390	296,506	346,827	557,649	273,854	14.8	14.8	22.2	12.5	1.2	0.1	1.3	0.1	1.1	0.3	1.1	0.6	-1.1	0.5	-1.1	0.3
				TLLVYDMNLR	2	94.5%	1																									
IPI00291175	VCL	isoform 1 of Vinculin	100.0%	22.1	17	17	20	2	33,925,934	34,040,132	33,909,789	38,342,938	2,336,237	1,414,036	2,562,161	732,210	15.4	9.3	16.9	4.3	1.0	1	-1.0	1	1.1	0.1	-1.0	1	1.1	0.03	1.1	0.2
IPI00307162	VCL	isoform 2 of Vinculin	100.0%	20.7	17	17	20	2	33,925,934	34,040,132	33,909,789	38,342,938	2,336,237	1,414,036	2,562,161	732,210	15.4	9.3	16.9	4.3	1.0	1	-1.0	1	1.1	0.1	-1.0	1	1.1	0.03	1.1	0.2
				AGEVINQPMMMAAR	2	99.0%	1																									
				AIPDLTAPVAAVQAAVSNLVR	2	100.0%	2																									
				AVAGNISDPGLQK	2	100.0%	2																									
				GILSGTSDLLLTFDEAEVR	2	100.0%	1																									
				GILSGTSDLLLTFDEAEVRK	3	99.1%	1																									
				ILSTVK	1	89.2%	1																									
				LLAVAATAPPDAPNREEVFDER	3	96.5%	1																									
				MLGQMTDQVADLR	2	99.7%	1																									
				MSAEINEIIR	2	99.9%	1																									
				MTGLVDEAIDTK	2	100.0%	1																									
				NQWIDNVEK	2	90.5%	1																									
				SLLDASEEAIKK	2	99.7%	1																									
				TNISDEESEQATEMLVHNAQNLMQSVK	3	100.0%	1																									
				VAMANIQPQMLVAGATSIAR	2	100.0%	1																									
				VLQLTSWDEDAWASK	2	100.0%	1																									
				VMLVNSMNTVK	2	100.0%	1																									
				WIDNPTVDDR	2	98.7%	2																									
IPI00291200	NUP133	Nuclear pore complex protein Nup133	98.8%	1.0	1	1	1	3	2,223,643	2,020,253	1,515,357	2,202,697	470,044	219,271	151,462	245,947	47.3	24.3	22.4	25.0	-1.1	0.7	-1.5	0.2	-1.0	1	-1.3	0.09	1.1	0.6	1.5	0.04
IPI00514905	NUP133	Uncharacterized protein	98.8%	1.1	1	1	1	3	2,223,643	2,020,253	1,515,357	2,202,697	470,044	219,271	151,462	245,947	47.3	24.3	22.4	25.0	-1.1	0.7	-1.5	0.2	-1.0	1	-1.3	0.09	1.1	0.6	1.5	0.04
IPI01015229	NUP133	cDNA FLJ55448, highly similar to Nuclear pore complex protein Nup133	98.8%	1.1	1	1	1	3	2,223,643	2,020,253	1,515,357	2,202,697	470,044	219,271	151,462	245,947	47.3	24.3	22.4	25.0	-1.1	0.7	-1.5	0.2	-1.0	1	-1.3	0.09	1.1	0.6	1.5	0.04
				DLLQADQLGSLK	2	98.1%	1																									
IPI00291215	PARP14	isoform 6 of Poly [ADP-ribose] polymerase 14	93.1%	0.4	1	1	1	4	1,167,110	1,442,273	1,388,278	1,420,748	89,109	99,981	125,123	78,997	17.1	15.5	20.2	12.4	1.2	0.07	1.2	0.2	1.2	0.07	-1.0	0.7	-1.0	0.9	1.0	0.8
IPI00783216	PARP14	isoform 1 of Poly [ADP-ribose] polymerase 14	93.1%	0.4	1	1	1	4	1,167,110	1,442,273	1,388,278	1,420,748	89,109	99,981	125,123	78,997	17.1	15.5	20.2	12.4	1.2	0.07	1.2	0.2	1.2	0.07	-1.0	0.7	-1.0	0.9	1.0	0.8
IPI00783683	PARP14	isoform 4 of Poly [ADP-ribose] polymerase 14	93.1%	0.4	1	1	1	4	1,167,110	1,442,273	1,388,278	1,420,748	89,109	99,981	125,123	78,997	17.1	15.5	20.2	12.4	1.2	0.07	1.2	0.2	1.2	0.07	-1.0	0.7	-1.0	0.9	1.0	0.8
IPI00783883	PARP14	isoform 3 of Poly [ADP-ribose] polymerase 14	93.1%	0.5	1	1	1	4	1,167,110	1,442,273	1,388,278	1,420,748	89,109	99,981	125,123	78,997	17.1	15.5	20.2	12.4	1.2	0.07	1.2	0.2	1.2	0.07	-1.0	0.7	-1.0	0.9	1.0	0.8
				EVNETYK	2	91.2%	1																									
IPI00291328	NDUFV2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	100.0%	4.8	1	1	1	2	2,517,115	2,593,360	2,438,930	2,694,225	188,910	239,892	222,677	137,617	16.8	20.7	20.4	11.4	1.0	0.8	-1.0	0.8	1.1	0.5	-1.1	0.6	1.0	0.7	1.1	0.4
IPI00646556	NDUFV2	Uncharacterized protein	100.0%	4.8	1	1	1	2	2,517,115	2,593,360	2,438,930	2,694,225	188,910	239,892	222,677	137,617	16.8	20.7	20.4	11.4	1.0	0.8	-1.0	0.8	1.1	0.5	-1.1	0.6	1.0	0.7	1.1	0.4
				QNGWLPISAMNK	2	93.4%	1																									
IPI00291398	TIA1	isoform Long of Nucleolysin TIA-1 isoform p40	100.0%	3.4	1	1	2	3	325,238	333,202	319,688	328,583	17,121	29,093	9,529	9,234	11.8	19.5	6.7	6.3	1.0	0.8	-1.0	0.8	1.0	0.9	-1.0	0.7	-1.0	0.9	1.0	0.5
IPI00926358	TIA1	Uncharacterized protein	100.0%	3.4	1	1	2	3	325,238	333,202	319,688	328,583	17,121	29,093	9,529	9,234	11.8	19.5	6.7	6.3	1.0	0.8	-1.0	0.8	1.0	0.9	-1.0	0.7	-1.0	0.9	1.0	0.5
IPI00926546	TIA1	13 kDa protein	100.0%	11.4	1	1	2	3	325,238	333,202	319,688	328,583	17,121	29,093	9,529	9,234	11.8	19.5	6.7	6.3	1.0	0.8	-1.0	0.8	1.0	0.9	-1.0	0.7	-1.0	0.9	1.0	0.5
				QTFSPFGQIMEIR	2	100.0%	2																									
IPI00291467	SLC25A6	ADP/ATP translocase 3	100.0%	17.1	5	5	7	1	9,139,262	9,222,855	10,001,785	10,743,375	670,426	421,017	567,507	607,642	16.4	10.2	12.7	12.7	1.0	0.9	1.1	0.4	1.2	0.1	1.1	0.3	1.2	0.07	1.1	0.4
				DFLAGGIAAAISK	2	100.0%	2																									
				EQGVLSFWR	2	99.7%	1																									
				LLLQVQHASK	2	95.3%	1																									
				MMMQSGR	2	98.9%	1																									
				YFPTQALNFAFK	2	100.0%	2																									
IPI00291483	AKR1C3	Aldo-keto reductase family 1 member C3	100.0%	32.8	7	8	9	1	21,640,090	22,284,117	21,287,769	24,675,519	1,826,789	1,030,528	1,513,214	983,648	18.9	10.3	15.9	8.9	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.6	1.1	0.1	1.2	0.1
				HIDSAHLYNNEEQVGLAIR	3	100.0%	1																									
				LAIEAGFR	2	97.8%	1																									
				NLHYFNSDSFASHPNYPYSDEY	3	98.5%	1																									
				QLEMILNKPGLK	2	99.1%	1																									
				QLEMILNKPGLK	3	81.8%	1																									
				TPALIALR	2	99.8%	2																									
				VIFDIVDLCTTWEAMEK	2	100.0%	1																									
				WVDPNSPVLLEDPVLCALAK	2	100.0%	1																									
IPI00291510	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	100.0%	21.0	7	7	7	1	19,030,332	19,227,852	18,190,039	20,996,822	1,447,658	686,802	555,946	617,388	17.0	8.0	6.8	6.6	1.0	0.9	-1.0	0.6	1.1	0.2	-1.1	0.3	1.1	0.09	1.2	0.01
				DKYPNLQVIGGNVVTAAQAK	3	97.6%	1																									
				GMGSLDAMDK	2	99.6%	1																									
				HGFCGIPITDTGR	2	99.8%	1																									
				LPIVNEDDELVAIIAR	2	100.0%	1																									
				REDLVVAPAGITLK	2	96.1%	1																									
				RFGVPVIADGGIQNVGHIAK	3	99.9%	1																									
				YEQGFITDPVVLSPK	2	100.0%	1																									
IPI00291544	SQLE	Squalene monooxygenase	99.5%	2.6	1	1	1	3	1,265,003	1,228,217	1,390,033	1,385,097	97,499	76,814	62,629	44,937	17.2	14.0	10.1	7.3	-1.0	0.8	1.1	0.3	1.1	0.3	1.1	0.1	1.1	0.1	-1.0	1
IPI00976058	SQLE	18 kDa protein	99.5%	9.2	1	1	1	3	1,265,003	1,228,217	1,390,033	1,385,097	97,499	76,814	62,629	44,937	17.2	14.0	10.1	7.3	-1.0	0.8	1.1	0.3	1.1	0.3	1.1	0.1	1.1	0.1	-1.0	1
IPI00978981	SQLE	Uncharacterized protein	99.5%	3.1	1	1	1	3	1,265,003	1,228,217	1,390,033	1,385,097	97,499	76,814	62,629	44,937	17.2	14.0	10.1	7.3	-1.0	0.8	1.1	0.3	1.1	0.3	1.1	0.1	1.1	0.1	-1.0	1
				GIPDLYDDAAIFEAK	2	99.5%	1																									
IPI00291802	LMO7	isoform 3 of LIM domain only protein 7	100.0%	14.3	13	13	16	2	7,319,381	7,443,474	7,288,048	8,290,865	896,891	563,230	495,914	299,761	27.4	16.9	15.2	8.1	1.0	0.9	-1.0	1	1.1	0.4	-1.0	0.8	1.1	0.2	1.1	0.1
IPI00985430	LMO7	Uncharacterized protein	100.0%	15.1	13	13	16	2	7,319,381	7,443,474	7,288,048	8,290,865	896,891	563,230	495,914	299,761	27.4	16.9	15.2	8.1	1.0	0.9	-1.0	1	1.1	0.4	-1.0	0.8	1.1	0.2	1.1	0.1
				EPSLATWEATWSEGSK	2	100.0%	1																									
				FSYNDSKEWEEAMAK	3	98.4%	1																									
				GAAMIIESLGLCYHLHCFK	2	90.3%	1																									
				ISINQTPGK	2	99.3%	2																									
				KWEQQLQEEQEQKR	3	92.3%	1																									
				NPSSSVPPPSAGSVK	2	98.4%	1																									
				QQILQEMR	2	97.2%	1																									
				SMSDVSAEDVQNLR	2	100.0%	2																									
				SWASPVYTEADGTFSR	2	100.0%	1																									
				TEEASSGFLPGDR	2	99.7%	1																									
				TPNNVVSTPAPSPDASQLASSLSSQK	3	100.0%	1																									
				TSTTGVATTQSPTPR	2	100.0%	1																									
				WIDATSGIYNSEK	2	100.0%	2																									
IPI00291922	PSMA5	Proteasome subunit alpha type-5	100.0%	46.5	8	9	11	1	41,320,870	43,070,573	41,920,832	45,997,105	3,362,492	1,282,441	2,366,887	949,294	18.2	6.7	12.6	4.6	1.0	0.6	1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.1	1.1	0.1
				AIGSASEGAQSSLQEVYHK	2	100.0%	1																									
				AIGSASEGAQSSLQEVYHK	3	99.6%	1																									
				EELEEVIKDI	2	87.3%	1																									
				GPQLFHMDPSGTFVQCDAR	3	99.9%	1																									
				GVNTFSPEGR	2	99.9%	1																									
				ITSPLMEPSSIEK	2	100.0%	2																									
				LFQVEYAIEAIK	2	100.0%	2																									
				LNATNIELATVQPGQNFHMFTK	3	100.0%	1																									
				SSLIILK	2	94.4%	1																									
IPI00291928	RAB14	Ras-related protein Rab-14	100.0%	14.4	2	2	2	2	15,864,940	15,831,900	14,141,830	17,634,400	1,079,805	607,416	1,261,380	638,874	15.2	8.6	19.9	8.1	-1.0	1	-1.1	0.3	1.1	0.2	-1.1	0.3	1.1	0.08	1.2	0.04
IPI00646415	RAB14	20 kDa protein	100.0%	17.1	2	2	2	2	15,864,940	15,831,900	14,141,830	17,634,400	1,079,805	607,416	1,261,380	638,874	15.2	8.6	19.9	8.1	-1.0	1	-1.1	0.3	1.1	0.2	-1.1	0.3	1.1	0.08	1.2	0.04
				FMADCPHTIGVEFGTR	3	91.5%	1																									
				TGENVEDAFLEAAKK	3	99.9%	1																									
IPI00291930	CLINT1	isoform 1 of Clathrin interactor 1	100.0%	13.4	6	8	10	1	22,191,834	22,680,888	21,949,799	25,488,633	1,672,744	861,405	1,467,221	583,495	16.9	8.5	15.0	5.1	1.0	0.8	-1.0	0.9	1.1	0.1	-1.0	0.7	1.1	0.03	1.2	0.06
				ATFMYEQFPELMNMLWSR	2	100.0%	1																									
				ATFMYEQFPELMNMLWSR	3	100.0%	1																									
				ATNVVMNYSEIESK	2	100.0%	2																									
				HIHITQATETTTTR	2	96.6%	1																									
				HIHITQATETTTTR	3	100.0%	1																									
				IGSTIDDTISK	2	100.0%	1																									
				TIDLGAAAHYTGDK	2	99.9%	1																									
				YVGVSSDSVGGFR	2	100.0%	2																									
IPI00291939	SMC1A	Structural maintenance of chromosomes protein 1A	100.0%	5.1	5	5	5	1	25,144,135	25,538,670	24,186,815	28,284,460	2,034,852	724,120	1,829,745	1,228,663	18.1	6.3	16.9	9.7	1.0	0.9	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.09	1.2	0.1
				IIDETMAQLQDLK	2	93.1%	1																									
				LNEQQSVLQR	2	86.6%	1																									
				MNQVEDEVFEEFCR	2	95.3%	1																									
				NFLVFQGAVESIAMK	2	99.6%	1																									
				NMDAIIVDSEK	2	99.4%	1																									
IPI00291946	USP10	Ubiquitin carboxyl-terminal hydrolase 10	99.4%	3.2	2	2	2	3	6,660,327	7,970,877	8,062,650	9,234,503	533,644	173,239	578,348	465,242	17.9	4.9	16.0	11.3	1.2	0.07	1.2	0.1	1.4	0.007	1.0	0.9	1.2	0.05	1.1	0.2
IPI00941385	USP10	isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10	99.4%	3.2	2	2	2	3	6,660,327	7,970,877	8,062,650	9,234,503	533,644	173,239	578,348	465,242	17.9	4.9	16.0	11.3	1.2	0.07	1.2	0.1	1.4	0.007	1.0	0.9	1.2	0.05	1.1	0.2
IPI00955965	USP10	isoform 2 of Ubiquitin carboxyl-terminal hydrolase 10	99.4%	3.1	2	2	2	3	6,660,327	7,970,877	8,062,650	9,234,503	533,644	173,239	578,348	465,242	17.9	4.9	16.0	11.3	1.2	0.07	1.2	0.1	1.4	0.007	1.0	0.9	1.2	0.05	1.1	0.2
				EGLVPVSEDPVAIK	2	87.9%	1																									
				TVQDALESLVAR	2	91.1%	1																									
IPI00292000	PRPF31	isoform 1 of U4/U6 small nuclear ribonucleoprotein Prp31	99.6%	10.8	3	3	4	2	9,895,674	11,925,821	9,818,396	14,187,337	1,080,085	891,809	1,179,891	1,029,479	24.4	16.7	26.9	16.2	1.2	0.2	-1.0	1	1.4	0.02	-1.2	0.2	1.2	0.1	1.4	0.02
IPI00657721	PRPF31	Uncharacterized protein	99.6%	11.0	3	3	4	2	9,895,674	11,925,821	9,818,396	14,187,337	1,080,085	891,809	1,179,891	1,029,479	24.4	16.7	26.9	16.2	1.2	0.2	-1.0	1	1.4	0.02	-1.2	0.2	1.2	0.1	1.4	0.02
				IMGVAGGLTNLSK	2	99.4%	2																									
				MSFGEIEEDAYQEDLGFSLGHLGK	3	99.3%	1																									
				RFPELESLVPNALDYIR	2	91.5%	1																									
IPI00292020	SRM	Spermidine synthase	100.0%	7.0	2	2	2	1	19,371,320	19,044,960	18,350,480	21,488,190	1,591,966	1,092,699	1,419,238	473,063	18.4	12.8	17.3	4.9	-1.0	0.9	-1.1	0.6	1.1	0.3	-1.0	0.7	1.1	0.07	1.2	0.09
				VLIIGGGDGGVLR	2	95.8%	1																									
				YQDILVFR	2	99.0%	1																									

IPI00292056	PIK3C2B	Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing subunit beta	99.7%	1.1	2	2	2	2	3,991,240	4,038,330	3,966,535	4,629,370	416,242	228,521	323,520	203,221	23.3	12.7	18.2	9.8	1.0	0.9	-1.0	1	1.2	0.2	-1.0	0.9	1.1	0.09	1.2	0.1
IPI00647314	PIK3C2B	Phosphoinositide-3-kinase, class 2, beta polypeptide	99.7%	1.1	2	2	2	2	3,991,240	4,038,330	3,966,535	4,629,370	416,242	228,521	323,520	203,221	23.3	12.7	18.2	9.8	1.0	0.9	-1.0	1	1.2	0.2	-1.0	0.9	1.1	0.09	1.2	0.1
				FTSPPGDK	1	80.7%	1																									
				HNPGEDEYEK	2	98.5%	1																									
IPI00796556	-	43 kDa protein	99.8%	5.4	2	2	2	4	1,847,899	1,783,935	1,715,349	2,016,687	130,183	77,353	91,826	70,535	15.8	9.7	12.0	7.8	-1.0	0.7	-1.1	0.4	1.1	0.3	-1.0	0.6	1.1	0.06	1.2	0.03
IPI00797253	-	46 kDa protein	99.8%	5.2	2	2	2	4	1,847,899	1,783,935	1,715,349	2,016,687	130,183	77,353	91,826	70,535	15.8	9.7	12.0	7.8	-1.0	0.7	-1.1	0.4	1.1	0.3	-1.0	0.6	1.1	0.06	1.2	0.03
IPI00292290	EPB49	isoform Long of Dematin	99.8%	5.2	2	2	2	4	1,847,899	1,783,935	1,715,349	2,016,687	130,183	77,353	91,826	70,535	15.8	9.7	12.0	7.8	-1.0	0.7	-1.1	0.4	1.1	0.3	-1.0	0.6	1.1	0.06	1.2	0.03
IPI01015007	EPB49	isoform Short of Dematin	99.8%	5.5	2	2	2	4	1,847,899	1,783,935	1,715,349	2,016,687	130,183	77,353	91,826	70,535	15.8	9.7	12.0	7.8	-1.0	0.7	-1.1	0.4	1.1	0.3	-1.0	0.6	1.1	0.06	1.2	0.03
				HLSAEDFSR	2	91.7%	1																									
				SPGIISQASAPR	2	99.6%	1																									
IPI00292496	TUBB8	Tubulin beta-8 chain	99.7%	11.0	2	2	2	1	10,430,623	14,267,823	9,842,823	15,420,110	2,040,098	1,797,176	1,898,777	1,409,896	43.7	28.2	43.1	20.4	1.4	0.2	-1.1	0.8	1.5	0.08	-1.4	0.1	1.1	0.6	1.6	0.05
				EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK	3	89.7%	1																									
				MSATFIGNNTAIQELFK	2	97.3%	1																									
IPI00292499	HSPA14	Heat shock 70 kDa protein 14	98.7%	2.8	1	1	1	1	5,684,030	6,046,940	6,098,560	6,641,810	582,395	312,876	248,336	437,080	22.9	11.6	9.1	14.7	1.1	0.6	1.1	0.5	1.2	0.2	1.0	0.9	1.1	0.3	1.1	0.3
				FTVLFPSGTPLPAR	2	98.7%	1																									
IPI00292657	PTGR1	Prostaglandin reductase 1	100.0%	14.3	3	4	4	2	3,544,943	3,668,611	4,210,531	3,813,075	252,198	248,488	151,540	127,347	15.9	15.2	8.1	7.5	1.0	0.7	1.2	0.05	1.1	0.4	1.1	0.1	1.0	0.6	-1.1	0.08
IPI00642248	PTGR1	prostaglandin reductase 1 isoform 2	100.0%	15.6	3	4	4	2	3,544,943	3,668,611	4,210,531	3,813,075	252,198	248,488	151,540	127,347	15.9	15.2	8.1	7.5	1.0	0.7	1.2	0.05	1.1	0.4	1.1	0.1	1.0	0.6	-1.1	0.08
				GGETVMVNAAAGAVGSVVGQIAK	2	98.3%	1																									
				GGETVMVNAAAGAVGSVVGQIAK	3	100.0%	1																									
				HFVGYPTNSDFELK	2	99.5%	1																									
				LGFDVVFNYK	2	100.0%	1																									
IPI00292771	NUMA1	isoform 1 of Nuclear mitotic apparatus protein 1	100.0%	13.6	18	18	21	1	83,553,392	84,921,065	80,605,892	95,608,557	5,809,875	1,716,947	6,005,490	3,550,488	15.6	4.5	16.7	8.3	1.0	0.8	-1.0	0.7	1.1	0.1	-1.1	0.5	1.1	0.03	1.2	0.06
				AQELGHSQSALASAQR	3	99.9%	1																									
				DAQIAMMQQR	2	98.9%	1																									
				DSALETLQGQLEEK	2	100.0%	1																									
				HQVEQLSSSLK	2	98.5%	1																									
				INQLSEENGDLSFK	2	100.0%	2																									
				LADDLSTLQEK	2	100.0%	1																									
				LDFVCSFLQK	2	88.6%	1																									
				LEILQQQLQVANEAR	2	100.0%	2																									
				LGHELQQAGLK	2	82.8%	1																									
				LQAQLNELQAQLSQK	2	100.0%	2																									
				LTAQVASLTSELTTLNATIQQQDQELAGLK	3	99.9%	1																									
				LTAQVEQLEVFQR	3	97.8%	1																									
				NSLISSLEEEVSILNR	2	100.0%	1																									
				QEATRQDHAQQLATAAEEREASLR	3	94.9%	1																									
				SLEAQVAHADQQLR	2	94.6%	1																									
				SQAPLESSLDSLGDVFLDSGR	2	100.0%	1																									
				VASENLRQELTSQAERAEELGQELK	3	90.1%	1																									
				VEFATLQEALAHALTEK	3	100.0%	1																									
IPI00292791	CNTN3	Contactin-3	91.6%	2.0	1	1	1	1	664,125	821,964	796,276	841,868	159,524	115,303	138,054	86,346	53.7	31.4	38.8	22.9	1.2	0.4	1.2	0.5	1.3	0.4	-1.0	0.9	1.0	0.9	1.1	0.8
				KGDVSVQEHERISLLNDGGLK	3	86.6%	1																									
IPI00292819	KIAA1456	Putative methyltransferase KIAA1456	91.5%	6.8	1	1	1	3	1,096,793	1,053,860	1,165,853	1,044,720	42,264	54,422	44,716	37,542	8.6	11.6	8.6	8.0	-1.0	0.6	1.1	0.3	-1.0	0.4	1.1	0.2	-1.0	0.9	-1.1	0.07
IPI00938379	KIAA1456	hypothetical protein LOC57604 isoform 2	91.5%	9.5	1	1	1	3	1,096,793	1,053,860	1,165,853	1,044,720	42,264	54,422	44,716	37,542	8.6	11.6	8.6	8.0	-1.0	0.6	1.1	0.3	-1.0	0.4	1.1	0.2	-1.0	0.9	-1.1	0.07
IPI01011454	KIAA1456	Uncharacterized protein	91.5%	8.5	1	1	1	3	1,096,793	1,053,860	1,165,853	1,044,720	42,264	54,422	44,716	37,542	8.6	11.6	8.6	8.0	-1.0	0.6	1.1	0.3	-1.0	0.4	1.1	0.2	-1.0	0.9	-1.1	0.07
				NGGGNFLDSTNTGVNCVDAGNIEDDNPSASK	3	91.5%	1																									
IPI00292894	TSR1	Pre-rRNA-processing protein TSR1 homolog	99.3%	1.9	1	1	1	1	2,126,550	2,187,230	2,269,620	2,557,130	286,630	139,728	258,222	72,996	30.1	14.3	25.4	6.4	1.0	0.9	1.1	0.7	1.2	0.2	1.0	0.8	1.2	0.05	1.1	0.3
				WTYDPYVPEPVPWLK	2	99.0%	1																									
IPI00293078	DDX27	Probable ATP-dependent RNA helicase DDX27	98.9%	1.3	1	1	1	1	3,258,060	3,575,210	3,227,050	4,177,740	507,526	289,325	179,838	56,037	34.8	18.1	12.5	3.0	1.1	0.6	-1.0	1	1.3	0.1	-1.1	0.3	1.2	0.1	1.3	0.004
				ALQEFDLALR	2	98.2%	1																									
IPI00293088	GAA	Lysosomal alpha-glucosidase	100.0%	2.9	2	2	2	1	18,129,980	18,181,790	19,458,570	18,922,900	601,423	804,003	640,524	997,881	7.4	9.9	7.4	11.8	1.0	1	1.1	0.2	1.0	0.5	1.1	0.2	1.0	0.6	-1.0	0.7
				GELFWDDGESLEVLER	2	99.6%	1																									
				VTSEGAGLQLQK	2	90.6%	1																									
IPI00293126	TBCB	Tubulin-folding cofactor B	100.0%	13.9	2	2	2	1	4,595,800	5,437,201	4,854,686	5,279,307	344,225	491,663	310,203	288,499	16.8	20.2	14.3	12.2	1.2	0.2	1.1	0.6	1.1	0.2	-1.1	0.3	-1.0	0.8	1.1	0.3
				LGEYEDVSR	2	99.2%	1																									
				YGAFVKPAVVTVGDFPEEDYGLDEI	2	100.0%	1																									
IPI00293162	SUGP2	isoform 3 of SURP and G-patch domain-containing protein 2	91.0%	1.7	1	1	1	2	205,029	208,189	254,890	261,952	13,629	14,709	17,910	14,018	14.9	15.8	15.7	12.0	1.0	0.9	1.2	0.06	1.3	0.02	1.2	0.08	1.3	0.03	1.0	0.8
IPI00554438	SUGP2	isoform 4 of SURP and G-patch domain-containing protein 2	91.0%	1.8	1	1	1	2	205,029	208,189	254,890	261,952	13,629	14,709	17,910	14,018	14.9	15.8	15.7	12.0	1.0	0.9	1.2	0.06	1.3	0.02	1.2	0.08	1.3	0.03	1.0	0.8
				EAELESPEASSGTCFPRK	2	87.6%	1																									
IPI00293260	DNAJC10	isoform 1 of DnaJ homolog subfamily C member 10	97.8%	2.1	1	1	1	5	468,366	464,404	500,978	478,828	26,570	13,403	51,631	42,818	12.7	6.5	23.1	20.0	-1.0	0.9	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.8	-1.0	0.7
IPI00844115	DNAJC10	isoform 2 of DnaJ homolog subfamily C member 10	97.8%	2.3	1	1	1	5	468,366	464,404	500,978	478,828	26,570	13,403	51,631	42,818	12.7	6.5	23.1	20.0	-1.0	0.9	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.8	-1.0	0.7
IPI00873764	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10, isoform CRA_b	97.8%	5.1	1	1	1	5	468,366	464,404	500,978	478,828	26,570	13,403	51,631	42,818	12.7	6.5	23.1	20.0	-1.0	0.9	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.8	-1.0	0.7
IPI01012003	DNAJC10	21 kDa protein	97.8%	9.6	1	1	1	5	468,366	464,404	500,978	478,828	26,570	13,403	51,631	42,818	12.7	6.5	23.1	20.0	-1.0	0.9	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.8	-1.0	0.7
IPI01016006	DNAJC10	Uncharacterized protein	97.8%	6.2	1	1	1	5	468,366	464,404	500,978	478,828	26,570	13,403	51,631	42,818	12.7	6.5	23.1	20.0	-1.0	0.9	1.1	0.6	1.0	0.8	1.1	0.5	1.0	0.8	-1.0	0.7
				YDFGIYDDDPEIITLER	2	97.8%	1																									
IPI00293276	MIF	Macrophage migration inhibitory factor	100.0%	26.1	2	2	4	1	25,658,910	24,886,390	25,039,670	31,499,030	2,801,375	2,003,327	2,132,847	2,451,021	24.4	18.0	19.1	17.4	-1.0	0.8	-1.0	0.9	1.2	0.2	1.0	1	1.3	0.07	1.3	0.08
				LLCGLLAER	2	100.0%	2																									
				VYINYYDMNAANVGWNNSTFA	2	100.0%	2																									
IPI00293303	LGMN	Legumain	98.4%	3.9	1	1	1	4	690,338	652,825	759,373	790,973	46,681	29,915	52,094	53,034	15.1	10.3	15.3	15.0	-1.1	0.5	1.1	0.4	1.1	0.2	1.2	0.1	1.2	0.05	1.0	0.7
IPI00384155	LGMN	Full-length cDNA clone CS0DI002YH20 of Placenta of Homo sapiens	98.4%	4.6	1	1	1	4	690,338	652,825	759,373	790,973	46,681	29,915	52,094	53,034	15.1	10.3	15.3	15.0	-1.1	0.5	1.1	0.4	1.1	0.2	1.2	0.1	1.2	0.05	1.0	0.7
IPI00384156	LGMN	Full-length cDNA clone CS0DB001YK19 of Neuroblastoma of Homo sapiens	98.4%	4.5	1	1	1	4	690,338	652,825	759,373	790,973	46,681	29,915	52,094	53,034	15.1	10.3	15.3	15.0	-1.1	0.5	1.1	0.4	1.1	0.2	1.2	0.1	1.2	0.05	1.0	0.7
IPI01013028	LGMN	cDNA FLJ53066, highly similar to Legumain	98.4%	4.2	1	1	1	4	690,338	652,825	759,373	790,973	46,681	29,915	52,094	53,034	15.1	10.3	15.3	15.0	-1.1	0.5	1.1	0.4	1.1	0.2	1.2	0.1	1.2	0.05	1.0	0.7
				DYTGEDVTPQNFLAVLR	2	98.4%	1																									
IPI00293307	PLIN2	Perilipin-2	100.0%	31.6	9	9	10	1	38,308,705	38,696,080	40,188,315	43,965,610	3,706,017	1,824,991	2,325,918	225,196	21.6	10.6	12.9	1.2	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.6	1.1	0.04	1.1	0.2
				AYQQALSR	2	99.3%	1																									
				DAVTTTVTGAK	2	100.0%	1																									
				DSVASTITGVMDK	2	100.0%	1																									
				EVSDSLLTSSK	2	98.6%	1																									
				LPILNQPSTQIVANAK	2	100.0%	1																									
				MMQLVSSGVENALTK	2	100.0%	1																									
				NLTQQLQTTCHTLLSNIQGVPQNIQDQAK	3	85.9%	1																									
				SELLVEQYLPLTEEELEKEAK	3	99.9%	1																									
				SVVSGSINTVLGSR	2	100.0%	2																									
IPI00293327	P2RX4	P2X purinoceptor 4	93.5%	3.9	1	1	1	4	629,118	587,545	587,273	717,330	67,355	20,694	52,073	39,203	23.9	7.9	19.8	12.2	-1.1	0.6	-1.1	0.6	1.1	0.3	-1.0	1	1.2	0.02	1.2	0.08
IPI00478728	P2RX4	P2X purinoceptor	93.5%	4.2	1	1	1	4	629,118	587,545	587,273	717,330	67,355	20,694	52,073	39,203	23.9	7.9	19.8	12.2	-1.1	0.6	-1.1	0.6	1.1	0.3	-1.0	1	1.2	0.02	1.2	0.08
IPI00790278	P2RX4	P2X purinoceptor	93.5%	5.2	1	1	1	4	629,118	587,545	587,273	717,330	67,355	20,694	52,073	39,203	23.9	7.9	19.8	12.2	-1.1	0.6	-1.1	0.6	1.1	0.3	-1.0	1	1.2	0.02	1.2	0.08
IPI01013466	P2RX4	45 kDa protein	93.5%	3.7	1	1	1	4	629,118	587,545	587,273	717,330	67,355	20,694	52,073	39,203	23.9	7.9	19.8	12.2	-1.1	0.6	-1.1	0.6	1.1	0.3	-1.0	1	1.2	0.02	1.2	0.08
				YVEDYEQGLASELDQ	2	93.5%	1																									
IPI00937434	-	Disrupted in schizophrenia 1 isoform 51	99.8%	10.1	2	2	2	3	2,292,213	2,371,810	2,105,520	2,561,480	209,333	143,721	118,782	116,870	20.4	13.6	12.6	10.2	1.0	0.8	-1.1	0.5	1.1	0.3	-1.1	0.2	1.1	0.3	1.2	0.03
IPI00293350	TSNAX	Translin-associated protein X	99.8%	6.6	2	2	2	3	2,292,213	2,371,810	2,105,520	2,561,480	209,333	143,721	118,782	116,870	20.4	13.6	12.6	10.2	1.0	0.8	-1.1	0.5	1.1	0.3	-1.1	0.2	1.1	0.3	1.2	0.03
IPI00647395	TSNAX	Disrupted in schizophrenia 1 isoform 54	99.8%	10.2	2	2	2	3	2,292,213	2,371,810	2,105,520	2,561,480	209,333	143,721	118,782	116,870	20.4	13.6	12.6	10.2	1.0	0.8	-1.1	0.5	1.1	0.3	-1.1	0.2	1.1	0.3	1.2	0.03
				SFQQELDAR	2	97.2%	1																									
				SLISMDEINK	2	99.7%	1																									
IPI00293434	SRP14	Signal recognition particle 14 kDa protein	99.6%	9.6	1	1	1	2	1,661,085	1,918,250	1,783,960	1,914,935	233,120	215,144	236,705	182,433	31.4	25.1	29.7	21.3	1.2	0.4	1.1	0.7	1.2	0.4	-1.1	0.7	-1.0	1	1.1	0.7
IPI00790432	SRP14	10 kDa protein	99.6%	15.1	1	1	1	2	1,661,085	1,918,250	1,783,960	1,914,935	233,120	215,144	236,705	182,433	31.4	25.1	29.7	21.3	1.2	0.4	1.1	0.7	1.2	0.4	-1.1	0.7	-1.0	1	1.1	0.7
				KGTVEGFEPADNK	2	99.6%	1																									
IPI00293464	DDB1	DNA damage-binding protein 1	100.0%	13.0	12	12	12	2	83,269,031	89,951,398	86,931,916	102,387,097	9,953,942	5,491,096	7,073,444	4,021,089	26.7	13.7	18.2	8.8	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.7	1.1	0.1	1.2	0.09
IPI00977083	DDB1;LOC10029033	cDNA FLJ56068, highly similar to DNA damage-binding protein 1	100.0%	13.6	12	12	12	2	83,269,031	89,951,398	86,931,916	102,387,097	9,953,942	5,491,096	7,073,444	4,021,089	26.7	13.7	18.2	8.8	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.7	1.1	0.1	1.2	0.09
				DLLFILTAK	2	99.6%	1																									
				EMLGGEIIPR	2	97.9%	1																									
				GAVYSMVEFNGK	2	96.1%	1																									
				IEVQDTSGGTTALRPSASTQALSSSVSSSK	3	100.0%	1																									
				LEELHVIDVK	3	85.2%	1																									
				LPSFELLHK	3	96.8%	1																									
				LVFSNVNLK	2	99.8%	1																									
				QSGESIDIITR	2	98.1%	1																									
				SVLLLAYKPMEGNFEEIAR	3	100.0%	1																									
				VTLGTQPTVLR	2	92.6%	1																									
				YLLGDMEGR	2	98.5%	1																									
				YNACILEYK	2	99.4%	1																									
IPI00293533	NUP62	Nuclear pore glycoprotein p62	98.8%	4.6	2	2	2	1	5,107,810	4,355,618	4,698,935	4,848,740	237,314	115,481	194,450	372,441	10.4	5.9	9.3	17.2	-1.2	0.02	-1.1	0.2	-1.1	0.6	1.1	0.2	1.1	0.3	1.0	0.7
				HFLQQATQVNAWDR	2	94.8%	1																									
				LAENIDAQLK	2	93.1%	1																									
IPI00293564	HMGCL	Hydroxymethylglutaryl-CoA lyase, mitochondrial	100.0%	20.0	5	5	5	2	7,414,159	7,587,573	7,256,867	8,250,312	594,690	294,370	495,653	321,471	17.9	8.7	15.3	8.7	1.0	0.8	-1.0	0.8	1.1	0.3	-1.0	0.6	1.1	0.2	1.1	0.1
IPI01011849	HMGCL	cDNA FLJ16378 fis, clone TKIDN2016399, highly similar to Hydroxymethylglutaryl-C	100.0%	21.7	5	5	5	2	7,414,159	7,587,573	7,256,867	8,250,312	594,690	294,370	495,653	321,471	17.9	8.7	15.3	8.7	1.0	0.8	-1.0	0.8	1.1	0.3	-1.0	0.6	1.1	0.2	1.1	0.1
				AAQSANISVR	2	99.3%	1																									
				EVVIFGAASELFTK	2	100.0%	1																									
				IVEVGPR	2	94.4%	1																									
				LIDMLSEAGLSVIETTSFVSPK	2	99.9%	1																									
				NINCSIEESFQR	2	99.9%	1																									
IPI00293590	MGLL	monoglyceride lipase isoform 1	99.9%	12.8	3	3	3	3	1,314,279	1,396,693	1,670,203	1,633,445	117,152	73,055	131,931	85,331	19.9	11.7	17.7	11.7	1.1	0.6	1.3	0.08	1.2	0.06	1.2	0.1	1.2	0.07	-1.0	0.8
IPI00455206	MGLL	Monoglyceride lipase	99.9%	13.2	3	3	3	3	1,314,279	1,396,693	1,670,203	1,633,445	117,152	73,055	131,931	85,331	19.9	11.7	17.7	11.7	1.1	0.6	1.3	0.08	1.2	0.06	1.2	0.1	1.2	0.07	-1.0	0.8
IPI01013572	MGLL	34 kDa protein	99.9%	12.8	3	3	3	3	1,314,279	1,396,693	1,670,203	1,633,445	117,152	73,055	131,931	85,331	19.9	11.7	17.7	11.7	1.1	0.6	1.3	0.08	1.2	0.06	1.2	0.1	1.2	0.07	-1.0	0.8
				VCFGIQLLNAVSR	2	99.9%	1																									
				VLNLVLPNLSLGPIDSSVLSR	2	100.0%	1																									
				YEELAR	1	94.8%	1																									
IPI00293616	DDX3Y	ATP-dependent RNA helicase DDX3Y	100.0%	2.9	2	2	2	3	2,229,845	2,435,715	2,239,935	2,659,085	199,262	74,673	225,999	136,760	20.0	6.9	22.6	11.5	1.1	0.4	1.0	1	1.2	0.1	-1.1	0.4	1.1	0.2	1.2	0.2
IPI00646152	DDX3Y	cDNA FLJ50912, highly similar to ATP-dependent RNA helicase DDX3Y	100.0%	2.9	2	2	2	3	2,229,845	2,435,715	2,239,935	2,659,085	199,262	74,673	225,999	136,760	20.0	6.9	22.6	11.5	1.1	0.4	1.0	1	1.2	0.1	-1.1	0.4	1.1	0.2	1.2	0.2
IPI00908506	DDX3Y	cDNA FLJ53122, highly similar to ATP-dependent RNA helicase DDX3Y	100.0%	4.7	2	2	2	3	2,229,845	2,435,715	2,239,935	2,659,085	199,262	74,673	225,999	136,760	20.0	6.9	22.6	11.5	1.1	0.4	1.0	1	1.2	0.1	-1.1	0.4	1.1	0.2	1.2	0.2
				EIQMLAR	2	87.7%	1																									
				SPILVATAVAAR	2	100.0%	1																									
IPI00293655	DDX1	ATP-dependent RNA helicase DDX1	100.0%	20.7	10	12	14	1	18,767,639	18,642,703	18,087,421	20,765,770	1,417,912	901,104	1,200,464	732,656	16.9	10.8	14.8	7.9	-1.0	0.9	-1.0	0.7	1.1	0.2	-1.0	0.7	1.1	0.1	1.1	0.09
				DQLSVLENGVDIVVGTPGR	2	97.4%	1																									
				EAQTSFLHLGYLPNQLFR	2	97.9%	1																									
				ELAEQTLNNIK	2	100.0%	2																									
				FGFGFGGTGK	2	99.6%	1																									
				FLVLDEADGLLSQGYSDFINR	2	100.0%	2																									
				FLVLDEADGLLSQGYSDFINR	3	100.0%	1																									
				GHVDILAPTVQELAALEK	2	83.1%	1																									
				GHVDILAPTVQELAALEK	3	100.0%	1																									
				GSAFAIGSDGLCCQSR	2	99.9%	1																									
				NQALFPACVLK	2	99.9%	1																									
				TGAFSIPVIQIVYETLKDQQEGK	3	98.6%	1																									
				YIDNPK	2	91.3%	1																									
IPI00293721	AKR7A3	Aflatoxin B1 aldehyde reductase member 3	100.0%	20.9	6	6	7	1	35,319,428	38,262,064	33,102,313	44,407,301	4,839,469	2,011,908	3,159,992	2,888,050	30.6	11.8	21.4	14.5	1.1	0.6	-1.1	0.7	1.3	0.1	-1.2	0.2	1.2	0.1	1.3	0.03
				ALQAAYGASAPSMTSATLR	2	100.0%	1																									
				ARPATVLGAMEMGR	2	99.8%	1																									

				FQLETSLKR	2	96.5%	1																									
				FYAFNPLAGGLLTGK	2	100.0%	2																									
				MDAPTSAAVTR	2	99.5%	1																									
				RMDAPTSAAVTR	2	100.0%	1																									
IPI00293867	DDT	D-dopachrome decarboxylase	100.0%	33.1	4	4	5	2	10,816,323	11,275,847	10,258,120	11,801,292	1,102,716	580,601	625,867	716,396	22.8	11.5	13.6	13.6	1.0	0.7	-1.1	0.7	1.1	0.5	-1.1	0.3	1.0	0.6	1.2	0.1
IPI00878984	DDT	14 kDa protein	100.0%	29.6	4	4	5	2	10,816,323	11,275,847	10,258,120	11,801,292	1,102,716	580,601	625,867	716,396	22.8	11.5	13.6	13.6	1.0	0.7	-1.1	0.7	1.1	0.5	-1.1	0.3	1.0	0.6	1.2	0.1
				FFPLESWQIGK	2	100.0%	2																									
				LCAAAASILGKPADR	2	99.8%	1																									
				RLCAAAASILGKPADR	3	99.8%	1																									
				SHSAHFFEFLTK	3	99.6%	1																									
IPI00293946	UBXN4	UBX domain-containing protein 4	95.0%	3.2	1	1	1	5	585,874	552,910	508,120	674,842	66,642	27,839	75,004	32,692	25.4	11.3	33.0	10.8	-1.1	0.7	-1.2	0.5	1.2	0.3	-1.1	0.6	1.2	0.02	1.3	0.08
IPI00448916	UBXN4	UBXN4 protein	95.0%	16.8	1	1	1	5	585,874	552,910	508,120	674,842	66,642	27,839	75,004	32,692	25.4	11.3	33.0	10.8	-1.1	0.7	-1.2	0.5	1.2	0.3	-1.1	0.6	1.2	0.02	1.3	0.08
IPI00916552	UBXN4	Uncharacterized protein	95.0%	13.7	1	1	1	5	585,874	552,910	508,120	674,842	66,642	27,839	75,004	32,692	25.4	11.3	33.0	10.8	-1.1	0.7	-1.2	0.5	1.2	0.3	-1.1	0.6	1.2	0.02	1.3	0.08
IPI00917307	UBXN4	7 kDa protein	95.0%	24.6	1	1	1	5	585,874	552,910	508,120	674,842	66,642	27,839	75,004	32,692	25.4	11.3	33.0	10.8	-1.1	0.7	-1.2	0.5	1.2	0.3	-1.1	0.6	1.2	0.02	1.3	0.08
IPI01014872	UBXN4	cDNA FLJ38083 fis, clone CTONG2016408, highly similar to UBX domain-containin	95.0%	3.3	1	1	1	5	585,874	552,910	508,120	674,842	66,642	27,839	75,004	32,692	25.4	11.3	33.0	10.8	-1.1	0.7	-1.2	0.5	1.2	0.3	-1.1	0.6	1.2	0.02	1.3	0.08
				MLWFQGAIPAAIATAK	2	95.0%	1																									
IPI00293963	CDYL	isoform 1 of Chromodomain Y-like protein	92.3%	4.0	1	1	1	4	1,807,830	1,820,648	1,569,068	1,606,560	205,745	198,657	59,030	97,566	25.5	24.4	8.4	13.6	1.0	1	-1.2	0.3	-1.1	0.4	-1.2	0.3	-1.1	0.4	1.0	0.8
IPI00334502	CDYL	isoform 4 of Chromodomain Y-like protein	92.3%	5.8	1	1	1	4	1,807,830	1,820,648	1,569,068	1,606,560	205,745	198,657	59,030	97,566	25.5	24.4	8.4	13.6	1.0	1	-1.2	0.3	-1.1	0.4	-1.2	0.3	-1.1	0.4	1.0	0.8
IPI00655922	CDYL	isoform 2 of Chromodomain Y-like protein	92.3%	4.4	1	1	1	4	1,807,830	1,820,648	1,569,068	1,606,560	205,745	198,657	59,030	97,566	25.5	24.4	8.4	13.6	1.0	1	-1.2	0.3	-1.1	0.4	-1.2	0.3	-1.1	0.4	1.0	0.8
IPI00942198	CDYL	isoform 3 of Chromodomain Y-like protein	92.3%	7.8	1	1	1	4	1,807,830	1,820,648	1,569,068	1,606,560	205,745	198,657	59,030	97,566	25.5	24.4	8.4	13.6	1.0	1	-1.2	0.3	-1.1	0.4	-1.2	0.3	-1.1	0.4	1.0	0.8
				AWFQTPYTTFGQSPDGCSTVMFPK	3	92.3%	1																									
IPI00294158	BLVRA	Biliverdin reductase A	93.8%	3.4	1	1	1	3	3,027,757	3,228,753	3,006,180	4,303,783	222,960	380,798	406,265	435,270	16.5	26.4	30.2	22.6	1.1	0.7	-1.0	1	1.4	0.03	-1.1	0.7	1.3	0.1	1.4	0.06
IPI00925847	BLVRA	14 kDa protein	93.8%	7.9	1	1	1	3	3,027,757	3,228,753	3,006,180	4,303,783	222,960	380,798	406,265	435,270	16.5	26.4	30.2	22.6	1.1	0.7	-1.0	1	1.4	0.03	-1.1	0.7	1.3	0.1	1.4	0.06
IPI00926066	BLVRA	Uncharacterized protein	93.8%	9.8	1	1	1	3	3,027,757	3,228,753	3,006,180	4,303,783	222,960	380,798	406,265	435,270	16.5	26.4	30.2	22.6	1.1	0.7	-1.0	1	1.4	0.03	-1.1	0.7	1.3	0.1	1.4	0.06
				FGVVVVGVGR	2	93.8%	1																									
IPI00294178	PPP2R1B	isoform 1 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A b	100.0%	3.0	1	1	2	8	489,755	606,742	568,590	533,662	119,010	123,078	60,265	41,350	54.3	45.4	23.7	17.3	1.2	0.5	1.2	0.6	1.1	0.7	-1.1	0.8	-1.1	0.6	-1.1	0.6
IPI00335449	PPP2R1B	isoform 2 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A b	100.0%	2.7	1	1	2	8	489,755	606,742	568,590	533,662	119,010	123,078	60,265	41,350	54.3	45.4	23.7	17.3	1.2	0.5	1.2	0.6	1.1	0.7	-1.1	0.8	-1.1	0.6	-1.1	0.6
IPI00909011	PPP2R1B	serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform is	100.0%	3.8	1	1	2	8	489,755	606,742	568,590	533,662	119,010	123,078	60,265	41,350	54.3	45.4	23.7	17.3	1.2	0.5	1.2	0.6	1.1	0.7	-1.1	0.8	-1.1	0.6	-1.1	0.6
IPI00910814	PPP2R1B	serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform is	100.0%	3.2	1	1	2	8	489,755	606,742	568,590	533,662	119,010	123,078	60,265	41,350	54.3	45.4	23.7	17.3	1.2	0.5	1.2	0.6	1.1	0.7	-1.1	0.8	-1.1	0.6	-1.1	0.6
IPI00939356	PPP2R1B	serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform is	100.0%	3.0	1	1	2	8	489,755	606,742	568,590	533,662	119,010	123,078	60,265	41,350	54.3	45.4	23.7	17.3	1.2	0.5	1.2	0.6	1.1	0.7	-1.1	0.8	-1.1	0.6	-1.1	0.6
IPI00973793	PPP2R1B	cDNA FLJ55030, highly similar to Serine/threonine-protein phosphatase 2A 65 kDa r	100.0%	4.0	1	1	2	8	489,755	606,742	568,590	533,662	119,010	123,078	60,265	41,350	54.3	45.4	23.7	17.3	1.2	0.5	1.2	0.6	1.1	0.7	-1.1	0.8	-1.1	0.6	-1.1	0.6
IPI00978397	PPP2R1B	Protein	100.0%	8.0	1	1	2	8	489,755	606,742	568,590	533,662	119,010	123,078	60,265	41,350	54.3	45.4	23.7	17.3	1.2	0.5	1.2	0.6	1.1	0.7	-1.1	0.8	-1.1	0.6	-1.1	0.6
IPI01013427	PPP2R1B	cDNA FLJ54667, highly similar to Serine/threonine-protein phosphatase 2A 65 kDa r	100.0%	4.1	1	1	2	8	489,755	606,742	568,590	533,662	119,010	123,078	60,265	41,350	54.3	45.4	23.7	17.3	1.2	0.5	1.2	0.6	1.1	0.7	-1.1	0.8	-1.1	0.6	-1.1	0.6
				QLSQSLLPAIVELAEDAK	2	100.0%	2																									
IPI00294218	ZNF470	isoform 2 of Zinc finger protein 470	97.4%	5.0	1	1	1	2	819,569	868,319	1,196,085	1,109,360	96,971	108,131	181,706	94,003	26.5	27.9	34.0	19.0	1.1	0.7	1.5	0.1	1.4	0.06	1.4	0.2	1.3	0.1	-1.1	0.7
IPI00791472	ZNF470	isoform 1 of Zinc finger protein 470	97.4%	4.2	1	1	1	2	819,569	868,319	1,196,085	1,109,360	96,971	108,131	181,706	94,003	26.5	27.9	34.0	19.0	1.1	0.7	1.5	0.1	1.4	0.06	1.4	0.2	1.3	0.1	-1.1	0.7
				QSVHLAHHQRIHTGESSVILSSALPYHQVL	3	97.4%	1																									
IPI00294250	EPHA1	Ephrin type-A receptor 1	98.0%	3.0	2	2	2	1	18,486,090	18,389,040	20,585,890	20,232,150	2,413,453	985,040	2,634,327	672,269	29.2	12.0	28.6	7.4	-1.0	1	1.1	0.6	1.1	0.5	1.1	0.5	1.1	0.2	-1.0	0.9
				SPGANLTYELHVLNQDEER	3	85.5%	1																									
				WEPPADTGGR	2	86.7%	1																									
IPI00294386	MYO1A	Myosin-Ia	100.0%	2.6	2	2	3	3	1,208,723	1,395,025	1,248,938	1,387,806	148,392	132,461	106,400	88,016	27.5	21.2	19.1	14.2	1.2	0.4	1.0	0.8	1.1	0.3	-1.1	0.4	-1.0	1	1.1	0.3
IPI00793284	MYO1B	Uncharacterized protein	100.0%	8.8	2	2	3	3	1,208,723	1,395,025	1,248,938	1,387,806	148,392	132,461	106,400	88,016	27.5	21.2	19.1	14.2	1.2	0.4	1.0	0.8	1.1	0.3	-1.1	0.4	-1.0	1	1.1	0.3
IPI00917840	MYO1B	Uncharacterized protein	100.0%	16.6	2	2	3	3	1,208,723	1,395,025	1,248,938	1,387,806	148,392	132,461	106,400	88,016	27.5	21.2	19.1	14.2	1.2	0.4	1.0	0.8	1.1	0.3	-1.1	0.4	-1.0	1	1.1	0.3
				LLQSNPVLEAFGNAK	2	100.0%	2																									
				LVMSYVAAVCGK	2	95.7%	1																									
IPI00294398	HADH	isoform 1 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	100.0%	22.3	4	4	4	3	2,650,589	3,586,444	2,470,861	3,794,492	363,224	263,052	293,045	288,525	30.6	16.4	26.5	17.0	1.4	0.07	-1.1	0.7	1.4	0.04	-1.5	0.02	1.1	0.6	1.5	0.01
IPI00298406	HADH	isoform 2 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	100.0%	18.0	4	4	4	3	2,650,589	3,586,444	2,470,861	3,794,492	363,224	263,052	293,045	288,525	30.6	16.4	26.5	17.0	1.4	0.07	-1.1	0.7	1.4	0.04	-1.5	0.02	1.1	0.6	1.5	0.01
IPI00902588	HADH	cDNA FLJ38699 fis, clone KIDNE2002168, highly similar to Short chain 3-hydroxyac	100.0%	22.0	4	4	4	3	2,650,589	3,586,444	2,470,861	3,794,492	363,224	263,052	293,045	288,525	30.6	16.4	26.5	17.0	1.4	0.07	-1.1	0.7	1.4	0.04	-1.5	0.02	1.1	0.6	1.5	0.01
				FIVDGWHEMDAENPLHQPSPSLNK	3	96.4%	1																									
				GDASKEDIDTAMK	2	99.9%	1																									
				LGAGYPMGPFELLDYVGLDTTK	3	100.0%	1																									
				LLVPYLMEAIR	2	99.9%	1																									
IPI00294536	STRAP	cDNA FLJ51909, highly similar to Serine-threonine kinase receptor-associatedprotei	100.0%	34.7	8	8	9	2	17,771,416	17,586,619	17,288,478	19,961,950	1,379,168	731,707	1,148,716	483,383	17.4	9.3	14.9	5.4	-1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.03	1.2	0.06
IPI00941907	STRAP	Serine-threonine kinase receptor-associated protein	100.0%	36.0	8	8	9	2	17,771,416	17,586,619	17,288,478	19,961,950	1,379,168	731,707	1,148,716	483,383	17.4	9.3	14.9	5.4	-1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.03	1.2	0.06
				FSPDGELYASGSEDGTLR	2	100.0%	1																									
				GAVWGATLNK	2	93.0%	1																									
				LWQTVVGK	2	98.3%	1																									
				QGDTGDWIGTFLGHK	3	99.9%	1																									
				SFEAPATINSASLHPEKEFLVAGGEDFK	3	100.0%	1																									
				TVDFTQDSNYLLTGGQDK	2	100.0%	2																									
				VWDAVSGDELMTLAHK	3	100.0%	1																									
				YDYNSGEELESYK	2	100.0%	1																									
IPI00294578	TGM2	isoform 1 of Protein-glutamine gamma-glutamyltransferase 2	100.0%	10.5	4	4	4	3	6,313,105	6,743,712	6,704,628	8,345,521	1,562,704	957,808	962,252	201,696	55.4	31.8	32.1	5.4	1.1	0.8	1.1	0.8	1.3	0.3	-1.0	1	1.2	0.2	1.2	0.2
IPI01013011	TGM2	cDNA FLJ57198, highly similar to Protein-glutamine gamma-glutamyltransferase 2	100.0%	11.5	4	4	4	3	6,313,105	6,743,712	6,704,628	8,345,521	1,562,704	957,808	962,252	201,696	55.4	31.8	32.1	5.4	1.1	0.8	1.1	0.8	1.3	0.3	-1.0	1	1.2	0.2	1.2	0.2
IPI01013460	TGM2	cDNA FLJ58187, highly similar to Protein-glutamine gamma-glutamyltransferase 2	100.0%	11.9	4	4	4	3	6,313,105	6,743,712	6,704,628	8,345,521	1,562,704	957,808	962,252	201,696	55.4	31.8	32.1	5.4	1.1	0.8	1.1	0.8	1.3	0.3	-1.0	1	1.2	0.2	1.2	0.2
				ALLVEPVINSYLLAER	2	100.0%	1																									
				LLLCARTVSYNGILGPECGTK	3	95.2%	1																									
				WDNNYGDGVSPMSWIGSVDILR	2	99.9%	1																									
				YLLNLNLEPFSEK	2	100.0%	1																									
IPI00294619	TFG	Protein TFG	100.0%	26.0	5	5	5	2	5,858,866	6,248,273	6,027,978	6,575,737	422,899	233,380	498,886	236,652	16.1	8.4	18.5	8.1	1.1	0.4	1.0	0.8	1.1	0.2	-1.0	0.7	1.1	0.4	1.1	0.4
IPI00788849	TFG	protein TFG isoform 2	100.0%	26.3	5	5	5	2	5,858,866	6,248,273	6,027,978	6,575,737	422,899	233,380	498,886	236,652	16.1	8.4	18.5	8.1	1.1	0.4	1.0	0.8	1.1	0.2	-1.0	0.7	1.1	0.4	1.1	0.4
				LLDSLEPPGEPGPSTNIPENDTVDGREEK	3	100.0%	1																									
				LLSNDEVTIK	2	100.0%	1																									
				NRPPFGQGYTQPGPGYR	3	100.0%	1																									
				NVMSAFGLTDDQVSGPPSAPAEDR	2	100.0%	1																									
				QSTQVMAASMSAFDPLKNQDEINK	3	97.0%	1																									
IPI00294627	SF1	isoform 2 of Splicing factor 1	100.0%	9.3	4	4	4	6	2,153,841	2,103,243	2,057,587	2,346,851	154,709	66,256	152,139	109,226	16.1	7.0	16.5	10.4	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	0.8	1.1	0.09	1.1	0.2
IPI00386114	SF1	isoform 1 of Splicing factor 1	100.0%	9.2	4	4	4	6	2,153,841	2,103,243	2,057,587	2,346,851	154,709	66,256	152,139	109,226	16.1	7.0	16.5	10.4	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	0.8	1.1	0.09	1.1	0.2
IPI00386117	SF1	isoform 3 of Splicing factor 1	100.0%	9.5	4	4	4	6	2,153,841	2,103,243	2,057,587	2,346,851	154,709	66,256	152,139	109,226	16.1	7.0	16.5	10.4	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	0.8	1.1	0.09	1.1	0.2
IPI00386119	SF1	isoform 5 of Splicing factor 1	100.0%	7.7	4	4	4	6	2,153,841	2,103,243	2,057,587	2,346,851	154,709	66,256	152,139	109,226	16.1	7.0	16.5	10.4	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	0.8	1.1	0.09	1.1	0.2
IPI00386120	SF1	isoform 6 of Splicing factor 1	100.0%	10.3	4	4	4	6	2,153,841	2,103,243	2,057,587	2,346,851	154,709	66,256	152,139	109,226	16.1	7.0	16.5	10.4	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	0.8	1.1	0.09	1.1	0.2
IPI00941553	SF1	Uncharacterized protein	100.0%	9.5	4	4	4	6	2,153,841	2,103,243	2,057,587	2,346,851	154,709	66,256	152,139	109,226	16.1	7.0	16.5	10.4	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	0.8	1.1	0.09	1.1	0.2
				AYIVQLQIEDLTR	2	99.9%	1																									
				TVIPGMPTVIPPGLTR	2	93.5%	1																									
				VMIPQDEYPEINFVGLLIGPR	3	100.0%	1																									
				WNQDTMEQK	2	99.9%	1																									
IPI00294739	SAMHD1	isoform 1 of SAM domain and HD domain-containing protein 1	97.4%	2.4	1	1	1	2	172,663	151,729	193,825	185,791	9,658	9,619	25,928	11,137	12.5	14.2	29.9	13.4	-1.1	0.2	1.1	0.5	1.1	0.4	1.3	0.2	1.2	0.05	-1.0	0.8
IPI00943982	SAMHD1	isoform 2 of SAM domain and HD domain-containing protein 1	97.4%	2.5	1	1	1	2	172,663	151,729	193,825	185,791	9,658	9,619	25,928	11,137	12.5	14.2	29.9	13.4	-1.1	0.2	1.1	0.5	1.1	0.4	1.3	0.2	1.2	0.05	-1.0	0.8
				VGNIIDTMITDAFLK	2	97.4%	1																									
IPI00294742	LARP7	isoform 1 of La-related protein 7	94.7%	2.6	1	1	1	4	1,145,210	1,148,575	1,204,955	1,571,370	113,574	130,598	134,973	73,331	22.2	25.4	25.1	10.4	1.0	1	1.1	0.7	1.4	0.01	1.0	0.8	1.4	0.02	1.3	0.04
IPI00395536	LARP7	La-related protein 7	94.7%	2.6	1	1	1	4	1,145,210	1,148,575	1,204,955	1,571,370	113,574	130,598	134,973	73,331	22.2	25.4	25.1	10.4	1.0	1	1.1	0.7	1.4	0.01	1.0	0.8	1.4	0.02	1.3	0.04
IPI00964251	LARP7	Uncharacterized protein	94.7%	9.7	1	1	1	4	1,145,210	1,148,575	1,204,955	1,571,370	113,574	130,598	134,973	73,331	22.2	25.4	25.1	10.4	1.0	1	1.1	0.7	1.4	0.01	1.0	0.8	1.4	0.02	1.3	0.04
IPI00967723	LARP7	Protein	94.7%	4.5	1	1	1	4	1,145,210	1,148,575	1,204,955	1,571,370	113,574	130,598	134,973	73,331	22.2	25.4	25.1	10.4	1.0	1	1.1	0.7	1.4	0.01	1.0	0.8	1.4	0.02	1.3	0.04
				VNATGPQFVSGVIVK	2	94.7%	1																									
IPI00294834	ASPH	isoform 1 of Aspartyl/asparaginyl beta-hydroxylase	99.9%	4.0	2	2	2	2	1,616,807	1,633,175	1,548,723	1,655,635	110,998	113,411	102,280	83,148	15.4	15.5	14.8	11.2	1.0	0.9	-1.0	0.7	1.0	0.8	-1.1	0.6	1.0	0.9	1.1	0.4
IPI00944640	ASPH	aspartyl/asparaginyl beta-hydroxylase isoform f	99.9%	4.1	2	2	2	2	1,616,807	1,633,175	1,548,723	1,655,635	110,998	113,411	102,280	83,148	15.4	15.5	14.8	11.2	1.0	0.9	-1.0	0.7	1.0	0.8	-1.1	0.6	1.0	0.9	1.1	0.4
				LGIYDADGDGDFDVDDAK	2	100.0%	1																									
				LIRDEGLAVMDK	2	81.9%	1																									
IPI00294879	RANGAP1	Ran GTPase-activating protein 1	100.0%	12.6	5	5	6	1	17,134,060	19,011,805	18,174,565	21,906,915	575,952	306,969	1,117,838	856,017	7.5	3.6	13.8	8.7	1.1	0.02	1.1	0.4	1.3	0.002	-1.0	0.5	1.2	0.02	1.2	0.03
				AFNSSSFNSNTFLTR	2	81.6%	1																									
				LNNCGMGIGGGK	2	97.7%	1																									
				LNTAEDAKDVIKEIEDFDSLEALR	3	100.0%	1																									
				TQVAGGQLSFK	2	99.6%	1																									
				VINLNDNTFTEK	2	100.0%	2																									
IPI00294911	SDHB	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	97.7%	2.1	1	1	1	1	4,359,950	3,507,050	3,347,640	4,870,940	600,025	469,283	364,722	274,011	30.8	29.9	24.4	12.6	-1.2	0.3	-1.3	0.2	1.1	0.5	-1.0	0.8	1.4	0.04	1.5	0.01
				WMIDSR	2	91.3%	1																									
IPI00294955	LSM4	U6 snRNA-associated Sm-like protein LSm4	99.2%	11.5	1	1	1	1	3,858,260	3,426,920	4,244,900	3,814,790	438,587	281,062	498,421	264,215	25.4	18.3	26.3	15.5	-1.1	0.4	1.1	0.6	-1.0	0.9	1.2	0.2	1.1	0.3	-1.1	0.5
				IPDEIIDMVKEEVVAK	3	99.2%	1																									
IPI00294962	SH3KBP1	isoform 1 of SH3 domain-containing kinase-binding protein 1	100.0%	14.6	7	7	7	5	8,035,931	8,521,328	8,054,233	9,252,832	734,543	486,233	493,754	422,065	20.4	12.8	13.7	10.2	1.1	0.6	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.3	1.1	0.1
IPI00477897	SH3KBP1	isoform 2 of SH3 domain-containing kinase-binding protein 1	100.0%	15.5	7	7	7	5	8,035,931	8,521,328	8,054,233	9,252,832	734,543	486,233	493,754	422,065	20.4	12.8	13.7	10.2	1.1	0.6	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.3	1.1	0.1
IPI00643458	SH3KBP1	SH3 domain-containing kinase-binding protein 1 isoform c	100.0%	22.7	7	7	7	5	8,035,931	8,521,328	8,054,233	9,252,832	734,543	486,233	493,754	422,065	20.4	12.8	13.7	10.2	1.1	0.6	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.3	1.1	0.1
IPI00645893	SH3KBP1	Uncharacterized protein	100.0%	14.9	7	7	7	5	8,035,931	8,521,328	8,054,233	9,252,832	734,543	486,233	493,754	422,065	20.4	12.8	13.7	10.2	1.1	0.6	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.3	1.1	0.1
IPI01014751	SH3KBP1	cDNA FLJ59425, highly similar to SH3-domain kinase-binding protein 1	100.0%	24.0	7	7	7	5	8,035,931	8,521,328	8,054,233	9,252,832	734,543	486,233	493,754	422,065	20.4	12.8	13.7	10.2	1.1	0.6	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.3	1.1	0.1
				ANSPSLFGTEGKPK	2	97.8%	1																									
				EGDIVTLINK	2	88.1%	1																									
				IDLAGSSLSGILDKDLSDR	3	100.0%	1																									
				MEPAASSQAAVEELR	2	99.2%	1																									
				RGVFPDNFVK	2	95.1%	1																									
				SNDIDLEGFDSVVSSTEK	2	100.0%	1																									
				TVTISQVSDNK	2	100.0%	1																									
IPI00295022	NKTR	NK-tumor recognition protein	99.2%	1.2	1	1	1	1	5,232,470	6,733,920	4,972,570	7,039,810	782,314	307,608	290,094	725,110	33.4	10.2	13.0	23.0	1.3	0.1	-1.1	0.8	1.3	0.1	-1.4	0.003	1.0	0.7	1.4	0.03
				TSTSDSEGSCSNSENNR	3	81.2%	1																									
IPI00295209	SNX5	Sorting nexin-5	99.5%	5.9	2	2	2	2	5,507,220	5,725,193	5,379,793	6,261,253	481,352	211,273	339,236	256,603	19.5	8.3	14.1	9.2	1.0	0.7	-1.0	0.8	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.07
IPI00513893	SNX5	Uncharacterized protein	99.5%	6.5	2	2	2	2	5,507,220	5,725,193	5,379,793	6,261,253	481,352	211,273	339,236	256,603	19.5	8.3	14.1	9.2	1.0	0.7	-1.0	0.8	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.07
				NNVSLLQSCIDLFK	2	92.2%	1																									
				YYMLNIEAAK	2	99.5%	1																									
IPI00295386	CBR1	Carbonyl reductase [NADPH] 1	100.0%	37.9	8	10	12	1	32,116,092	32,717,829	33,086,427	37,078,508	2,406,362	1,268,892	2,689,115	939,323	16.8	8.7	18.2	5.7	1.0	0.8	1.0	0.8	1.2	0.1	1.0	0.9	1.1	0.02	1.1	0.2
				EYGGLDVLVNNAGIAFK	2	100.0%	2																									
				EYGGLDVLVNNAGIAFK	3	100.0%	1																									
				FHQLDIDDLQSIR	2	100.0%	1																									
				FHQLDIDDLQSIR	3	99.9%	1																									
				FRSETITEEELVGLMNK	3	100.0%	1																									
				GQAAVQQLQAEGLSPR	2	100.0%	2																									
				KEYGGLDVLVNNAGIAFK	3	99.7%	1																									
				LFSGDVVLTAR	2	99.8%	1																									
				SETITEEELVGLMNK	2	100.0%	1																									
				SPEEGAETPVYLALLPPDAEGPHGQFVSEK	3	100.0%	1																									
IPI00295400	WARS	isoform 1 of Tryptophanyl-tRNA synthetase, cytoplasmic	100.0%	22.9	7	7	7	1	12,387,775	13,506,125	12,830,140	15,136,420	728,470	614,133	850,284	557,432	13.2	10.2	14.8	8.2	1.1	0.3	1.0	0.7	1.2	0.02	-1.1	0.5	1.1	0.08	1.2	0.05
				AGNASKDEIDSAVK	3	97.7%	1																									
				ALIEVLQPLIAEHQAR	2	99.1%	1																									
				DIIACGFDINK	2	95.1%	1																									
				DLTLDQAYSYAVENAK	2	100.0%	1																									
				DMNQVLDAYENK	2	99.9%	1																									
				ISFPAIQAAPSFSNSFPQIFR	3	100.0%	1																									
				TFIFSDLDYMGMSSGFYK	2	99.5%	1																									
IPI00295437	LAMB4	isoform 1 of Laminin subunit beta-4	99.9%	1.9	2	2	2	1	8,009,521	11,217,421	10,517,946	11,308,818	1,452,321	1,193,435	557,843	887,107	40.6	23.8	11.9	17.5	1.4	0.1	1.3	0.2	1.4	0.09	-1.1	0.6	1.0	1	1.1	0.5
				GPGCHGSLTLSTNALQKAQEAK	2	97.8%	1																									

				KIQDLNLSRQAK	2	94.1%	1																									
IPI00295494	CCDC39	isoform 2 of Coiled-coil domain-containing protein 39	97.6%	1.3	1	1	1	2	1,077,965	961,825	1,284,067	1,099,407	117,038	91,141	157,718	214,154	24.3	21.2	27.5	43.6	-1.1	0.5	1.2	0.3	1.0	0.9	1.3	0.1	1.1	0.6	-1.2	0.5
IPI00790221	CCDC39	isoform 1 of Coiled-coil domain-containing protein 39	97.6%	1.1	1	1	1	2	1,077,965	961,825	1,284,067	1,099,407	117,038	91,141	157,718	214,154	24.3	21.2	27.5	43.6	-1.1	0.5	1.2	0.3	1.0	0.9	1.3	0.1	1.1	0.6	-1.2	0.5
				AEEVLSLEKR	2	97.6%	1																									
IPI00295542	NUCB1	Nucleobindin-1	100.0%	5.2	2	2	2	1	1,925,867	1,965,352	2,389,643	2,100,113	130,723	237,348	115,482	76,183	15.2	27.0	10.8	8.1	1.0	0.9	1.2	0.03	1.1	0.3	1.2	0.1	1.1	0.6	-1.1	0.07
				DLELLIQTATR	2	99.8%	1																									
				LVTLEEFLASTQR	2	99.4%	1																									
IPI00295598	CBARA1	isoform 3 of Calcium uptake protein 1, mitochondrial	95.8%	4.4	1	1	1	5	145,651	148,646	150,276	186,138	13,444	20,142	31,533	17,665	20.6	30.3	46.9	21.2	1.0	0.9	1.0	0.9	1.3	0.1	1.0	1	1.3	0.2	1.2	0.4
IPI00872133	CBARA1	isoform 1 of Calcium uptake protein 1, mitochondrial	95.8%	4.4	1	1	1	5	145,651	148,646	150,276	186,138	13,444	20,142	31,533	17,665	20.6	30.3	46.9	21.2	1.0	0.9	1.0	0.9	1.3	0.1	1.0	1	1.3	0.2	1.2	0.4
IPI00873942	CBARA1	55 kDa protein	95.8%	4.4	1	1	1	5	145,651	148,646	150,276	186,138	13,444	20,142	31,533	17,665	20.6	30.3	46.9	21.2	1.0	0.9	1.0	0.9	1.3	0.1	1.0	1	1.3	0.2	1.2	0.4
IPI00888290	CBARA1	isoform 2 of Calcium uptake protein 1, mitochondrial	95.8%	5.2	1	1	1	5	145,651	148,646	150,276	186,138	13,444	20,142	31,533	17,665	20.6	30.3	46.9	21.2	1.0	0.9	1.0	0.9	1.3	0.1	1.0	1	1.3	0.2	1.2	0.4
IPI00981358	CBARA1	Uncharacterized protein	95.8%	5.1	1	1	1	5	145,651	148,646	150,276	186,138	13,444	20,142	31,533	17,665	20.6	30.3	46.9	21.2	1.0	0.9	1.0	0.9	1.3	0.1	1.0	1	1.3	0.2	1.2	0.4
				LMMVAFLGASAVTASTGLLWK	2	95.8%	1																									
IPI00295701	ALS2CR8	isoform 1 of Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 8 p	92.3%	1.8	1	1	1	3	3,845,803	4,167,767	3,908,997	4,599,000	368,044	135,102	246,150	68,982	21.4	7.3	14.1	3.4	1.1	0.4	1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.02	1.2	0.05
IPI00924961	ALS2CR8	cDNA FLJ59114, highly similar to Amyotrophic lateral sclerosis 2 chromosomalregio	92.3%	2.0	1	1	1	3	3,845,803	4,167,767	3,908,997	4,599,000	368,044	135,102	246,150	68,982	21.4	7.3	14.1	3.4	1.1	0.4	1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.02	1.2	0.05
IPI00925234	ALS2CR8	cDNA FLJ59532, highly similar to Amyotrophic lateral sclerosis 2 chromosomalregio	92.3%	2.0	1	1	1	3	3,845,803	4,167,767	3,908,997	4,599,000	368,044	135,102	246,150	68,982	21.4	7.3	14.1	3.4	1.1	0.4	1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.02	1.2	0.05
				HNLSFFPTVNDIK	3	92.3%	1																									
IPI00295741	CTSB	Cathepsin B	100.0%	30.1	7	8	10	2	19,297,820	19,215,438	19,130,864	21,532,503	1,261,064	476,560	1,120,581	430,821	14.6	5.6	13.1	4.5	-1.0	1	-1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.007	1.1	0.1
IPI00909303	CTSB	Uncharacterized protein	100.0%	37.1	7	8	10	2	19,297,820	19,215,438	19,130,864	21,532,503	1,261,064	476,560	1,120,581	430,821	14.6	5.6	13.1	4.5	-1.0	1	-1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.007	1.1	0.1
				DQGSCGSCWAFGAVEAISDR	2	100.0%	1																									
				DQGSCGSCWAFGAVEAISDR	3	98.3%	1																									
				EQWPQCPTIK	2	99.9%	1																									
				GQDHCGIESEVVAGIPR	2	100.0%	2																									
				ICEPGYSPTYK	2	99.4%	1																									
				LPASFDAR	2	98.1%	1																									
				NGPVEGAFSVYSDFLLYK	2	100.0%	1																									
				SGVYQHVTGEMMGGHAIR	3	100.0%	2																									
IPI00295772	CYP51A1	lanosterol 14-alpha demethylase isoform 1	99.9%	4.7	2	2	2	2	2,649,495	2,527,654	2,888,218	2,834,003	380,609	162,520	232,473	139,404	32.1	14.4	18.0	11.0	-1.0	0.8	1.1	0.6	1.1	0.7	1.1	0.2	1.1	0.2	-1.0	0.8
IPI01013163	CYP51A1	cDNA FLJ34004 fis, clone FCBBF1000232, highly similar to Cytochrome P450 51A1	99.9%	5.4	2	2	2	2	2,649,495	2,527,654	2,888,218	2,834,003	380,609	162,520	232,473	139,404	32.1	14.4	18.0	11.0	-1.0	0.8	1.1	0.6	1.1	0.7	1.1	0.2	1.1	0.2	-1.0	0.8
				NEDLNAEDVYSR	2	99.8%	1																									
				SPIEFLENAYEK	2	98.5%	1																									
IPI00295851	COPB1	Coatomer subunit beta	100.0%	15.7	10	10	10	1	52,196,910	53,406,860	55,987,780	60,172,970	5,049,046	818,815	2,954,479	1,042,619	21.6	3.4	11.8	3.9	1.0	0.8	1.1	0.5	1.2	0.2	1.0	0.4	1.1	0.0009	1.1	0.2
				CIYNLLQSSSPAVK	2	100.0%	1																									
				EAGELKPEEEITVGPVQK	3	99.8%	1																									
				KPITDDDVDR	2	87.2%	1																									
				LVEKPSPLTLAPHDFANIK	3	100.0%	1																									
				NVTVQPDDPISFMQLTAK	2	100.0%	1																									
				QMWAEFEWENK	2	97.4%	1																									
				SQGMALSLGDK	2	100.0%	1																									
				TLQLALDLVSSR	2	100.0%	1																									
				VTVNTNMVDLNDYLQHILK	3	100.0%	1																									
				YEAAGTLVTLSSAPTAIK	2	100.0%	1																									
IPI00295857	COPA	isoform 1 of Coatomer subunit alpha	100.0%	5.3	5	5	5	2	10,793,390	11,209,515	12,000,125	12,805,925	743,116	330,356	904,111	448,444	15.4	6.6	16.9	7.8	1.0	0.6	1.1	0.3	1.2	0.05	1.1	0.4	1.1	0.02	1.1	0.4
IPI00646493	COPA	isoform 2 of Coatomer subunit alpha	100.0%	5.3	5	5	5	2	10,793,390	11,209,515	12,000,125	12,805,925	743,116	330,356	904,111	448,444	15.4	6.6	16.9	7.8	1.0	0.6	1.1	0.3	1.2	0.05	1.1	0.4	1.1	0.02	1.1	0.4
				EYIVGLSVETER	2	95.7%	1																									
				GVNWAAFHPTMPLIVSGADDR	3	100.0%	1																									
				LVGQSIIAYLQK	2	100.0%	1																									
				TLDLPIYVTR	2	97.5%	1																									
				VLTIDPTEFK	2	96.9%	1																									
IPI00296053	FH	isoform Mitochondrial of Fumarate hydratase, mitochondrial	100.0%	20.6	5	5	6	2	8,323,947	8,057,353	8,368,485	9,327,525	962,741	321,786	720,192	360,558	25.9	8.9	19.2	8.6	-1.0	0.8	1.0	1	1.1	0.4	1.0	0.7	1.2	0.03	1.1	0.3
IPI00759715	FH	isoform Cytoplasmic of Fumarate hydratase, mitochondrial	100.0%	22.5	5	5	6	2	8,323,947	8,057,353	8,368,485	9,327,525	962,741	321,786	720,192	360,558	25.9	8.9	19.2	8.6	-1.0	0.8	1.0	1	1.1	0.4	1.0	0.7	1.2	0.03	1.1	0.3
				AAAEVNQDYGLDPK	2	100.0%	1																									
				ETAIELGYLTAEQFDEWVKPK	3	100.0%	1																									
				LMNESLMLVTALNPHIGYDK	3	100.0%	1																									
				LNDHFPLVVWQTGSGTQTNMNVNEVISNR	3	100.0%	2																									
				SGLGELILPENEPGSSIMPGK	2	100.0%	1																									
IPI00646889	C10orf57;C10orf58	Uncharacterized protein	100.0%	10.6	2	2	2	3	1,808,358	1,847,269	1,842,861	1,972,857	54,250	92,176	89,070	146,189	6.7	11.2	10.8	16.6	1.0	0.7	1.0	0.7	1.1	0.3	-1.0	1	1.1	0.5	1.1	0.5
IPI00296190	C10orf58	UPF0765 protein C10orf58	100.0%	10.0	2	2	2	3	1,808,358	1,847,269	1,842,861	1,972,857	54,250	92,176	89,070	146,189	6.7	11.2	10.8	16.6	1.0	0.7	1.0	0.7	1.1	0.3	-1.0	1	1.1	0.5	1.1	0.5
IPI00646289	C10orf58	25 kDa protein	100.0%	10.3	2	2	2	3	1,808,358	1,847,269	1,842,861	1,972,857	54,250	92,176	89,070	146,189	6.7	11.2	10.8	16.6	1.0	0.7	1.0	0.7	1.1	0.3	-1.0	1	1.1	0.5	1.1	0.5
				AALEYLEDIDLK	2	99.1%	1																									
				VNLLSVLEAAK	2	96.1%	1																									
IPI00296215	EPCAM	Epithelial cell adhesion molecule	100.0%	11.8	3	3	3	2	8,448,050	8,436,012	8,576,830	9,557,243	792,116	655,789	645,850	338,440	21.0	17.4	16.8	7.9	-1.0	1	1.0	0.9	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.2
IPI00893715	EPCAM	Uncharacterized protein	100.0%	10.8	3	3	3	2	8,448,050	8,436,012	8,576,830	9,557,243	792,116	655,789	645,850	338,440	21.0	17.4	16.8	7.9	-1.0	1	1.0	0.9	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.2
				APEFSMQGLK	2	99.2%	1																									
				LAVNCFVNNNR	2	100.0%	1																									
				TQNDVDIADVAYYFEK	2	100.0%	1																									
IPI00296259	TMED4	isoform 1 of Transmembrane emp24 domain-containing protein 4	99.9%	7.5	1	2	2	5	1,047,470	1,185,090	1,094,508	1,128,188	99,529	34,953	91,798	48,658	21.3	6.6	18.8	9.6	1.1	0.2	1.0	0.7	1.1	0.5	-1.1	0.4	-1.1	0.4	1.0	0.8
IPI00914891	TMED4	isoform 2 of Transmembrane emp24 domain-containing protein 4	99.9%	8.1	1	2	2	5	1,047,470	1,185,090	1,094,508	1,128,188	99,529	34,953	91,798	48,658	21.3	6.6	18.8	9.6	1.1	0.2	1.0	0.7	1.1	0.5	-1.1	0.4	-1.1	0.4	1.0	0.8
IPI00914908	TMED4	isoform 3 of Transmembrane emp24 domain-containing protein 4	99.9%	9.1	1	2	2	5	1,047,470	1,185,090	1,094,508	1,128,188	99,529	34,953	91,798	48,658	21.3	6.6	18.8	9.6	1.1	0.2	1.0	0.7	1.1	0.5	-1.1	0.4	-1.1	0.4	1.0	0.8
IPI00925777	TMED4	Uncharacterized protein	99.9%	9.6	1	2	2	5	1,047,470	1,185,090	1,094,508	1,128,188	99,529	34,953	91,798	48,658	21.3	6.6	18.8	9.6	1.1	0.2	1.0	0.7	1.1	0.5	-1.1	0.4	-1.1	0.4	1.0	0.8
IPI00953634	TMED4	Uncharacterized protein	99.9%	8.1	1	2	2	5	1,047,470	1,185,090	1,094,508	1,128,188	99,529	34,953	91,798	48,658	21.3	6.6	18.8	9.6	1.1	0.2	1.0	0.7	1.1	0.5	-1.1	0.4	-1.1	0.4	1.0	0.8
				CFIEEIPDETMVIGNYR	2	99.9%	1																									
				CFIEEIPDETMVIGNYR	3	91.6%	1																									
IPI00786995	LOC731751	DNA-dependent protein kinase catalytic subunit-like	97.1%	0.5	2	2	2	3	2,938,213	3,340,553	3,008,657	3,378,000	287,931	133,149	245,569	129,099	21.9	8.9	18.3	8.6	1.1	0.2	1.0	0.9	1.1	0.2	-1.1	0.3	1.0	0.8	1.1	0.2
IPI00296337	PRKDC	isoform 1 of DNA-dependent protein kinase catalytic subunit	97.1%	0.5	2	2	2	3	2,938,213	3,340,553	3,008,657	3,378,000	287,931	133,149	245,569	129,099	21.9	8.9	18.3	8.6	1.1	0.2	1.0	0.9	1.1	0.2	-1.1	0.3	1.0	0.8	1.1	0.2
IPI00376215	PRKDC	isoform 2 of DNA-dependent protein kinase catalytic subunit	97.1%	0.5	2	2	2	3	2,938,213	3,340,553	3,008,657	3,378,000	287,931	133,149	245,569	129,099	21.9	8.9	18.3	8.6	1.1	0.2	1.0	0.9	1.1	0.2	-1.1	0.3	1.0	0.8	1.1	0.2
				DDWLVSWVQSYCR	2	85.4%	1																									
				LNSNEARLK	2	89.2%	1																									
IPI00296340	JMJD5	isoform 1 of Lysine-specific demethylase 8	92.0%	4.6	1	1	1	4	1,055,058	1,043,920	1,086,068	1,123,650	90,476	62,410	60,114	91,110	19.2	13.4	12.4	18.1	-1.0	0.9	1.0	0.8	1.1	0.6	1.0	0.6	1.1	0.5	1.0	0.7
IPI00435577	JMJD5	isoform 2 of Lysine-specific demethylase 8	92.0%	8.6	1	1	1	4	1,055,058	1,043,920	1,086,068	1,123,650	90,476	62,410	60,114	91,110	19.2	13.4	12.4	18.1	-1.0	0.9	1.0	0.8	1.1	0.6	1.0	0.6	1.1	0.5	1.0	0.7
IPI00922284	JMJD5	isoform 3 of Lysine-specific demethylase 8	92.0%	4.2	1	1	1	4	1,055,058	1,043,920	1,086,068	1,123,650	90,476	62,410	60,114	91,110	19.2	13.4	12.4	18.1	-1.0	0.9	1.0	0.8	1.1	0.6	1.0	0.6	1.1	0.5	1.0	0.7
IPI01009611	JMJD5	cDNA FLJ61151	92.0%	13.0	1	1	1	4	1,055,058	1,043,920	1,086,068	1,123,650	90,476	62,410	60,114	91,110	19.2	13.4	12.4	18.1	-1.0	0.9	1.0	0.8	1.1	0.6	1.0	0.6	1.1	0.5	1.0	0.7
				APFLSCILSPGEILFIPVK	3	92.0%	1																									
IPI00296365	CENPE	isoform 1 of Centromere-associated protein E	97.1%	0.9	2	2	2	2	4,733,197	4,467,865	4,166,917	4,988,532	445,150	151,331	218,809	254,482	21.0	7.6	11.7	11.4	-1.1	0.6	-1.1	0.3	1.1	0.6	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00619925	CENPE	isoform 3 of Centromere-associated protein E	97.1%	1.0	2	2	2	2	4,733,197	4,467,865	4,166,917	4,988,532	445,150	151,331	218,809	254,482	21.0	7.6	11.7	11.4	-1.1	0.6	-1.1	0.3	1.1	0.6	-1.1	0.3	1.1	0.1	1.2	0.04
				ANLSLPYLQTK	2	87.7%	1																									
				NELQQMLESVIAEK	2	97.1%	1																									
IPI00296370	LCMT1	Uncharacterized protein	99.8%	3.6	1	1	1	3	2,485,290	2,482,793	2,362,320	2,591,260	264,960	128,587	202,406	220,579	23.8	11.6	19.2	19.0	-1.0	1	-1.1	0.7	1.0	0.8	-1.1	0.6	1.0	0.7	1.1	0.5
IPI00414463	LCMT1	isoform 2 of Leucine carboxyl methyltransferase 1	99.8%	3.4	1	1	1	3	2,485,290	2,482,793	2,362,320	2,591,260	264,960	128,587	202,406	220,579	23.8	11.6	19.2	19.0	-1.0	1	-1.1	0.7	1.0	0.8	-1.1	0.6	1.0	0.7	1.1	0.5
IPI00651717	LCMT1	leucine carboxyl methyltransferase 1 isoform b	99.8%	4.3	1	1	1	3	2,485,290	2,482,793	2,362,320	2,591,260	264,960	128,587	202,406	220,579	23.8	11.6	19.2	19.0	-1.0	1	-1.1	0.7	1.0	0.8	-1.1	0.6	1.0	0.7	1.1	0.5
				YFEVDFPMIVTR	2	98.9%	1																									
IPI00296432	IWS1	isoform 1 of Protein IWS1 homolog	100.0%	5.4	3	3	3	4	2,792,155	3,517,465	3,141,328	3,423,888	302,252	253,947	522,909	198,161	24.2	16.1	37.2	12.9	1.3	0.1	1.1	0.6	1.2	0.1	-1.1	0.5	-1.0	0.8	1.1	0.6
IPI00386012	IWS1	isoform 3 of Protein IWS1 homolog	100.0%	7.2	3	3	3	4	2,792,155	3,517,465	3,141,328	3,423,888	302,252	253,947	522,909	198,161	24.2	16.1	37.2	12.9	1.3	0.1	1.1	0.6	1.2	0.1	-1.1	0.5	-1.0	0.8	1.1	0.6
IPI00908727	IWS1	cDNA FLJ53983, highly similar to IWS1 homolog	100.0%	6.0	3	3	3	4	2,792,155	3,517,465	3,141,328	3,423,888	302,252	253,947	522,909	198,161	24.2	16.1	37.2	12.9	1.3	0.1	1.1	0.6	1.2	0.1	-1.1	0.5	-1.0	0.8	1.1	0.6
IPI00909451	IWS1	isoform 2 of Protein IWS1 homolog	100.0%	5.7	3	3	3	4	2,792,155	3,517,465	3,141,328	3,423,888	302,252	253,947	522,909	198,161	24.2	16.1	37.2	12.9	1.3	0.1	1.1	0.6	1.2	0.1	-1.1	0.5	-1.0	0.8	1.1	0.6
				DGGTFISDADDVVSAMIVK	2	99.2%	1																									
				ETFIDSGVMSAIK	2	98.4%	1																									
				TIASDSEEEAGK	2	92.1%	1																									
IPI00296441	ADA	Adenosine deaminase	99.1%	10.7	2	2	2	2	14,996,940	15,457,560	14,325,180	16,508,195	1,259,647	855,309	1,123,821	935,093	18.8	12.4	17.5	12.7	1.0	0.8	-1.0	0.7	1.1	0.4	-1.1	0.4	1.1	0.4	1.2	0.2
IPI01012449	ADA	38 kDa protein	99.1%	11.5	2	2	2	2	14,996,940	15,457,560	14,325,180	16,508,195	1,259,647	855,309	1,123,821	935,093	18.8	12.4	17.5	12.7	1.0	0.8	-1.0	0.7	1.1	0.4	-1.1	0.4	1.1	0.4	1.2	0.2
				ELLDLLYK	2	91.6%	1																									
				VEPIPWNQAEGDLTPDEVVALVGQGLQEGER	3	90.2%	1																									
IPI00296528	ANXA10	Annexin A10	100.0%	17.0	5	5	6	2	15,273,495	15,505,585	14,309,175	16,539,920	1,278,595	852,848	615,147	460,204	18.7	12.3	9.6	6.2	1.0	0.9	-1.1	0.5	1.1	0.4	-1.1	0.3	1.1	0.3	1.2	0.02
IPI00873355	ANXA10	Uncharacterized protein	100.0%	17.0	5	5	6	2	15,273,495	15,505,585	14,309,175	16,539,920	1,278,595	852,848	615,147	460,204	18.7	12.3	9.6	6.2	1.0	0.9	-1.1	0.5	1.1	0.4	-1.1	0.3	1.1	0.3	1.2	0.02
				DTLMNLVQGTR	2	94.8%	1																									
				GVGTDENCLIEILASR	2	100.0%	2																									
				SEIDLLTIR	2	94.2%	1																									
				TMLQMILCNK	2	100.0%	1																									
				TNGEIFQMR	2	90.3%	1																									
IPI00296863	DCTD	isoform 1 of Deoxycytidylate deaminase	99.3%	6.2	1	1	1	4	552,448	424,095	520,295	621,380	94,062	35,518	51,559	46,907	38.1	18.7	22.2	16.9	-1.3	0.3	-1.1	0.8	1.1	0.5	1.2	0.2	1.5	0.01	1.2	0.2
IPI00554705	DCTD	isoform 2 of Deoxycytidylate deaminase	99.3%	5.8	1	1	1	4	552,448	424,095	520,295	621,380	94,062	35,518	51,559	46,907	38.1	18.7	22.2	16.9	-1.3	0.3	-1.1	0.8	1.1	0.5	1.2	0.2	1.5	0.01	1.2	0.2
IPI00910904	DCTD	cDNA FLJ52248, highly similar to Deoxycytidylate deaminase	99.3%	9.2	1	1	1	4	552,448	424,095	520,295	621,380	94,062	35,518	51,559	46,907	38.1	18.7	22.2	16.9	-1.3	0.3	-1.1	0.8	1.1	0.5	1.2	0.2	1.5	0.01	1.2	0.2
IPI00968301	DCTD	Uncharacterized protein	99.3%	6.5	1	1	1	4	552,448	424,095	520,295	621,380	94,062	35,518	51,559	46,907	38.1	18.7	22.2	16.9	-1.3	0.3	-1.1	0.8	1.1	0.5	1.2	0.2	1.5	0.01	1.2	0.2
				LLFNMAGVTFR	2	99.3%	1																									
IPI00296907	ACOX1	isoform 1 of Peroxisomal acyl-coenzyme A oxidase 1	100.0%	5.5	2	2	2	2	2,033,608	2,292,135	2,335,545	2,301,755	136,667	235,591	165,968	114,027	15.0	23.0	15.9	11.1	1.1	0.4	1.1	0.2	1.1	0.2	1.0	0.9	1.0	1	-1.0	0.9
IPI00477729	ACOX1	isoform 2 of Peroxisomal acyl-coenzyme A oxidase 1	100.0%	5.5	2	2	2	2	2,033,608	2,292,135	2,335,545	2,301,755	136,667	235,591	165,968	114,027	15.0	23.0	15.9	11.1	1.1	0.4	1.1	0.2	1.1	0.2	1.0	0.9	1.0	1	-1.0	0.9
				EIENMILNDPDFQHEDLNFLTR	3	99.6%	1																									
				YDGNVYENLFEWAK	2	100.0%	1																									
IPI00296913	NUDT5	ADP-sugar pyrophosphatase	100.0%	14.2	3	3	5	4	4,314,633	4,543,422	4,609,097	5,174,923	440,130	124,152	442,976	170,093	22.8	6.1	21.5	7.4	1.1	0.6	1.1	0.6	1.2	0.1	1.0	0.9	1.1	0.02	1.1	0.3
IPI00646762	NUDT5	Uncharacterized protein	100.0%	13.4	3	3	5	4	4,314,633	4,543,422	4,609,097	5,174,923	440,130	124,152	442,976	170,093	22.8	6.1	21.5	7.4	1.1	0.6	1.1	0.6	1.2	0.1	1.0	0.9	1.1	0.02	1.1	0.3
IPI00646261	NUDT5	Uncharacterized protein	100.0%	16.4	3	3	5	4	4,314,633	4,543,422	4,609,097	5,174,923	440,130	124,152	442,976	170,093	22.8	6.1	21.5	7.4	1.1	0.6	1.1	0.6	1.2	0.1	1.0	0.9	1.1	0.02	1.1	0.3
IPI00647797	NUDT5	Uncharacterized protein	100.0%	16.7	3	3	5	4	4,314,633	4,543,422	4,609,097	5,174,923	440,130	124,152	442,976	170,093	22.8	6.1	21.5	7.4	1.1	0.6	1.1	0.6	1.2	0.1	1.0	0.9	1.1	0.02	1.1	0.3
				EQTADGVAVIPVLQR	2	100.0%	2																									
				PGDGEFVEVISLPK	2	100.0%	2																									
				PKPGDGEFVEVISLPK	3	99.8%	1																									
IPI00297045	MKLN1	isoform 1 of Muskelin	95.5%	1.5	1	1	1	6	673,607	678,997	686,657	780,738	59,114	15,994	46,728	23,204	19.6	5.3	15.2	6.7	1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.9	1.1	0.007	1.1	0.1
IPI00815995	MKLN1	muskelin isoform 1	95.5%	1.5	1	1	1	6	673,607	678,997	686,657	780,738	59,114	15,994	46,728	23,204	19.6	5.3	15.2	6.7	1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.9	1.1	0.007	1.1	0.1
IPI00924627	MKLN1	Uncharacterized protein	95.5%	14.1	1	1	1	6	673,607	678,997	686,657	780,738	59,114	15,994	46,728	23,204	19.6	5.3	15.2	6.7	1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.9	1.1	0.007	1.1	0.1
IPI00924849	MKLN1	Uncharacterized protein	95.5%	11.3	1	1	1	6	673,607	678,997	686,657	780,738	59,114	15,994	46,728	23,204	19.6	5.3	15.2	6.7	1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.9	1.1	0.007	1.1	0.1
IPI00925287	MKLN1	Uncharacterized protein	95.5%	8.7	1	1	1	6	673,607	678,997	686,657	780,738	59,114	15,994	46,728	23,204	19.6	5.3	15.2	6.7	1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.9	1.1	0.007	1.1	0.1
IPI00926744	MKLN1	20 kDa protein	95.5%	6.5	1	1	1	6	673,607	678,997	686,657	780,738	59,114	15,994	46,728	23,204	19.6	5.3	15.2	6.7	1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.9	1.1	0.007	1.1	0.1
				NDYNKETFTLK	2	95.5%	1																									
IPI00297084	DDOST	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	99.9%	5.7	2	2	2	2	6,206,735	6,485,295	6,216,660	7,243,895	629,567	407,057	341,367	289,802	22.7	14.0	12.3	9.0	1.0	0.7	1.0	1	1.2	0.2	-1.0	0.6	1.1	0.2	1.2	0.05
IPI00910419	DDOST	cDNA FLJ52929, highly similar to Dolichyl-diphosphooligosaccharide--proteinglycosy	99.9%	6.2	2	2	2	2	6,206,735	6,485,295	6,216,660	7,243,895	629,567	407,057	341,367	289,802	22.7	14.0	12.3	9.0	1.0	0.7	1.0	1	1.2	0.2	-1.0	0.6	1.1	0.2	1.2	0.05
				TLVLLDNLNVR	2	99.3%	1																									
				YSQTGNYELAVALSR	2	99.9%	1																									
IPI00297160	CD44	isoform 12 of CD44 antigen	99.6%	3.6	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00305064	CD44	isoform 1 of CD44 antigen	99.6%	1.8	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00418465	CD44	isoform 4 of CD44 antigen	99.6%	1.9	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00419219	CD44	isoform 10 of CD44 antigen	99.6%	2.6	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00827650	CD44	isoform 3 of CD44 antigen	99.6%	1.8	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00827795	CD44	isoform 8 of CD44 antigen	99.6%	1.9	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00827893	CD44	isoform 11 of CD44 antigen	99.6%	3.0	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00827937	CD44	isoform 14 of CD44 antigen	99.6%	3.3	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00827982	CD44	isoform 13 of CD44 antigen	99.6%	3.1	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00828056	CD44	isoform 16 of CD44 antigen	99.6%	2.0	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00828064	CD44	isoform 6 of CD44 antigen	99.6%	1.9	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2

IPI00828192	CD44	isoform 17 of CD44 antigen	99.6%	1.9	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00918020	CD44	cDNA FLJ52702, highly similar to Homo sapiens CD44 antigen (homing function and	99.6%	4.0	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00922478	CD44	CD44 antigen isoform 7 precursor	99.6%	3.8	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00956122	CD44	isoform 5 of CD44 antigen	99.6%	1.8	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00974500	CD44	31 kDa protein	99.6%	4.5	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00982553	CD44	20 kDa protein	99.6%	7.0	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00982959	CD44	9 kDa protein	99.6%	15.9	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
IPI00984539	CD44	isoform 7 of CD44 antigen	99.6%	1.8	1	1	1	19	960,847	957,679	932,911	999,858	34,279	23,050	38,399	21,787	8.0	5.4	9.2	4.9	-1.0	0.9	-1.0	0.6	1.0	0.4	-1.0	0.6	1.0	0.2	1.1	0.2
				LVINSGNGAVEDR	2	99.6%	1																									
IPI00297241	URB1	Nucleolar pre-ribosomal-associated protein 1	99.5%	1.6	2	2	2	1	8,845,370	7,505,000	11,004,970	8,199,640	364,956	950,515	533,247	430,845	9.2	28.3	10.8	11.8	-1.2	0.2	1.2	0.01	-1.1	0.3	1.5	0.01	1.1	0.5	-1.3	0.003
				MLLTAVQLLYSPESSVR	3	86.9%	1																									
				RPESETMLIFQVFEAILLR	2	96.1%	1																									
IPI00297322	ARFGAP2	ADP-ribosylation factor GTPase-activating protein 2	100.0%	5.6	2	2	2	3	1,931,487	1,577,049	1,443,728	1,681,360	158,173	172,229	142,588	169,737	18.3	24.4	22.1	22.6	-1.2	0.2	-1.3	0.05	-1.1	0.3	-1.1	0.6	1.1	0.7	1.2	0.3
IPI00937554	ARFGAP2	cDNA FLJ58830, highly similar to Homo sapiens zinc finger protein 289, ID1 regulate	100.0%	7.6	2	2	2	3	1,931,487	1,577,049	1,443,728	1,681,360	158,173	172,229	142,588	169,737	18.3	24.4	22.1	22.6	-1.2	0.2	-1.3	0.05	-1.1	0.3	-1.1	0.6	1.1	0.7	1.2	0.3
IPI00941529	ARFGAP2	cDNA FLJ53674, highly similar to Homo sapiens zinc finger protein 289, ID1 regulate	100.0%	7.0	2	2	2	3	1,931,487	1,577,049	1,443,728	1,681,360	158,173	172,229	142,588	169,737	18.3	24.4	22.1	22.6	-1.2	0.2	-1.3	0.05	-1.1	0.3	-1.1	0.6	1.1	0.7	1.2	0.3
				SQLDLFDDVGTFASGPPK	2	100.0%	1																									
				VSSQSFSEIER	2	99.9%	1																									
IPI00297452	TFG	Tyrosine-protein kinase receptor	100.0%	7.9	3	3	3	1	3,389,612	3,424,013	3,356,771	3,678,802	268,432	110,703	283,234	69,155	17.7	7.2	18.9	4.2	1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	0.8	1.1	0.09	1.1	0.3
				LLDSLEPPGEPGPSTNIPENDTVDGREEK	3	100.0%	1																									
				LLSNDEVTIK	2	100.0%	1																									
				QSTQVMAASMSAFDPLKNQDEINK	3	97.0%	1																									
IPI00985462	-	cDNA FLJ58398, highly similar to A-kinase anchor protein 8	98.5%	2.2	1	1	1	2	2,925,785	2,723,605	2,890,945	2,815,665	144,756	194,179	199,611	154,958	11.1	15.9	15.4	12.3	-1.1	0.4	-1.0	0.9	-1.0	0.6	1.1	0.6	1.0	0.7	-1.0	0.8
IPI00297455	AKAP8L	A-kinase anchor protein 8-like	98.5%	2.0	1	1	1	2	2,925,785	2,723,605	2,890,945	2,815,665	144,756	194,179	199,611	154,958	11.1	15.9	15.4	12.3	-1.1	0.4	-1.0	0.9	-1.0	0.6	1.1	0.6	1.0	0.7	-1.0	0.8
				QTADFLQEYVTNK	2	98.5%	1																									
IPI00297477	SNRPA1	U2 small nuclear ribonucleoprotein A'	99.9%	10.2	2	2	2	1	8,973,850	9,023,720	7,877,470	8,983,520	1,071,316	675,411	445,551	735,042	26.7	16.7	12.7	18.3	1.0	1	-1.1	0.4	1.0	1	-1.1	0.2	-1.0	1	1.1	0.2
				NAIANASTLAEVER	2	86.4%	1																									
				TFNPGAGLPTDK	2	99.6%	1																									
IPI00297487	CTSH	Cathepsin H	98.7%	3.9	1	1	1	3	719,707	693,657	661,197	728,690	99,174	21,235	71,433	21,791	30.8	6.9	24.2	6.7	-1.0	0.8	-1.1	0.6	1.0	0.9	-1.0	0.7	1.1	0.3	1.1	0.4
IPI00375426	CTSH	Uncharacterized protein	98.7%	4.0	1	1	1	3	719,707	693,657	661,197	728,690	99,174	21,235	71,433	21,791	30.8	6.9	24.2	6.7	-1.0	0.8	-1.1	0.6	1.0	0.9	-1.0	0.7	1.1	0.3	1.1	0.4
IPI00982637	CTSH	Uncharacterized protein	98.7%	9.7	1	1	1	3	719,707	693,657	661,197	728,690	99,174	21,235	71,433	21,791	30.8	6.9	24.2	6.7	-1.0	0.8	-1.1	0.6	1.0	0.9	-1.0	0.7	1.1	0.3	1.1	0.4
				GIMGEDTYPYQGK	2	98.7%	1																									
IPI00297579	CBX3	Chromobox protein homolog 3	100.0%	30.1	4	5	7	1	22,950,516	26,821,083	24,910,264	27,304,764	4,011,874	1,653,065	1,450,998	1,931,398	39.1	13.8	13.0	15.8	1.2	0.4	1.1	0.7	1.2	0.4	-1.1	0.4	1.0	0.9	1.1	0.4
				IIGATDSSGELMFLMK	2	100.0%	2																									
				KVEEAEPEEFVVEK	2	100.0%	1																									
				KVEEAEPEEFVVEK	3	99.9%	1																									
				LTWHSCPEDEAQ	2	100.0%	2																									
				WKDSDEADLVLAK	3	99.9%	1																									
IPI00297626	STXBP3	Syntaxin-binding protein 3	97.6%	2.9	1	1	1	1	604,690	476,746	567,451	657,401	35,947	32,826	41,732	42,123	13.3	15.4	16.4	14.3	-1.3	0.03	-1.1	0.5	1.1	0.4	1.2	0.1	1.4	0.01	1.2	0.2
				MTDLLEEGITVVENIYK	2	97.6%	1																									
IPI00297646	COL1A1	Collagen alpha-1(I) chain	92.2%	2.1	1	1	1	1	1,251,622	1,368,083	1,482,340	1,219,441	141,626	71,478	111,747	219,142	25.3	11.7	16.9	40.2	1.1	0.5	1.2	0.2	-1.0	0.9	1.1	0.4	-1.1	0.5	-1.2	0.3
				GETGPAGPTGPVGPVGARGPAGPQGPRGDK	3	92.2%	1																									
IPI00297779	CCT2	T-complex protein 1 subunit beta	100.0%	53.5	22	26	34	1	58,037,873	57,755,220	58,176,718	66,079,802	3,900,664	1,490,840	3,718,344	1,801,724	15.0	5.8	14.3	6.1	-1.0	0.9	1.0	1	1.1	0.1	1.0	0.9	1.1	0.007	1.1	0.09
				AAHSEGNTTAGLDMR	2	100.0%	1																									
				AAHSEGNTTAGLDMR	3	95.2%	1																									
				DASLMVTNDGATILK	2	100.0%	2																									
				EGTIGDMAILGITESFQVK	2	100.0%	1																									
				FRQDLMNIAGTTLSSK	3	99.9%	1																									
				GATQQILDEAER	2	100.0%	2																									
				GSGNLEAIHIIK	2	87.3%	1																									
				ILIANTGMDTDK	2	90.4%	1																									
				KIGVNQPK	2	86.4%	1																									
				KLGGSLADSYLDEGFLLDKK	3	100.0%	1																									
				LALVTGGEIASTFDHPELVK	2	100.0%	1																									
				LAVEAVLR	2	89.1%	1																									
				LGGSLADSYLDEGFLLDK	2	100.0%	1																									
				LGGSLADSYLDEGFLLDKK	2	100.0%	1																									
				LGGSLADSYLDEGFLLDKK	3	100.0%	2																									
				LIEEVMIGEDK	2	100.0%	1																									
				LKGSGNLEAIHIIK	3	98.0%	1																									
				LTSFIGAIAIGDLVK	2	100.0%	2																									
				MLPTIIADNAGYDSADLVAQLR	2	100.0%	2																									
				MLPTIIADNAGYDSADLVAQLR	3	100.0%	2																									
				QDLMNIAGTTLSSK	2	100.0%	1																									
				QLIYNYPEQLFGAAGVMAIEHADFAGVER	3	99.6%	1																									
				QVLLSAAEAAEVILR	3	99.9%	1																									
				SLHDALCVLAQTVK	2	97.5%	1																									
				VQDDEVGDGTTSVTVLAAELLR	2	100.0%	2																									
				VQDDEVGDGTTSVTVLAAELLR	3	100.0%	2																									
IPI00297900	DDX10	Probable ATP-dependent RNA helicase DDX10	92.2%	2.1	1	1	1	2	1,243,590	1,346,380	1,613,775	1,168,135	152,089	53,386	206,902	60,898	27.4	8.9	28.7	11.7	1.1	0.6	1.3	0.2	-1.1	0.7	1.2	0.3	-1.2	0.06	-1.4	0.1
IPI00982941	DDX10	Uncharacterized protein	92.2%	2.2	1	1	1	2	1,243,590	1,346,380	1,613,775	1,168,135	152,089	53,386	206,902	60,898	27.4	8.9	28.7	11.7	1.1	0.6	1.3	0.2	-1.1	0.7	1.2	0.3	-1.2	0.06	-1.4	0.1
				LQWTSTDGLGVLIISPTR	2	89.8%	1																									
IPI00900305	-	isoform 1 of Eukaryotic translation initiation factor 2 subunit 3-like protein	94.2%	6.4	2	2	2	2	3,101,170	2,953,822	2,961,819	3,212,150	188,126	140,943	223,731	149,666	13.6	10.7	16.9	10.4	-1.0	0.5	-1.0	0.6	1.0	0.7	1.0	1	1.1	0.2	1.1	0.4
IPI00297982	EIF2S3	Eukaryotic translation initiation factor 2 subunit 3	94.2%	6.4	2	2	2	2	3,101,170	2,953,822	2,961,819	3,212,150	188,126	140,943	223,731	149,666	13.6	10.7	16.9	10.4	-1.0	0.5	-1.0	0.6	1.0	0.7	1.0	1	1.1	0.2	1.1	0.4
				IVLTNPVCTEVGEK	2	94.2%	1																									
				NEVLMVNIGSLSTGGR	2	92.7%	1																									
IPI00298007	MB21D1	isoform 1 of Protein MB21D1	96.8%	4.6	1	1	1	2	705,844	683,017	663,735	762,540	85,070	57,883	59,868	55,222	27.0	19.0	20.2	16.2	-1.0	0.8	-1.1	0.7	1.1	0.6	-1.0	0.8	1.1	0.3	1.1	0.3
IPI00607846	MB21D1	isoform 2 of Protein MB21D1	96.8%	5.4	1	1	1	2	705,844	683,017	663,735	762,540	85,070	57,883	59,868	55,222	27.0	19.0	20.2	16.2	-1.0	0.8	-1.1	0.7	1.1	0.6	-1.0	0.8	1.1	0.3	1.1	0.3
				AQDTQPSDATSAPGAEGLEPPAAR	2	86.7%	1																									
IPI00298057	PPL	Periplakin	100.0%	9.6	13	13	13	1	72,963,140	74,198,100	71,186,765	87,317,345	8,687,682	2,797,949	5,680,078	3,012,553	26.6	8.4	17.8	7.7	1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.6	1.2	0.01	1.2	0.04
				DMSIQELAVLVSGQK	2	91.0%	1																									
				EVDPQVNWAALVEEK	2	100.0%	1																									
				FSIEEALQSGR	2	91.9%	1																									
				LLYVLEADAAIAK	2	96.9%	1																									
				LQNDPQLEAEYQQLQEDHQR	3	99.8%	1																									
				LQNLEFALNLLR	2	99.5%	1																									
				LSELEFHNSK	2	91.8%	1																									
				NQGPQESVVR	2	98.4%	1																									
				NQLLQEELEALQLQLR	2	99.9%	1																									
				SLLDLENGR	2	95.9%	1																									
				SLLGEVEQNLQAAK	2	97.2%	1																									
				SQECDWEEISVK	2	93.5%	1																									
				VVLQQDPQQAR	2	99.4%	1																									
IPI00298058	SUPT5H	isoform 1 of Transcription elongation factor SPT5	98.7%	1.8	2	2	2	3	3,810,335	3,156,699	3,323,958	3,729,383	136,871	93,760	103,400	273,630	8.0	6.6	7.0	16.4	-1.2	0.004	-1.1	0.02	-1.0	0.8	1.1	0.3	1.2	0.1	1.1	0.2
IPI00655641	SUPT5H	isoform 2 of Transcription elongation factor SPT5	98.7%	1.8	2	2	2	3	3,810,335	3,156,699	3,323,958	3,729,383	136,871	93,760	103,400	273,630	8.0	6.6	7.0	16.4	-1.2	0.004	-1.1	0.02	-1.0	0.8	1.1	0.3	1.2	0.1	1.1	0.2
IPI01010195	SUPT5H	cDNA FLJ55629, highly similar to Transcription elongation factor SPT5	98.7%	1.8	2	2	2	3	3,810,335	3,156,699	3,323,958	3,729,383	136,871	93,760	103,400	273,630	8.0	6.6	7.0	16.4	-1.2	0.004	-1.1	0.02	-1.0	0.8	1.1	0.3	1.2	0.1	1.1	0.2
				ILNLRFLGK	2	98.1%	1																									
				QAIEGVGNLR	2	91.4%	1																									
IPI00298067	PDZK1	Na(+)/H(+) exchange regulatory cofactor NHE-RF3	99.9%	4.8	2	2	2	2	2,647,707	2,416,635	3,239,405	2,544,901	170,057	87,523	321,433	121,633	14.4	8.1	22.2	10.7	-1.1	0.3	1.2	0.1	-1.0	0.6	1.3	0.06	1.1	0.4	-1.3	0.1
IPI00908590	PDZK1	Na(+)/H(+) exchange regulatory cofactor NHE-RF3 isoform 2	99.9%	6.1	2	2	2	2	2,647,707	2,416,635	3,239,405	2,544,901	170,057	87,523	321,433	121,633	14.4	8.1	22.2	10.7	-1.1	0.3	1.2	0.1	-1.0	0.6	1.3	0.06	1.1	0.4	-1.3	0.1
				DIDSGSPAEEAGLK	2	97.2%	1																									
				IEKDTEGHLVR	3	82.1%	1																									
IPI00298176	GPX2	Glutathione peroxidase 2	100.0%	19.5	3	3	3	1	20,144,540	18,739,800	18,571,810	21,337,510	2,346,185	488,721	2,523,886	858,855	26.0	5.8	30.4	9.0	-1.1	0.6	-1.1	0.7	1.1	0.7	-1.0	1	1.1	0.03	1.1	0.3
				DFTQLNELQCR	2	93.8%	1																									
				DKLPYPYDDPFSLMTDPKLIIWSPVR	3	86.0%	1																									
				LPYPYDDPFSLMTDPK	2	97.3%	1																									
IPI00298237	TPP1	cDNA FLJ56402, highly similar to Tripeptidyl-peptidase 1	100.0%	7.9	2	2	2	1	2,210,723	2,186,263	2,359,973	2,554,530	170,179	171,410	173,050	132,218	17.2	17.5	16.4	11.6	-1.0	0.9	1.1	0.6	1.2	0.1	1.1	0.5	1.2	0.1	1.1	0.4
				AYPDVAALSDGYWVVSNR	3	100.0%	1																									
				VPIPWVSGTSASTPVFGGILSLINEHR	3	100.0%	1																									
IPI00298281	LAMC1	Laminin subunit gamma-1	99.1%	1.1	1	1	1	1	3,578,190	3,742,970	4,313,090	4,247,570	276,592	206,739	377,083	249,467	17.3	12.4	19.6	13.1	1.0	0.6	1.2	0.2	1.2	0.1	1.2	0.2	1.1	0.2	-1.0	0.9
				TFAEVTDLDNEVNNMLK	2	99.1%	1																									
IPI00298348	OXR1	isoform 2 of Oxidation resistance protein 1	94.1%	1.3	1	1	1	3	1,865,260	1,492,210	1,657,053	1,671,797	304,526	93,049	160,920	171,831	36.5	13.9	21.7	23.0	-1.2	0.3	-1.1	0.6	-1.1	0.6	1.1	0.4	1.1	0.4	1.0	1
IPI00927650	OXR1	Uncharacterized protein	94.1%	12.6	1	1	1	3	1,865,260	1,492,210	1,657,053	1,671,797	304,526	93,049	160,920	171,831	36.5	13.9	21.7	23.0	-1.2	0.3	-1.1	0.6	-1.1	0.6	1.1	0.4	1.1	0.4	1.0	1
IPI00973351	OXR1	Uncharacterized protein	94.1%	27.5	1	1	1	3	1,865,260	1,492,210	1,657,053	1,671,797	304,526	93,049	160,920	171,831	36.5	13.9	21.7	23.0	-1.2	0.3	-1.1	0.6	-1.1	0.6	1.1	0.4	1.1	0.4	1.0	1
				LLGFGGGGEAR	2	94.1%	1																									
IPI00298520	ARCN1	Coatomer subunit delta variant 2	100.0%	14.0	7	7	7	2	21,797,021	22,737,360	22,046,667	24,593,319	1,437,161	868,552	1,295,484	911,151	14.7	8.5	13.1	8.3	1.0	0.6	1.0	0.9	1.1	0.1	-1.0	0.7	1.1	0.2	1.1	0.1
IPI00514053	ARCN1	Coatomer subunit delta	100.0%	15.1	7	7	7	2	21,797,021	22,737,360	22,046,667	24,593,319	1,437,161	868,552	1,295,484	911,151	14.7	8.5	13.1	8.3	1.0	0.6	1.0	0.9	1.1	0.1	-1.0	0.7	1.1	0.2	1.1	0.1
				ENVNLAQIR	2	98.4%	1																									
				GKEVDNFVDK	2	91.3%	1																									
				LFTAESLIGLK	2	99.1%	1																									
				QHTFVETESVR	2	83.5%	1																									
				SEGETIMSSSMGK	2	99.4%	1																									
				SFPVNSDVGVLK	2	99.5%	1																									
				TFTEMDSHEEK	2	99.9%	1																									
IPI00298547	PARK7	Protein DJ-1	100.0%	84.1	11	14	17	1	96,884,916	93,871,916	89,327,953	106,729,470	8,551,895	2,144,634	5,671,363	4,302,756	19.7	5.1	14.2	9.0	-1.0	0.7	-1.1	0.5	1.1	0.3	-1.1	0.5	1.1	0.03	1.2	0.04
				ALVILAK	2	99.9%	1																									
				APLVLKD	2	99.7%	2																									
				DGLILTSR	2	87.4%	1																									
				DVVICPDASLEDAKK	2	100.0%	2																									
				EGPYDVVVLPGGNLGAQNLSESAAVK	2	100.0%	2																									
				EGPYDVVVLPGGNLGAQNLSESAAVK	3	100.0%	1																									
				GAEEMETVIPVDVMR	2	100.0%	1																									
				GLIAAICAGPTALLAHEIGFGSK	2	100.0%	1																									
				GLIAAICAGPTALLAHEIGFGSK	3	100.0%	1																									
				GPGTSFEFALAIVEALNGKEVAAQVK	3	100.0%	1																									
				MMNGGHYTYSENR	3	99.9%	1																									
				MMNGGHYTYSENRVEK	3	99.9%	1																									
				VTVAGLAGKDPVQCSR	2	100.0%	1																									
				VTVAGLAGKDPVQCSR	3	100.0%	1																									
IPI00298558	PDCD10	Programmed cell death protein 10	99.6%	11.3	1	1	1	7	912,830	970,083	866,380	1,032,571	55,331	64,978	73,411	76,797	13.6	15.0	19.0	16.6	1.1	0.5	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.6	1.2	0.2
IPI00790953	PDCD10	Uncharacterized protein	99.6%	17.9	1	1	1	7	912,830	970,083	866,380	1,032,571	55,331	64,978	73,411	76,797	13.6	15.0	19.0	16.6	1.1	0.5	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.6	1.2	0.2
IPI00791474	PDCD10	Uncharacterized protein	99.6%	16.1	1	1	1	7	912,830	970,083	866,380	1,032,571	55,331	64,978	73,411	76,797	13.6	15.0	19.0	16.6	1.1	0.5	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.6	1.2	0.2
IPI00793671	PDCD10	Protein	99.6%	19.7	1	1	1	7	912,830	970,083	866,380	1,032,571	55,331	64,978	73,411	76,797	13.6	15.0	19.0	16.6	1.1	0.5	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.6	1.2	0.2
IPI00945696	PDCD10	Uncharacterized protein	99.6%	12.9	1	1	1	7	912,830	970,083	866,380	1,032,571	55,331	64,978	73,411	76,797	13.6	15.0	19.0	16.6	1.1	0.5	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.6	1.2	0.2
IPI00946434	PDCD10	Uncharacterized protein	99.6%	11.9	1	1	1	7	912,830	970,083	866,380	1,032,571	55,331	64,978	73,411	76,797	13.6	15.0	19.0	16.6	1.1	0.5	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.6	1.2	0.2
IPI00947286	PDCD10	Uncharacterized protein	99.6%	16.4	1	1	1	7	912,830	970,083	866,380	1,032,571	55,331	64,978	73,411	76,797	13.6	15.0	19.0	16.6	1.1	0.5	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.6	1.2	0.2
				MAADDVEEYMIERPEPEFQDLNEK	3	99.6%	1																									
IPI00298788	ILF3	isoform 1 of Interleukin enhancer-binding factor 3	100.0%	25.2	18	18	21	2	22,143,549	22,077,669	21,437,760	25,682,123	1,381,209	1,103,572	1,374,914	1,281,135	14.0	11.2	14.3	11.2	-1.0	1	-1.0	0.7	1.2	0.1	-1.0	0.7	1.2	0.07	1.2	0.05

IPI00418313	ILF3	interleukin enhancer-binding factor 3 isoform d	100.0%	25.1	18	18	21	2	22,143,549	22,077,669	21,437,760	25,682,123	1,381,209	1,103,572	1,374,914	1,281,135	14.0	11.2	14.3	11.2	-1.0	1	-1.0	0.7	1.2	0.1	-1.0	0.7	1.2	0.07	1.2	0.05
				AEPPQAMNALMR	2	98.0%	1																									
				AVSDWIDEQEK	2	99.9%	1																									
				AYAALAALEK	2	99.8%	1																									
				EDITQSAQHALR	2	96.0%	1																									
				FNYSGSGGR	2	96.3%	1																									
				FVMEVEVDGQK	2	100.0%	1																									
				GDLDLELVLLCK	2	100.0%	1																									
				HSSVYPTQEELEAVQNMVSHTER	3	100.0%	2																									
				IFVNDDR	2	89.9%	1																									
				LAAFGQLHK	2	96.3%	1																									
				LNQLKPGLQYK	2	99.9%	1																									
				QQREDITQSAQHALR	3	80.8%	1																									
				VADNLAIQLAAVTEDKYEILQSVDDAAIVIK	3	99.9%	1																									
				VLAGETLSVNDPPDVLDR	2	100.0%	2																									
				VLGMDPLPSK	2	99.9%	1																									
				VLQDMGLPTGAEGR	2	100.0%	2																									
				VPTWGPLR	2	95.4%	1																									
				YELISETGGSHDKR	2	100.0%	1																									
IPI00298860	LTF	cDNA FLJ78440, highly similar to Human lactoferrin	99.6%	1.7	1	1	1	3	3,512,220	3,958,967	3,619,530	4,064,880	182,394	204,919	393,367	397,584	11.6	11.6	24.3	21.9	1.1	0.1	1.0	0.8	1.2	0.2	-1.1	0.5	1.0	0.8	1.1	0.4
IPI00903112	LTF	cDNA FLJ36533 fis, clone TRACH2004428, highly similar to Lactotransferrin (Fragm	99.6%	1.7	1	1	1	3	3,512,220	3,958,967	3,619,530	4,064,880	182,394	204,919	393,367	397,584	11.6	11.6	24.3	21.9	1.1	0.1	1.0	0.8	1.2	0.2	-1.1	0.5	1.0	0.8	1.1	0.4
IPI00925547	LTF	Uncharacterized protein	99.6%	1.7	1	1	1	3	3,512,220	3,958,967	3,619,530	4,064,880	182,394	204,919	393,367	397,584	11.6	11.6	24.3	21.9	1.1	0.1	1.0	0.8	1.2	0.2	-1.1	0.5	1.0	0.8	1.1	0.4
				CGLVPVLAENYK	2	99.6%	1																									
IPI00298961	XPO1	Exportin-1	100.0%	9.1	6	8	10	1	32,353,525	40,897,441	38,476,726	42,861,104	4,254,831	3,176,152	5,115,818	2,665,755	29.4	17.4	29.7	13.9	1.3	0.1	1.2	0.4	1.3	0.07	-1.1	0.7	1.0	0.6	1.1	0.5
				EFAGEDTSDLFLEER	2	100.0%	1																									
				LDINLLDNVVNCLYHGEGAQQR	3	100.0%	1																									
				LLSEEVFDFSSGQITQVK	2	99.9%	1																									
				LLSEEVFDFSSGQITQVK	3	100.0%	1																									
				NVDILKDPETVK	2	99.7%	1																									
				YMLLPNQVWDSIIQQATK	2	100.0%	2																									
				YMLLPNQVWDSIIQQATK	3	100.0%	1																									
				YYGLQILENVIK	2	100.0%	2																									
IPI00298971	VTN	Vitronectin	100.0%	8.8	3	3	4	1	6,962,200	8,224,880	7,510,225	9,426,160	459,162	448,046	432,644	376,601	14.8	12.2	12.9	8.9	1.2	0.08	1.1	0.4	1.4	0.003	-1.1	0.3	1.1	0.07	1.3	0.01
				DVWGIEGPIDAAFTR	2	100.0%	2																									
				FEDGVLDPDYPR	2	98.1%	1																									
				SIAQYWLGCPAPGHL	2	99.9%	1																									
IPI00298994	TLN1	Talin-1	100.0%	19.1	28	28	31	1	69,343,418	70,730,199	68,238,273	80,149,153	5,650,898	2,586,684	4,649,185	1,780,485	18.2	8.2	15.2	5.0	1.0	0.8	-1.0	0.9	1.2	0.1	-1.0	0.7	1.1	0.02	1.2	0.06
				AAAFEEQENETVVVK	2	100.0%	1																									
				AIAVTVQEMVTK	2	100.0%	2																									
				ALDGAFTEENR	2	99.7%	1																									
				ALSTDPAAPNLK	2	99.7%	1																									
				AQEACGPLEMDSALSVVQNLEKDLQEVK	3	98.4%	1																									
				AVSSAIAQLLGEVAQGNENYAGIAAR	3	100.0%	1																									
				CTQDLGNSTK	2	98.3%	1																									
				DHFGLEGDEESTMLEDSVSPKK	3	99.4%	1																									
				EADESLNFEEQILEAAK	2	100.0%	1																									
				GVAALTSDPAVQAIVLDTASDVLDK	2	100.0%	1																									
				GVGAAATAVTQALNELLQHVK	3	100.0%	1																									
				ILAQATSDLVNAIK	2	100.0%	2																									
				LAQAAQSSVATITR	2	100.0%	1																									
				LASEAKPAAVAAENEEIGSHIK	3	86.0%	1																									
				LHTDDELNWLDHGR	3	98.0%	1																									
				LNEAAAGLNQAATELVQASR	2	100.0%	1																									
				MVAAATNNLCEAANAAVQGHASQEK	3	100.0%	1																									
				NCGQMSEIEAK	2	89.1%	1																									
				NGNLPEFGDAISTASK	2	99.7%	1																									
				QAAASATQTIAAAQHAASTPK	3	100.0%	2																									
				QEDVIATANLSR	2	99.9%	1																									
				QELAVFCSPEPPAK	2	86.5%	1																									
				VAGSVTELIQAAEAMK	2	98.3%	1																									
				VGAIPANALDDGQWSQGLISAAR	3	100.0%	1																									
				VGDDPAVWQLK	2	99.8%	1																									
				VMVTNVTSLLK	2	99.6%	1																									
				VSQMAQYFEPLTLAAVGAASK	2	99.9%	1																									
				VVAPTISSPVCQEQLVEAGR	3	99.2%	1																									
IPI00299000	PA2G4	Proliferation-associated protein 2G4	100.0%	42.9	15	15	18	1	81,447,045	86,921,015	81,461,090	93,535,865	9,547,269	4,097,102	6,142,041	2,178,311	26.2	10.5	16.9	5.2	1.1	0.6	1.0	1	1.1	0.3	-1.1	0.5	1.1	0.2	1.1	0.1
				AAHLCAEAALR	3	81.1%	1																									
				AFFSEVER	2	99.6%	1																									
				ALLQSSASR	2	100.0%	2																									
				EGEFVAQFK	2	98.4%	1																									
				FTVLLMPNGPMR	2	96.9%	1																									
				GDAMIMEETGK	2	100.0%	2																									
				GIAFPTSISVNNCVCHFSPLK	3	99.6%	1																									
				HELLQPFNVLYEK	2	100.0%	1																									
				ITSGPFEPDLYK	2	100.0%	1																									
				ITSGPFEPDLYKSEMEVQDAELK	3	81.4%	1																									
				KGIAFPTSISVNNCVCHFSPLK	3	92.9%	1																									
				LVKPGNQNTQVTEAWNK	3	100.0%	2																									
				MGVVECAK	2	98.2%	1																									
				SDQDYILK	2	98.1%	1																									
				SLVEASSSGVSVLSLCEK	2	99.3%	1																									
IPI00299003	WASF3	Wiskott-Aldrich syndrome protein family member 3	100.0%	2.6	1	1	1	2	152,714	171,248	166,690	214,695	10,220	27,623	22,618	32,526	15.0	36.1	30.3	33.9	1.1	0.6	1.1	0.6	1.4	0.1	-1.0	0.9	1.3	0.3	1.3	0.3
IPI00384347	WASF3	WASF3 protein	100.0%	2.6	1	1	1	2	152,714	171,248	166,690	214,695	10,220	27,623	22,618	32,526	15.0	36.1	30.3	33.9	1.1	0.6	1.1	0.6	1.4	0.1	-1.0	0.9	1.3	0.3	1.3	0.3
				FYTDPSYFFDLWK	2	100.0%	1																									
IPI00299024	BASP1	isoform 1 of Brain acid soluble protein 1	99.2%	6.2	1	1	1	2	860,172	1,191,150	1,042,086	1,300,695	166,005	119,011	145,262	172,128	43.2	22.3	31.2	29.6	1.4	0.1	1.2	0.4	1.5	0.1	-1.1	0.5	1.1	0.6	1.2	0.3
IPI00908521	BASP1	isoform 2 of Brain acid soluble protein 1	99.2%	8.1	1	1	1	2	860,172	1,191,150	1,042,086	1,300,695	166,005	119,011	145,262	172,128	43.2	22.3	31.2	29.6	1.4	0.1	1.2	0.4	1.5	0.1	-1.1	0.5	1.1	0.6	1.2	0.3
				ETPAATEAPSSTPK	2	99.2%	1																									
IPI00299033	KPNA3	Importin subunit alpha-3	99.5%	5.2	2	2	2	1	6,216,375	6,821,690	6,778,065	7,620,865	473,190	230,179	324,736	565,842	17.0	7.5	10.7	16.6	1.1	0.3	1.1	0.4	1.2	0.09	-1.0	0.9	1.1	0.2	1.1	0.2
				DSQVVQVVLDGLK	2	98.4%	1																									
				EAAWAISNLTISGR	2	99.5%	1																									
IPI00299086	SDCBP	isoform 1 of Syntenin-1	100.0%	13.8	2	2	2	2	1,309,026	1,403,548	1,389,461	1,543,811	72,890	82,811	119,190	72,520	12.5	13.2	19.2	10.5	1.1	0.4	1.1	0.6	1.2	0.05	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00478874	SDCBP	isoform 3 of Syntenin-1	100.0%	14.0	2	2	2	2	1,309,026	1,403,548	1,389,461	1,543,811	72,890	82,811	119,190	72,520	12.5	13.2	19.2	10.5	1.1	0.4	1.1	0.6	1.2	0.05	-1.0	0.9	1.1	0.2	1.1	0.3
				ANVAVVSGAPLQGQLVAR	2	82.9%	1																									
				SIDNGIFVQLVQANSPASLVGLR	2	98.8%	1																									
IPI00299095	SNX2	Sorting nexin-2	100.0%	13.9	6	6	6	2	21,884,043	25,530,000	22,890,615	29,516,940	4,215,838	1,904,085	1,901,104	1,136,897	43.1	16.7	18.6	8.6	1.2	0.5	1.0	0.8	1.3	0.1	-1.1	0.4	1.2	0.1	1.3	0.02
IPI00964716	SNX2	cDNA FLJ51799, highly similar to Sorting nexin-2	100.0%	17.9	6	6	6	2	21,884,043	25,530,000	22,890,615	29,516,940	4,215,838	1,904,085	1,901,104	1,136,897	43.1	16.7	18.6	8.6	1.2	0.5	1.0	0.8	1.3	0.1	-1.1	0.4	1.2	0.1	1.3	0.02
				ALSQLAEVEEK	2	99.9%	1																									
				AVNTQALSGAGILR	2	100.0%	1																									
				HPTLLQDPDLR	2	99.3%	1																									
				QQQFENLDQQLR	2	99.3%	1																									
				YLESLVQTQQQLIK	2	99.8%	1																									
				YWEAFLPEAK	2	99.9%	1																									
IPI00299116	PODXL	Podocalyxin-like isoform 2 precursor	100.0%	2.5	1	1	1	5	1,094,800	1,164,724	1,180,976	1,264,952	103,918	56,037	57,291	66,373	21.2	10.8	10.9	11.7	1.1	0.6	1.1	0.5	1.2	0.2	1.0	0.8	1.1	0.3	1.1	0.4
IPI00604773	PODXL	PODXL protein	100.0%	2.3	1	1	1	5	1,094,800	1,164,724	1,180,976	1,264,952	103,918	56,037	57,291	66,373	21.2	10.8	10.9	11.7	1.1	0.6	1.1	0.5	1.2	0.2	1.0	0.8	1.1	0.3	1.1	0.4
IPI00926191	PODXL	55 kDa protein	100.0%	2.5	1	1	1	5	1,094,800	1,164,724	1,180,976	1,264,952	103,918	56,037	57,291	66,373	21.2	10.8	10.9	11.7	1.1	0.6	1.1	0.5	1.2	0.2	1.0	0.8	1.1	0.3	1.1	0.4
IPI01012180	PODXL	54 kDa protein	100.0%	2.5	1	1	1	5	1,094,800	1,164,724	1,180,976	1,264,952	103,918	56,037	57,291	66,373	21.2	10.8	10.9	11.7	1.1	0.6	1.1	0.5	1.2	0.2	1.0	0.8	1.1	0.3	1.1	0.4
IPI01012590	PODXL	59 kDa protein	100.0%	2.3	1	1	1	5	1,094,800	1,164,724	1,180,976	1,264,952	103,918	56,037	57,291	66,373	21.2	10.8	10.9	11.7	1.1	0.6	1.1	0.5	1.2	0.2	1.0	0.8	1.1	0.3	1.1	0.4
				LASVPGSQTVVVK	2	99.8%	1																									
IPI00299147	SUMO3	Small ubiquitin-related modifier 3	100.0%	20.4	2	2	3	4	1,877,359	1,825,342	1,702,303	2,137,196	99,980	91,758	75,657	61,460	11.9	11.2	9.9	6.4	-1.0	0.7	-1.1	0.2	1.1	0.06	-1.1	0.3	1.2	0.02	1.3	0.002
IPI00793687	SUMO3	Uncharacterized protein	100.0%	15.6	2	2	3	4	1,877,359	1,825,342	1,702,303	2,137,196	99,980	91,758	75,657	61,460	11.9	11.2	9.9	6.4	-1.0	0.7	-1.1	0.2	1.1	0.06	-1.1	0.3	1.2	0.02	1.3	0.002
IPI00798011	SUMO3	Uncharacterized protein	100.0%	14.3	2	2	3	4	1,877,359	1,825,342	1,702,303	2,137,196	99,980	91,758	75,657	61,460	11.9	11.2	9.9	6.4	-1.0	0.7	-1.1	0.2	1.1	0.06	-1.1	0.3	1.2	0.02	1.3	0.002
IPI00909492	SUMO3	cDNA FLJ57440, moderately similar to Small ubiquitin-related modifier 3	100.0%	14.9	2	2	3	4	1,877,359	1,825,342	1,702,303	2,137,196	99,980	91,758	75,657	61,460	11.9	11.2	9.9	6.4	-1.0	0.7	-1.1	0.2	1.1	0.06	-1.1	0.3	1.2	0.02	1.3	0.002
				TENDHINLK	2	91.0%	1																									
				VAGQDGSVVQFK	2	100.0%	2																									
IPI00299149	SUMO2	Small ubiquitin-related modifier 2	100.0%	23.2	2	2	3	4	1,946,282	2,070,592	2,228,755	2,442,943	163,181	106,635	240,594	142,530	18.8	11.5	24.1	13.1	1.1	0.5	1.1	0.4	1.3	0.05	1.1	0.6	1.2	0.07	1.1	0.5
IPI00745893	SUMO2	small ubiquitin-related modifier 2 isoform b precursor	100.0%	31.0	2	2	3	4	1,946,282	2,070,592	2,228,755	2,442,943	163,181	106,635	240,594	142,530	18.8	11.5	24.1	13.1	1.1	0.5	1.1	0.4	1.3	0.05	1.1	0.6	1.2	0.07	1.1	0.5
IPI00790142	LOC728825;SUMO2	10 kDa protein	100.0%	24.2	2	2	3	4	1,946,282	2,070,592	2,228,755	2,442,943	163,181	106,635	240,594	142,530	18.8	11.5	24.1	13.1	1.1	0.5	1.1	0.4	1.3	0.05	1.1	0.6	1.2	0.07	1.1	0.5
IPI00973977	SUMO2	small ubiquitin-related modifier 2 isoform a precursor	100.0%	23.2	2	2	3	4	1,946,282	2,070,592	2,228,755	2,442,943	163,181	106,635	240,594	142,530	18.8	11.5	24.1	13.1	1.1	0.5	1.1	0.4	1.3	0.05	1.1	0.6	1.2	0.07	1.1	0.5
				TENNDHINLK	2	99.9%	1																									
				VAGQDGSVVQFK	2	100.0%	2																									
IPI00299155	PSMA4	Proteasome subunit alpha type-4	100.0%	26.8	6	6	7	2	8,124,566	8,460,122	7,957,143	9,823,416	753,730	259,522	588,468	373,621	20.7	6.9	16.5	8.5	1.0	0.7	-1.0	0.9	1.2	0.08	-1.1	0.5	1.2	0.02	1.2	0.03
IPI00790207	PSMA4	27 kDa protein	100.0%	29.8	6	6	7	2	8,124,566	8,460,122	7,957,143	9,823,416	753,730	259,522	588,468	373,621	20.7	6.9	16.5	8.5	1.0	0.7	-1.0	0.9	1.2	0.08	-1.1	0.5	1.2	0.02	1.2	0.03
				ATCIGNNSAAAVSMLK	2	100.0%	1																									
				HYGFQLYQSDPSGNYGGWK	3	96.3%	1																									
				LLDEVFFSEK	2	100.0%	2																									
				SALALAIK	2	99.7%	1																									
				TTIFSPEGR	2	98.2%	1																									
				VEIATLTR	2	88.9%	1																									
IPI00299166	TANK	isoform Long of TRAF family member-associated NF-kappa-B activator	90.5%	5.2	1	1	1	4	244,431	269,751	303,378	337,332	14,893	30,273	39,902	40,696	13.6	25.1	29.4	27.0	1.1	0.5	1.2	0.2	1.4	0.08	1.1	0.5	1.3	0.2	1.1	0.6
IPI00893061	TANK	22 kDa protein	90.5%	11.1	1	1	1	4	244,431	269,751	303,378	337,332	14,893	30,273	39,902	40,696	13.6	25.1	29.4	27.0	1.1	0.5	1.2	0.2	1.4	0.08	1.1	0.5	1.3	0.2	1.1	0.6
IPI00894040	TANK	Uncharacterized protein	90.5%	5.4	1	1	1	4	244,431	269,751	303,378	337,332	14,893	30,273	39,902	40,696	13.6	25.1	29.4	27.0	1.1	0.5	1.2	0.2	1.4	0.08	1.1	0.5	1.3	0.2	1.1	0.6
IPI00917956	TANK	31 kDa protein	90.5%	8.0	1	1	1	4	244,431	269,751	303,378	337,332	14,893	30,273	39,902	40,696	13.6	25.1	29.4	27.0	1.1	0.5	1.2	0.2	1.4	0.08	1.1	0.5	1.3	0.2	1.1	0.6
				TEETLFEIQGIDPIASAIQNLK	2	90.5%	1																									
IPI00299254	EIF5B	Eukaryotic translation initiation factor 5B	100.0%	2.5	2	2	3	1	7,482,160	9,395,080	8,225,540	10,246,490	673,394	812,553	762,900	622,952	20.1	19.3	20.7	13.6	1.3	0.1	1.1	0.5	1.4	0.02	-1.1	0.3	1.1	0.4	1.2	0.07
				HFEATDILVSK	2	99.8%	2																									
				IPGMLIIDTPGHESFSNLR	3	99.9%	1																									
IPI00299571	PDIA6	isoform 2 of Protein disulfide-isomerase A6	100.0%	43.5	15	17	27	4	25,619,210	25,313,518	24,992,645	28,486,268	1,696,410	757,463	1,394,258	1,179,575	14.8	6.7	12.5	9.3	-1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.05	1.1	0.09
IPI00644989	PDIA6	isoform 1 of Protein disulfide-isomerase A6	100.0%	48.6	15	17	27	4	25,619,210	25,313,518	24,992,645	28,486,268	1,696,410	757,463	1,394,258	1,179,575	14.8	6.7	12.5	9.3	-1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.05	1.1	0.09
IPI01011902	PDIA6	Uncharacterized protein	100.0%	48.1	15	17	27	4	25,619,210	25,313,518	24,992,645	28,486,268	1,696,410	757,463	1,394,258	1,179,575	14.8	6.7	12.5	9.3	-1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.05	1.1	0.09
IPI01013559	PDIA6	cDNA FLJ58502, highly similar to Protein disulfide-isomerase A6	100.0%	49.0	15	17	27	4	25,619,210	25,313,518	24,992,645	28,486,268	1,696,410	757,463	1,394,258	1,179,575	14.8	6.7	12.5	9.3	-1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.05	1.1	0.09
				AATALKDVVK	2	98.5%	1																									
				ALDLFSDNAPPPELLEIINEDIAK	2	100.0%	2																									
				ALDLFSDNAPPPELLEIINEDIAK	3	100.0%	2																									
				ALDLFSDNAPPPELLEIINEDIAKR	3	100.0%	2																									
				DGELPVEDDIDLSDVELDDLGKDEL	2	100.0%	2																									
				EPWDGRDGELPVEDDIDLSDVELDDLGKDEL	3	100.0%	1																									
				GESPVDYDGGR	2	100.0%	2																									

				GSFSEQGINEFLR	2	100.0%	2																									
				GSTAPVGGGAFPTIVER	2	100.0%	1																									
				IFGSNK	1	90.8%	1																									
				LAAVDATVNQVLASR	2	100.0%	2																									
				NLEPEWAAAASEVK	2	100.0%	2																									
				NSYLEVLLK	2	99.9%	2																									
				TCEEHQLCVVAVLPHILDTGAAGR	3	100.0%	1																									
				TGEAIVDAALSALR	2	100.0%	2																									
				TGEAIVDAALSALR	3	100.0%	1																									
				VGAVDADKHHSLGGQYGVQGFPTIK	3	100.0%	1																									
IPI00299573	RPL7A	60S ribosomal protein L7a	100.0%	15.0	3	3	4	1	7,294,922	8,655,583	7,878,539	9,205,704	565,172	575,365	390,218	463,366	17.3	14.9	11.1	11.3	1.2	0.1	1.1	0.4	1.3	0.03	-1.1	0.3	1.1	0.5	1.2	0.06
				AGVNTVTTLVENK	2	100.0%	2																									
				LKVPPAINQFTQALDR	3	100.0%	1																									
				NFGIGQDIQPK	2	99.6%	1																									
IPI00299608	PSMD1	isoform 1 of 26S proteasome non-ATPase regulatory subunit 1	100.0%	9.2	5	5	5	2	6,357,548	6,588,357	6,996,430	7,347,605	825,210	130,263	576,750	411,170	29.0	4.4	18.4	12.5	1.0	0.8	1.1	0.5	1.2	0.3	1.1	0.5	1.1	0.1	1.1	0.6
IPI00456695	PSMD1	isoform 2 of 26S proteasome non-ATPase regulatory subunit 1	100.0%	9.5	5	5	5	2	6,357,548	6,588,357	6,996,430	7,347,605	825,210	130,263	576,750	411,170	29.0	4.4	18.4	12.5	1.0	0.8	1.1	0.5	1.2	0.3	1.1	0.5	1.1	0.1	1.1	0.6
				MITSAAGIISLLDEDEPQLK	2	98.7%	1																									
				NNNTDLMILK	2	96.6%	1																									
				TNLYQDDAVTGEAAGLALGLVMLGSK	2	97.8%	1																									
				TPEQCPSVVSLLSESYNPHVR	3	100.0%	1																									
				VSTAVLSITAK	2	95.9%	1																									
IPI00299946	KCNH7	isoform 1 of Potassium voltage-gated channel subfamily H member 7	98.9%	2.1	2	2	2	1	21,371,250	19,762,220	19,971,580	18,575,580	2,836,502	1,159,981	1,571,796	1,248,829	29.7	13.1	17.6	15.0	-1.1	0.6	-1.1	0.7	-1.2	0.4	1.0	0.9	-1.1	0.5	-1.1	0.5
				ESLCSIR	2	89.8%	1																									
				SNADVRALTYCDLHKIQR	3	89.4%	1																									
IPI00299977	PHPT1	14 kDa phosphohistidine phosphatase	100.0%	26.4	4	4	5	1	37,575,831	35,621,270	39,273,130	43,790,309	5,436,767	1,870,209	2,844,254	2,544,260	32.4	11.7	16.2	13.0	-1.1	0.7	1.0	0.8	1.2	0.3	1.1	0.3	1.2	0.03	1.1	0.3
				AKYPDYEVTWANDGY	2	100.0%	2																									
				WAEYHADIYDK	2	99.9%	1																									
				WAEYHADIYDKVSGDMQK	3	85.6%	1																									
				YPDYEVTWANDGY	2	100.0%	1																									
IPI00300018	AIFM1	isoform 2 of Apoptosis-inducing factor 1, mitochondrial	100.0%	8.3	2	2	2	1	2,713,717	2,842,013	2,550,423	2,923,437	276,493	81,918	187,146	57,436	22.8	6.5	16.4	4.4	1.0	0.7	-1.1	0.6	1.1	0.5	-1.1	0.2	1.0	0.4	1.1	0.1
				ALGTEVIQLFPEK	2	96.6%	1																									
				TGGLEIDSDFGGFR	2	99.2%	1																									
IPI00300074	FARSB	Phenylalanyl-tRNA synthetase beta chain	99.6%	1.9	1	1	1	2	2,542,180	2,327,330	2,710,050	2,532,820	183,596	124,659	128,533	96,274	16.2	12.0	10.6	8.5	-1.1	0.4	1.1	0.5	-1.0	1	1.2	0.07	1.1	0.2	-1.1	0.3
IPI01009249	FARSB	55 kDa protein	99.6%	2.2	1	1	1	2	2,542,180	2,327,330	2,710,050	2,532,820	183,596	124,659	128,533	96,274	16.2	12.0	10.6	8.5	-1.1	0.4	1.1	0.5	-1.0	1	1.2	0.07	1.1	0.2	-1.1	0.3
				ASEGPAFFPGR	2	99.6%	1																									
IPI00300078	PWP2	Periodic tryptophan protein 2 homolog	91.3%	1.7	1	1	1	1	3,429,100	3,445,060	4,039,040	3,445,200	139,075	175,375	340,524	302,599	9.1	11.4	18.9	19.6	1.0	0.9	1.2	0.1	1.0	1	1.2	0.2	1.0	1	-1.2	0.2
				VLFDPFELDTSVTPGR	2	91.3%	1																									
IPI00300086	QPRT	Nicotinate-nucleotide pyrophosphorylase [carboxylating]	100.0%	22.2	6	6	6	1	28,063,837	26,352,785	26,482,145	28,787,844	2,069,492	1,344,653	970,512	1,227,123	16.5	11.4	8.2	9.5	-1.1	0.5	-1.1	0.5	1.0	0.8	1.0	0.9	1.1	0.2	1.1	0.2
				CSGIASAAAAAVEAAR	2	100.0%	1																									
				DNHVVAAGGVEK	3	86.4%	1																									
				EVAPVPK	1	91.4%	1																									
				GPAHCLLLGER	3	86.4%	1																									
				VALNTLAR	2	99.8%	1																									
				YGLLVGGAASHR	3	99.4%	1																									
IPI00300127	NAT10	N-acetyltransferase 10	99.5%	3.1	2	2	2	2	11,129,270	11,117,952	10,191,475	12,820,758	1,167,637	615,559	877,198	581,834	23.5	12.4	19.3	10.2	-1.0	1	-1.1	0.5	1.2	0.2	-1.1	0.4	1.2	0.08	1.3	0.04
IPI00921516	NAT10	N-acetyltransferase 10 isoform b	99.5%	3.4	2	2	2	2	11,129,270	11,117,952	10,191,475	12,820,758	1,167,637	615,559	877,198	581,834	23.5	12.4	19.3	10.2	-1.0	1	-1.1	0.5	1.2	0.2	-1.1	0.4	1.2	0.08	1.3	0.04
				AGPNASIISLK	2	85.7%	1																									
				LGQAELVVIDEAAAIPLPLVK	2	98.9%	1																									
IPI00300299	SPCS3	Signal peptidase complex subunit 3	100.0%	12.8	2	2	3	1	30,269,550	31,671,910	28,624,520	31,408,260	2,907,556	1,714,371	1,680,618	2,408,222	21.5	12.1	13.1	17.2	1.0	0.7	-1.1	0.6	1.0	0.8	-1.1	0.2	-1.0	0.9	1.1	0.4
				NNALNQVVLWDK	2	100.0%	1																									
				YFFFDDGNGLK	2	99.3%	2																									
IPI00300341	TCEB1	Transcription elongation factor B polypeptide 1	100.0%	21.4	2	2	3	2	513,480	479,238	519,498	559,927	48,630	18,726	35,997	9,085	21.2	8.7	15.5	3.6	-1.1	0.5	1.0	0.9	1.1	0.4	1.1	0.4	1.2	0.005	1.1	0.3
IPI00982721	TCEB1	Uncharacterized protein	100.0%	27.0	2	2	3	2	513,480	479,238	519,498	559,927	48,630	18,726	35,997	9,085	21.2	8.7	15.5	3.6	-1.1	0.5	1.0	0.9	1.1	0.4	1.1	0.4	1.2	0.005	1.1	0.3
				EHALTSGTIK	1	100.0%	1																									
				TYGGCEGPDAMYVK	2	100.0%	2																									
IPI00300371	SF3B3	isoform 1 of Splicing factor 3B subunit 3	100.0%	11.4	11	11	13	1	79,190,895	78,098,355	70,839,935	89,237,460	8,562,810	3,800,415	5,285,724	3,888,085	24.2	10.9	16.7	9.7	-1.0	0.9	-1.1	0.4	1.1	0.3	-1.1	0.3	1.1	0.07	1.3	0.02
				AGNGQWASVIR	2	99.9%	1																									
				FLAVGLVDNTVR	2	100.0%	2																									
				HIANYISGIQTIGHR	3	100.0%	1																									
				ITLETDEDMVTEIR	2	98.3%	1																									
				IVILEYQPSK	2	100.0%	1																									
				IVPGQFLAVDPK	2	98.8%	1																									
				LTISSPLEAHK	3	97.4%	1																									
				NENQLIIFADDTYPR	2	100.0%	1																									
				NFGDQPDIR	2	94.9%	1																									
				TPVEEVPAAIAPFQGR	2	99.8%	2																									
				VIVSDVQESFIWVR	2	100.0%	1																									
IPI00300504	UPF2	isoform 1 of Regulator of nonsense transcripts 2	94.2%	1.5	1	1	1	2	1,785,925	1,866,605	1,665,030	1,977,915	182,002	122,107	128,708	212,330	22.8	14.6	17.3	24.0	1.0	0.7	-1.1	0.6	1.1	0.5	-1.1	0.3	1.1	0.7	1.2	0.2
IPI00472081	UPF2	isoform 2 of Regulator of nonsense transcripts 2	94.2%	3.3	1	1	1	2	1,785,925	1,866,605	1,665,030	1,977,915	182,002	122,107	128,708	212,330	22.8	14.6	17.3	24.0	1.0	0.7	-1.1	0.6	1.1	0.5	-1.1	0.3	1.1	0.7	1.2	0.2
				LLDEQEQEDEEASTGSHLK	3	94.2%	1																									
IPI00300567	ECI1	isoform 1 of Enoyl-CoA delta isomerase 1, mitochondrial	99.9%	11.9	3	3	4	1	5,923,645	6,448,485	5,809,690	6,437,495	397,713	356,056	482,748	400,486	15.0	12.4	18.6	13.9	1.1	0.4	-1.0	0.9	1.1	0.4	-1.1	0.3	-1.0	1	1.1	0.3
				DADVQNFVSFISK	2	99.5%	2																									
				SLQMYLER	2	98.5%	1																									
				VLVEPDAGAGVAVMK	2	99.8%	1																									
IPI00300631	SAFB	Scaffold attachment factor B1	100.0%	6.6	3	3	4	5	1,758,388	1,778,148	1,844,933	2,095,730	235,514	153,645	159,142	95,780	30.0	19.3	19.3	10.2	1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.1	1.1	0.2
IPI00646058	SAFB	scaffold attachment factor B1 isoform 2	100.0%	6.6	3	3	4	5	1,758,388	1,778,148	1,844,933	2,095,730	235,514	153,645	159,142	95,780	30.0	19.3	19.3	10.2	1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.1	1.1	0.2
IPI00941773	SAFB	scaffold attachment factor B1 isoform 4	100.0%	7.1	3	3	4	5	1,758,388	1,778,148	1,844,933	2,095,730	235,514	153,645	159,142	95,780	30.0	19.3	19.3	10.2	1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.1	1.1	0.2
IPI00983392	SAFB	scaffold attachment factor B1 isoform 1	100.0%	6.5	3	3	4	5	1,758,388	1,778,148	1,844,933	2,095,730	235,514	153,645	159,142	95,780	30.0	19.3	19.3	10.2	1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.1	1.1	0.2
IPI01013398	SAFB	cDNA FLJ59523, highly similar to Scaffold attachment factor B	100.0%	7.4	3	3	4	5	1,758,388	1,778,148	1,844,933	2,095,730	235,514	153,645	159,142	95,780	30.0	19.3	19.3	10.2	1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.1	1.1	0.2
				AIEDEGGNPDEIEITSEGNKK	3	99.8%	1																									
				NFWVSGLSSTTR	2	100.0%	2																									
				SEPVKEESSELEQPFAQDTSSVGPDRK	3	99.3%	1																									
IPI00300990	CHTOP	isoform 1 of Chromatin target of PRMT1 protein	99.5%	5.2	1	1	1	4	726,240	899,118	1,022,103	1,297,238	74,996	27,555	189,722	121,285	23.1	6.9	41.5	20.9	1.2	0.08	1.4	0.2	1.8	0.004	1.1	0.6	1.4	0.03	1.3	0.3
IPI00470438	CHTOP	24 kDa protein	99.5%	5.8	1	1	1	4	726,240	899,118	1,022,103	1,297,238	74,996	27,555	189,722	121,285	23.1	6.9	41.5	20.9	1.2	0.08	1.4	0.2	1.8	0.004	1.1	0.6	1.4	0.03	1.3	0.3
IPI00644245	CHTOP	isoform 3 of Chromatin target of PRMT1 protein	99.5%	6.4	1	1	1	4	726,240	899,118	1,022,103	1,297,238	74,996	27,555	189,722	121,285	23.1	6.9	41.5	20.9	1.2	0.08	1.4	0.2	1.8	0.004	1.1	0.6	1.4	0.03	1.3	0.3
IPI00719040	CHTOP	isoform 2 of Chromatin target of PRMT1 protein	99.5%	5.2	1	1	1	4	726,240	899,118	1,022,103	1,297,238	74,996	27,555	189,722	121,285	23.1	6.9	41.5	20.9	1.2	0.08	1.4	0.2	1.8	0.004	1.1	0.6	1.4	0.03	1.3	0.3
				EQLDNQLDAYMSK	2	99.5%	1																									
IPI00301021	SSR1	isoform 1 of Translocon-associated protein subunit alpha	100.0%	8.0	2	2	2	6	1,607,573	1,660,442	1,562,485	1,824,422	146,520	85,875	134,484	42,754	20.4	11.6	19.3	5.2	1.0	0.8	-1.0	0.8	1.1	0.2	-1.1	0.6	1.1	0.1	1.2	0.1
IPI00945633	SSR1	Uncharacterized protein	100.0%	7.7	2	2	2	6	1,607,573	1,660,442	1,562,485	1,824,422	146,520	85,875	134,484	42,754	20.4	11.6	19.3	5.2	1.0	0.8	-1.0	0.8	1.1	0.2	-1.1	0.6	1.1	0.1	1.2	0.1
IPI00945795	SSR1	Uncharacterized protein	100.0%	8.7	2	2	2	6	1,607,573	1,660,442	1,562,485	1,824,422	146,520	85,875	134,484	42,754	20.4	11.6	19.3	5.2	1.0	0.8	-1.0	0.8	1.1	0.2	-1.1	0.6	1.1	0.1	1.2	0.1
IPI00946676	SSR1	Uncharacterized protein	100.0%	8.7	2	2	2	6	1,607,573	1,660,442	1,562,485	1,824,422	146,520	85,875	134,484	42,754	20.4	11.6	19.3	5.2	1.0	0.8	-1.0	0.8	1.1	0.2	-1.1	0.6	1.1	0.1	1.2	0.1
IPI00946839	SSR1	Uncharacterized protein	100.0%	7.9	2	2	2	6	1,607,573	1,660,442	1,562,485	1,824,422	146,520	85,875	134,484	42,754	20.4	11.6	19.3	5.2	1.0	0.8	-1.0	0.8	1.1	0.2	-1.1	0.6	1.1	0.1	1.2	0.1
IPI00449669	SSR1	isoform 2 of Translocon-associated protein subunit alpha	100.0%	8.9	2	2	2	6	1,607,573	1,660,442	1,562,485	1,824,422	146,520	85,875	134,484	42,754	20.4	11.6	19.3	5.2	1.0	0.8	-1.0	0.8	1.1	0.2	-1.1	0.6	1.1	0.1	1.2	0.1
				FLVGFTNK	2	89.9%	1																									
				GTEDFIVESLDASFR	2	100.0%	1																									
IPI00301058	VASP	Vasodilator-stimulated phosphoprotein	100.0%	20.8	5	6	8	1	69,473,571	70,917,286	65,551,586	78,953,962	5,745,186	1,591,117	5,058,104	2,629,194	18.5	5.0	17.3	7.5	1.0	0.8	-1.1	0.6	1.1	0.2	-1.1	0.4	1.1	0.03	1.2	0.05
				MQPDQQVVINCAIVR	2	99.9%	2																									
				QQPGPSEHIER	3	96.2%	1																									
				SGGGGLMEEMNAMLAR	2	100.0%	2																									
				SSSSVTTSETQPCTPSSSDYSDLQR	3	99.4%	1																									
				YNQATPNFHQWR	2	86.5%	1																									
				YNQATPNFHQWR	3	98.6%	1																									
IPI00301107	IPO11	Importin-11	98.6%	1.4	1	1	1	5	321,882	340,108	341,623	350,254	41,045	29,584	29,500	16,053	28.5	19.5	19.3	10.3	1.1	0.7	1.1	0.7	1.1	0.5	1.0	1	1.0	0.8	1.0	0.8
IPI00913938	IPO11	importin-11 isoform 1	98.6%	1.4	1	1	1	5	321,882	340,108	341,623	350,254	41,045	29,584	29,500	16,053	28.5	19.5	19.3	10.3	1.1	0.7	1.1	0.7	1.1	0.5	1.0	1	1.0	0.8	1.0	0.8
IPI00917511	IPO11	100 kDa protein	98.6%	1.6	1	1	1	5	321,882	340,108	341,623	350,254	41,045	29,584	29,500	16,053	28.5	19.5	19.3	10.3	1.1	0.7	1.1	0.7	1.1	0.5	1.0	1	1.0	0.8	1.0	0.8
IPI00965368	IPO11	Uncharacterized protein	98.6%	9.4	1	1	1	5	321,882	340,108	341,623	350,254	41,045	29,584	29,500	16,053	28.5	19.5	19.3	10.3	1.1	0.7	1.1	0.7	1.1	0.5	1.0	1	1.0	0.8	1.0	0.8
IPI01009690	IPO11	Uncharacterized protein	98.6%	8.6	1	1	1	5	321,882	340,108	341,623	350,254	41,045	29,584	29,500	16,053	28.5	19.5	19.3	10.3	1.1	0.7	1.1	0.7	1.1	0.5	1.0	1	1.0	0.8	1.0	0.8
				QWPELIPTLIESVK	2	94.3%	1																									
IPI00301109	PPA2	isoform 1 of Inorganic pyrophosphatase 2, mitochondrial	100.0%	16.8	3	3	3	5	1,226,620	1,142,331	1,527,283	1,277,394	132,348	60,936	204,361	50,652	24.1	11.9	29.9	8.9	-1.1	0.6	1.2	0.3	1.0	0.7	1.3	0.1	1.1	0.1	-1.2	0.3
IPI00413014	PPA2	inorganic pyrophosphatase 2, mitochondrial isoform 3 precursor	100.0%	24.1	3	3	3	5	1,226,620	1,142,331	1,527,283	1,277,394	132,348	60,936	204,361	50,652	24.1	11.9	29.9	8.9	-1.1	0.6	1.2	0.3	1.0	0.7	1.3	0.1	1.1	0.1	-1.2	0.3
IPI00470502	PPA2	isoform 2 of Inorganic pyrophosphatase 2, mitochondrial	100.0%	16.1	3	3	3	5	1,226,620	1,142,331	1,527,283	1,277,394	132,348	60,936	204,361	50,652	24.1	11.9	29.9	8.9	-1.1	0.6	1.2	0.3	1.0	0.7	1.3	0.1	1.1	0.1	-1.2	0.3
IPI00470503	PPA2	isoform 3 of Inorganic pyrophosphatase 2, mitochondrial	100.0%	18.4	3	3	3	5	1,226,620	1,142,331	1,527,283	1,277,394	132,348	60,936	204,361	50,652	24.1	11.9	29.9	8.9	-1.1	0.6	1.2	0.3	1.0	0.7	1.3	0.1	1.1	0.1	-1.2	0.3
IPI00654717	PPA2	Uncharacterized protein	100.0%	17.7	3	3	3	5	1,226,620	1,142,331	1,527,283	1,277,394	132,348	60,936	204,361	50,652	24.1	11.9	29.9	8.9	-1.1	0.6	1.2	0.3	1.0	0.7	1.3	0.1	1.1	0.1	-1.2	0.3
				FKPGYLEATLNWFR	3	99.9%	1																									
				ILGILALIDEGETDWK	2	100.0%	1																									
				SLVESVSSSPNKESNEEEQVWHFLGK	3	99.8%	1																									
IPI00301204	RDH13	isoform 1 of Retinol dehydrogenase 13	98.7%	5.7	1	1	1	2	275,160	283,789	375,798	357,396	16,963	38,280	42,072	26,438	13.8	30.2	25.0	16.5	1.0	0.8	1.4	0.06	1.3	0.03	1.3	0.1	1.3	0.2	-1.1	0.7
IPI01013743	RDH13	24 kDa protein	98.7%	8.6	1	1	1	2	275,160	283,789	375,798	357,396	16,963	38,280	42,072	26,438	13.8	30.2	25.0	16.5	1.0	0.8	1.4	0.06	1.3	0.03	1.3	0.1	1.3	0.2	-1.1	0.7
				YLLPLSALGTVAGAAVLLK	2	98.7%	1																									
IPI00301250	EPS8L1	isoform 1 of Epidermal growth factor receptor kinase substrate 8-like protein 1	100.0%	11.8	6	6	6	2	3,975,716	4,188,202	3,917,397	4,749,377	332,428	120,874	163,841	245,958	18.7	6.5	9.4	11.6	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.2	1.1	0.07	1.2	0.02
IPI01015233	EPS8L1	cDNA FLJ60287, highly similar to Epidermal growth factor receptor kinase substrate	100.0%	12.9	6	6	6	2	3,975,716	4,188,202	3,917,397	4,749,377	332,428	120,874	163,841	245,958	18.7	6.5	9.4	11.6	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.2	1.1	0.07	1.2	0.02
				APEPQLSPGSDASEVR	2	99.5%	1																									
				DLEPESEPQLESETAGK	2	100.0%	1																									
				EVDILNHVFDDVESFVSR	3	99.9%	1																									
				GPDLAVLQAER	2	99.8%	1																									
				RAAGEGLLTLR	2	95.4%	1																									
				SLLLLVCQEPER	2	98.0%	1																									
IPI00301263	CAD	CAD protein	99.6%	0.5	1	1	1	2	2,117,790	2,004,820	1,957,865	2,327,355	240,011	222,801	130,294	233,169	25.3	24.9	14.9	22.4	-1.1	0.7	-1.1	0.6	1.1	0.5	-1.0	0.9	1.2	0.3	1.2	0.2
IPI00893035	CAD	Putative uncharacterized protein CAD	99.6%	0.6	1	1	1	2	2,117,790	2,004,820	1,957,865	2,327,355	240,011	222,801	130,294	233,169	25.3	24.9	14.9	22.4	-1.1	0.7	-1.1	0.6	1.1	0.5	-1.0	0.9	1.2	0.3	1.2	0.2
				TLGVDLVALATR	2	99.6%	1																									
IPI00301323	DDX18	ATP-dependent RNA helicase DDX18	97.2%	3.9	2	2	2	1	3,568,365	3,532,659	3,281,229	4,044,403	376,097	165,161	357,078	309,392	23.6	10.5	24.3	17.1	-1.0	0.9	-1.1	0.6	1.1	0.4	-1.1	0.5	1.1	0.2	1.2	0.1
				TLAFLIPAVELIVK	2	96.7%	1																									
				VPLSEFDFSWSK	2	97.2%	1																									
IPI00301346	POLR3B	DNA-directed RNA polymerase III subunit RPC2	95.9%	1.2	1	1	1	2	1,063,545	1,052,719	1,042,570	1,073,300	211,517	108,929	28,289	190,531	44.5	23.1	6.1	39.7	-1.0	1	-1.0	0.9	1.0	1	-1.0	0.9	1.0	0.9	1.0	0.9
IPI00930490	POLR3B	DNA-directed RNA polymerase III subunit RPC2 isoform 2	95.9%	1.3	1	1	1	2	1,063,545	1,052,719	1,042,570	1,073,300	211,517	108,929	28,289	190,531	44.5	23.1	6.1	39.7	-1.0	1	-1.0	0.9	1.0	1	-1.0	0.9	1.0	0.9	1.0	0.9
				ELLASTILTHVPVK	2	94.9%	1																									
IPI00301364	SKP1	isoform 1 of S-phase kinase-associated protein 1	100.0%	36.8	5	5	5	2	9,277,013	9,450,368	9,118,896	10,575,384	797,055	363,166	749,649	440,135	19.2	8.6	18.4	9.3	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.08	1.2	0.1
IPI00974176	SKP1	Uncharacterized protein	100.0%	36.8	5	5	5	2	9,277,013	9,450,368	9,118,896	10,575,384	797,055	363,166	749,649	440,135	19.2	8.6	18.4	9.3	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.08	1.2	0.1
				LQSSDGEIFEVDVEIAK	2	100.0%	1																									
				RTDDIPVWDQEFLK	2	100.0%	1																									
				TDDIPVWDQEFLK	2	99.6%	1																									
				TMLEDLGMDDEGDDDPVPLPNVNAAILK	2	99.9%	1																									
				TMLEDLGMDDEGDDDPVPLPNVNAAILKK	3	100.0%	1																									
IPI00301395	CPVL	Probable serine carboxypeptidase CPVL	95.9%	2.9	1	1	1	4	1,011,245	1,078,673	979,658	1,025,023	59,068	28,312	90,631	123,457	13.1	5.9	20.7	26.9	1.1	0.3	-1.0	0.8	1.0	0.9	-1.1	0.3	-1.1	0.7	1.0	0.8
IPI00915961	CPVL	Uncharacterized protein	95.9%	9.9	1	1	1	4	1,011,245	1,078,673	979,658	1,025,023	59,068	28,312	90,631	123,457	13.1	5.9	20.7	26.9	1.1	0.3	-1.0	0.8	1.0	0.9	-1.1	0.3	-1.1	0.7	1.0	0.8
IPI00916887	CPVL	Uncharacterized bone marrow protein BM031	95.9%	6.0	1	1	1	4	1,011,245	1,078,673	979,658	1,025,023	59,068	28,312	90,631	123,457	13.1	5.9	20.7	26.9	1.1	0.3	-1.0	0.8	1.0	0.9	-1.1	0.3	-1.1	0.7	1.0	0.8
IPI00917290	CPVL	Uncharacterized protein	95.9%	5.7	1	1	1	4	1,011,245	1,078,673	979,658	1,025,023	59,068	28,312	90,631	123,457	13.1	5.9	20.7	26.9	1.1	0.3	-1.0	0.8	1.0	0.9	-1.1	0.3	-1.1	0.7	1.0	0.8

				NNDFYVTGESYAGK	2	95.9%	1																									
IPI00301434	BOLA2;BOLA2B	BolA-like protein 2	99.8%	10.5	1	1	1	2	2,847,210	2,644,565	2,637,190	2,965,025	456,281	128,072	290,644	248,181	35.8	10.8	24.6	18.7	-1.1	0.7	-1.1	0.7	1.0	0.8	-1.0	1	1.1	0.3	1.1	0.4
IPI00410226	BOLA2;BOLA2B	isoform 2 of BolA-like protein 2	99.8%	27.6	1	1	1	2	2,847,210	2,644,565	2,637,190	2,965,025	456,281	128,072	290,644	248,181	35.8	10.8	24.6	18.7	-1.1	0.7	-1.1	0.7	1.0	0.8	-1.0	1	1.1	0.3	1.1	0.4
				DLEAEHVEVEDTTLNR	3	99.8%	1																									
IPI00301503	TRA2B	isoform 1 of Transformer-2 protein homolog beta	100.0%	17.4	4	4	5	3	6,403,493	6,730,596	6,677,757	7,755,923	425,979	252,208	433,646	157,703	14.9	8.4	14.5	4.6	1.1	0.5	1.0	0.7	1.2	0.03	-1.0	0.9	1.2	0.009	1.2	0.07
IPI00472633	TRA2B	isoform 3 of Transformer-2 protein homolog beta	100.0%	26.6	4	4	5	3	6,403,493	6,730,596	6,677,757	7,755,923	425,979	252,208	433,646	157,703	14.9	8.4	14.5	4.6	1.1	0.5	1.0	0.7	1.2	0.03	-1.0	0.9	1.2	0.009	1.2	0.07
IPI00555647	TRA2B	Uncharacterized protein	100.0%	17.3	4	4	5	3	6,403,493	6,730,596	6,677,757	7,755,923	425,979	252,208	433,646	157,703	14.9	8.4	14.5	4.6	1.1	0.5	1.0	0.7	1.2	0.03	-1.0	0.9	1.2	0.009	1.2	0.07
				AAQDRDQIYR	3	96.7%	1																									
				GFAFVYFENVDDAK	2	100.0%	1																									
				GYDDRDYYSR	2	90.9%	1																									
				YGPIADVSIVYDQQSR	2	100.0%	2																									
IPI00301676	LRRC16B	isoform 1 of Leucine-rich repeat-containing protein 16B	94.8%	2.0	1	1	1	2	2,218,995	2,459,290	3,432,630	2,666,205	345,134	408,451	498,750	184,724	34.8	37.1	32.5	15.5	1.1	0.7	1.5	0.08	1.2	0.3	1.4	0.2	1.1	0.7	-1.3	0.2
IPI00886998	LRRC16B	isoform 3 of Leucine-rich repeat-containing protein 16B	94.8%	16.2	1	1	1	2	2,218,995	2,459,290	3,432,630	2,666,205	345,134	408,451	498,750	184,724	34.8	37.1	32.5	15.5	1.1	0.7	1.5	0.08	1.2	0.3	1.4	0.2	1.1	0.7	-1.3	0.2
				ALESNHTLRFMSFPVSDISQAYRSAPER	3	94.8%	1																									
IPI00301865	TMEM132A	isoform 1 of Transmembrane protein 132A	96.3%	1.1	1	1	1	4	664,495	600,380	691,778	642,680	34,827	21,112	13,578	19,685	11.7	7.9	4.4	6.9	-1.1	0.2	1.0	0.5	-1.0	0.6	1.2	0.007	1.1	0.2	-1.1	0.07
IPI00383814	TMEM132A	isoform 2 of Transmembrane protein 132A	96.3%	1.1	1	1	1	4	664,495	600,380	691,778	642,680	34,827	21,112	13,578	19,685	11.7	7.9	4.4	6.9	-1.1	0.2	1.0	0.5	-1.0	0.6	1.2	0.007	1.1	0.2	-1.1	0.07
IPI00845309	TMEM132A	isoform 4 of Transmembrane protein 132A	96.3%	1.4	1	1	1	4	664,495	600,380	691,778	642,680	34,827	21,112	13,578	19,685	11.7	7.9	4.4	6.9	-1.1	0.2	1.0	0.5	-1.0	0.6	1.2	0.007	1.1	0.2	-1.1	0.07
IPI01015162	TMEM132A	Protein	96.3%	7.2	1	1	1	4	664,495	600,380	691,778	642,680	34,827	21,112	13,578	19,685	11.7	7.9	4.4	6.9	-1.1	0.2	1.0	0.5	-1.0	0.6	1.2	0.007	1.1	0.2	-1.1	0.07
				LTVWAPLLPLR	3	96.3%	1																									
IPI00301869	CDHR5	isoform 2 of Cadherin-related family member 5	99.4%	5.7	2	2	2	3	5,256,283	5,892,560	5,536,942	6,262,522	397,725	477,668	537,601	184,964	16.9	18.1	21.7	6.6	1.1	0.3	1.1	0.7	1.2	0.05	-1.1	0.6	1.1	0.5	1.1	0.3
IPI00336112	CDHR5	isoform 1 of Cadherin-related family member 5	99.4%	4.4	2	2	2	3	5,256,283	5,892,560	5,536,942	6,262,522	397,725	477,668	537,601	184,964	16.9	18.1	21.7	6.6	1.1	0.3	1.1	0.7	1.2	0.05	-1.1	0.6	1.1	0.5	1.1	0.3
IPI00409619	CDHR5	isoform 3 of Cadherin-related family member 5	99.4%	4.4	2	2	2	3	5,256,283	5,892,560	5,536,942	6,262,522	397,725	477,668	537,601	184,964	16.9	18.1	21.7	6.6	1.1	0.3	1.1	0.7	1.2	0.05	-1.1	0.6	1.1	0.5	1.1	0.3
				APEPQPQGFDNQAFLPDHK	3	98.6%	1																									
				VFVSVLDVNDNAPEFPFK	2	99.4%	1																									
IPI00301936	ELAVL1	cDNA FLJ60076, highly similar to ELAV-like protein 1	100.0%	18.7	4	5	6	2	10,336,461	10,612,162	10,849,523	12,862,572	989,758	328,401	978,388	389,481	21.4	6.9	20.2	6.8	1.0	0.8	1.0	0.7	1.2	0.06	1.0	0.8	1.2	0.002	1.2	0.09
IPI00940851	ELAVL1	ELAV-like protein 1	100.0%	20.3	4	5	6	2	10,336,461	10,612,162	10,849,523	12,862,572	989,758	328,401	978,388	389,481	21.4	6.9	20.2	6.8	1.0	0.8	1.0	0.7	1.2	0.06	1.0	0.8	1.2	0.002	1.2	0.09
				GFGFVTMTNYEEAAMAIASLNGYR	2	100.0%	1																									
				GFGFVTMTNYEEAAMAIASLNGYR	3	100.0%	1																									
				SLFSSIGEVESAK	2	99.9%	1																									
				TNLIVNYLPQNMTQDELR	2	100.0%	1																									
				VLVDQTTGLSR	2	100.0%	2																									
IPI00302047	CAST	cDNA FLJ77737, highly similar to Homo sapiens calpastatin (CAST), transcript varia	100.0%	16.2	3	3	3	1	942,636	990,917	903,667	1,093,327	62,204	44,225	46,065	46,900	14.8	10.0	11.4	9.6	1.1	0.5	-1.0	0.6	1.2	0.09	-1.1	0.2	1.1	0.2	1.2	0.02
				EQLPPMSEDFLLDALSEDFSGPQNASSLK	3	99.8%	1																									
				GTVPDDAVEALADSLGK	2	99.8%	1																									
				LAAAISEVVSQTPASTTQAGAPPR	3	99.3%	1																									
IPI00302238	AATF	Protein AATF	100.0%	2.3	1	1	1	1	2,156,220	1,996,460	2,261,770	2,028,780	131,188	89,322	192,549	143,188	13.6	10.0	19.0	15.8	-1.1	0.3	1.0	0.7	-1.1	0.5	1.1	0.2	1.0	0.9	-1.1	0.4
				NQIALWDQLLEGR	2	100.0%	1																									
IPI00302318	SDCBP2	isoform 1 of Syntenin-2	100.0%	7.2	2	2	2	1	3,629,595	3,787,298	3,732,927	4,121,857	376,018	215,895	194,819	273,946	23.2	12.8	11.7	14.9	1.0	0.7	1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.4	1.1	0.3
				FGDQLLQIDGR	2	100.0%	1																									
				VDQAIQAQVR	2	100.0%	1																									
IPI00302383	CFTR	Cystic fibrosis transmembrane conductance regulator ATP-binding cassette sub-fam	91.3%	1.3	1	1	1	4	893,668	766,660	828,613	995,473	80,953	60,468	85,052	65,190	20.3	17.6	23.0	14.6	-1.2	0.2	-1.1	0.6	1.1	0.4	1.1	0.6	1.3	0.03	1.2	0.2
IPI00815998	CFTR	isoform 1 of Cystic fibrosis transmembrane conductance regulator	91.3%	1.3	1	1	1	4	893,668	766,660	828,613	995,473	80,953	60,468	85,052	65,190	20.3	17.6	23.0	14.6	-1.2	0.2	-1.1	0.6	1.1	0.4	1.1	0.6	1.3	0.03	1.2	0.2
IPI00816790	CFTR	isoform 2 of Cystic fibrosis transmembrane conductance regulator	91.3%	1.3	1	1	1	4	893,668	766,660	828,613	995,473	80,953	60,468	85,052	65,190	20.3	17.6	23.0	14.6	-1.2	0.2	-1.1	0.6	1.1	0.4	1.1	0.6	1.3	0.03	1.2	0.2
IPI01010813	CFTR	Cystic fibrosis transmembrane conductance regulator ATP-binding cassette sub-fam	91.3%	1.3	1	1	1	4	893,668	766,660	828,613	995,473	80,953	60,468	85,052	65,190	20.3	17.6	23.0	14.6	-1.2	0.2	-1.1	0.6	1.1	0.4	1.1	0.6	1.3	0.03	1.2	0.2
				QSVLNLMTHSVNQGQNIHR	3	91.4%	1																									
IPI00302436	HDHD1	isoform 1 of Pseudouridine-5'-monophosphatase	99.4%	12.3	1	1	1	4	93,437	95,159	115,576	133,700	18,612	9,499	14,389	12,052	44.5	22.3	27.8	20.2	1.0	0.9	1.2	0.4	1.4	0.1	1.2	0.3	1.4	0.04	1.2	0.4
IPI00913889	HDHD1	pseudouridine-5'-monophosphatase isoform a	99.4%	11.2	1	1	1	4	93,437	95,159	115,576	133,700	18,612	9,499	14,389	12,052	44.5	22.3	27.8	20.2	1.0	0.9	1.2	0.4	1.4	0.1	1.2	0.3	1.4	0.04	1.2	0.4
IPI01013783	HDHD1	27 kDa protein	99.4%	11.5	1	1	1	4	93,437	95,159	115,576	133,700	18,612	9,499	14,389	12,052	44.5	22.3	27.8	20.2	1.0	0.9	1.2	0.4	1.4	0.1	1.2	0.3	1.4	0.04	1.2	0.4
IPI00922433	HDHD1	pseudouridine-5'-monophosphatase isoform c	99.4%	13.5	1	1	1	4	93,437	95,159	115,576	133,700	18,612	9,499	14,389	12,052	44.5	22.3	27.8	20.2	1.0	0.9	1.2	0.4	1.4	0.1	1.2	0.3	1.4	0.04	1.2	0.4
				ALEAAQIIIDVLQLPMSKEELVEESQTK	3	99.4%	1																									
IPI00302458	XPO7	Exportin-7	98.8%	1.5	1	1	1	2	18,062,900	18,610,300	17,541,300	24,624,800	3,713,884	1,705,433	2,964,626	1,496,644	46.0	20.5	37.8	13.6	1.0	0.9	-1.0	0.9	1.4	0.1	-1.1	0.8	1.3	0.03	1.4	0.07
IPI00855940	XPO7	Uncharacterized protein	98.8%	1.5	1	1	1	2	18,062,900	18,610,300	17,541,300	24,624,800	3,713,884	1,705,433	2,964,626	1,496,644	46.0	20.5	37.8	13.6	1.0	0.9	-1.0	0.9	1.4	0.1	-1.1	0.8	1.3	0.03	1.4	0.07
				LYGDDALDNALQTFIK	2	98.8%	1																									
IPI00302592	FLNA	isoform 2 of Filamin-A	100.0%	10.0	15	15	16	4	20,961,450	23,026,453	20,710,051	25,437,595	2,076,059	706,354	1,836,836	754,768	22.2	6.9	19.8	6.6	1.1	0.4	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.05	1.2	0.04
IPI00333541	FLNA	isoform 1 of Filamin-A	100.0%	10.0	15	15	16	4	20,961,450	23,026,453	20,710,051	25,437,595	2,076,059	706,354	1,836,836	754,768	22.2	6.9	19.8	6.6	1.1	0.4	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.05	1.2	0.04
IPI00553169	FLNA	Uncharacterized protein	100.0%	11.4	15	15	16	4	20,961,450	23,026,453	20,710,051	25,437,595	2,076,059	706,354	1,836,836	754,768	22.2	6.9	19.8	6.6	1.1	0.4	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.05	1.2	0.04
IPI00644576	FLNA	Filamin A, alpha	100.0%	10.1	15	15	16	4	20,961,450	23,026,453	20,710,051	25,437,595	2,076,059	706,354	1,836,836	754,768	22.2	6.9	19.8	6.6	1.1	0.4	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.05	1.2	0.04
				AFGPGLQGGSAGSPAR	2	100.0%	1																									
				AWGPGLEGGVVGK	2	95.5%	1																									
				CSYQPTMEGVHTVHVTFAGVPIPR	3	89.4%	1																									
				EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	3	97.1%	1																									
				LDVQFSGLTK	2	88.6%	1																									
				LIALLEVLSQK	2	100.0%	2																									
				LLGWIQNK	2	98.6%	1																									
				QMQLENVSVALEFLDRESIK	3	99.2%	1																									
				SADFVVEAIGDDVGTLGFSVEGPSQAKIECDDK	3	91.6%	1																									
				SPFSVAVSPSLDLSK	2	99.5%	1																									
				VANPSGNLTETYVQDR	2	100.0%	1																									
				VEPGLGADNSVVR	2	84.5%	1																									
				VHSPSGALEECYVTEIDQDKYAVR	3	98.0%	1																									
				VTYTPMAPGSYLISIK	2	96.6%	1																									
				YGGQPVPNFPSK	2	94.7%	1																									
IPI00302641	FAT2	Protocadherin Fat 2	96.0%	0.2	1	1	1	1	5,654,530	4,917,580	5,273,100	5,500,390	181,866	201,800	431,889	253,023	7.2	9.2	18.3	10.3	-1.1	0.03	-1.1	0.4	-1.0	0.6	1.1	0.5	1.1	0.1	1.0	0.7
				KHLDSSYNLR	2	94.5%	1																									
IPI00302688	ECHDC1	isoform 1 of Enoyl-CoA hydratase domain-containing protein 1	99.5%	6.2	1	1	1	6	487,308	456,413	446,638	481,162	33,221	19,838	28,891	28,985	15.2	9.7	14.5	13.5	-1.1	0.4	-1.1	0.4	-1.0	0.9	-1.0	0.8	1.1	0.5	1.1	0.4
IPI00479537	ECHDC1	Uncharacterized protein	99.5%	6.6	1	1	1	6	487,308	456,413	446,638	481,162	33,221	19,838	28,891	28,985	15.2	9.7	14.5	13.5	-1.1	0.4	-1.1	0.4	-1.0	0.9	-1.0	0.8	1.1	0.5	1.1	0.4
IPI00513761	ECHDC1	Uncharacterized protein	99.5%	7.0	1	1	1	6	487,308	456,413	446,638	481,162	33,221	19,838	28,891	28,985	15.2	9.7	14.5	13.5	-1.1	0.4	-1.1	0.4	-1.0	0.9	-1.0	0.8	1.1	0.5	1.1	0.4
IPI00550928	ECHDC1	isoform 2 of Enoyl-CoA hydratase domain-containing protein 1	99.5%	6.3	1	1	1	6	487,308	456,413	446,638	481,162	33,221	19,838	28,891	28,985	15.2	9.7	14.5	13.5	-1.1	0.4	-1.1	0.4	-1.0	0.9	-1.0	0.8	1.1	0.5	1.1	0.4
IPI00645630	ECHDC1	enoyl-CoA hydratase domain-containing protein 1 isoform 3	99.5%	8.4	1	1	1	6	487,308	456,413	446,638	481,162	33,221	19,838	28,891	28,985	15.2	9.7	14.5	13.5	-1.1	0.4	-1.1	0.4	-1.0	0.9	-1.0	0.8	1.1	0.5	1.1	0.4
IPI00973756	ECHDC1	Novel enoyl-CoA hydratase/isomerase family protein (Fragment)	99.5%	8.9	1	1	1	6	487,308	456,413	446,638	481,162	33,221	19,838	28,891	28,985	15.2	9.7	14.5	13.5	-1.1	0.4	-1.1	0.4	-1.0	0.9	-1.0	0.8	1.1	0.5	1.1	0.4
				NALNIGMVEEVLQSSDETK	2	99.5%	1																									
IPI00302840	ATP1A3	Sodium/potassium-transporting ATPase subunit alpha-3	99.7%	1.9	1	1	1	4	326,386	304,365	364,000	352,684	22,307	31,305	28,679	15,163	15.3	23.0	17.6	9.6	-1.1	0.6	1.1	0.3	1.1	0.4	1.2	0.2	1.2	0.2	-1.0	0.7
IPI00647099	ATP1A3	Na+/K+ transporting ATPase alpha 3 polypeptide	99.7%	1.9	1	1	1	4	326,386	304,365	364,000	352,684	22,307	31,305	28,679	15,163	15.3	23.0	17.6	9.6	-1.1	0.6	1.1	0.3	1.1	0.4	1.2	0.2	1.2	0.2	-1.0	0.7
IPI00790327	ATP1A3	cDNA FLJ59513, highly similar to Sodium/potassium-transporting ATPase alpha-3 c	99.7%	1.9	1	1	1	4	326,386	304,365	364,000	352,684	22,307	31,305	28,679	15,163	15.3	23.0	17.6	9.6	-1.1	0.6	1.1	0.3	1.1	0.4	1.2	0.2	1.2	0.2	-1.0	0.7
IPI01014473	ATP1A3	cDNA FLJ59485, highly similar to Sodium/potassium-transporting ATPase alpha-3 c	99.7%	2.1	1	1	1	4	326,386	304,365	364,000	352,684	22,307	31,305	28,679	15,163	15.3	23.0	17.6	9.6	-1.1	0.6	1.1	0.3	1.1	0.4	1.2	0.2	1.2	0.2	-1.0	0.7
				TVNDLEDSYGQQWTYEQRK	2	88.1%	1																									
IPI00302850	SNRPD1	Small nuclear ribonucleoprotein Sm D1	100.0%	34.5	2	3	4	1	5,565,765	5,962,599	5,885,675	4,757,583	590,311	444,360	304,347	420,491	23.7	16.7	11.6	19.8	1.1	0.6	1.1	0.6	-1.2	0.3	-1.0	0.9	-1.3	0.08	-1.2	0.06
				NGTQVHGTITGVDVSMNTHLK	3	99.9%	1																									
				YFILPDSLPLDTLLVDVEPK	2	100.0%	2																									
				YFILPDSLPLDTLLVDVEPK	3	100.0%	1																									
IPI00302925	CCT8	59 kDa protein	100.0%	36.4	18	18	23	1	44,486,443	44,482,470	42,433,903	49,527,464	3,776,105	1,793,262	2,750,238	1,426,015	19.0	9.0	14.5	6.4	-1.0	1	-1.0	0.7	1.1	0.3	-1.0	0.6	1.1	0.06	1.2	0.05
				APGFAQMLK	2	100.0%	1																									
				AVDDGVNTFK	2	100.0%	1																									
				DMLEAGILDTYLGK	2	100.0%	2																									
				EDGAISTIVLR	2	82.4%	1																									
				ELEVQHPAAK	2	99.4%	1																									
				FAEAFEAIPR	2	100.0%	1																									
				GEENLMDAQVK	2	100.0%	2																									
				GSTDNLMDDIER	2	100.0%	2																									
				HFSGLEEAVYR	2	99.3%	1																									
				IAVYSCPFDGMITETK	2	97.7%	1																									
				LATNAAVTVLR	2	100.0%	2																									
				LFVTNDAATILR	2	100.0%	1																									
				LVPGGGATEIELAK	2	88.3%	1																									
				MVINHLEK	2	85.5%	1																									
				NVGLDIEAEVPAVK	2	100.0%	2																									
				TAEELMNFSK	2	100.0%	1																									
				TVGATALPR	2	98.5%	1																									
				YNIMLVR	2	99.0%	1																									
IPI00302927	CCT4	T-complex protein 1 subunit delta	100.0%	25.6	11	13	14	1	16,090,961	18,396,470	18,006,171	19,290,217	1,166,097	1,032,807	1,565,995	434,807	16.2	12.6	19.5	5.0	1.1	0.2	1.1	0.4	1.2	0.05	-1.0	0.8	1.0	0.4	1.1	0.5
				DALSDLALHFLNK	2	100.0%	1																									
				DALSDLALHFLNK	3	88.5%	1																									
				GDVTITNDGATILK	2	95.2%	1																									
				IDDVVNTR	2	99.4%	2																									
				KLGGTIDDCELVEGLVLTQKVSNSGITR	3	98.0%	1																									
				LGGTIDDCELVEGLVLTQK	2	100.0%	1																									
				LGGTIDDCELVEGLVLTQK	3	99.3%	1																									
				MIQDGKGDVTITNDGATILK	3	100.0%	1																									
				QMQVLHPAAR	2	98.6%	1																									
				TDMDNQIVVSDYAQMDR	2	100.0%	1																									
				TGCNVLLIQK	2	99.8%	1																									
				VIDPATATSVDLR	2	100.0%	1																									
				VVSQYSSLLSPMSVNAVMK	2	100.0%	1																									
IPI00303174	HGD	Homogentisate 1,2-dioxygenase	95.2%	2.3	1	1	1	4	1,495,000	1,581,888	1,548,600	1,522,920	61,685	90,020	83,590	33,025	9.2	12.7	12.1	4.9	1.1	0.4	1.0	0.6	1.0	0.7	-1.0	0.8	-1.0	0.6	-1.0	0.8
IPI00640411	HGD	Uncharacterized protein	95.2%	3.0	1	1	1	4	1,495,000	1,581,888	1,548,600	1,522,920	61,685	90,020	83,590	33,025	9.2	12.7	12.1	4.9	1.1	0.4	1.0	0.6	1.0	0.7	-1.0	0.8	-1.0	0.6	-1.0	0.8
IPI00794948	HGD	Protein	95.2%	11.4	1	1	1	4	1,495,000	1,581,888	1,548,600	1,522,920	61,685	90,020	83,590	33,025	9.2	12.7	12.1	4.9	1.1	0.4	1.0	0.6	1.0	0.7	-1.0	0.8	-1.0	0.6	-1.0	0.8
IPI00947534	HGD	Uncharacterized protein	95.2%	5.7	1	1	1	4	1,495,000	1,581,888	1,548,600	1,522,920	61,685	90,020	83,590	33,025	9.2	12.7	12.1	4.9	1.1	0.4	1.0	0.6	1.0	0.7	-1.0	0.8	-1.0	0.6	-1.0	0.8
				FSIDVFEETR	2	95.2%	1																									
IPI00303207	ABCE1	ATP-binding cassette sub-family E member 1	100.0%	11.4	5	5	5	1	14,232,538	15,489,792	15,068,275	15,969,440	1,014,871	936,544	821,372	273,239	15.9	13.5	12.2	3.8	1.1	0.4	1.1	0.5	1.1	0.2	-1.0	0.7	1.0	0.6	1.1	0.3
				ADIFMFDEPSSYLDVK	2	100.0%	1																									
				CPFGALSIVNLPSNLEK	2	99.0%	1																									
				FLSQLEITFR	2	96.1%	1																									
				IAIVNHDK	2	95.7%	1																									
				VAETANEEEVKKMCMYK	3	82.5%	1																									
IPI00303292	KPNA1	Importin subunit alpha-1	98.4%	2.6	1	1	2	2	602,042	649,568	601,138	765,703	49,700	66,832	62,217	68,564	18.5	23.0	23.1	20.0	1.1	0.6	-1.0	1	1.3	0.09	-1.1	0.6	1.2	0.3	1.3	0.1
IPI00642306	KPNA5	Karyopherin alpha 5	98.4%	11.5	1	1	2	2	602,042	649,568	601,138	765,703	49,700	66,832	62,217	68,564	18.5	23.0	23.1	20.0	1.1	0.6	-1.0	1	1.3	0.09	-1.1	0.6	1.2	0.3	1.3	0.1
				IVQVALNGLENILR	2	98.4%	2																									
IPI00303318	FAM49B	Protein FAM49B	100.0%	15.4	4	4	5	1	9,499,064	10,386,654	9,884,161	11,580,520	827,922	418,410	1,347,369	608,383	19.5	9.0	30.5	11.8	1.1	0.4	1.0	0.8	1.2	0.08	-1.1	0.7	1.1	0.1	1.2	0.3
				DAEGILEDLQSYR	2	100.0%	2																									
				DQPPNSVEGLLNALR	2	95.3%	1																									
				INNVPAEGENEVNNELANR	3	93.4%	1																									
				VLKDQPPNSVEGLLNALR	3	99.9%	1																									
IPI00303335	NEB	Nebulin	99.4%	0.4	2	2	2	4	2,003,898	1,970,257	1,764,495	2,447,549	208,054	157,792	133,087	197,438	23.2	17.9	16.9	18.0	-1.0	0.9	-1.1	0.4	1.2	0.2	-1.1	0.3	1.2	0.1	1.4	0.02
IPI00914847	NEB	nebulin isoform 1	99.4%	0.3	2	2	2	4	2,003,898	1,970,257	1,764,495	2,447,549	208,054	157,792	133,087	197,438	23.2	17.9	16.9	18.0	-1.0	0.9	-1.1	0.4	1.2	0.2	-1.1	0.3	1.2	0.1	1.4	0.02
IPI00917728	NEB	nebulin isoform 2	99.4%	0.3	2	2	2	4	2,003,898	1,970,257	1,764,495	2,447,549	208,054	157,792	133,087	197,438	23.2	17.9	16.9	18.0	-1.0	0.9	-1.1	0.4	1.2	0.2	-1.1	0.3	1.2	0.1	1.4	0.02
IPI01015244	NEB	773 kDa protein	99.4%	0.4	2	2	2	4	2,003,898	1,970,257	1,764,495	2,447,549	208,054	157,792	133,087	197,438	23.2	17.9	16.9	18.0	-1.0	0.9	-1.1	0.4	1.2	0.2	-1.1	0.3	1.2	0.1	1.4	0.02
				QVSDILYK	2	81.8%	1																									

				SREQSRSASALSISGGEEK	3	96.8%	1																									
IPI00303397	SPAG9	isoform 6 of C-Jun-amino-terminal kinase-interacting protein 4	99.3%	1.3	1	1	1	3	234,005	292,576	285,545	323,348	40,675	36,142	39,599	36,575	38.9	27.6	31.0	25.3	1.3	0.3	1.2	0.4	1.4	0.1	-1.0	0.9	1.1	0.6	1.1	0.5
IPI00385301	SPAG9	Uncharacterized protein	99.3%	1.3	1	1	1	3	234,005	292,576	285,545	323,348	40,675	36,142	39,599	36,575	38.9	27.6	31.0	25.3	1.3	0.3	1.2	0.4	1.4	0.1	-1.0	0.9	1.1	0.6	1.1	0.5
IPI00748244	SPAG9	isoform 7 of C-Jun-amino-terminal kinase-interacting protein 4	99.3%	2.3	1	1	1	3	234,005	292,576	285,545	323,348	40,675	36,142	39,599	36,575	38.9	27.6	31.0	25.3	1.3	0.3	1.2	0.4	1.4	0.1	-1.0	0.9	1.1	0.6	1.1	0.5
				HIEVQVAQETR	2	99.3%	1																									
IPI00303476	ATP5B	ATP synthase subunit beta, mitochondrial	100.0%	50.1	18	22	31	1	130,166,088	132,845,147	133,187,170	149,162,508	########	3,263,857	7,984,230	5,172,561	17.9	5.5	13.4	7.8	1.0	0.8	1.0	0.8	1.1	0.1	1.0	1	1.1	0.03	1.1	0.1
				AIAELGIYPAVDPLDSTSR	3	99.2%	1																									
				EGNDLYHEMIESGVINLK	2	100.0%	1																									
				EGNDLYHEMIESGVINLK	3	100.0%	1																									
				FTQAGSEVSALLGR	2	100.0%	2																									
				IGLFGGAGVGK	2	100.0%	2																									
				ILQDYK	2	94.2%	1																									
				IMDPNIVGSEHYDVAR	3	99.9%	1																									
				IMNVIGEPIDER	2	100.0%	1																									
				IPSAVGYQPTLATDMGTMQER	2	100.0%	2																									
				IPVGPETLGR	2	97.6%	1																									
				LVLEVAQHLGESTVR	2	100.0%	2																									
				LVLEVAQHLGESTVR	3	100.0%	1																									
				QFAPIHAEAPEFMEMSVEQEILVTGIK	3	100.0%	1																									
				SLQDIIAILGMDELSEEDKLTVSR	2	100.0%	1																									
				SLQDIIAILGMDELSEEDKLTVSR	3	100.0%	1																									
				TIAMDGTEGLVR	2	100.0%	2																									
				TVLIMELINNVAK	2	100.0%	2																									
				VALTGLTVAEYFR	2	100.0%	2																									
				VALVYGQMNEPPGAR	2	100.0%	3																									
				VLDSGAPIKIPVGPETLGR	2	94.8%	1																									
				VLDSGAPIKIPVGPETLGR	3	100.0%	1																									
				VVDLLAPYAK	2	99.9%	1																									
IPI00303568	PTGES2	Prostaglandin E synthase 2	98.8%	2.1	1	1	1	2	1,345,920	1,538,675	1,472,795	1,574,380	119,688	114,543	76,859	131,650	19.9	16.7	11.7	18.7	1.1	0.3	1.1	0.4	1.2	0.2	-1.0	0.6	1.0	0.8	1.1	0.5
IPI00947368	PTGES2	Protein	98.8%	2.6	1	1	1	2	1,345,920	1,538,675	1,472,795	1,574,380	119,688	114,543	76,859	131,650	19.9	16.7	11.7	18.7	1.1	0.3	1.1	0.4	1.2	0.2	-1.0	0.6	1.0	0.8	1.1	0.5
				YWLMLNEK	2	95.2%	1																									
IPI00303722	FAM136A	Protein FAM136A	100.0%	17.4	2	2	3	2	2,999,783	2,960,797	2,670,593	3,040,770	290,867	124,050	156,656	113,731	21.7	9.4	13.1	8.4	-1.0	0.9	-1.1	0.3	1.0	0.9	-1.1	0.2	1.0	0.6	1.1	0.09
IPI00927933	FAM136A	Uncharacterized protein	100.0%	9.8	2	2	3	2	2,999,783	2,960,797	2,670,593	3,040,770	290,867	124,050	156,656	113,731	21.7	9.4	13.1	8.4	-1.0	0.9	-1.1	0.3	1.0	0.9	-1.1	0.2	1.0	0.6	1.1	0.09
				CVDDHMHLIPTMTK	2	98.9%	2																									
				VQEAVESMVK	2	99.1%	1																									
IPI00303832	RTF1	RNA polymerase-associated protein RTF1 homolog	98.7%	1.7	1	1	1	1	7,986,460	8,913,730	7,610,590	9,225,280	837,714	510,990	379,302	610,653	23.5	12.8	11.1	14.8	1.1	0.4	-1.0	0.7	1.2	0.3	-1.2	0.07	1.0	0.7	1.2	0.05
				VAEITGVVETAK	2	98.7%	1																									
IPI00303882	PLIN3	isoform B of Perilipin-3	100.0%	52.5	13	14	19	1	18,647,492	19,763,093	19,046,788	22,566,199	1,672,228	940,466	1,377,022	728,078	20.1	10.6	16.2	7.2	1.1	0.6	1.0	0.9	1.2	0.06	-1.0	0.7	1.1	0.05	1.2	0.05
				DIAQQLQATCTSLGSSIQGLPTNVKDQVQQAR	3	100.0%	1																									
				DTVATQLSEAVDATR	2	100.0%	1																									
				EALDHMVEYVAQNTPVTWLVGPFAPGITEK	3	100.0%	1																									
				ELVSSKVSGAQEMVSSAKDTVATQLSEAVDATR	3	95.6%	1																									
				IATSLDGFDVASVQQQR	2	100.0%	2																									
				IATSLDGFDVASVQQQR	3	95.3%	1																									
				LGQMVLSGVDTVLGK	2	100.0%	2																									
				QEQSYFVR	2	99.9%	2																									
				QLQGPEKEPPKPEQVESR	3	99.9%	1																									
				QVEDLQATFSSIHSFQDLSSSILAQSR	3	94.0%	1																									
				SEEWADNHLPLTDAELAR	3	100.0%	1																									
				SVVTGGVQSVMGSR	2	100.0%	1																									
				TLTAAAVSGAQPILSK	2	100.0%	2																									
				VSGAQEMVSSAK	2	100.0%	2																									
IPI00303887	OR10J5	Olfactory receptor 10J5	95.4%	9.1	1	1	1	1	1,733,990	1,631,330	1,762,160	1,848,000	174,196	120,129	181,165	187,871	22.5	16.5	23.0	22.7	-1.1	0.6	1.0	0.9	1.1	0.7	1.1	0.6	1.1	0.4	1.0	0.8
				KTFATCVSHLTVVIVHCGCASIAYLKPK	3	95.4%	1																									
IPI00303933	ACAA1	3-ketoacyl-CoA thiolase, peroxisomal isoform b	100.0%	20.2	4	4	4	1	11,782,246	12,491,994	13,432,369	14,731,047	1,717,303	973,639	1,293,050	566,028	32.6	17.4	21.5	8.6	1.1	0.7	1.1	0.5	1.3	0.2	1.1	0.6	1.2	0.08	1.1	0.4
				GGFKDTTPDELLSAVMTAVLK	3	100.0%	1																									
				IAQFLSDIPETVPLSTVNR	2	98.2%	1																									
				QCSSGLQAVASIAGGIR	2	100.0%	1																									
				QVITLLNELK	2	96.5%	1																									
IPI00304071	ACSF2	Acyl-CoA synthetase family member 2, mitochondrial	100.0%	3.7	2	2	2	4	2,597,337	2,906,185	1,908,721	3,100,530	381,652	301,548	230,634	236,846	32.9	23.2	27.0	17.1	1.1	0.5	-1.4	0.2	1.2	0.3	-1.5	0.03	1.1	0.6	1.6	0.007
IPI00909579	ACSF2	cDNA FLJ51819, weakly similar to Long-chain-fatty-acid--CoA ligase	100.0%	3.6	2	2	2	4	2,597,337	2,906,185	1,908,721	3,100,530	381,652	301,548	230,634	236,846	32.9	23.2	27.0	17.1	1.1	0.5	-1.4	0.2	1.2	0.3	-1.5	0.03	1.1	0.6	1.6	0.007
IPI00967282	ACSF2	cDNA FLJ54351, weakly similar to Long-chain-fatty-acid--CoA ligase	100.0%	3.8	2	2	2	4	2,597,337	2,906,185	1,908,721	3,100,530	381,652	301,548	230,634	236,846	32.9	23.2	27.0	17.1	1.1	0.5	-1.4	0.2	1.2	0.3	-1.5	0.03	1.1	0.6	1.6	0.007
IPI01015394	ACSF2	cDNA FLJ50666, weakly similar to Long-chain-fatty-acid--CoA ligase	100.0%	4.0	2	2	2	4	2,597,337	2,906,185	1,908,721	3,100,530	381,652	301,548	230,634	236,846	32.9	23.2	27.0	17.1	1.1	0.5	-1.4	0.2	1.2	0.3	-1.5	0.03	1.1	0.6	1.6	0.007
				IMNMEAGTLAK	2	99.9%	1																									
				TVGQCLETTAQR	2	99.6%	1																									
IPI00304082	ISOC1	Isochorismatase domain-containing protein 1	100.0%	10.1	2	2	2	3	1,000,055	925,990	860,541	934,748	145,635	16,477	71,109	44,019	32.6	4.0	18.5	10.5	-1.1	0.6	-1.2	0.4	-1.1	0.7	-1.1	0.4	1.0	0.9	1.1	0.4
IPI00884070	ISOC1	CGI-111 protein	100.0%	15.1	2	2	2	3	1,000,055	925,990	860,541	934,748	145,635	16,477	71,109	44,019	32.6	4.0	18.5	10.5	-1.1	0.6	-1.2	0.4	-1.1	0.7	-1.1	0.4	1.0	0.9	1.1	0.4
IPI00966364	ISOC1	Uncharacterized protein	100.0%	12.6	2	2	2	3	1,000,055	925,990	860,541	934,748	145,635	16,477	71,109	44,019	32.6	4.0	18.5	10.5	-1.1	0.6	-1.2	0.4	-1.1	0.7	-1.1	0.4	1.0	0.9	1.1	0.4
				FSMVLPEVEAALAEIPGVR	3	99.7%	1																									
				YFGDIISVGQR	2	99.9%	1																									
IPI00304189	OPTN	isoform 1 of Optineurin	96.7%	2.3	1	1	1	3	422,018	368,848	524,130	446,383	41,954	57,280	34,507	56,343	22.2	34.7	14.7	28.2	-1.1	0.5	1.2	0.1	1.1	0.7	1.4	0.05	1.2	0.4	-1.2	0.3
IPI00514792	OPTN	isoform 3 of Optineurin	96.7%	2.5	1	1	1	3	422,018	368,848	524,130	446,383	41,954	57,280	34,507	56,343	22.2	34.7	14.7	28.2	-1.1	0.5	1.2	0.1	1.1	0.7	1.4	0.05	1.2	0.4	-1.2	0.3
IPI00554537	OPTN	isoform 2 of Optineurin	96.7%	2.3	1	1	1	3	422,018	368,848	524,130	446,383	41,954	57,280	34,507	56,343	22.2	34.7	14.7	28.2	-1.1	0.5	1.2	0.1	1.1	0.7	1.4	0.05	1.2	0.4	-1.2	0.3
				ADLLGIVSELQLK	2	96.7%	1																									
IPI00304232	WDR12	Ribosome biogenesis protein WDR12	99.3%	3.1	1	1	1	1	3,598,660	3,637,130	3,664,910	4,284,370	241,437	203,316	276,109	341,486	15.0	12.5	16.9	17.8	1.0	0.9	1.0	0.9	1.2	0.1	1.0	0.9	1.2	0.1	1.2	0.2
				GAEEWILTGSYDK	2	99.3%	1																									
IPI00304273	APOA4	Apolipoprotein A-IV	98.3%	3.5	1	1	1	1	3,393,080	3,368,380	3,467,720	3,758,370	204,606	176,092	281,442	91,892	13.5	11.7	18.2	5.5	-1.0	0.9	1.0	0.8	1.1	0.1	1.0	0.8	1.1	0.09	1.1	0.4
				SELTQQLNALFQDK	2	98.3%	1																									
IPI00304409	CARHSP1	Calcium-regulated heat stable protein 1	100.0%	18.4	2	2	2	1	12,507,340	14,756,800	12,187,440	14,571,910	1,022,775	755,160	844,573	651,781	18.3	11.4	15.5	10.0	1.2	0.1	-1.0	0.8	1.2	0.1	-1.2	0.05	-1.0	0.9	1.2	0.06
				HETWSGHVISS	2	99.9%	1																									
				LQAVEVVITHLAPGTK	2	100.0%	1																									
IPI00304435	NIPSNAP1	Protein NipSnap homolog 1	100.0%	8.8	2	2	2	2	2,287,510	2,326,015	2,280,298	2,530,863	285,378	88,221	166,400	96,056	27.9	8.5	16.3	8.5	1.0	0.9	-1.0	1	1.1	0.5	-1.0	0.8	1.1	0.2	1.1	0.2
IPI00894205	NIPSNAP1	protein NipSnap homolog 1 isoform 2	100.0%	9.5	2	2	2	2	2,287,510	2,326,015	2,280,298	2,530,863	285,378	88,221	166,400	96,056	27.9	8.5	16.3	8.5	1.0	0.9	-1.0	1	1.1	0.5	-1.0	0.8	1.1	0.2	1.1	0.2
				KDAHSTLLSK	2	99.9%	1																									
				LKPGTMIEWGNNWAR	3	100.0%	1																									
IPI00304589	TNKS1BP1	isoform 1 of 182 kDa tankyrase-1-binding protein	100.0%	11.6	14	14	14	1	74,221,601	79,086,988	73,780,578	86,013,788	7,130,820	2,709,649	5,430,541	3,421,731	21.5	7.7	16.5	8.9	1.1	0.6	-1.0	1	1.2	0.2	-1.1	0.4	1.1	0.2	1.2	0.09
				ESAVGQMGWSGGLSLR	2	100.0%	1																									
				FAATTVEEILAK	2	100.0%	1																									
				GPLAELPSAR	2	97.2%	1																									
				GVGQADWTPDLGLR	2	95.0%	1																									
				GWVGEFSLSVGPQR	2	93.9%	1																									
				HNGSLSPGLEAR	2	99.9%	1																									
				QQAGAQGPGSADLEDGEMGKR	3	99.2%	1																									
				SFGTRPLSSGFSPEEAQQQDEEFEK	3	100.0%	1																									
				SKDLAEVGEGGGHSQAR	3	100.0%	1																									
				SQEADVQDWEFR	2	99.9%	1																									
				SYQFGIIGNDR	2	97.8%	1																									
				VNLFPGLSPSALK	2	99.3%	1																									
				VVGKPAQLGTQR	3	88.1%	1																									
				WSDQGPAQTSR	2	92.8%	1																									
IPI00304596	NONO	Non-POU domain-containing octamer-binding protein	100.0%	33.1	15	16	19	1	71,569,373	70,856,581	67,452,285	79,892,376	5,067,730	2,498,803	3,845,799	2,876,976	15.8	7.9	12.8	8.1	-1.0	0.9	-1.1	0.5	1.1	0.2	-1.1	0.5	1.1	0.05	1.2	0.03
				AAPGAEFAPNK	2	96.7%	1																									
				AAPGAEFAPNKR	2	100.0%	2																									
				AGEVFIHK	2	99.7%	1																									
				AVVIVDDR	2	98.5%	1																									
				EKLEMEMEAAR	2	99.9%	1																									
				FACHSASLTVR	3	100.0%	1																									
				FAQPGSFEYEYAMR	2	100.0%	2																									
				FGQAATMEGIGAIGGTPPAFNR	2	100.0%	1																									
				FGQAATMEGIGAIGGTPPAFNR	3	100.0%	1																									
				HEHQVMLMR	2	88.5%	1																									
				LFVGNLPPDITEEEMR	2	100.0%	1																									
				MEELHNQEVQKRK	2	99.0%	1																									
				MGQMAMGGAMGINNR	2	94.2%	1																									
				RMEELHNQEVQK	3	100.0%	1																									
				TLAEIAK	1	98.8%	1																									
				VELDNMPLR	2	100.0%	2																									
IPI00432865	RPL13AP3	Putative 60S ribosomal protein L13a-like MGC87657	99.8%	18.6	2	2	2	2	13,107,960	12,625,360	11,406,220	14,451,755	1,633,772	688,552	690,132	597,537	27.9	12.2	13.5	9.3	-1.0	0.8	-1.1	0.4	1.1	0.5	-1.1	0.2	1.1	0.08	1.3	0.01
IPI00304612	SNORD32A;RPL13A	60S ribosomal protein L13a	99.8%	9.4	2	2	2	2	13,107,960	12,625,360	11,406,220	14,451,755	1,633,772	688,552	690,132	597,537	27.9	12.2	13.5	9.3	-1.0	0.8	-1.1	0.4	1.1	0.5	-1.1	0.2	1.1	0.08	1.3	0.01
				MVVPAALK	2	80.3%	1																									
				YQAVTATLEEK	2	98.7%	1																									
IPI00304692	RBMX	Heterogeneous nuclear ribonucleoprotein G	100.0%	29.9	12	13	15	1	29,871,431	32,225,742	32,675,431	36,705,548	2,186,431	1,561,566	1,944,697	1,461,773	16.4	10.8	13.3	8.9	1.1	0.4	1.1	0.4	1.2	0.03	1.0	0.9	1.1	0.07	1.1	0.1
				AIKVEQATKPSFESGR	3	95.9%	1																									
				ALEAVFGK	2	99.9%	1																									
				DRDYSDHPSGGSYR	3	97.3%	1																									
				DSYESYGNSR	2	100.0%	1																									
				GFAFVTFESPADAK	2	100.0%	2																									
				GPPPSYGGSSR	2	100.0%	1																									
				IVEVLLMK	2	99.5%	1																									
				LFIGGLNTETNEK	2	100.0%	2																									
				REPLPSR	2	92.6%	1																									
				SDLYSSGR	2	99.3%	1																									
				VEQATKPSFESGR	2	100.0%	1																									
				VEQATKPSFESGR	3	99.9%	1																									
				YDDYSSSR	2	98.5%	1																									
IPI00304693	AGFG1	isoform 2 of Arf-GAP domain and FG repeats-containing protein 1	98.9%	1.9	1	1	1	7	537,681	606,413	561,783	709,213	78,043	35,608	61,844	89,207	32.5	13.1	24.6	28.1	1.1	0.4	1.0	0.8	1.3	0.2	-1.1	0.5	1.2	0.3	1.3	0.2
IPI00607616	AGFG1	isoform 1 of Arf-GAP domain and FG repeats-containing protein 1	98.9%	1.8	1	1	1	7	537,681	606,413	561,783	709,213	78,043	35,608	61,844	89,207	32.5	13.1	24.6	28.1	1.1	0.4	1.0	0.8	1.3	0.2	-1.1	0.5	1.2	0.3	1.3	0.2
IPI00736669	AGFG1	isoform 3 of Arf-GAP domain and FG repeats-containing protein 1	98.9%	1.8	1	1	1	7	537,681	606,413	561,783	709,213	78,043	35,608	61,844	89,207	32.5	13.1	24.6	28.1	1.1	0.4	1.0	0.8	1.3	0.2	-1.1	0.5	1.2	0.3	1.3	0.2
IPI00903328	AGFG1	arf-GAP domain and FG repeats-containing protein 1 isoform 1	98.9%	1.7	1	1	1	7	537,681	606,413	561,783	709,213	78,043	35,608	61,844	89,207	32.5	13.1	24.6	28.1	1.1	0.4	1.0	0.8	1.3	0.2	-1.1	0.5	1.2	0.3	1.3	0.2
IPI00915778	AGFG1	Uncharacterized protein	98.9%	4.2	1	1	1	7	537,681	606,413	561,783	709,213	78,043	35,608	61,844	89,207	32.5	13.1	24.6	28.1	1.1	0.4	1.0	0.8	1.3	0.2	-1.1	0.5	1.2	0.3	1.3	0.2
IPI00916083	AGFG1	Uncharacterized protein	98.9%	1.9	1	1	1	7	537,681	606,413	561,783	709,213	78,043	35,608	61,844	89,207	32.5	13.1	24.6	28.1	1.1	0.4	1.0	0.8	1.3	0.2	-1.1	0.5	1.2	0.3	1.3	0.2
IPI01013774	AGFG1	59 kDa protein	98.9%	1.8	1	1	1	7	537,681	606,413	561,783	709,213	78,043	35,608	61,844	89,207	32.5	13.1	24.6	28.1	1.1	0.4	1.0	0.8	1.3	0.2	-1.1	0.5	1.2	0.3	1.3	0.2
				QIWLGLFDDR	2	98.9%	1																									
IPI00304814	GPX4	isoform Mitochondrial of Phospholipid hydroperoxide glutathione peroxidase, mitoch	99.9%	15.2	3	3	3	3	4,642,197	4,513,954	4,145,946	4,804,476	739,501	213,166	231,970	294,322	35.6	10.6	12.5	13.7	-1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.1	0.4	1.2	0.1
IPI00745335	GPX4	isoform Cytoplasmic of Phospholipid hydroperoxide glutathione peroxidase, mitocho	99.9%	17.7	3	3	3	3	4,642,197	4,513,954	4,145,946	4,804,476	739,501	213,166	231,970	294,322	35.6	10.6	12.5	13.7	-1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.1	0.4	1.2	0.1
IPI00884192	GPX4	phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform C precurs	99.9%	12.8	3	3	3	3	4,642,197	4,513,954	4,145,946	4,804,476	739,501	213,166	231,970	294,322	35.6	10.6	12.5	13.7	-1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.1	0.4	1.2	0.1
				ILAFPCNQFGK	2	93.2%	1																									

				YAECGLR	2	82.9%	1																									
				YGPMEEPLVIEK	2	98.9%	1																									
IPI00304911	ATP6V1B1	V-type proton ATPase subunit B, kidney isoform	98.5%	2.0	1	1	1	5	615,346	697,471	741,996	709,549	57,526	74,910	65,534	49,925	20.9	24.0	19.8	15.7	1.1	0.4	1.2	0.2	1.2	0.3	1.1	0.7	1.0	0.9	-1.0	0.7
IPI00924887	ATP6V1B1	cDNA FLJ57632, highly similar to Vacuolar ATP synthase subunit B, kidney isoform	98.5%	2.1	1	1	1	5	615,346	697,471	741,996	709,549	57,526	74,910	65,534	49,925	20.9	24.0	19.8	15.7	1.1	0.4	1.2	0.2	1.2	0.3	1.1	0.7	1.0	0.9	-1.0	0.7
IPI00925534	ATP6V1B1	Uncharacterized protein	98.5%	4.0	1	1	1	5	615,346	697,471	741,996	709,549	57,526	74,910	65,534	49,925	20.9	24.0	19.8	15.7	1.1	0.4	1.2	0.2	1.2	0.3	1.1	0.7	1.0	0.9	-1.0	0.7
IPI00925827	ATP6V1B1	Uncharacterized protein	98.5%	4.0	1	1	1	5	615,346	697,471	741,996	709,549	57,526	74,910	65,534	49,925	20.9	24.0	19.8	15.7	1.1	0.4	1.2	0.2	1.2	0.3	1.1	0.7	1.0	0.9	-1.0	0.7
IPI00926751	ATP6V1B1	Uncharacterized protein	98.5%	2.0	1	1	1	5	615,346	697,471	741,996	709,549	57,526	74,910	65,534	49,925	20.9	24.0	19.8	15.7	1.1	0.4	1.2	0.2	1.2	0.3	1.1	0.7	1.0	0.9	-1.0	0.7
				TPVSEDMLGR	2	98.5%	1																									
IPI00304925	HSPA1A;HSPA1B	Heat shock 70 kDa protein 1A/1B	100.0%	48.7	26	28	34	1	86,415,915	90,715,726	87,747,172	101,665,317	7,316,820	3,136,585	6,389,184	3,542,641	18.9	7.7	16.3	7.8	1.0	0.6	1.0	0.9	1.2	0.1	-1.0	0.7	1.1	0.05	1.2	0.09
				AFYPEEISSMVLTK	2	100.0%	2																									
				ARFEELCSDLFR	2	96.6%	1																									
				ATAGDTHLGGEDFDNR	2	100.0%	2																									
				ATAGDTHLGGEDFDNR	3	99.9%	1																									
				CQEVISWLDANTLAEKDEFEHK	3	99.9%	1																									
				DAGVIAGLNVLR	2	100.0%	1																									
				DNNLLGR	2	96.6%	1																									
				ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK	3	99.9%	1																									
				FEELCSDLFR	2	100.0%	1																									
				FELSGIPPAPR	2	98.9%	1																									
				FGDPVVQSDMK	2	99.9%	1																									
				GGSGSGPTIEEVD	1	88.5%	1																									
				HWPFQVINDGDKPK	3	100.0%	2																									
				ITITNDKGR	2	99.5%	1																									
				KFGDPVVQSDMK	2	100.0%	2																									
				LLQDFFNGR	2	95.2%	1																									
				LVNHFVEEFK	2	100.0%	2																									
				LVNHFVEEFK	3	99.9%	1																									
				LVNHFVEEFKR	3	100.0%	1																									
				MKEIAEAYLGYPVTNAVITVPAYFNDSQR	3	100.0%	1																									
				NALESYAFNMK	2	100.0%	1																									
				NAVITVPAYFNDSQR	2	99.9%	1																									
				NQVALNPQNTVFDAK	2	100.0%	2																									
				SAVEDEGLK	2	95.9%	1																									
				SINPDEAVAYGAAVQAAILMGDK	2	100.0%	1																									
				TTPSYVAFTDTER	2	100.0%	1																									
				VQVSYKGETK	2	99.7%	1																									
				YKAEDEVQR	2	99.9%	1																									
IPI00305152	SEC31A	isoform 3 of Protein transport protein Sec31A	100.0%	2.8	2	2	3	10	448,537	462,381	538,414	584,189	29,437	26,280	56,980	31,551	14.7	12.7	23.7	12.1	1.0	0.7	1.2	0.2	1.3	0.01	1.2	0.3	1.3	0.02	1.1	0.5
IPI00445429	SEC31A	isoform 7 of Protein transport protein Sec31A	100.0%	3.2	2	2	3	10	448,537	462,381	538,414	584,189	29,437	26,280	56,980	31,551	14.7	12.7	23.7	12.1	1.0	0.7	1.2	0.2	1.3	0.01	1.2	0.3	1.3	0.02	1.1	0.5
IPI00515103	SEC31A	isoform 4 of Protein transport protein Sec31A	100.0%	2.6	2	2	3	10	448,537	462,381	538,414	584,189	29,437	26,280	56,980	31,551	14.7	12.7	23.7	12.1	1.0	0.7	1.2	0.2	1.3	0.01	1.2	0.3	1.3	0.02	1.1	0.5
IPI00746182	SEC31A	isoform 1 of Protein transport protein Sec31A	100.0%	2.5	2	2	3	10	448,537	462,381	538,414	584,189	29,437	26,280	56,980	31,551	14.7	12.7	23.7	12.1	1.0	0.7	1.2	0.2	1.3	0.01	1.2	0.3	1.3	0.02	1.1	0.5
IPI00795507	SEC31A	isoform 2 of Protein transport protein Sec31A	100.0%	2.6	2	2	3	10	448,537	462,381	538,414	584,189	29,437	26,280	56,980	31,551	14.7	12.7	23.7	12.1	1.0	0.7	1.2	0.2	1.3	0.01	1.2	0.3	1.3	0.02	1.1	0.5
IPI00853220	SEC31A	isoform 6 of Protein transport protein Sec31A	100.0%	2.9	2	2	3	10	448,537	462,381	538,414	584,189	29,437	26,280	56,980	31,551	14.7	12.7	23.7	12.1	1.0	0.7	1.2	0.2	1.3	0.01	1.2	0.3	1.3	0.02	1.1	0.5
IPI00953506	SEC31A	Uncharacterized protein	100.0%	3.2	2	2	3	10	448,537	462,381	538,414	584,189	29,437	26,280	56,980	31,551	14.7	12.7	23.7	12.1	1.0	0.7	1.2	0.2	1.3	0.01	1.2	0.3	1.3	0.02	1.1	0.5
IPI00965105	SEC31A	Uncharacterized protein	100.0%	2.5	2	2	3	10	448,537	462,381	538,414	584,189	29,437	26,280	56,980	31,551	14.7	12.7	23.7	12.1	1.0	0.7	1.2	0.2	1.3	0.01	1.2	0.3	1.3	0.02	1.1	0.5
IPI00965360	SEC31A	SEC31A protein	100.0%	2.7	2	2	3	10	448,537	462,381	538,414	584,189	29,437	26,280	56,980	31,551	14.7	12.7	23.7	12.1	1.0	0.7	1.2	0.2	1.3	0.01	1.2	0.3	1.3	0.02	1.1	0.5
IPI00966405	SEC31A	protein transport protein Sec31A isoform 5	100.0%	2.6	2	2	3	10	448,537	462,381	538,414	584,189	29,437	26,280	56,980	31,551	14.7	12.7	23.7	12.1	1.0	0.7	1.2	0.2	1.3	0.01	1.2	0.3	1.3	0.02	1.1	0.5
				MADAIILAIAGGQELLAR	2	82.1%	1																									
				NPAVLSAASFDGR	2	99.9%	2																									
IPI00305166	SDHA	cDNA FLJ61478, highly similar to Succinate dehydrogenase (ubiquinone) flavoprote	100.0%	10.0	4	4	5	1	4,156,910	3,588,838	4,286,008	4,605,903	467,273	94,422	338,098	386,904	25.1	5.9	17.6	18.8	-1.2	0.3	1.0	0.8	1.1	0.5	1.2	0.1	1.3	0.06	1.1	0.6
				GEGGILINSQGER	2	100.0%	1																									
				LGANSLLDLVVFGR	2	100.0%	2																									
				NTVVATGGYGR	2	100.0%	1																									
				VSDSISAQYPVVDHEFDAVVVGAGGAGLR	3	93.8%	1																									
IPI00305267	GOLGA3	isoform 1 of Golgin subfamily A member 3	99.7%	0.8	1	1	1	2	6,152,930	7,328,700	6,651,000	6,815,500	298,912	173,268	440,775	235,279	10.9	5.3	14.8	7.7	1.2	0.009	1.1	0.4	1.1	0.1	-1.1	0.2	-1.1	0.1	1.0	0.8
IPI00333419	GOLGA3	Similar to Golgin subfamily A member 3	99.7%	0.8	1	1	1	2	6,152,930	7,328,700	6,651,000	6,815,500	298,912	173,268	440,775	235,279	10.9	5.3	14.8	7.7	1.2	0.009	1.1	0.4	1.1	0.1	-1.1	0.2	-1.1	0.1	1.0	0.8
				VLELEDELQESR	2	99.7%	1																									
IPI00305374	THOC1	isoform 1 of THO complex subunit 1	96.5%	4.3	1	1	1	2	170,431	196,681	206,029	260,389	19,796	10,537	24,183	36,821	26.0	12.0	26.3	31.6	1.2	0.3	1.2	0.3	1.5	0.06	1.0	0.7	1.3	0.2	1.3	0.3
IPI00645740	THOC1	18 kDa protein	96.5%	18.5	1	1	1	2	170,431	196,681	206,029	260,389	19,796	10,537	24,183	36,821	26.0	12.0	26.3	31.6	1.2	0.3	1.2	0.3	1.5	0.06	1.0	0.7	1.3	0.2	1.3	0.3
				EHMPTLEEFFEEAIEQADPENMVENEYK	3	96.5%	1																									
IPI00305383	UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial	100.0%	8.6	3	3	3	1	12,724,775	13,339,710	11,371,111	14,700,437	1,061,915	382,099	1,490,468	1,225,334	18.7	6.4	29.3	18.6	1.0	0.6	-1.1	0.5	1.2	0.3	-1.2	0.3	1.1	0.3	1.3	0.1
				NALANPLYCPDYR	2	100.0%	1																									
				QVAEQFLNMR	2	99.9%	1																									
				TIAQGNLSNTDVQAAK	2	100.0%	1																									
IPI00305461	ITIH2	Inter-alpha (Globulin) inhibitor H2, isoform CRA_a	96.9%	1.2	1	1	1	3	2,387,967	2,568,623	2,642,807	3,206,510	168,470	143,160	215,679	193,976	15.8	12.5	18.3	13.5	1.1	0.4	1.1	0.4	1.3	0.01	1.0	0.8	1.2	0.03	1.2	0.09
IPI00645038	ITIH2	Inter-alpha (Globulin) inhibitor H2	96.9%	1.2	1	1	1	3	2,387,967	2,568,623	2,642,807	3,206,510	168,470	143,160	215,679	193,976	15.8	12.5	18.3	13.5	1.1	0.4	1.1	0.4	1.3	0.01	1.0	0.8	1.2	0.03	1.2	0.09
IPI00910636	ITIH2	cDNA FLJ53848, highly similar to Inter-alpha-trypsin inhibitor heavy chain H2	96.9%	2.0	1	1	1	3	2,387,967	2,568,623	2,642,807	3,206,510	168,470	143,160	215,679	193,976	15.8	12.5	18.3	13.5	1.1	0.4	1.1	0.4	1.3	0.01	1.0	0.8	1.2	0.03	1.2	0.09
				FYNQVSTPLLR	2	96.9%	1																									
IPI00305469	CRK	adapter molecule crk isoform b	100.0%	21.6	3	3	4	2	3,062,769	3,281,013	3,194,990	3,818,687	293,444	165,651	303,534	91,475	21.4	11.3	21.2	5.4	1.1	0.5	1.0	0.8	1.2	0.06	-1.0	0.8	1.2	0.02	1.2	0.1
IPI00399054	CRK	isoform Crk-I of Adapter molecule crk	100.0%	21.6	3	3	4	2	3,062,769	3,281,013	3,194,990	3,818,687	293,444	165,651	303,534	91,475	21.4	11.3	21.2	5.4	1.1	0.5	1.0	0.8	1.2	0.06	-1.0	0.8	1.2	0.02	1.2	0.1
				ALFDFNGNDEEDLPFK	2	100.0%	1																									
				IGDQEFDSLPALLEFYK	2	100.0%	2																									
				QEAVALLQGQR	2	99.7%	1																									
IPI00305551	GNA11	Guanine nucleotide-binding protein subunit alpha-11	100.0%	9.5	2	3	4	1	3,805,115	4,262,915	4,446,354	4,421,025	472,082	397,766	546,139	246,514	27.7	20.9	27.5	12.5	1.1	0.5	1.2	0.4	1.2	0.3	1.0	0.8	1.0	0.7	-1.0	1
				IATLGYLPTQQDVLR	2	98.9%	1																									
				VPTTGIIEYPFDLENIIFR	2	100.0%	2																									
				VPTTGIIEYPFDLENIIFR	3	100.0%	1																									
IPI00305692	TXNL1	Thioredoxin-like protein 1	100.0%	9.0	2	2	2	2	7,179,066	7,243,463	7,238,069	8,206,632	695,584	324,226	671,187	207,287	21.7	10.0	20.7	5.7	1.0	0.9	1.0	1	1.1	0.2	-1.0	1	1.1	0.04	1.1	0.2
IPI00642032	TXNL1	cDNA, FLJ94230, highly similar to Homo sapiens thioredoxin-like 1 (TXNL1), mRNA	100.0%	8.0	2	2	2	2	7,179,066	7,243,463	7,238,069	8,206,632	695,584	324,226	671,187	207,287	21.7	10.0	20.7	5.7	1.0	0.9	1.0	1	1.1	0.2	-1.0	1	1.1	0.04	1.1	0.2
				GYMDLMPFINK	2	99.9%	1																									
				IDQYQGADAVGLEEK	2	100.0%	1																									
IPI00305978	AKR7A2	Aflatoxin B1 aldehyde reductase member 2	100.0%	19.2	6	6	8	2	13,740,153	14,058,550	13,670,462	15,125,846	950,453	776,195	1,012,010	376,774	15.5	12.4	16.6	5.6	1.0	0.8	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.3	1.1	0.2
IPI00946527	AKR7A2	35 kDa protein	100.0%	22.0	6	6	8	2	13,740,153	14,058,550	13,670,462	15,125,846	950,453	776,195	1,012,010	376,774	15.5	12.4	16.6	5.6	1.0	0.8	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.3	1.1	0.2
				ALQAAYGASAPSVTSAALR	2	100.0%	1																									
				FFGNSWAETYR	2	100.0%	2																									
				FYAYNPLAGGLLTGK	2	100.0%	1																									
				MDAPASAAAVR	2	99.9%	1																									
				RMDAPASAAAVR	2	99.9%	1																									
				VASVLGTMEMGR	2	100.0%	2																									
IPI00306280	DENR	Density-regulated protein	100.0%	14.7	2	2	2	1	14,202,040	14,180,790	15,855,540	15,869,820	1,361,894	1,032,427	1,191,850	505,745	21.4	16.3	16.8	7.1	-1.0	1	1.1	0.4	1.1	0.3	1.1	0.3	1.1	0.2	1.0	1
				VCGLATFEIDLK	2	99.9%	1																									
				WPEVDDDSIEDLGEVKK	3	99.6%	1																									
IPI00306301	PDHA1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial i	100.0%	4.7	2	2	2	4	5,795,508	4,733,023	5,436,893	4,986,088	1,140,962	114,600	944,781	117,060	44.0	5.4	38.9	5.3	-1.2	0.4	-1.1	0.8	-1.2	0.5	1.1	0.5	1.1	0.2	-1.1	0.7
IPI00643575	PDHA1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial i	100.0%	5.0	2	2	2	4	5,795,508	4,733,023	5,436,893	4,986,088	1,140,962	114,600	944,781	117,060	44.0	5.4	38.9	5.3	-1.2	0.4	-1.1	0.8	-1.2	0.5	1.1	0.5	1.1	0.2	-1.1	0.7
IPI00922697	PDHA1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	100.0%	5.1	2	2	2	4	5,795,508	4,733,023	5,436,893	4,986,088	1,140,962	114,600	944,781	117,060	44.0	5.4	38.9	5.3	-1.2	0.4	-1.1	0.8	-1.2	0.5	1.1	0.5	1.1	0.2	-1.1	0.7
IPI00955815	PDHA1	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial i	100.0%	5.6	2	2	2	4	5,795,508	4,733,023	5,436,893	4,986,088	1,140,962	114,600	944,781	117,060	44.0	5.4	38.9	5.3	-1.2	0.4	-1.1	0.8	-1.2	0.5	1.1	0.5	1.1	0.2	-1.1	0.7
				GPILMELQTYR	2	99.7%	1																									
				RGDFIPGLR	2	99.2%	1																									
IPI00306354	PLEKHA1	Pleckstrin homology domain-containing family A member 1	95.1%	2.7	1	1	1	4	1,004,915	1,040,478	1,139,215	1,157,570	46,025	55,209	109,481	44,755	10.2	11.9	21.5	8.7	1.0	0.6	1.1	0.3	1.2	0.04	1.1	0.4	1.1	0.1	1.0	0.9
IPI00555801	PLEKHA1	Pleckstrin homology domain containing, family A (Phosphoinositide binding specific)	95.1%	4.8	1	1	1	4	1,004,915	1,040,478	1,139,215	1,157,570	46,025	55,209	109,481	44,755	10.2	11.9	21.5	8.7	1.0	0.6	1.1	0.3	1.2	0.04	1.1	0.4	1.1	0.1	1.0	0.9
IPI00644920	PLEKHA1	Pleckstrin homology domain containing, family A (Phosphoinositide binding specific)	95.1%	2.9	1	1	1	4	1,004,915	1,040,478	1,139,215	1,157,570	46,025	55,209	109,481	44,755	10.2	11.9	21.5	8.7	1.0	0.6	1.1	0.3	1.2	0.04	1.1	0.4	1.1	0.1	1.0	0.9
IPI00646101	PLEKHA1	pleckstrin homology domain-containing family A member 1 isoform 2	95.1%	3.3	1	1	1	4	1,004,915	1,040,478	1,139,215	1,157,570	46,025	55,209	109,481	44,755	10.2	11.9	21.5	8.7	1.0	0.6	1.1	0.3	1.2	0.04	1.1	0.4	1.1	0.1	1.0	0.9
				DNLFEIVTTSR	2	95.1%	1																									
IPI00306369	NSUN2	tRNA (cytosine-5-)-methyltransferase NSUN2	100.0%	10.2	5	5	5	2	9,822,456	10,088,118	10,461,110	11,959,896	430,999	228,387	523,889	361,387	9.8	5.1	11.2	6.8	1.0	0.6	1.1	0.4	1.2	0.005	1.0	0.5	1.2	0.002	1.1	0.05
IPI00966877	NSUN2	tRNA (cytosine-5-)-methyltransferase NSUN2 isoform 2	100.0%	10.7	5	5	5	2	9,822,456	10,088,118	10,461,110	11,959,896	430,999	228,387	523,889	361,387	9.8	5.1	11.2	6.8	1.0	0.6	1.1	0.4	1.2	0.005	1.0	0.5	1.2	0.002	1.1	0.05
				DGQWFTDWDAVPHSR	3	100.0%	1																									
				EGVILTNESAASTGQPDNDVTEGQR	3	84.9%	1																									
				FHQFLVSETESGNISR	3	99.0%	1																									
				ILDMCAAPGSK	2	98.7%	1																									
				ILLTQENPFFR	2	96.5%	1																									
IPI00306380	GNL3;SNORD19B	isoform 1 of Guanine nucleotide-binding protein-like 3	96.0%	1.3	1	1	1	1	9,784,460	10,185,690	8,237,950	10,175,790	743,923	489,465	302,227	761,428	17.0	10.8	8.2	16.7	1.0	0.7	-1.2	0.09	1.0	0.7	-1.2	0.01	-1.0	1	1.2	0.05
				RMTCHKR	2	84.7%	1																									
IPI00306382	SCAMP3	isoform 1 of Secretory carrier-associated membrane protein 3	100.0%	8.7	2	2	2	1	8,728,970	9,019,120	9,047,420	10,437,240	1,700,132	846,981	271,377	561,665	43.6	21.0	6.7	12.0	1.0	0.9	1.0	0.9	1.2	0.4	1.0	1	1.2	0.2	1.2	0.06
				QYATLDVYNPFETR	2	99.9%	1																									
				TAAANAAAGAAENAFR	2	99.5%	1																									
IPI00306383	SCAMP3	isoform 2 of Secretory carrier-associated membrane protein 3	99.5%	5.0	1	1	1	1	3,523,310	4,303,820	3,501,350	5,156,090	1,130,304	868,088	240,757	523,390	71.7	45.1	15.4	22.7	1.2	0.6	-1.0	1	1.5	0.2	-1.2	0.4	1.2	0.4	1.5	0.02
				TAAANAAAGAAENAFR	2	99.5%	1																									
IPI00306413	TPPP3	Tubulin polymerization-promoting protein family member 3	100.0%	20.5	3	3	3	1	14,676,600	14,835,630	13,947,790	15,488,410	1,003,014	828,795	823,420	837,827	15.3	12.5	13.2	12.1	1.0	0.9	-1.1	0.6	1.1	0.6	-1.1	0.5	1.0	0.6	1.1	0.2
				ALEELATKR	2	84.4%	1																									
				QDILDDSGYVSAYK	2	100.0%	1																									
				SVTGTDVDIVFSK	2	99.4%	1																									
IPI00306661	KCMF1	E3 ubiquitin-protein ligase KCMF1	100.0%	8.1	2	2	3	1	741,393	844,279	889,933	1,090,565	64,230	80,820	125,725	50,854	19.4	21.4	31.6	10.4	1.1	0.3	1.2	0.3	1.5	0.003	1.1	0.8	1.3	0.03	1.2	0.2
				EAMDPIAELLSQLSGVR	2	100.0%	1																									
				SLFVQELLLSTLVR	2	99.9%	2																									
IPI00306825	TPD52L2	isoform 1 of Tumor protein D54	100.0%	54.4	7	7	9	3	6,605,024	6,227,423	6,292,862	7,614,212	550,340	360,618	436,279	385,117	18.6	13.0	15.5	11.3	-1.1	0.6	-1.0	0.7	1.2	0.2	1.0	0.9	1.2	0.03	1.2	0.05
IPI00399265	TPD52L2	tumor protein D54 isoform a	100.0%	48.9	7	7	9	3	6,605,024	6,227,423	6,292,862	7,614,212	550,340	360,618	436,279	385,117	18.6	13.0	15.5	11.3	-1.1	0.6	-1.0	0.7	1.2	0.2	1.0	0.9	1.2	0.03	1.2	0.05
IPI00399267	TPD52L2	tumor protein D54 isoform c	100.0%	50.9	7	7	9	3	6,605,024	6,227,423	6,292,862	7,614,212	550,340	360,618	436,279	385,117	18.6	13.0	15.5	11.3	-1.1	0.6	-1.0	0.7	1.2	0.2	1.0	0.9	1.2	0.03	1.2	0.05
				GLLSDSMTDVPVDTGVAAR	2	100.0%	2																									
				LGLSTLGELK	2	100.0%	2																									
				SWHDVQVSSAYVK	2	100.0%	1																									
				TPAVEGLTEAEEEELRAELTK	3	97.6%	1																									
				TPAVEGLTEAEEEELRAELTKVEEEIVTLR	3	100.0%	1																									
				TQETLSQAGQK	2	100.0%	1																									
				VVGDRENGSDNLPSSAGSGDKPLSDPAPF	3	100.0%	1																									
IPI00306960	NARS	Asparaginyl-tRNA synthetase, cytoplasmic	100.0%	14.2	6	6	6	1	37,058,757	36,504,152	36,672,762	43,697,887	3,563,343	1,972,751	2,978,358	1,474,526	21.5	12.1	18.2	7.6	-1.0	0.9	-1.0	0.9	1.2	0.1	1.0	1	1.2	0.02	1.2	0.07
				IFDSEEILAGYK	2	100.0%	1																									
				IGALEGYR	2	99.8%	1																									
				LMTDTINEPILLCR	2	99.9%	1																									
				MNYSDAIVWLK	2	100.0%	1																									
				SPAGSIVHELNPNFQPPK	3	98.0%	1																									
				YGTCPHGGYGLGLER	3	100.0%	1																									
IPI00307039	SNX22	Sorting nexin-22	95.1%	3.1	1	1	1	3	1,278,873	1,313,730	1,538,513	1,671,470	159,878	104,739	129,891	103,362	28.0	17.8	18.9	13.8	1.0	0.9	1.2	0.2	1.3	0.07	1.2	0.2	1.3	0.04	1.1	0.4
IPI00445063	SNX22	cDNA FLJ44699 fis, clone BRACE3016020	95.1%	3.5	1	1	1	3	1,278,873	1,313,730	1,538,513	1,671,470	159,878	104,739	129,891	103,362	28.0	17.8	18.9	13.8	1.0	0.9	1.2	0.2	1.3	0.07	1.2	0.2	1.3	0.04	1.1	0.4
IPI00789828	SNX22	SNX22 protein	95.1%	5.0	1	1	1	3	1,278,873	1,313,730	1,538,513	1,671,470	159,878	104,739	129,891	103,362	28.0	17.8	18.9	13.8	1.0	0.9	1.2	0.2	1.3	0.07	1.2	0.2	1.3	0.04	1.1	0.4
				RLPNWR	2	95.1%	1																									
IPI00307155	ROCK2	Rho-associated protein kinase 2	99.4%	1.0	1	1	1	2	1,151,595	1,244,430	1,353,520	1,378,905	99,589	101,589	109,660	157,394	19.3	18.3	18.1	25.5	1.1	0.5	1.2	0.2	1.2	0.3	1.1	0.5	1.1	0.5	1.0	0.9
IPI00894514	ROCK2	Uncharacterized protein	99.4%	1.2	1	1	1	2	1,151,595	1,244,430	1,353,520	1,378,905	99,589	101,589	109,660	157,394	19.3	18.3	18.1	25.5	1.1	0.5	1.2	0.2	1.2	0.3	1.1	0.5	1.1	0.5	1.0	0.9

				NLLLLANSTEEQQK	2	99.4%	1																									
IPI00307257	TBC1D9B	isoform 1 of TBC1 domain family member 9B	99.3%	1.3	1	1	1	2	952,600	1,028,290	1,165,245	1,088,670	130,768	54,455	121,110	59,792	30.7	11.8	23.2	12.3	1.1	0.6	1.2	0.3	1.1	0.4	1.1	0.3	1.1	0.5	-1.1	0.6
IPI00640908	TBC1D9B	isoform 2 of TBC1 domain family member 9B	99.3%	1.3	1	1	1	2	952,600	1,028,290	1,165,245	1,088,670	130,768	54,455	121,110	59,792	30.7	11.8	23.2	12.3	1.1	0.6	1.2	0.3	1.1	0.4	1.1	0.3	1.1	0.5	-1.1	0.6
				VVGALVDQGIFEELTR	2	99.3%	1																									
IPI00307545	TNS1	Tensin-1	97.7%	2.4	2	2	2	3	2,868,263	2,949,403	2,880,350	3,263,747	234,595	196,722	235,477	212,251	18.3	14.9	18.3	14.5	1.0	0.8	1.0	1	1.1	0.2	-1.0	0.8	1.1	0.3	1.1	0.3
IPI00925950	TNS1	Uncharacterized protein	97.7%	2.5	2	2	2	3	2,868,263	2,949,403	2,880,350	3,263,747	234,595	196,722	235,477	212,251	18.3	14.9	18.3	14.5	1.0	0.8	1.0	1	1.1	0.2	-1.0	0.8	1.1	0.3	1.1	0.3
IPI00926129	TNS1	Uncharacterized protein	97.7%	2.4	2	2	2	3	2,868,263	2,949,403	2,880,350	3,263,747	234,595	196,722	235,477	212,251	18.3	14.9	18.3	14.5	1.0	0.8	1.0	1	1.1	0.2	-1.0	0.8	1.1	0.3	1.1	0.3
				GAYGLAMKVSSPPPTIMQQNK	2	84.5%	1																									
				TDEPVPGASSATAALSPQEKR	2	85.4%	1																									
IPI00328089	HIVEP3	isoform 2 of Transcription factor HIVEP3	99.9%	0.9	2	2	2	2	66,483,875	61,309,249	67,120,260	66,132,519	2,961,675	2,590,033	3,094,004	3,932,733	10.0	9.5	10.3	13.3	-1.1	0.2	1.0	0.9	-1.0	0.9	1.1	0.2	1.1	0.3	-1.0	0.8
IPI00641105	HIVEP3	isoform 1 of Transcription factor HIVEP3	99.9%	0.9	2	2	2	2	66,483,875	61,309,249	67,120,260	66,132,519	2,961,675	2,590,033	3,094,004	3,932,733	10.0	9.5	10.3	13.3	-1.1	0.2	1.0	0.9	-1.0	0.9	1.1	0.2	1.1	0.3	-1.0	0.8
				KAEGSPRK	2	99.4%	1																									
				SVPSLEGPTGFQPR	3	86.2%	1																									
IPI00328097	SNX27	isoform 3 of Sorting nexin-27	99.9%	7.6	2	2	2	3	2,815,720	2,441,965	2,768,837	2,649,976	309,247	206,023	423,572	108,285	24.6	18.9	34.2	9.1	-1.2	0.3	-1.0	0.9	-1.1	0.6	1.1	0.5	1.1	0.4	-1.0	0.8
IPI00640980	SNX27	isoform 2 of Sorting nexin-27	99.9%	6.4	2	2	2	3	2,815,720	2,441,965	2,768,837	2,649,976	309,247	206,023	423,572	108,285	24.6	18.9	34.2	9.1	-1.2	0.3	-1.0	0.9	-1.1	0.6	1.1	0.5	1.1	0.4	-1.0	0.8
IPI00645303	SNX27	isoform 1 of Sorting nexin-27	99.9%	6.3	2	2	2	3	2,815,720	2,441,965	2,768,837	2,649,976	309,247	206,023	423,572	108,285	24.6	18.9	34.2	9.1	-1.2	0.3	-1.0	0.9	-1.1	0.6	1.1	0.5	1.1	0.4	-1.0	0.8
				KNSTTDQVYQAIAAK	2	98.1%	1																									
				LYIQNYTSAVPGTCLTIRK	3	97.2%	1																									
IPI00328154	UBA3	NEDD8-activating enzyme E1 catalytic subunit	98.3%	3.7	1	1	1	3	3,157,873	3,486,297	3,748,227	3,601,390	498,733	352,229	291,563	136,153	35.3	22.6	17.4	8.5	1.1	0.6	1.2	0.3	1.1	0.4	1.1	0.6	1.0	0.8	-1.0	0.7
IPI00375533	UBA3	NEDD8-activating enzyme E1 catalytic subunit isoform 2	98.3%	3.8	1	1	1	3	3,157,873	3,486,297	3,748,227	3,601,390	498,733	352,229	291,563	136,153	35.3	22.6	17.4	8.5	1.1	0.6	1.2	0.3	1.1	0.4	1.1	0.6	1.0	0.8	-1.0	0.7
IPI00917001	UBA3	cDNA, FLJ79439, highly similar to NEDD8-activating enzyme E1 catalytic subunit	98.3%	4.0	1	1	1	3	3,157,873	3,486,297	3,748,227	3,601,390	498,733	352,229	291,563	136,153	35.3	22.6	17.4	8.5	1.1	0.6	1.2	0.3	1.1	0.4	1.1	0.6	1.0	0.8	-1.0	0.7
				LQEVLDYLTNSASLQMK	2	98.3%	1																									
IPI00328170	MOGS	Mannosyl-oligosaccharide glucosidase	98.8%	1.4	1	1	1	2	2,525,155	2,766,240	3,200,745	2,788,945	210,482	69,581	134,803	221,268	18.6	5.6	9.4	17.7	1.1	0.3	1.3	0.03	1.1	0.4	1.2	0.02	1.0	0.9	-1.1	0.2
IPI00916474	MOGS	mannosyl-oligosaccharide glucosidase isoform 2	98.8%	1.6	1	1	1	2	2,525,155	2,766,240	3,200,745	2,788,945	210,482	69,581	134,803	221,268	18.6	5.6	9.4	17.7	1.1	0.3	1.3	0.03	1.1	0.4	1.2	0.02	1.0	0.9	-1.1	0.2
				LGPLLDILADSR	2	98.8%	1																									
IPI00328178	TOM1L2	isoform 3 of TOM1-like protein 2	99.4%	5.0	1	1	1	6	709,488	730,654	714,065	748,889	89,061	39,478	107,561	51,980	28.1	12.1	33.7	15.5	1.0	0.8	1.0	1	1.1	0.7	-1.0	0.9	1.0	0.8	1.0	0.8
IPI00651745	TOM1L2	isoform 2 of TOM1-like protein 2	99.4%	5.0	1	1	1	6	709,488	730,654	714,065	748,889	89,061	39,478	107,561	51,980	28.1	12.1	33.7	15.5	1.0	0.8	1.0	1	1.1	0.7	-1.0	0.9	1.0	0.8	1.0	0.8
IPI00828126	TOM1L2	isoform 4 of TOM1-like protein 2	99.4%	9.6	1	1	1	6	709,488	730,654	714,065	748,889	89,061	39,478	107,561	51,980	28.1	12.1	33.7	15.5	1.0	0.8	1.0	1	1.1	0.7	-1.0	0.9	1.0	0.8	1.0	0.8
IPI00922013	TOM1L2	cDNA FLJ52529, highly similar to Homo sapiens target of myb1-like 2 (TOM1L2), tra	99.4%	8.3	1	1	1	6	709,488	730,654	714,065	748,889	89,061	39,478	107,561	51,980	28.1	12.1	33.7	15.5	1.0	0.8	1.0	1	1.1	0.7	-1.0	0.9	1.0	0.8	1.0	0.8
IPI00922594	TOM1L2	cDNA FLJ54058, highly similar to Homo sapiens target of myb1-like 2 (TOM1L2), tra	99.4%	5.9	1	1	1	6	709,488	730,654	714,065	748,889	89,061	39,478	107,561	51,980	28.1	12.1	33.7	15.5	1.0	0.8	1.0	1	1.1	0.7	-1.0	0.9	1.0	0.8	1.0	0.8
IPI00922748	TOM1L2	cDNA FLJ54050, highly similar to Homo sapiens target of myb1-like 2 (TOM1L2), tra	99.4%	5.9	1	1	1	6	709,488	730,654	714,065	748,889	89,061	39,478	107,561	51,980	28.1	12.1	33.7	15.5	1.0	0.8	1.0	1	1.1	0.7	-1.0	0.9	1.0	0.8	1.0	0.8
				VSNEEVTEELLHVNDDLNNVFLR	3	99.4%	1																									
IPI00328230	SPTBN1	isoform Short of Spectrin beta chain, brain 1	100.0%	25.4	36	38	52	2	71,216,323	74,733,601	72,949,850	83,969,455	5,398,760	2,281,131	4,609,706	2,405,888	17.0	6.8	14.1	6.4	1.0	0.6	1.0	0.8	1.2	0.06	-1.0	0.7	1.1	0.02	1.2	0.07
IPI00333015	SPTBN1	isoform 2 of Spectrin beta chain, brain 1	100.0%	25.5	36	38	52	2	71,216,323	74,733,601	72,949,850	83,969,455	5,398,760	2,281,131	4,609,706	2,405,888	17.0	6.8	14.1	6.4	1.0	0.6	1.0	0.8	1.2	0.06	-1.0	0.7	1.1	0.02	1.2	0.07
				AFEDEMSGR	2	99.9%	1																									
				AQQYYFDAAEAEAWMSEQELYMMSEEK	3	80.0%	1																									
				DASVAEAWLLGQEPYLSSR	2	100.0%	1																									
				DASVAEAWLLGQEPYLSSR	3	100.0%	1																									
				DGMAFNALIHK	3	99.5%	1																									
				DLMLWMEDVIR	2	100.0%	2																									
				DVEDEILWVGER	2	100.0%	2																									
				DVSSVELLMNNHQGIK	2	100.0%	1																									
				EAEKLESEHPDQAQAILSR	3	100.0%	1																									
				EGMQLISEKPETEAVVK	3	99.3%	1																									
				EIEELQSQAQALSQEGK	2	100.0%	1																									
				EVVAGSHELGQDYEHVTMLQER	3	100.0%	1																									
				FATDGEGYKPCDPQVIR	3	99.3%	1																									
				FESLEPEMNNQASR	2	100.0%	1																									
				FFWEMAEEEGWIR	2	100.0%	2																									
				FMELLEPLNER	2	100.0%	2																									
				FQIQDISVETEDNKEK	3	99.9%	1																									
				HLLGVEDLLQK	2	100.0%	2																									
				HQILEQAVEDYAETVHQLSK	3	100.0%	1																									
				HRPDLIDFDK	3	98.3%	1																									
				ITDLYTDLR	2	99.8%	1																									
				LAEISDVWEEMK	2	100.0%	2																									
				LLEVLSGER	2	100.0%	2																									
				LLTQHENIKNEIDNYEEDYQK	3	100.0%	1																									
				LQALDTGWNELHK	2	100.0%	1																									
				LTTLELLEVR	2	100.0%	2																									
				LVSDGNINSDR	2	100.0%	2																									
				LVSQDNFGFDLPAVEAATK	2	100.0%	2																									
				MHTTFEHDIQALGTQVR	3	100.0%	1																									
				MLTAQDMSYDEAR	2	100.0%	2																									
				MWEVLESTTQTK	2	100.0%	2																									
				QAEAFLNNQEYVLAHTEMPTTLEGAEAAIK	3	100.0%	1																									
				SQNIVTDSSSLSAEAIR	2	100.0%	2																									
				SQNIVTDSSSLSAEAIR	3	99.8%	1																									
				TQTAIASEDMPNTLTEAEK	2	100.0%	2																									
				VDTVNHLADELINSGHSDAATIAEWK	3	100.0%	1																									
				VLDNAIETEK	2	100.0%	1																									
				VLVLSQDYGK	2	100.0%	1																									
IPI00328257	AP1B1	isoform A of AP-1 complex subunit beta-1	100.0%	15.8	11	11	12	3	8,702,089	9,062,416	8,544,256	10,499,904	797,639	402,486	782,447	567,659	20.5	9.9	20.5	12.1	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.6	1.2	0.07	1.2	0.08
IPI00413947	AP1B1	isoform B of AP-1 complex subunit beta-1	100.0%	15.9	11	11	12	3	8,702,089	9,062,416	8,544,256	10,499,904	797,639	402,486	782,447	567,659	20.5	9.9	20.5	12.1	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.6	1.2	0.07	1.2	0.08
IPI00940292	AP1B1	isoform C of AP-1 complex subunit beta-1	100.0%	16.0	11	11	12	3	8,702,089	9,062,416	8,544,256	10,499,904	797,639	402,486	782,447	567,659	20.5	9.9	20.5	12.1	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.6	1.2	0.07	1.2	0.08
				AAMIWIVGEYAER	2	100.0%	2																									
				CVSTLLDLIQTK	2	100.0%	1																									
				DCPLNAEAASSK	2	100.0%	1																									
				DIPNENEAQFQIR	2	97.6%	1																									
				FMEMLSK	2	93.5%	1																									
				GLEISGTFTR	2	99.9%	1																									
				LAPPLVTLLSAEPELQYVALR	3	100.0%	1																									
				LASQANIAQVLAELKEYATEVDVDFVR	3	100.0%	1																									
				MEPLNNLQVAVK	2	99.8%	1																									
				SQPDMAIMAVNTFVK	2	100.0%	1																									
				YNDPIYVK	2	99.7%	1																									
IPI00328293	SRRM1	cDNA FLJ61739, highly similar to Serine/arginine repetitive matrix protein 1	99.6%	4.4	3	3	3	2	17,302,043	19,008,780	19,563,457	19,381,987	2,054,380	1,524,672	1,714,935	1,013,816	26.6	17.9	19.6	11.7	1.1	0.5	1.1	0.4	1.1	0.4	1.0	0.8	1.0	0.8	-1.0	0.9
IPI00647720	SRRM1	isoform 1 of Serine/arginine repetitive matrix protein 1	99.6%	4.4	3	3	3	2	17,302,043	19,008,780	19,563,457	19,381,987	2,054,380	1,524,672	1,714,935	1,013,816	26.6	17.9	19.6	11.7	1.1	0.5	1.1	0.4	1.1	0.4	1.0	0.8	1.0	0.8	-1.0	0.9
				MAAADSVQQR	2	99.8%	1																									
				MMQINLTGFLNGK	2	99.6%	1																									
				VKEPSVQEATSTSDILK	3	98.2%	1																									
IPI00328308	ZNF804B	Zinc finger protein 804B	91.6%	1.3	1	1	1	1	851,780	1,083,004	842,687	966,666	142,018	89,703	123,854	63,822	37.3	18.5	32.9	14.8	1.3	0.2	-1.0	1	1.1	0.5	-1.3	0.2	-1.1	0.3	1.1	0.4
				NTKEDHNLEDLKTELGK	3	91.7%	1																									
IPI00328319	RBBP4	isoform 1 of Histone-binding protein RBBP4	100.0%	4.7	2	2	3	9	1,538,034	1,582,133	1,406,606	1,775,180	157,151	76,044	130,774	100,765	22.9	10.8	20.8	12.7	1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.06
IPI00645329	RBBP4	isoform 3 of Histone-binding protein RBBP4	100.0%	4.9	2	2	3	9	1,538,034	1,582,133	1,406,606	1,775,180	157,151	76,044	130,774	100,765	22.9	10.8	20.8	12.7	1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.06
IPI00877802	RBBP4	isoform 4 of Histone-binding protein RBBP4	100.0%	5.1	2	2	3	9	1,538,034	1,582,133	1,406,606	1,775,180	157,151	76,044	130,774	100,765	22.9	10.8	20.8	12.7	1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.06
IPI00877934	RBBP4	isoform 2 of Histone-binding protein RBBP4	100.0%	4.7	2	2	3	9	1,538,034	1,582,133	1,406,606	1,775,180	157,151	76,044	130,774	100,765	22.9	10.8	20.8	12.7	1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.06
IPI00980511	RBBP4	Protein	100.0%	9.7	2	2	3	9	1,538,034	1,582,133	1,406,606	1,775,180	157,151	76,044	130,774	100,765	22.9	10.8	20.8	12.7	1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.06
IPI00395865	RBBP7	Histone-binding protein RBBP7	100.0%	4.7	2	2	3	9	1,538,034	1,582,133	1,406,606	1,775,180	157,151	76,044	130,774	100,765	22.9	10.8	20.8	12.7	1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.06
IPI00552530	RBBP7	Uncharacterized protein	100.0%	4.9	2	2	3	9	1,538,034	1,582,133	1,406,606	1,775,180	157,151	76,044	130,774	100,765	22.9	10.8	20.8	12.7	1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.06
IPI00646512	RBBP7	histone-binding protein RBBP7 isoform 1	100.0%	4.3	2	2	3	9	1,538,034	1,582,133	1,406,606	1,775,180	157,151	76,044	130,774	100,765	22.9	10.8	20.8	12.7	1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.06
IPI00879702	RBBP7	Uncharacterized protein	100.0%	4.8	2	2	3	9	1,538,034	1,582,133	1,406,606	1,775,180	157,151	76,044	130,774	100,765	22.9	10.8	20.8	12.7	1.0	0.8	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.06
				LMIWDTR	2	97.5%	1																									
				TPSSDVLVFDYTK	2	100.0%	2																									
IPI00328328	1;SNORA4;SNORD2	isoform 1 of Eukaryotic initiation factor 4A-II	100.0%	38.6	10	12	16	2	15,800,195	17,175,118	15,794,545	19,229,238	1,922,444	1,104,601	1,400,946	755,326	27.2	14.4	19.8	8.8	1.1	0.6	-1.0	1	1.2	0.2	-1.1	0.5	1.1	0.2	1.2	0.06
IPI00409717	1;SNORA4;SNORD2	isoform 2 of Eukaryotic initiation factor 4A-II	100.0%	38.5	10	12	16	2	15,800,195	17,175,118	15,794,545	19,229,238	1,922,444	1,104,601	1,400,946	755,326	27.2	14.4	19.8	8.8	1.1	0.6	-1.0	1	1.2	0.2	-1.1	0.5	1.1	0.2	1.2	0.06
				DFTVSALHGDMDQK	2	100.0%	1																									
				DIETFYNTTVEEMPMNVADLI	2	100.0%	1																									
				DIETFYNTTVEEMPMNVADLI	3	90.0%	1																									
				EHGGPEGMDPDGVIESNWNEIVDNFDDMNLK	3	100.0%	2																									
				GIDVQQVSLVINYDLPTNR	2	100.0%	2																									
				GVAINFVTEEDKR	2	88.2%	1																									
				GYDVIAQAQSGTGK	2	100.0%	2																									
				LQAEAPHIVVGTPGR	2	99.3%	1																									
				LQAEAPHIVVGTPGR	3	99.9%	1																									
				MFVLDEADEMLSR	2	100.0%	2																									
				VFDMLNR	2	100.0%	1																									
				VLITTDLLAR	2	100.0%	1																									
IPI00328415	CYB5R3	isoform 1 of NADH-cytochrome b5 reductase 3	100.0%	12.3	2	2	2	3	1,798,143	2,075,053	2,237,847	2,021,077	83,772	107,042	169,883	84,156	10.4	11.5	17.0	9.3	1.2	0.08	1.2	0.05	1.1	0.1	1.1	0.4	-1.0	0.7	-1.1	0.3
IPI00446235	CYB5R3	isoform 2 of NADH-cytochrome b5 reductase 3	100.0%	13.3	2	2	2	3	1,798,143	2,075,053	2,237,847	2,021,077	83,772	107,042	169,883	84,156	10.4	11.5	17.0	9.3	1.2	0.08	1.2	0.05	1.1	0.1	1.1	0.4	-1.0	0.7	-1.1	0.3
IPI00954806	CYB5R3	NADH-cytochrome b5 reductase 3 isoform 3	100.0%	11.1	2	2	2	3	1,798,143	2,075,053	2,237,847	2,021,077	83,772	107,042	169,883	84,156	10.4	11.5	17.0	9.3	1.2	0.08	1.2	0.05	1.1	0.1	1.1	0.4	-1.0	0.7	-1.1	0.3
				APEAWDYGQGFVNEEMIR	2	100.0%	1																									
				SVGMIAGGTGITPMLQVIR	2	100.0%	1																									
IPI00328526	ARPP19	isoform ARPP-19 of cAMP-regulated phosphoprotein 19	100.0%	9.8	1	1	1	2	280,239	273,309	272,369	299,211	21,316	24,802	16,268	15,670	17.0	20.3	13.4	11.7	-1.0	0.8	-1.0	0.8	1.1	0.5	-1.0	1	1.1	0.4	1.1	0.3
IPI00745466	ARPP19	isoform ARPP-16 of cAMP-regulated phosphoprotein 19	100.0%	11.5	1	1	1	2	280,239	273,309	272,369	299,211	21,316	24,802	16,268	15,670	17.0	20.3	13.4	11.7	-1.0	0.8	-1.0	0.8	1.1	0.5	-1.0	1	1.1	0.4	1.1	0.3
				YFDSGDYNMAK	2	100.0%	1																									
IPI00328644	FPR1	fMet-Leu-Phe receptor	90.4%	5.7	1	1	1	1	4,859,430	4,565,610	5,032,680	4,672,400	130,657	202,188	261,136	501,586	6.0	9.9	11.6	24.0	-1.1	0.3	1.0	0.6	-1.0	0.7	1.1	0.2	1.0	0.8	-1.1	0.5
				KVIIGPWVMALLLTLPVIIR	3	90.4%	1																									
IPI00328658	ASH2L	isoform 1 of Set1/Ash2 histone methyltransferase complex subunit ASH2	98.7%	2.9	1	1	1	5	1,068,994	1,055,650	1,182,488	1,155,640	80,866	38,905	99,208	39,723	16.9	8.2	18.8	7.7	-1.0	0.9	1.1	0.4	1.1	0.4	1.1	0.3	1.1	0.1	-1.0	0.8
IPI00328659	ASH2L	isoform 2 of Set1/Ash2 histone methyltransferase complex subunit ASH2	98.7%	3.6	1	1	1	5	1,068,994	1,055,650	1,182,488	1,155,640	80,866	38,905	99,208	39,723	16.9	8.2	18.8	7.7	-1.0	0.9	1.1	0.4	1.1	0.4	1.1	0.3	1.1	0.1	-1.0	0.8
IPI00333837	ASH2L	isoform 3 of Set1/Ash2 histone methyltransferase complex subunit ASH2	98.7%	3.4	1	1	1	5	1,068,994	1,055,650	1,182,488	1,155,640	80,866	38,905	99,208	39,723	16.9	8.2	18.8	7.7	-1.0	0.9	1.1	0.4	1.1	0.4	1.1	0.3	1.1	0.1	-1.0	0.8
IPI00976113	ASH2L	cDNA FLJ57157, highly similar to Set1/Ash2 histone methyltransferase complex sub	98.7%	3.7	1	1	1	5	1,068,994	1,055,650	1,182,488	1,155,640	80,866	38,905	99,208	39,723	16.9	8.2	18.8	7.7	-1.0	0.9	1.1	0.4	1.1	0.4	1.1	0.3	1.1	0.1	-1.0	0.8
IPI00981787	ASH2L	Conserved hypothetical protein	98.7%	8.2	1	1	1	5	1,068,994	1,055,650	1,182,488	1,155,640	80,866	38,905	99,208	39,723	16.9	8.2	18.8	7.7	-1.0	0.9	1.1	0.4	1.1	0.4	1.1	0.3	1.1	0.1	-1.0	0.8
				LGWSQPLGNLQAPLGYDK	2	98.7%	1																									
IPI00328748	-	cDNA FLJ77177, highly similar to Homo sapiens arginine-rich, mutated in early stag	99.9%	26.5	4	4	4	2	21,520,975	26,138,760	19,969,045	27,351,800	2,314,590	1,731,848	1,819,908	1,773,435	24.1	14.8	20.4	14.5	1.2	0.1	-1.1	0.6	1.3	0.08	-1.3	0.04	1.0	0.6	1.4	0.02
IPI00980165	MANF	Mesencephalic astrocyte-derived neurotrophic factor	99.9%	26.9	4	4	4	2	21,520,975	26,138,760	19,969,045	27,351,800	2,314,590	1,731,848	1,819,908	1,773,435	24.1	14.8	20.4	14.5	1.2	0.1	-1.1	0.6	1.3	0.08	-1.3	0.04	1.0	0.6	1.4	0.02
				IINEVSKPLAHHIPVEK	3	87.6%	1																									
				INELMPK	2	84.1%	1																									
				LCYYIGATDDAATK	2	98.9%	1																									
				QIDLSTVDLKK	3	86.5%	1																									
IPI00328749	C20orf160	isoform 1 of Uncharacterized protein C20orf160	99.7%	6.3	2	2	2	1	4,901,661	6,412,502	5,348,304	6,630,208	628,845	290,903	838,811	240,679	28.7	10.1	35.1	8.1	1.3	0.06	1.1	0.7	1.4	0.05	-1.2	0.3	1.0	0.6	1.2	0.2
				HGGGGGGGAGKPGGSWERR	2	98.5%	1																									
				SYDGAAQRPEAQAFHR	2	82.8%	1																									
IPI00328753	KTN1	isoform 1 of Kinectin	99.9%	1.8	2	2	2	4	2,250,853	2,248,635	2,664,640	2,526,973	87,353	56,854	69,163	133,383	8.7	5.7	5.8	11.8	-1.0	1	1.2	0.006	1.1	0.1	1.2	0.002	1.1	0.09	-1.1	0.4
IPI00337736	KTN1	isoform 2 of Kinectin	99.9%	1.9	2	2	2	4	2,250,853	2,248,635	2,664,640	2,526,973	87,353	56,854	69,163	133,383	8.7	5.7	5.8	11.8	-1.0	1	1.2	0.006	1.1	0.1	1.2	0.002	1.1	0.09	-1.1	0.4
IPI00783726	KTN1	kinectin isoform b	99.9%	1.9	2	2	2	4	2,250,853	2,248,635	2,664,640	2,526,973	87,353	56,854	69,163	133,383	8.7	5.7	5.8	11.8	-1.0	1	1.2	0.006	1.1	0.1	1.2	0.002	1.1	0.09	-1.1	0.4
IPI00909030	KTN1	cDNA FLJ61494, highly similar to Kinectin	99.9%	1.9	2	2	2	4	2,250,853	2,248,635	2,664,640	2,526,973	87,353	56,854	69,163	133,383	8.7	5.7	5.8	11.8	-1.0	1	1.2	0.006	1.1	0.1	1.2	0.002	1.1	0.09	-1.1	0.4

				SVEELLEAELLK	2	99.8%	1																									
				WLQDLQEENESLK	2	88.7%	1																									
IPI00328840	THOC4	THO complex subunit 4	100.0%	25.0	4	5	6	2	11,924,249	13,540,363	12,440,964	13,725,015	1,156,352	680,093	481,829	216,723	21.7	11.2	8.7	3.5	1.1	0.3	1.0	0.7	1.2	0.2	-1.1	0.2	1.0	0.8	1.1	0.04
IPI01010794	THOC4	THO complex subunit 4	100.0%	25.7	4	5	6	2	11,924,249	13,540,363	12,440,964	13,725,015	1,156,352	680,093	481,829	216,723	21.7	11.2	8.7	3.5	1.1	0.3	1.0	0.7	1.2	0.2	-1.1	0.2	1.0	0.8	1.1	0.04
				LLVSNLDFGVSDADIQELFAEFGTLKK	3	100.0%	2																									
				MDMSLDDIIK	2	99.9%	1																									
				QQLSAEELDAQLDAYNAR	2	100.0%	1																									
				QQLSAEELDAQLDAYNAR	3	100.0%	1																									
				SLGTADVHFER	2	100.0%	1																									
IPI00328867	SRC	isoform 2 of Proto-oncogene tyrosine-protein kinase Src	100.0%	9.2	3	3	3	2	3,711,230	4,127,351	4,019,082	4,413,907	370,072	157,264	230,254	154,780	22.3	8.5	12.8	7.8	1.1	0.3	1.1	0.5	1.2	0.1	-1.0	0.7	1.1	0.2	1.1	0.2
IPI00641230	SRC	isoform 1 of Proto-oncogene tyrosine-protein kinase Src	100.0%	9.3	3	3	3	2	3,711,230	4,127,351	4,019,082	4,413,907	370,072	157,264	230,254	154,780	22.3	8.5	12.8	7.8	1.1	0.3	1.1	0.5	1.2	0.1	-1.0	0.7	1.1	0.2	1.1	0.2
				GPSAAFAPAAAEPK	2	99.9%	1																									
				LPQLVDMAAQIASGMAYVER	2	94.8%	1																									
				SDVWSFGILLTELTTK	2	90.7%	1																									
IPI00328885	IGFN1	immunoglobulin-like and fibronectin type III domain-containing protein 1	92.5%	0.4	1	1	1	1	4,474,680	5,180,970	4,613,030	4,557,210	519,122	218,745	309,303	291,234	25.9	9.4	15.0	14.3	1.2	0.2	1.0	0.8	1.0	0.9	-1.1	0.2	-1.1	0.1	-1.0	0.9
				KDLGVPEGIGSGSK	2	92.5%	1																									
IPI00329147	CCDC43	isoform 1 of Coiled-coil domain-containing protein 43	98.9%	4.9	1	1	1	2	2,445,160	2,271,285	2,047,540	2,538,775	281,815	206,014	277,335	150,193	25.8	20.3	30.3	13.2	-1.1	0.6	-1.2	0.3	1.0	0.8	-1.1	0.5	1.1	0.3	1.2	0.2
IPI00792109	CCDC43	CCDC43 protein	98.9%	4.9	1	1	1	2	2,445,160	2,271,285	2,047,540	2,538,775	281,815	206,014	277,335	150,193	25.8	20.3	30.3	13.2	-1.1	0.6	-1.2	0.3	1.0	0.8	-1.1	0.5	1.1	0.3	1.2	0.2
				NTNVEDVLNAR	2	98.9%	1																									
IPI00329208	PDXDC1	PDXDC1 protein	100.0%	8.8	3	3	3	2	2,894,268	3,076,071	2,889,613	3,316,468	259,844	78,806	220,164	114,210	20.1	5.7	17.0	7.7	1.1	0.5	-1.0	1	1.1	0.2	-1.1	0.5	1.1	0.1	1.1	0.1
IPI00384285	PDXDC1	isoform 2 of Pyridoxal-dependent decarboxylase domain-containing protein 1	100.0%	10.3	3	3	3	2	2,894,268	3,076,071	2,889,613	3,316,468	259,844	78,806	220,164	114,210	20.1	5.7	17.0	7.7	1.1	0.5	-1.0	1	1.1	0.2	-1.1	0.5	1.1	0.1	1.1	0.1
				FFQELPGSDPVFK	2	98.8%	1																									
				HDDPALTLVAGLTSNKPTDK	3	100.0%	1																									
				IADPTLAEMGK	2	88.0%	1																									
IPI00329331	UGP2	isoform 1 of UTP--glucose-1-phosphate uridylyltransferase	100.0%	29.7	11	13	16	2	21,029,585	21,340,515	20,253,703	23,608,475	1,319,557	578,537	984,297	689,048	14.0	6.1	10.9	6.5	1.0	0.8	-1.0	0.7	1.1	0.1	-1.1	0.4	1.1	0.04	1.2	0.02
IPI00873223	UGP2	cDNA FLJ56155, highly similar to UTP--glucose-1-phosphate uridylyltransferase 2	100.0%	29.2	11	13	16	2	21,029,585	21,340,515	20,253,703	23,608,475	1,319,557	578,537	984,297	689,048	14.0	6.1	10.9	6.5	1.0	0.8	-1.0	0.7	1.1	0.1	-1.1	0.4	1.1	0.04	1.2	0.02
				AMSQDGASQFQEVIR	2	99.7%	1																									
				CEFVMEVTNK	2	87.1%	1																									
				GLPDNISSVLNK	2	99.8%	2																									
				IQRPPEDSIQPYEK	3	99.7%	1																									
				LGSSFTK	2	94.3%	1																									
				LNGGLGTSMGCK	2	86.8%	1																									
				LVEIAQVPK	2	97.2%	1																									
				NENTFLDLTVQQIEHLNK	2	99.8%	1																									
				NENTFLDLTVQQIEHLNK	3	100.0%	2																									
				SFENSLGINVPR	2	100.0%	1																									
				TLDGGLNVIQLETAVGAAIK	2	100.0%	2																									
				TLDGGLNVIQLETAVGAAIK	3	99.7%	1																									
				TYNTDVPLVLMNSFNTDEDTKK	3	90.1%	1																									
IPI00329332	STX12	Syntaxin-12	100.0%	10.5	2	2	2	2	3,901,940	3,699,710	4,153,865	4,335,470	156,806	198,835	167,076	217,983	9.0	12.0	9.0	11.2	-1.1	0.4	1.1	0.3	1.1	0.1	1.1	0.1	1.2	0.06	1.0	0.5
IPI00513853	STX12	Uncharacterized protein	100.0%	9.7	2	2	2	2	3,901,940	3,699,710	4,153,865	4,335,470	156,806	198,835	167,076	217,983	9.0	12.0	9.0	11.2	-1.1	0.4	1.1	0.3	1.1	0.1	1.1	0.1	1.2	0.06	1.0	0.5
				ELGSLPLPLSTSEQR	2	99.8%	1																									
				QLEADILDVNQIFK	2	99.3%	1																									
IPI00329338	PCYT1A	Choline-phosphate cytidylyltransferase A	100.0%	7.4	2	2	2	3	5,090,790	6,077,270	5,639,320	6,486,437	462,914	167,288	418,858	199,251	20.3	6.2	16.6	6.9	1.2	0.1	1.1	0.4	1.3	0.02	-1.1	0.4	1.1	0.2	1.2	0.1
IPI00790032	PCYT1A	cDNA FLJ53135, highly similar to Choline-phosphate cytidylyltransferase A	100.0%	8.2	2	2	2	3	5,090,790	6,077,270	5,639,320	6,486,437	462,914	167,288	418,858	199,251	20.3	6.2	16.6	6.9	1.2	0.1	1.1	0.4	1.3	0.02	-1.1	0.4	1.1	0.2	1.2	0.1
IPI00924713	PCYT1A	Uncharacterized protein	100.0%	7.1	2	2	2	3	5,090,790	6,077,270	5,639,320	6,486,437	462,914	167,288	418,858	199,251	20.3	6.2	16.6	6.9	1.2	0.1	1.1	0.4	1.3	0.02	-1.1	0.4	1.1	0.2	1.2	0.1
				EFIGSFLEMFGPEGALK	2	99.9%	1																									
				ELNVSFINEK	2	99.1%	1																									
IPI00329352	NOMO1;NOMO3	Nodal modulator 1	100.0%	6.0	5	5	5	6	2,483,406	2,313,829	2,312,528	2,535,780	182,046	84,345	162,591	149,961	16.4	8.2	15.7	13.2	-1.1	0.4	-1.1	0.5	1.0	0.8	-1.0	1	1.1	0.2	1.1	0.3
IPI00413732	NOMO1;NOMO3	139 kDa protein	100.0%	5.8	5	5	5	6	2,483,406	2,313,829	2,312,528	2,535,780	182,046	84,345	162,591	149,961	16.4	8.2	15.7	13.2	-1.1	0.4	-1.1	0.5	1.0	0.8	-1.0	1	1.1	0.2	1.1	0.3
IPI00872411	NOMO1;NOMO3	Nodal modulator 3	100.0%	6.0	5	5	5	6	2,483,406	2,313,829	2,312,528	2,535,780	182,046	84,345	162,591	149,961	16.4	8.2	15.7	13.2	-1.1	0.4	-1.1	0.5	1.0	0.8	-1.0	1	1.1	0.2	1.1	0.3
IPI00941810	NOMO1;NOMO3	139 kDa protein	100.0%	5.8	5	5	5	6	2,483,406	2,313,829	2,312,528	2,535,780	182,046	84,345	162,591	149,961	16.4	8.2	15.7	13.2	-1.1	0.4	-1.1	0.5	1.0	0.8	-1.0	1	1.1	0.2	1.1	0.3
IPI00333985	NOMO2	isoform 2 of Nodal modulator 2	100.0%	6.0	5	5	5	6	2,483,406	2,313,829	2,312,528	2,535,780	182,046	84,345	162,591	149,961	16.4	8.2	15.7	13.2	-1.1	0.4	-1.1	0.5	1.0	0.8	-1.0	1	1.1	0.2	1.1	0.3
IPI00465432	NOMO2	isoform 1 of Nodal modulator 2	100.0%	5.8	5	5	5	6	2,483,406	2,313,829	2,312,528	2,535,780	182,046	84,345	162,591	149,961	16.4	8.2	15.7	13.2	-1.1	0.4	-1.1	0.5	1.0	0.8	-1.0	1	1.1	0.2	1.1	0.3
				EGYVLTAVEGTIGDFK	2	99.9%	1																									
				FEPSSQMIEVQEGQNLK	2	99.2%	1																									
				ITFDVAPSR	2	99.2%	1																									
				SDVEINYSLIEIK	2	97.6%	1																									
				VIEVGNNDIDDVNIIVFR	2	99.6%	1																									
IPI00647060	-	cDNA FLJ58603, highly similar to Actin-binding LIM protein 1	99.9%	6.3	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00329495	ABLIM1	isoform 1 of Actin-binding LIM protein 1	99.9%	3.1	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00455786	ABLIM1	Actin binding LIM protein 1	99.9%	3.4	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00456617	ABLIM1	isoform 2 of Actin-binding LIM protein 1	99.9%	3.3	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00515115	ABLIM1	Uncharacterized protein	99.9%	2.8	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00551038	ABLIM1	isoform 3 of Actin-binding LIM protein 1	99.9%	5.6	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00644747	ABLIM1	Actin binding LIM protein 1	99.9%	4.5	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00744789	ABLIM1	isoform 4 of Actin-binding LIM protein 1	99.9%	6.0	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00747332	ABLIM1	cDNA FLJ16546 fis, clone PERIC2006443, highly similar to Homo sapiens actin bind	99.9%	3.2	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00873424	ABLIM1	Uncharacterized protein	99.9%	3.4	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00883638	ABLIM1	actin-binding LIM protein 1 isoform s	99.9%	5.3	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00922144	ABLIM1	cDNA FLJ58674, highly similar to Actin-binding LIM protein 1	99.9%	3.7	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI00940368	ABLIM1	Uncharacterized protein	99.9%	3.3	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
IPI01009888	ABLIM1	52 kDa protein	99.9%	5.3	2	2	2	14	1,092,555	1,085,842	1,069,234	1,226,745	58,222	25,680	58,577	47,540	11.9	5.3	12.3	8.7	-1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.8	1.1	0.03	1.1	0.07
				HLAPEVFR	2	81.9%	1																									
				VDNEILDYKDLAAIPK	3	100.0%	1																									
IPI00329536	EEA1	Early endosome antigen 1	99.6%	4.0	5	5	5	2	20,312,588	21,236,368	20,042,083	24,588,193	2,038,554	1,086,549	1,964,427	731,326	22.4	11.4	21.9	6.7	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.6	1.2	0.03	1.2	0.08
IPI00941708	EEA1	Uncharacterized protein	99.6%	4.0	5	5	5	2	20,312,588	21,236,368	20,042,083	24,588,193	2,038,554	1,086,549	1,964,427	731,326	22.4	11.4	21.9	6.7	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.6	1.2	0.03	1.2	0.08
				AAQLATEIADIK	2	99.5%	1																									
				EQALQDLQQQR	2	99.2%	1																									
				ISVLQNNYEK	2	93.8%	1																									
				LSLAQEDLISNR	2	99.5%	1																									
				QDFETLSQETK	2	85.1%	1																									
IPI00329583	SPATA5	isoform 1 of Spermatogenesis-associated protein 5	99.7%	2.1	1	1	1	2	140,873	142,620	141,071	164,030	24,659	6,866	13,314	7,163	39.1	10.8	21.1	9.8	1.0	0.9	1.0	1	1.2	0.4	-1.0	0.9	1.2	0.06	1.2	0.2
IPI00890727	SPATA5	isoform 2 of Spermatogenesis-associated protein 5	99.7%	2.4	1	1	1	2	140,873	142,620	141,071	164,030	24,659	6,866	13,314	7,163	39.1	10.8	21.1	9.8	1.0	0.9	1.0	1	1.2	0.4	-1.0	0.9	1.2	0.06	1.2	0.2
				AVAPSIIFFDELDALAVER	2	99.7%	1																									
IPI00329633	TARS	Threonyl-tRNA synthetase, cytoplasmic	100.0%	26.0	16	16	19	1	29,358,293	31,108,701	29,448,997	35,661,693	2,758,487	928,602	1,583,795	486,619	21.0	6.7	12.0	3.1	1.1	0.6	1.0	1	1.2	0.08	-1.1	0.4	1.1	0.002	1.2	0.01
				AEHDSILAEK	2	99.5%	1																									
				AELNPWPEYIYTR	2	100.0%	1																									
				CGPLIDLCR	2	91.2%	1																									
				FLGDIEVWDQAEK	2	100.0%	2																									
				FMADIDLDPGCTLNK	2	99.6%	1																									
				FMADIDLDPGCTLNKK	3	99.0%	1																									
				GAYIYNALIEFIR	2	100.0%	2																									
				ISGTVNIR	2	81.4%	1																									
				IYGISFPDPK	2	99.9%	1																									
				LADFGVLHR	2	98.8%	1																									
				MIAILTENYGGK	2	99.7%	1																									
				NAQLAQYNFILVVGEK	2	99.3%	1																									
				NELSGALTGLTR	2	100.0%	2																									
				QVMVVPVGPTCDEYAQK	2	100.0%	1																									
				TTPYQIACGISQGLADNTVIAK	2	99.5%	1																									
				WPFWLSPR	2	100.0%	1																									
IPI00329719	MYO1D	Myosin-Id	100.0%	13.1	10	10	10	1	68,845,320	79,703,880	68,098,920	76,794,140	9,113,712	9,074,340	5,355,960	4,110,656	29.6	25.5	17.6	12.0	1.2	0.4	-1.0	0.9	1.1	0.4	-1.2	0.3	-1.0	0.8	1.1	0.2
				FVVDGDTPLIENGK	2	88.5%	1																									
				GIIAILDDACMNVGK	2	99.7%	1																									
				HIDYFNNQIIVDLVEQQHK	3	100.0%	1																									
				HLQVNVTNPVQCSLHGK	3	99.9%	1																									
				LMYNSSNPVLK	2	81.7%	1																									
				LNQPQPDFTK	2	97.8%	1																									
				LSITEVTK	2	88.6%	1																									
				NSMIALVDNLASK	2	100.0%	1																									
				SNCVLEAFGNAK	2	100.0%	1																									
				VTDEMFLEALNSK	2	99.9%	1																									
IPI00329791	DDX46	Probable ATP-dependent RNA helicase DDX46	99.5%	2.3	2	2	2	2	3,908,525	4,837,875	3,962,415	3,886,435	283,594	228,632	365,777	276,674	16.2	10.6	20.6	15.9	1.2	0.03	1.0	0.9	-1.0	1	-1.2	0.08	-1.2	0.03	-1.0	0.9
IPI00939523	DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46, isoform CRA_a	99.5%	2.3	2	2	2	2	3,908,525	4,837,875	3,962,415	3,886,435	283,594	228,632	365,777	276,674	16.2	10.6	20.6	15.9	1.2	0.03	1.0	0.9	-1.0	1	-1.2	0.08	-1.2	0.03	-1.0	0.9
				GYAYTFITEDQAR	2	96.8%	1																									
				VTYVVLDEADR	2	92.0%	1																									
IPI00329801	ANXA5	Annexin A5	100.0%	65.3	17	22	34	1	136,274,378	135,718,473	131,375,874	156,238,880	########	4,597,113	########	4,523,103	19.5	7.6	18.1	6.5	-1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.7	1.2	0.01	1.2	0.06
				ALLLLCGEDD	1	100.0%	2																									
				DLLDDLKSELTGKFEK	2	100.0%	1																									
				DLLDDLKSELTGKFEK	3	100.0%	2																									
				DPDAGIDEAQVEQDAQALFQAGELK	3	100.0%	1																									
				ETSGNLEQLLLAVVK	2	100.0%	2																									
				GAGTDDHTLIR	2	100.0%	3																									
				GLGTDEESILTLLTSR	2	100.0%	2																									
				GLGTDEESILTLLTSR	3	100.0%	1																									
				GTVTDFPGFDER	2	100.0%	2																									
				KNFATSLYSMIK	2	98.7%	1																									
				LIVALMKPSR	2	99.9%	1																									
				LIVALMKPSR	3	89.7%	1																									
				LYDAYELK	2	100.0%	2																									
				NFATSLYSMIK	2	100.0%	2																									
				QVYEEEYGSSLEDDVVGDTSGYYQR	2	100.0%	1																									
				SEIDLFNIR	2	99.1%	1																									
				SEIDLFNIRK	2	99.9%	1																									
				SEIDLFNIRK	3	99.8%	1																									
				SIPAYLAETLYYAMK	3	100.0%	1																									
				VLTEIIASR	2	100.0%	2																									
				WGTDEEKFITIFGTR	2	100.0%	2																									
				WGTDEEKFITIFGTR	3	100.0%	2																									
IPI00332091	RPP40	isoform 2 of Ribonuclease P protein subunit p40	95.8%	5.6	1	1	1	3	390,073	358,877	387,510	415,055	56,982	30,674	42,978	49,970	32.7	19.1	24.8	26.9	-1.1	0.6	-1.0	1	1.1	0.8	1.1	0.6	1.2	0.4	1.1	0.7
IPI00478496	RPP40	isoform 1 of Ribonuclease P protein subunit p40	95.8%	5.2	1	1	1	3	390,073	358,877	387,510	415,055	56,982	30,674	42,978	49,970	32.7	19.1	24.8	26.9	-1.1	0.6	-1.0	1	1.1	0.8	1.1	0.6	1.2	0.4	1.1	0.7
IPI01014400	RPP40	35 kDa protein	95.8%	6.3	1	1	1	3	390,073	358,877	387,510	415,055	56,982	30,674	42,978	49,970	32.7	19.1	24.8	26.9	-1.1	0.6	-1.0	1	1.1	0.8	1.1	0.6	1.2	0.4	1.1	0.7
				DTYEETGLQGHPSQFSGRK	3	95.8%	1																									
IPI00332187	MPI	isoform 2 of Mannose-6-phosphate isomerase	100.0%	26.5	6	6	6	1	5,710,388	6,023,847	6,023,495	6,476,484	430,326	304,325	344,515	222,719	16.9	11.3	12.8	7.7	1.1	0.6	1.1	0.6	1.1	0.2	-1.0	1	1.1	0.3	1.1	0.3
				FIDVPTLCEMLSYTPSSSK	2	100.0%	1																									
				SQEDPYLSIYDPPVPDFTIMK	2	100.0%	1																									

				TEVPGSVTEYK	2	80.4%	1																									
				TLSQWIAENQDSLGSK	2	100.0%	1																									
				VFPLSCAVQQYAWGK	2	100.0%	1																									
				VKDTFNGNLPFLFK	2	87.5%	1																									
IPI00332371	PFKL	isoform 1 of 6-phosphofructokinase, liver type	100.0%	26.3	15	17	18	1	82,742,157	89,639,085	84,090,395	96,539,640	9,003,091	2,859,853	7,555,248	1,427,215	24.3	7.1	20.1	3.3	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.06	1.1	0.2
				AIGVLTSGGDAQGMNAAVR	2	100.0%	2																									
				GQLESIVENIR	2	97.6%	1																									
				GQVQEVGWHDVAGWLGR	3	99.5%	1																									
				KAVAFSPVTELK	2	83.9%	1																									
				LNIIIIAEGAIDR	2	100.0%	1																									
				LPLMECVQMTK	2	100.0%	1																									
				MGIYVGAK	2	98.4%	1																									
				SNFSLAILNVGAPAAGMNAAVR	2	99.9%	1																									
				SNFSLAILNVGAPAAGMNAAVR	3	100.0%	1																									
				TFVLEVMGR	2	99.8%	1																									
				TGISHGHTVYVVHDGFEGLAK	2	93.4%	1																									
				TNVLGHLQQGGAPTPFDR	3	99.9%	1																									
				VFANAPDSACVIGLK	2	99.9%	1																									
				VFANAPDSACVIGLKK	2	91.4%	1																									
				VFLIYEGYEGLVEGGENIK	2	99.9%	1																									
				VFLIYEGYEGLVEGGENIK	3	99.0%	1																									
				VNVEHMTEK	2	99.6%	1																									
IPI00332453	TJP2	isoform A3 of Tight junction protein ZO-2	100.0%	8.6	6	6	6	2	8,146,611	8,599,628	7,385,509	9,346,157	662,210	265,999	622,486	496,250	18.2	6.9	18.9	11.9	1.1	0.5	-1.1	0.4	1.1	0.2	-1.2	0.1	1.1	0.2	1.3	0.04
IPI00797934	TJP2	isoform A2 of Tight junction protein ZO-2	100.0%	8.2	6	6	6	2	8,146,611	8,599,628	7,385,509	9,346,157	662,210	265,999	622,486	496,250	18.2	6.9	18.9	11.9	1.1	0.5	-1.1	0.4	1.1	0.2	-1.2	0.1	1.1	0.2	1.3	0.04
				AEQMASVQNAQR	2	99.9%	1																									
				AFEVMDEFDGR	2	100.0%	1																									
				GEMVTILAQSR	2	99.9%	1																									
				MSYLTAMGADYLSCDSR	2	99.9%	1																									
				RPVVLFGPIADIAMEK	2	85.0%	1																									
				TFLRPSPEDEAIYGPNTK	3	100.0%	1																									
IPI00332511	PPP2R2A	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	100.0%	16.1	6	6	7	2	7,892,964	8,250,958	7,842,732	9,057,931	594,694	474,154	700,660	370,616	16.9	12.9	20.0	9.2	1.0	0.7	-1.0	1	1.1	0.1	-1.1	0.6	1.1	0.2	1.2	0.2
IPI00798041	PPP2R2A	serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	100.0%	15.8	6	6	7	2	7,892,964	8,250,958	7,842,732	9,057,931	594,694	474,154	700,660	370,616	16.9	12.9	20.0	9.2	1.0	0.7	-1.0	1	1.1	0.1	-1.1	0.6	1.1	0.2	1.2	0.2
				LFEEPEDPSNR	2	98.8%	1																									
				NAAQFLLSTNDK	2	99.9%	1																									
				RPEGYNLK	2	87.7%	1																									
				SFFSEIISSISDVK	2	100.0%	2																									
				VPVFRPMDLMVEASPR	3	100.0%	1																									
				VVIFQQEQENK	2	100.0%	1																									
IPI00333215	TCEA1	isoform 1 of Transcription elongation factor A protein 1	100.0%	18.6	3	3	3	1	3,938,670	4,399,582	4,600,469	4,715,783	377,054	126,887	420,798	66,573	21.4	6.5	20.5	3.2	1.1	0.3	1.2	0.3	1.2	0.1	1.0	0.7	1.1	0.06	1.0	0.8
				MTAEEMASDELKEMR	3	91.6%	1																									
				NIPMTLELLQSTR	2	99.2%	1																									
				TGDDYIAIGADEEELGSQIEEAIYQEIR	3	99.9%	1																									
IPI00333317	PSIP1	isoform 2 of PC4 and SFRS1-interacting protein	100.0%	11.7	3	3	3	2	3,502,448	3,456,643	3,453,616	3,771,949	187,566	53,312	202,518	183,477	12.0	3.5	13.1	10.9	-1.0	0.8	-1.0	0.9	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.3
IPI00643781	PSIP1	PSIP1 protein	100.0%	11.9	3	3	3	2	3,502,448	3,456,643	3,453,616	3,771,949	187,566	53,312	202,518	183,477	12.0	3.5	13.1	10.9	-1.0	0.8	-1.0	0.9	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.3
				GFNEGLWEIDNNPK	2	99.9%	1																									
				GYPHWPAR	2	99.0%	1																									
				LPIFFFGTHETAFLGPK	3	99.5%	1																									
IPI00333558	ANK3	cDNA FLJ35042 fis, clone OCBBF2017489, highly similar to Homo sapiens ankyrin	100.0%	8.5	2	2	2	3	1,244,502	1,256,756	1,199,391	1,517,702	150,509	60,104	107,903	106,117	27.0	10.7	20.1	15.6	1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.7	1.2	0.06	1.3	0.07
IPI00964604	ANK3	Protein	100.0%	18.1	2	2	2	3	1,244,502	1,256,756	1,199,391	1,517,702	150,509	60,104	107,903	106,117	27.0	10.7	20.1	15.6	1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.7	1.2	0.06	1.3	0.07
IPI00964884	ANK3	Protein	100.0%	15.7	2	2	2	3	1,244,502	1,256,756	1,199,391	1,517,702	150,509	60,104	107,903	106,117	27.0	10.7	20.1	15.6	1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.7	1.2	0.06	1.3	0.07
				IDIVTLLEGPIFDYGNISGTR	2	99.9%	1																									
				NATTDALTSVLTK	2	99.3%	1																									
IPI00333763	GLRX5	Glutaredoxin-related protein 5, mitochondrial	97.9%	8.9	1	1	1	1	7,056,940	6,105,590	7,547,380	6,752,320	462,655	326,367	453,900	267,370	14.7	12.0	13.5	8.9	-1.2	0.1	1.1	0.5	-1.0	0.6	1.2	0.03	1.1	0.2	-1.1	0.2
				DYAAYNVLDDPELR	2	97.9%	1																									
IPI00333996	TIA1	isoform Short of Nucleolysin TIA-1 isoform p40	100.0%	9.6	2	2	3	2	1,014,160	982,898	949,102	1,070,255	122,226	87,240	45,078	86,882	27.0	19.9	10.6	18.2	-1.0	0.8	-1.1	0.6	1.1	0.7	-1.0	0.7	1.1	0.5	1.1	0.3
IPI00927286	TIA1	Uncharacterized protein	100.0%	12.6	2	2	3	2	1,014,160	982,898	949,102	1,070,255	122,226	87,240	45,078	86,882	27.0	19.9	10.6	18.2	-1.0	0.8	-1.1	0.6	1.1	0.7	-1.0	0.7	1.1	0.5	1.1	0.3
				DTSNHFHVFVGDLSPEITTEDIK	3	94.8%	1																									
				QTFSPFGQIMEIR	2	100.0%	2																									
IPI00334159	VBP1	von Hippel-Lindau binding protein 1, isoform CRA_b	100.0%	18.9	3	3	3	1	2,035,585	2,079,947	2,516,715	2,356,742	188,991	172,692	310,585	106,023	20.8	18.6	27.6	10.1	1.0	0.9	1.2	0.2	1.2	0.2	1.2	0.3	1.1	0.2	-1.1	0.6
				LHLGIPEAVFVEDVDSFMK	3	97.2%	1																									
				NLDSLEEDLDFLR	2	99.6%	1																									
				NLDSLEEDLDFLRDQFTTTEVNMAR	3	100.0%	1																									
IPI00334174	RAB1A	isoform 2 of Ras-related protein Rab-1A	100.0%	18.4	2	3	3	2	3,245,190	3,302,735	3,971,671	3,940,029	267,032	294,681	329,128	127,648	18.4	20.0	18.5	7.2	1.0	0.9	1.2	0.1	1.2	0.05	1.2	0.2	1.2	0.08	-1.0	0.9
IPI00917079	RAB1A	Uncharacterized protein	100.0%	15.0	2	3	3	2	3,245,190	3,302,735	3,971,671	3,940,029	267,032	294,681	329,128	127,648	18.4	20.0	18.5	7.2	1.0	0.9	1.2	0.1	1.2	0.05	1.2	0.2	1.2	0.08	-1.0	0.9
				KVVDYTTAK	2	97.5%	1																									
				NATNVEQSFMTMAAEIK	2	100.0%	1																									
				NATNVEQSFMTMAAEIK	3	100.0%	1																									
IPI00334190	STOML2	Stomatin-like protein 2	100.0%	20.5	4	4	5	2	4,543,030	4,356,839	5,151,447	5,406,110	481,739	207,333	528,076	336,963	23.7	10.6	22.9	13.9	-1.0	0.7	1.1	0.4	1.2	0.2	1.2	0.2	1.2	0.03	1.0	0.7
IPI00908723	STOML2	cDNA FLJ61039, highly similar to Stomatin-like protein 2	100.0%	23.5	4	4	5	2	4,543,030	4,356,839	5,151,447	5,406,110	481,739	207,333	528,076	336,963	23.7	10.6	22.9	13.9	-1.0	0.7	1.1	0.4	1.2	0.2	1.2	0.2	1.2	0.03	1.0	0.7
				DSNTILLPSNPGDVTSMVAQAMGVYGALTK	3	100.0%	1																									
				ESAINVAEGKK	2	95.0%	1																									
				ILEPGLNILIPVLDR	2	100.0%	2																									
				NTVVLFVPQQEAWVVER	2	98.2%	1																									
IPI00334282	FAM3C	Protein FAM3C	100.0%	12.8	2	2	2	3	2,926,393	3,025,903	2,892,879	3,167,201	159,485	115,651	197,138	88,897	12.2	8.6	15.2	6.3	1.0	0.6	-1.0	0.9	1.1	0.2	-1.0	0.6	1.0	0.4	1.1	0.2
IPI00925923	FAM3C	Uncharacterized protein	100.0%	26.6	2	2	2	3	2,926,393	3,025,903	2,892,879	3,167,201	159,485	115,651	197,138	88,897	12.2	8.6	15.2	6.3	1.0	0.6	-1.0	0.9	1.1	0.2	-1.0	0.6	1.0	0.4	1.1	0.2
IPI00926250	FAM3C	Uncharacterized protein	100.0%	19.2	2	2	2	3	2,926,393	3,025,903	2,892,879	3,167,201	159,485	115,651	197,138	88,897	12.2	8.6	15.2	6.3	1.0	0.6	-1.0	0.9	1.1	0.2	-1.0	0.6	1.0	0.4	1.1	0.2
				MASGAANVVGPK	2	99.9%	1																									
				YFDMWGGDVAPFIEFLK	2	100.0%	1																									
IPI00334410	MYO18A	isoform 2 of Myosin-XVIIIa	99.9%	2.4	4	4	4	8	2,710,974	2,718,525	2,572,344	2,979,372	502,917	148,135	182,879	180,086	41.5	12.2	15.9	13.5	1.0	1	-1.1	0.8	1.1	0.6	-1.1	0.6	1.1	0.3	1.2	0.2
IPI00760846	MYO18A	isoform 1 of Myosin-XVIIIa	99.9%	2.0	4	4	4	8	2,710,974	2,718,525	2,572,344	2,979,372	502,917	148,135	182,879	180,086	41.5	12.2	15.9	13.5	1.0	1	-1.1	0.8	1.1	0.6	-1.1	0.6	1.1	0.3	1.2	0.2
IPI00760925	MYO18A	isoform 3 of Myosin-XVIIIa	99.9%	2.1	4	4	4	8	2,710,974	2,718,525	2,572,344	2,979,372	502,917	148,135	182,879	180,086	41.5	12.2	15.9	13.5	1.0	1	-1.1	0.8	1.1	0.6	-1.1	0.6	1.1	0.3	1.2	0.2
IPI00827840	MYO18A	cDNA FLJ60372, highly similar to Myosin-18A	99.9%	2.5	4	4	4	8	2,710,974	2,718,525	2,572,344	2,979,372	502,917	148,135	182,879	180,086	41.5	12.2	15.9	13.5	1.0	1	-1.1	0.8	1.1	0.6	-1.1	0.6	1.1	0.3	1.2	0.2
IPI00828082	MYO18A	isoform 4 of Myosin-XVIIIa	99.9%	2.0	4	4	4	8	2,710,974	2,718,525	2,572,344	2,979,372	502,917	148,135	182,879	180,086	41.5	12.2	15.9	13.5	1.0	1	-1.1	0.8	1.1	0.6	-1.1	0.6	1.1	0.3	1.2	0.2
IPI01011327	MYO18A	227 kDa protein	99.9%	2.1	4	4	4	8	2,710,974	2,718,525	2,572,344	2,979,372	502,917	148,135	182,879	180,086	41.5	12.2	15.9	13.5	1.0	1	-1.1	0.8	1.1	0.6	-1.1	0.6	1.1	0.3	1.2	0.2
IPI01013806	MYO18A	233 kDa protein	99.9%	2.0	4	4	4	8	2,710,974	2,718,525	2,572,344	2,979,372	502,917	148,135	182,879	180,086	41.5	12.2	15.9	13.5	1.0	1	-1.1	0.8	1.1	0.6	-1.1	0.6	1.1	0.3	1.2	0.2
IPI01014006	MYO18A	isoform 5 of Myosin-XVIIIa	99.9%	2.6	4	4	4	8	2,710,974	2,718,525	2,572,344	2,979,372	502,917	148,135	182,879	180,086	41.5	12.2	15.9	13.5	1.0	1	-1.1	0.8	1.1	0.6	-1.1	0.6	1.1	0.3	1.2	0.2
				ISELTSELTDER	2	97.7%	1																									
				QMEVMEMEVMEAR	2	99.4%	1																									
				RLESLASR	2	98.4%	1																									
				TFVQELER	2	97.6%	1																									
IPI00334453	TMEM179B	Transmembrane protein 179B	99.6%	7.3	1	1	1	1	4,929,280	4,832,440	4,534,050	5,131,050	324,685	102,218	268,391	359,438	14.7	4.7	13.2	15.7	-1.0	0.8	-1.1	0.4	1.0	0.7	-1.1	0.3	1.1	0.5	1.1	0.2
				GDPEWSSETDALVGSR	2	99.6%	1																									
IPI00334513	SUMF2	isoform 2 of Sulfatase-modifying factor 2	100.0%	11.7	2	2	2	3	944,009	889,505	911,162	952,969	67,501	94,234	65,990	35,780	16.0	23.7	16.2	8.4	-1.1	0.7	-1.0	0.7	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.6
IPI00783919	SUMF2	Uncharacterized protein	100.0%	7.7	2	2	2	3	944,009	889,505	911,162	952,969	67,501	94,234	65,990	35,780	16.0	23.7	16.2	8.4	-1.1	0.7	-1.0	0.7	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.6
IPI00927565	SUMF2	cDNA FLJ59949, highly similar to Homo sapiens sulfatase modifying factor 2 (SUMF	100.0%	10.8	2	2	2	3	944,009	889,505	911,162	952,969	67,501	94,234	65,990	35,780	16.0	23.7	16.2	8.4	-1.1	0.7	-1.0	0.7	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.6
				MGNTPDSASDNLGFR	2	99.5%	1																									
				SVLWWLPVEK	2	99.9%	1																									
IPI00334514	SUMF2	sulfatase-modifying factor 2 isoform e precursor	100.0%	2.8	1	1	1	5	220,473	228,029	249,988	266,315	21,053	21,564	3,388	13,699	21.4	21.2	3.0	11.5	1.0	0.8	1.1	0.2	1.2	0.1	1.1	0.4	1.2	0.2	1.1	0.3
IPI00910862	SUMF2	cDNA FLJ54105, highly similar to Sulfatase-modifying factor 2	100.0%	5.5	1	1	1	5	220,473	228,029	249,988	266,315	21,053	21,564	3,388	13,699	21.4	21.2	3.0	11.5	1.0	0.8	1.1	0.2	1.2	0.1	1.1	0.4	1.2	0.2	1.1	0.3
IPI00926529	SUMF2	Uncharacterized protein	100.0%	2.8	1	1	1	5	220,473	228,029	249,988	266,315	21,053	21,564	3,388	13,699	21.4	21.2	3.0	11.5	1.0	0.8	1.1	0.2	1.2	0.1	1.1	0.4	1.2	0.2	1.1	0.3
IPI00926849	SUMF2	19 kDa protein	100.0%	6.1	1	1	1	5	220,473	228,029	249,988	266,315	21,053	21,564	3,388	13,699	21.4	21.2	3.0	11.5	1.0	0.8	1.1	0.2	1.2	0.1	1.1	0.4	1.2	0.2	1.1	0.3
IPI00972944	SUMF2	Uncharacterized protein	100.0%	3.4	1	1	1	5	220,473	228,029	249,988	266,315	21,053	21,564	3,388	13,699	21.4	21.2	3.0	11.5	1.0	0.8	1.1	0.2	1.2	0.1	1.1	0.4	1.2	0.2	1.1	0.3
				SVLWWLPVEK	2	99.9%	1																									
IPI00334587	HNRNPAB	isoform 2 of Heterogeneous nuclear ribonucleoprotein A/B	100.0%	24.7	6	7	11	5	6,279,650	6,655,913	6,546,794	7,638,270	716,042	235,035	596,779	290,740	25.5	7.9	20.4	8.5	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.03	1.2	0.1
IPI00334713	HNRNPAB	isoform 3 of Heterogeneous nuclear ribonucleoprotein A/B	100.0%	28.8	6	7	11	5	6,279,650	6,655,913	6,546,794	7,638,270	716,042	235,035	596,779	290,740	25.5	7.9	20.4	8.5	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.03	1.2	0.1
IPI00964686	HNRNPAB	Uncharacterized protein	100.0%	29.3	6	7	11	5	6,279,650	6,655,913	6,546,794	7,638,270	716,042	235,035	596,779	290,740	25.5	7.9	20.4	8.5	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.03	1.2	0.1
IPI00964992	HNRNPAB	Uncharacterized protein	100.0%	25.1	6	7	11	5	6,279,650	6,655,913	6,546,794	7,638,270	716,042	235,035	596,779	290,740	25.5	7.9	20.4	8.5	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.03	1.2	0.1
IPI00966854	HNRNPAB	Uncharacterized protein	100.0%	29.0	6	7	11	5	6,279,650	6,655,913	6,546,794	7,638,270	716,042	235,035	596,779	290,740	25.5	7.9	20.4	8.5	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.03	1.2	0.1
				EVYQQQQYGSGGR	2	100.0%	2																									
				EYFGEFGEIEAIELPMDPK	2	100.0%	2																									
				EYFGEFGEIEAIELPMDPK	3	99.6%	1																									
				GFGFILFK	2	100.0%	2																									
				GFVFITFKEEEPVKK	3	96.1%	1																									
				IFVGGLNPEATEEK	2	100.0%	2																									
				MFVGGLSWDTSKK	2	100.0%	1																									
IPI00334715	GRLF1	isoform 1 of Glucocorticoid receptor DNA-binding factor 1	99.9%	3.2	2	2	2	2	4,473,255	4,471,815	4,732,355	4,933,685	543,428	207,618	437,420	194,814	27.2	10.4	20.7	8.8	-1.0	1	1.1	0.7	1.1	0.5	1.1	0.6	1.1	0.1	1.0	0.7
IPI00718985	GRLF1	isoform 2 of Glucocorticoid receptor DNA-binding factor 1	99.9%	3.2	2	2	2	2	4,473,255	4,471,815	4,732,355	4,933,685	543,428	207,618	437,420	194,814	27.2	10.4	20.7	8.8	-1.0	1	1.1	0.7	1.1	0.5	1.1	0.6	1.1	0.1	1.0	0.7
				AFLCEVQDIIPIQLVALTDGAVDVLDNDLSR	3	90.3%	1																									
				LQCVFLDPASAGIGYGR	2	99.0%	1																									
IPI00335009	HMCN2	isoform 3 of Hemicentin-2	99.5%	1.3	2	2	2	3	4,428,793	4,644,273	5,100,263	5,440,896	280,211	192,170	461,781	113,906	14.2	9.3	20.3	4.7	1.0	0.5	1.2	0.2	1.2	0.01	1.1	0.4	1.2	0.007	1.1	0.5
IPI00936570	HMCN2	isoform 1 of Hemicentin-2	99.5%	1.1	2	2	2	3	4,428,793	4,644,273	5,100,263	5,440,896	280,211	192,170	461,781	113,906	14.2	9.3	20.3	4.7	1.0	0.5	1.2	0.2	1.2	0.01	1.1	0.4	1.2	0.007	1.1	0.5
IPI00964287	HMCN2	isoform 2 of Hemicentin-2	99.5%	1.4	2	2	2	3	4,428,793	4,644,273	5,100,263	5,440,896	280,211	192,170	461,781	113,906	14.2	9.3	20.3	4.7	1.0	0.5	1.2	0.2	1.2	0.01	1.1	0.4	1.2	0.007	1.1	0.5
				NYHVEVLIPPSISKDDPLGEVGVKEVK	3	94.8%	1																									
				TETVSQVAGSPLVLTCDVSGVPAPTVTWLK	3	92.4%	1																									
IPI00335069	PSMD12	26S proteasome non-ATPase regulatory subunit 12 isoform 2	100.0%	8.0	2	2	2	1	2,927,805	3,414,800	2,080,754	2,742,610	188,912	223,428	239,139	297,671	14.4	14.6	25.7	24.3	1.2	0.1	-1.4	0.02	-1.1	0.6	-1.6	0.004	-1.2	0.1	1.3	0.1
				DPNNLLNDWSQK	2	99.6%	1																									
				MAQLLDLSVDESEAFLSNLVVNK	3	98.3%	1																									
IPI00335168	MYL6	isoform Non-muscle of Myosin light polypeptide 6	100.0%	73.5	9	11	17	1	33,147,083	34,412,505	33,310,923	38,860,043	2,625,597	1,350,456	2,299,236	1,147,477	17.7	8.8	15.4	6.6	1.0	0.7	1.0	1	1.2	0.08	-1.0	0.7	1.1	0.04	1.2	0.06
				ALGQNPTNAEVLK	2	100.0%	2																									
				DQGTYEDYVEGLR	2	100.0%	2																									
				EAFQLFDR	2	88.6%	1																									
				EGNGTVMGAEIR	2	95.8%	1																									
				HVLVTLGEK	2	100.0%	2																									
				ILYSQCGDVMR	2	100.0%	2																									
				MTEEEVEMLVAGHEDSNGCINYEAFVR	3	100.0%	1																									
				NKDQGTYEDYVEGLR	2	100.0%	2																									
				NKDQGTYEDYVEGLR	3	100.0%	1																									
				VLDFEHFLPMLQTVAK	2	100.0%	1																									
				VLDFEHFLPMLQTVAK	3	100.0%	2																									
IPI00335280	LOC729020;RPE	isoform 1 of Ribulose-phosphate 3-epimerase	99.4%	17.5	2	2	2	5	2,496,027	2,418,573	2,331,827	2,767,400	158,623	85,935	166,303	93,903	14.2	7.9	16.0	7.6	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.05
IPI00373788	LOC729020;RPE	isoform 2 of Ribulose-phosphate 3-epimerase	99.4%	18.2	2	2	2	5	2,496,027	2,418,573	2,331,827	2,767,400	158,623	85,935	166,303	93,903	14.2	7.9	16.0	7.6	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.05
IPI00925376	LOC729020;RPE	Ribulose-phosphate 3-epimerase	99.4%	17.8	2	2	2	5	2,496,027	2,418,573	2,331,827	2,767,400	158,623	85,935	166,303	93,903	14.2	7.9	16.0	7.6	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.05
IPI00927031	LOC729020;RPE	Uncharacterized protein	99.4%	20.9	2	2	2	5	2,496,027	2,418,573	2,331,827	2,767,400	158,623	85,935	166,303	93,903	14.2	7.9	16.0	7.6	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.05
IPI00983692	LOC729020;RPE	Ribulose-phosphate 3-epimerase	99.4%	18.2	2	2	2	5	2,496,027	2,418,573	2,331,827	2,767,400	158,623	85,935	166,303	93,903	14.2	7.9	16.0	7.6	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.7	1.1	0.03	1.2	0.05
				IGPSILNSDLANLGAECLR	2	95.5%	1																									
				TQFPSLDIEVDGGVGPDTVHK	3	99.4%	1																									
IPI00335385	DCPS	Scavenger mRNA-decapping enzyme DcpS	100.0%	11.3	2	2	3	1	8,502,500	8,412,454	8,349,630	11,333,578	1,396,080	764,528	974,191	741,859	36.7	20.3	26.1	14.6	-1.0	1	-1.0	0.9	1.3	0.1	-1.0	1	1.3	0.03	1.4	0.04

				IVFENPDPSDGFVLIPDLK	2	100.0%	2																									
				VNEASGDGDGEDAVVILEK	3	80.1%	1																									
IPI00335437	ANKZF1	Ankyrin repeat and zinc finger domain-containing protein 1	90.1%	3.0	1	1	1	2	4,028,150	4,575,435	4,799,050	4,198,555	1,187,456	1,055,979	793,988	839,705	65.9	51.6	37.0	44.7	1.1	0.7	1.2	0.6	1.0	0.9	1.0	0.9	-1.1	0.8	-1.1	0.6
IPI00916311	ANKZF1	Uncharacterized protein	90.1%	4.3	1	1	1	2	4,028,150	4,575,435	4,799,050	4,198,555	1,187,456	1,055,979	793,988	839,705	65.9	51.6	37.0	44.7	1.1	0.7	1.2	0.6	1.0	0.9	1.0	0.9	-1.1	0.8	-1.1	0.6
				RLAAQLGAPTSPIPDSAIVNTR	2	90.1%	1																									
IPI00335961	EWSR1	RNA-binding protein EWS isoform 5	100.0%	6.8	1	1	1	2	923,343	996,493	948,624	1,055,650	74,314	22,916	41,125	31,705	18.0	5.1	9.7	6.7	1.1	0.4	1.0	0.8	1.1	0.1	-1.1	0.3	1.1	0.2	1.1	0.07
IPI00956178	EWSR1	31 kDa protein	100.0%	8.2	1	1	1	2	923,343	996,493	948,624	1,055,650	74,314	22,916	41,125	31,705	18.0	5.1	9.7	6.7	1.1	0.4	1.0	0.8	1.1	0.1	-1.1	0.3	1.1	0.2	1.1	0.07
				QDHPSSMGVYGQESGGFSGPGENR	3	100.0%	1																									
IPI00336094	HSD17B10	isoform 2 of 3-hydroxyacyl-CoA dehydrogenase type-2	100.0%	30.2	4	4	5	1	10,556,328	12,789,615	11,939,203	13,424,343	1,961,486	702,437	680,820	279,663	41.6	12.3	12.8	4.7	1.2	0.3	1.1	0.5	1.3	0.2	-1.1	0.4	1.0	0.4	1.1	0.08
				GGIVGMTLPIAR	2	100.0%	2																									
				LGDPAEYAHLVQAIIENPFLNGEVIR	3	100.0%	1																									
				LVGQGASAVLLDLPNSGGEAQAK	2	100.0%	1																									
				VDVAVNCAGIAVASK	2	100.0%	1																									
IPI00337315	RBBP6	isoform 1 of E3 ubiquitin-protein ligase RBBP6	90.7%	0.6	1	1	1	2	1,636,095	1,796,690	1,673,470	1,964,175	192,591	111,682	84,344	81,559	26.3	13.9	11.3	9.3	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.3	1.2	0.04
IPI00376283	RBBP6	isoform 2 of E3 ubiquitin-protein ligase RBBP6	90.7%	0.6	1	1	1	2	1,636,095	1,796,690	1,673,470	1,964,175	192,591	111,682	84,344	81,559	26.3	13.9	11.3	9.3	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.3	1.2	0.04
				REDYVGGQSHR	3	88.0%	1																									
IPI00337328	ASTE1	Protein asteroid homolog 1	99.3%	3.7	1	1	1	4	720,568	747,213	723,610	863,930	79,594	30,361	94,993	27,942	24.7	9.1	29.4	7.2	1.0	0.8	1.0	1	1.2	0.2	-1.0	0.8	1.2	0.02	1.2	0.2
IPI00790409	ASTE1	cDNA FLJ60917	99.3%	6.3	1	1	1	4	720,568	747,213	723,610	863,930	79,594	30,361	94,993	27,942	24.7	9.1	29.4	7.2	1.0	0.8	1.0	1	1.2	0.2	-1.0	0.8	1.2	0.02	1.2	0.2
IPI00790975	ASTE1	cDNA FLJ52104	99.3%	4.8	1	1	1	4	720,568	747,213	723,610	863,930	79,594	30,361	94,993	27,942	24.7	9.1	29.4	7.2	1.0	0.8	1.0	1	1.2	0.2	-1.0	0.8	1.2	0.02	1.2	0.2
IPI00965138	ASTE1	Uncharacterized protein	99.3%	3.6	1	1	1	4	720,568	747,213	723,610	863,930	79,594	30,361	94,993	27,942	24.7	9.1	29.4	7.2	1.0	0.8	1.0	1	1.2	0.2	-1.0	0.8	1.2	0.02	1.2	0.2
				GTQNYIPAKCFSLDAFCHHFSNMNK	3	99.3%	1																									
IPI00337335	MYH14	isoform 1 of Myosin-14	100.0%	31.1	44	48	58	2	63,333,025	64,655,266	61,740,410	71,038,262	5,044,713	2,599,849	3,460,992	2,223,034	17.8	9.0	12.5	7.0	1.0	0.8	-1.0	0.8	1.1	0.2	-1.0	0.5	1.1	0.1	1.2	0.05
IPI01012558	MYH14	232 kDa protein	100.0%	30.5	44	48	58	2	63,333,025	64,655,266	61,740,410	71,038,262	5,044,713	2,599,849	3,460,992	2,223,034	17.8	9.0	12.5	7.0	1.0	0.8	-1.0	0.8	1.1	0.2	-1.0	0.5	1.1	0.1	1.2	0.05
				AELEALLSSKDDVGK	2	99.9%	1																									
				AELSSLQTAR	2	99.9%	1																									
				AGVLAQLEEER	2	100.0%	2																									
				AMEAEAAGLREQLEEEAAAR	3	100.0%	1																									
				AQAELENVSGALNEAESK	2	100.0%	2																									
				AQVTELEDELTAAEDAK	2	100.0%	2																									
				AQVTELEDELTAAEDAK	3	100.0%	1																									
				DLGEELEALRGELEDTLDSTNAQQELR	3	100.0%	1																									
				DQADFSVLHYAGK	2	97.2%	1																									
				EAQAALAEAQEDLESER	2	100.0%	2																									
				EAQAALAEAQEDLESER	3	99.9%	1																									
				ELEDVTESAESMNR	2	100.0%	2																									
				ELFQETLESLR	2	99.7%	1																									
				ELQTAQAQLSEWR	2	100.0%	1																									
				ELSSTEAQLHDAQELLQEETR	2	100.0%	1																									
				ELSSTEAQLHDAQELLQEETR	3	100.0%	1																									
				EQEVTELKK	2	99.3%	1																									
				GPSAGGGPGSGTSPQVEWTAR	2	100.0%	1																									
				HEVPPHVYAVTEGAYR	3	100.0%	1																									
				HGQALGELAEQLEQAR	2	100.0%	1																									
				KEEELQAALAR	2	99.9%	2																									
				KQELELVVSELEAR	2	100.0%	1																									
				LALEAEVSELR	2	100.0%	2																									
				LALEAEVSELRAELSSLQTAR	3	98.9%	1																									
				LAQAEEQLEQETR	2	100.0%	2																									
				LELQLQEVQGR	2	99.9%	1																									
				LKYEATIADMEDR	2	99.9%	1																									
				LLGLGVTDFSR	2	100.0%	2																									
				LLLQVESLTTELSAER	2	100.0%	1																									
				LMATLSNTNPSFVR	2	100.0%	1																									
				LQEELAASDR	2	100.0%	1																									
				LQQELDDATMDLEQQR	2	100.0%	1																									
				LQQELDDATMDLEQQR	3	100.0%	1																									
				LQQHIQELEAHLEAEEGAR	3	100.0%	1																									
				MIQALELDPNLYR	2	100.0%	2																									
				MVSAVLQFGNIALK	2	100.0%	1																									
				NMDPLNDNVAALLHQSTDR	3	99.8%	1																									
				NTDQATMPDNTAAQK	2	100.0%	1																									
				QAQQDRDEMADEVANGNLSK	3	99.9%	1																									
				QLPIYTEAIVEMYR	2	98.2%	1																									
				RLDGESSELQEQMVEQQQR	3	100.0%	1																									
				RRQEEEAGALEAGEEAR	3	98.9%	1																									
				TSREEIFSQNR	2	88.9%	1																									
				VAQLEEER	2	94.3%	1																									
				VKPLLQVTR	3	98.4%	1																									
				VQELQQQSAR	2	99.8%	1																									
				VTDIIVSFQAAAR	2	99.8%	1																									
				YEILTPNAIPK	2	96.3%	1																									
IPI00337370	NAMPT	42 kDa protein	100.0%	9.5	2	2	2	2	2,389,703	2,391,060	2,397,167	2,660,297	112,328	162,206	188,203	161,463	10.5	15.2	17.6	13.6	1.0	1	1.0	1	1.1	0.2	1.0	1	1.1	0.3	1.1	0.3
IPI00922378	NAMPT	cDNA FLJ55038, highly similar to Nicotinamide phosphoribosyltransferase	100.0%	14.5	2	2	2	2	2,389,703	2,391,060	2,397,167	2,660,297	112,328	162,206	188,203	161,463	10.5	15.2	17.6	13.6	1.0	1	1.0	1	1.1	0.2	1.0	1	1.1	0.3	1.1	0.3
				GVSSQETAGIGASAHLVNFK	3	98.4%	1																									
				YLLETSGNLDGLEYK	2	100.0%	1																									
IPI00337385	PRPF40A	isoform 1 of Pre-mRNA-processing factor 40 homolog A	100.0%	5.3	3	3	3	2	2,412,201	2,368,181	2,410,459	2,593,053	186,270	165,620	209,660	168,799	17.3	15.6	19.5	14.6	-1.0	0.9	-1.0	1	1.1	0.5	1.0	0.9	1.1	0.4	1.1	0.5
IPI00337387	PRPF40A	isoform 3 of Pre-mRNA-processing factor 40 homolog A	100.0%	5.4	3	3	3	2	2,412,201	2,368,181	2,410,459	2,593,053	186,270	165,620	209,660	168,799	17.3	15.6	19.5	14.6	-1.0	0.9	-1.0	1	1.1	0.5	1.0	0.9	1.1	0.4	1.1	0.5
				FTNMLGQPGSTALDLFK	2	100.0%	1																									
				FVKEPAFEDITLESER	3	99.9%	1																									
				QAAPPIELDAVWEDIRER	3	94.2%	1																									
IPI00337386	PRPF40A	isoform 2 of Pre-mRNA-processing factor 40 homolog A	100.0%	6.5	4	4	4	2	5,032,275	4,693,605	4,421,805	5,200,123	286,128	108,403	429,965	446,692	12.7	5.2	21.7	19.2	-1.1	0.3	-1.1	0.3	1.0	0.8	-1.1	0.6	1.1	0.3	1.2	0.2
IPI01010316	PRPF40A	cDNA, FLJ96168, Homo sapiens formin binding protein 3 (FNBP3), mRNA	100.0%	7.3	4	4	4	2	5,032,275	4,693,605	4,421,805	5,200,123	286,128	108,403	429,965	446,692	12.7	5.2	21.7	19.2	-1.1	0.3	-1.1	0.3	1.0	0.8	-1.1	0.6	1.1	0.3	1.2	0.2
				FTNMLGQPGSTALDLFK	2	100.0%	1																									
				FVKEPAFEDITLESER	3	99.9%	1																									
				LAFNSLLEK	2	99.7%	1																									
				QAAPPIELDAVWEDIRER	3	94.2%	1																									
IPI00337494	SLC25A24	isoform 1 of Calcium-binding mitochondrial carrier protein SCaMC-1	99.4%	2.7	1	1	1	2	4,185,160	4,111,965	4,793,095	4,431,630	280,958	157,192	142,278	208,253	15.0	8.6	6.6	10.5	-1.0	0.8	1.1	0.09	1.1	0.5	1.2	0.01	1.1	0.3	-1.1	0.2
IPI00412742	SLC25A24	isoform 2 of Calcium-binding mitochondrial carrier protein SCaMC-1	99.4%	2.8	1	1	1	2	4,185,160	4,111,965	4,793,095	4,431,630	280,958	157,192	142,278	208,253	15.0	8.6	6.6	10.5	-1.0	0.8	1.1	0.09	1.1	0.5	1.2	0.01	1.1	0.3	-1.1	0.2
				QLLAGGIAGAVSR	2	99.4%	1																									
IPI00337495	PLOD2	isoform 2 of Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	100.0%	11.2	6	6	7	3	6,845,953	6,905,940	7,111,579	7,639,076	751,236	289,358	497,389	266,276	24.5	9.4	15.6	7.8	1.0	0.9	1.0	0.8	1.1	0.4	1.0	0.7	1.1	0.1	1.1	0.4
IPI00472165	PLOD2	isoform 1 of Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	100.0%	11.5	6	6	7	3	6,845,953	6,905,940	7,111,579	7,639,076	751,236	289,358	497,389	266,276	24.5	9.4	15.6	7.8	1.0	0.9	1.0	0.8	1.1	0.4	1.0	0.7	1.1	0.1	1.1	0.4
IPI00947400	PLOD2	Uncharacterized protein	100.0%	12.1	6	6	7	3	6,845,953	6,905,940	7,111,579	7,639,076	751,236	289,358	497,389	266,276	24.5	9.4	15.6	7.8	1.0	0.9	1.0	0.8	1.1	0.4	1.0	0.7	1.1	0.1	1.1	0.4
				GGDGINSIGGGQK	2	92.4%	1																									
				ISGGYENVPTDDIHMK	3	100.0%	1																									
				IVGPEENLSQAEAR	2	100.0%	1																									
				LWSNFWGALSPDGYYAR	2	99.9%	1																									
				QVDLENVWLHFIR	3	99.8%	1																									
				SEDYVDIVQGNR	2	100.0%	2																									
IPI00337541	NNT	NAD(P) transhydrogenase, mitochondrial	99.1%	1.6	1	1	1	3	2,123,007	1,996,167	2,133,877	2,217,603	90,126	44,148	79,360	85,491	9.5	5.0	8.3	8.6	-1.1	0.2	1.0	0.9	1.0	0.5	1.1	0.2	1.1	0.05	1.0	0.5
IPI00963871	NNT	Uncharacterized protein	99.1%	7.8	1	1	1	3	2,123,007	1,996,167	2,133,877	2,217,603	90,126	44,148	79,360	85,491	9.5	5.0	8.3	8.6	-1.1	0.2	1.0	0.9	1.0	0.5	1.1	0.2	1.1	0.05	1.0	0.5
IPI00967459	NNT	Uncharacterized protein	99.1%	8.5	1	1	1	3	2,123,007	1,996,167	2,133,877	2,217,603	90,126	44,148	79,360	85,491	9.5	5.0	8.3	8.6	-1.1	0.2	1.0	0.9	1.0	0.5	1.1	0.2	1.1	0.05	1.0	0.5
				APMVNPTLGVHEADLLK	3	99.1%	1																									
IPI00337602	ZNF326	cDNA FLJ50345, highly similar to Zinc finger protein 326	99.5%	3.3	1	1	1	1	1,203,293	1,257,277	1,214,963	1,388,217	140,815	103,835	131,787	170,215	26.2	18.5	24.3	27.4	1.0	0.8	1.0	1	1.2	0.4	-1.0	0.8	1.1	0.5	1.1	0.4
				ESVLTATSILNNPIVK	2	99.5%	1																									
IPI00337741	APEH	Acylamino-acid-releasing enzyme	100.0%	7.1	5	5	6	2	13,637,061	14,630,686	14,225,114	16,817,372	1,311,866	603,988	1,298,628	525,859	21.5	9.2	20.4	7.0	1.1	0.5	1.0	0.8	1.2	0.05	-1.0	0.8	1.1	0.03	1.2	0.1
IPI00926648	APEH	Uncharacterized protein	100.0%	7.1	5	5	6	2	13,637,061	14,630,686	14,225,114	16,817,372	1,311,866	603,988	1,298,628	525,859	21.5	9.2	20.4	7.0	1.1	0.5	1.0	0.8	1.2	0.05	-1.0	0.8	1.1	0.03	1.2	0.1
				ALDVSASDDEIAR	2	100.0%	1																									
				LLLYPK	2	85.4%	1																									
				SALYYVDLIGGK	2	100.0%	1																									
				SFNLSALEK	2	90.2%	1																									
				TPLLLMLGQEDR	2	100.0%	2																									
IPI00339269	HSPA6	Heat shock 70 kDa protein 6	100.0%	10.3	6	8	10	1	48,701,434	48,757,100	46,243,506	54,371,498	3,000,302	1,994,859	2,808,120	1,594,643	13.8	9.2	13.6	6.6	1.0	1	-1.1	0.6	1.1	0.1	-1.1	0.5	1.1	0.06	1.2	0.04
				ARFEELCSDLFR	2	96.6%	1																									
				ATAGDTHLGGEDFDNR	2	100.0%	2																									
				ATAGDTHLGGEDFDNR	3	99.9%	1																									
				DNNLLGR	2	96.6%	1																									
				FELSGIPPAPR	2	98.9%	1																									
				LLQDFFNGK	2	100.0%	2																									
				VEILANDQGNR	1	98.1%	1																									
				VEILANDQGNR	2	91.1%	1																									
IPI01015210	PDXDC1	LP8165	100.0%	6.4	1	1	1	2	682,026	727,353	626,568	763,626	52,896	40,188	55,139	27,348	17.3	12.4	19.7	8.0	1.1	0.5	-1.1	0.5	1.1	0.2	-1.2	0.2	1.0	0.5	1.2	0.06
IPI00373856	PDXDC2P	Pyridoxal-dependent decarboxylase domain-containing protein 2	100.0%	2.8	1	1	1	2	682,026	727,353	626,568	763,626	52,896	40,188	55,139	27,348	17.3	12.4	19.7	8.0	1.1	0.5	-1.1	0.5	1.1	0.2	-1.2	0.2	1.0	0.5	1.2	0.06
				FFQELPGSDPVFK	2	98.8%	1																									
IPI00373870	SNORA69;CHD3	isoform 1 of Chromodomain-helicase-DNA-binding protein 3	97.2%	0.5	1	1	1	3	866,977	1,008,550	875,280	1,060,043	80,369	67,958	69,238	87,990	20.7	15.1	17.7	18.6	1.2	0.2	1.0	0.9	1.2	0.1	-1.2	0.2	1.1	0.7	1.2	0.1
IPI00411592	SNORA69;CHD3	isoform 2 of Chromodomain-helicase-DNA-binding protein 3	97.2%	0.5	1	1	1	3	866,977	1,008,550	875,280	1,060,043	80,369	67,958	69,238	87,990	20.7	15.1	17.7	18.6	1.2	0.2	1.0	0.9	1.2	0.1	-1.2	0.2	1.1	0.7	1.2	0.1
IPI00465222	SNORA69;CHD3	chromodomain-helicase-DNA-binding protein 3 isoform 3	97.2%	0.4	1	1	1	3	866,977	1,008,550	875,280	1,060,043	80,369	67,958	69,238	87,990	20.7	15.1	17.7	18.6	1.2	0.2	1.0	0.9	1.2	0.1	-1.2	0.2	1.1	0.7	1.2	0.1
				KGEGDGGQK	2	88.6%	1																									
IPI00373877	ZNF326	isoform 1 of Zinc finger protein 326	99.5%	6.7	2	2	2	2	1,758,673	1,855,830	1,843,190	2,016,563	176,975	127,484	143,001	232,274	22.5	15.4	17.4	25.8	1.1	0.7	1.0	0.7	1.1	0.4	-1.0	0.9	1.1	0.6	1.1	0.5
IPI01012540	ZNF326	Uncharacterized protein	99.5%	6.7	2	2	2	2	1,758,673	1,855,830	1,843,190	2,016,563	176,975	127,484	143,001	232,274	22.5	15.4	17.4	25.8	1.1	0.7	1.0	0.7	1.1	0.4	-1.0	0.9	1.1	0.6	1.1	0.5
				ESVLTATSILNNPIVK	2	99.5%	1																									
				SMDSYLNQSYGMDNHSGGGGGSR	3	98.3%	1																									
IPI00374054	ENAH	isoform 2 of Protein enabled homolog	99.6%	3.9	1	1	1	5	597,648	698,096	712,030	748,166	51,696	51,170	68,276	60,541	19.3	16.4	21.4	18.1	1.2	0.2	1.2	0.2	1.3	0.1	1.0	0.9	1.1	0.5	1.1	0.7
IPI00411623	ENAH	isoform 1 of Protein enabled homolog	99.6%	3.7	1	1	1	5	597,648	698,096	712,030	748,166	51,696	51,170	68,276	60,541	19.3	16.4	21.4	18.1	1.2	0.2	1.2	0.2	1.3	0.1	1.0	0.9	1.1	0.5	1.1	0.7
IPI00646954	ENAH	89 kDa protein	99.6%	2.7	1	1	1	5	597,648	698,096	712,030	748,166	51,696	51,170	68,276	60,541	19.3	16.4	21.4	18.1	1.2	0.2	1.2	0.2	1.3	0.1	1.0	0.9	1.1	0.5	1.1	0.7
IPI00749432	ENAH	cDNA FLJ44946 fis, clone BRAMY4001863, highly similar to Mus musculus enabled	99.6%	7.4	1	1	1	5	597,648	698,096	712,030	748,166	51,696	51,170	68,276	60,541	19.3	16.4	21.4	18.1	1.2	0.2	1.2	0.2	1.3	0.1	1.0	0.9	1.1	0.5	1.1	0.7
IPI00976226	ENAH	Enabled-like protein variant hMenaDv6	99.6%	4.1	1	1	1	5	597,648	698,096	712,030	748,166	51,696	51,170	68,276	60,541	19.3	16.4	21.4	18.1	1.2	0.2	1.2	0.2	1.3	0.1	1.0	0.9	1.1	0.5	1.1	0.7
				GNGPLPLGGSGLMEEMSALLAR	2	99.6%	1																									
IPI00374273	C5orf34	Uncharacterized protein C5orf34	92.0%	0.9	1	1	1	1	1,370,125	1,524,659	2,144,168	1,803,096	249,735	197,559	404,849	309,628	40.8	29.0	42.2	38.4	1.1	0.6	1.6	0.1	1.3	0.3	1.4	0.2	1.2	0.5	-1.2	0.5
				VSIALK	1	89.7%	1																									
IPI00374519	RAB1C	Putative Ras-related protein Rab-1C	100.0%	8.5	1	2	3	1	1,241,140	1,247,450	1,401,491	1,216,511	141,146	65,990	81,995	62,454	25.4	11.8	13.1	11.5	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.2	-1.0	0.7	-1.2	0.1
				NATNVEQAFMTMAAEIK	2	100.0%	2																									
				NATNVEQAFMTMAAEIK	3	100.0%	1																									
IPI00374563	AGRN	Agrin	100.0%	5.1	8	8	8	1	41,481,153	44,731,803	40,105,957	49,089,120	4,475,578	1,908,100	2,825,183	1,671,440	24.1	9.5	15.8	7.6	1.1	0.5	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.1	1.2	0.03
				AAAVSSGFDGAIQLVSLGGR	3	83.0%	1																									
				FGALCEAETGR	2	99.9%	1																									
				GPSGLLLYNGQK	2	85.3%	1																									
				LELGIGPGAATR	2	89.4%	1																									

				SAGDVDTLAFDGR	2	99.9%	1																									
				SIESTLDDLFR	2	100.0%	1																									
				TEATQGLVLWSGK	2	98.4%	1																									
				VLGAPVPAFEGR	2	98.1%	1																									
IPI00374748	TMC3	isoform 1 of Transmembrane channel-like protein 3	97.8%	1.6	1	1	1	1	2,371,600	2,570,150	2,444,050	2,445,000	214,773	333,858	93,105	179,108	20.3	29.1	8.5	16.4	1.1	0.6	1.0	0.8	1.0	0.8	-1.1	0.7	-1.1	0.7	1.0	1
				SGQELTVDLDDLICSDV	3	97.8%	1																									
IPI00374970	SEP10	isoform 1 of Septin-10	100.0%	4.4	2	2	2	5	1,665,290	1,809,228	1,714,699	1,801,507	99,137	126,698	145,427	51,979	13.3	15.7	19.0	6.5	1.1	0.4	1.0	0.8	1.1	0.3	-1.1	0.6	-1.0	1	1.1	0.6
IPI00872036	SEP10	septin-10 isoform 2	100.0%	4.6	2	2	2	5	1,665,290	1,809,228	1,714,699	1,801,507	99,137	126,698	145,427	51,979	13.3	15.7	19.0	6.5	1.1	0.4	1.0	0.8	1.1	0.3	-1.1	0.6	-1.0	1	1.1	0.6
IPI00873459	SEP10	Uncharacterized protein	100.0%	3.7	2	2	2	5	1,665,290	1,809,228	1,714,699	1,801,507	99,137	126,698	145,427	51,979	13.3	15.7	19.0	6.5	1.1	0.4	1.0	0.8	1.1	0.3	-1.1	0.6	-1.0	1	1.1	0.6
IPI00926875	SEP10	Uncharacterized protein	100.0%	4.2	2	2	2	5	1,665,290	1,809,228	1,714,699	1,801,507	99,137	126,698	145,427	51,979	13.3	15.7	19.0	6.5	1.1	0.4	1.0	0.8	1.1	0.3	-1.1	0.6	-1.0	1	1.1	0.6
IPI00927054	SEP10	Uncharacterized protein	100.0%	4.4	2	2	2	5	1,665,290	1,809,228	1,714,699	1,801,507	99,137	126,698	145,427	51,979	13.3	15.7	19.0	6.5	1.1	0.4	1.0	0.8	1.1	0.3	-1.1	0.6	-1.0	1	1.1	0.6
				LLEEEIIAFSK	2	100.0%	1																									
				VNIIPVIAK	2	99.2%	1																									
IPI00375127	EIF4H	Similar to mKIAA0038 protein	100.0%	11.6	2	2	2	1	6,065,350	6,703,880	4,265,615	5,873,750	754,303	701,523	500,628	643,333	27.8	23.4	26.2	24.5	1.1	0.6	-1.4	0.08	-1.0	0.9	-1.6	0.02	-1.1	0.4	1.4	0.08
				EALTYDGALLGDR	2	99.9%	1																									
				TVATPLNQVANPNSAIFGGAR	2	100.0%	1																									
IPI00375226	-	Similar to ribosomal protein L18	99.6%	5.8	1	1	1	1	24,043,500	24,038,700	23,801,600	26,933,000	2,006,979	1,039,801	1,589,425	1,249,758	18.7	9.7	14.9	10.4	-1.0	1	-1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.1	1.1	0.2
				NLTFDQLALDSPK	2	99.6%	1																									
IPI00411635	-	180 kDa protein	90.1%	1.4	2	2	2	6	4,807,563	4,988,133	4,858,547	5,769,567	548,946	192,502	363,313	253,806	25.5	8.6	16.7	9.8	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.8	1.2	0.04	1.2	0.07
IPI00375286	KIAA0802	isoform 4 of Uncharacterized protein KIAA0802	90.1%	2.3	2	2	2	6	4,807,563	4,988,133	4,858,547	5,769,567	548,946	192,502	363,313	253,806	25.5	8.6	16.7	9.8	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.8	1.2	0.04	1.2	0.07
IPI00477620	KIAA0802	isoform 3 of Uncharacterized protein KIAA0802	90.1%	1.4	2	2	2	6	4,807,563	4,988,133	4,858,547	5,769,567	548,946	192,502	363,313	253,806	25.5	8.6	16.7	9.8	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.8	1.2	0.04	1.2	0.07
IPI00792611	KIAA0802	isoform 1 of Uncharacterized protein KIAA0802	90.1%	1.2	2	2	2	6	4,807,563	4,988,133	4,858,547	5,769,567	548,946	192,502	363,313	253,806	25.5	8.6	16.7	9.8	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.8	1.2	0.04	1.2	0.07
IPI00794856	KIAA0802	Uncharacterized protein	90.1%	1.3	2	2	2	6	4,807,563	4,988,133	4,858,547	5,769,567	548,946	192,502	363,313	253,806	25.5	8.6	16.7	9.8	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.8	1.2	0.04	1.2	0.07
IPI00829780	KIAA0802	isoform 2 of Uncharacterized protein KIAA0802	90.1%	1.4	2	2	2	6	4,807,563	4,988,133	4,858,547	5,769,567	548,946	192,502	363,313	253,806	25.5	8.6	16.7	9.8	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.8	1.2	0.04	1.2	0.07
				AGGGATPVSSPSR	2	90.2%	1																									
				QNIFLFYVK	2	86.2%	1																									
IPI00375306	PRDX5	peroxiredoxin-5, mitochondrial isoform b precursor	100.0%	62.4	10	10	13	1	18,440,864	17,995,014	18,241,177	20,824,996	1,517,181	323,784	986,319	767,908	18.4	4.0	12.1	8.3	-1.0	0.8	-1.0	0.9	1.1	0.2	1.0	0.8	1.2	0.009	1.1	0.07
				ALNVEPDGTGLTCSLAPNIISQL	2	100.0%	1																									
				ETDLLLDDSLVSIFGNR	2	100.0%	1																									
				FSMVVQDGIVK	2	100.0%	2																									
				GVLFGVPGAFTPGCSK	2	100.0%	2																									
				KGVLFGVPGAFTPGCSK	2	99.5%	1																									
				LLADPTGAFGK	2	100.0%	1																									
				LLADPTGAFGKETDLLLDDSLVSIFGNR	3	89.3%	1																									
				RFSMVVQDGIVK	2	100.0%	1																									
				VGDAIPAVEVFEGEPGNK	2	100.0%	2																									
				VNLAELFK	2	100.0%	1																									
IPI00375370	SEC13	SEC13-like 1 isoform b variant	100.0%	19.1	4	5	6	5	8,404,892	7,860,423	9,211,279	8,622,017	314,900	541,461	427,380	394,637	8.4	15.4	10.4	10.2	-1.1	0.4	1.1	0.2	1.0	0.7	1.2	0.09	1.1	0.3	-1.1	0.3
IPI00479141	SEC13	Protein SEC13 homolog	100.0%	19.3	4	5	6	5	8,404,892	7,860,423	9,211,279	8,622,017	314,900	541,461	427,380	394,637	8.4	15.4	10.4	10.2	-1.1	0.4	1.1	0.2	1.0	0.7	1.2	0.09	1.1	0.3	-1.1	0.3
IPI00789755	SEC13	protein SEC13 homolog isoform 2	100.0%	20.1	4	5	6	5	8,404,892	7,860,423	9,211,279	8,622,017	314,900	541,461	427,380	394,637	8.4	15.4	10.4	10.2	-1.1	0.4	1.1	0.2	1.0	0.7	1.2	0.09	1.1	0.3	-1.1	0.3
IPI00845335	SEC13	Uncharacterized protein	100.0%	20.1	4	5	6	5	8,404,892	7,860,423	9,211,279	8,622,017	314,900	541,461	427,380	394,637	8.4	15.4	10.4	10.2	-1.1	0.4	1.1	0.2	1.0	0.7	1.2	0.09	1.1	0.3	-1.1	0.3
IPI00853598	SEC13	cDNA FLJ56334, highly similar to SEC13-related protein	100.0%	16.9	4	5	6	5	8,404,892	7,860,423	9,211,279	8,622,017	314,900	541,461	427,380	394,637	8.4	15.4	10.4	10.2	-1.1	0.4	1.1	0.2	1.0	0.7	1.2	0.09	1.1	0.3	-1.1	0.3
				DVAWAPSIGLPTSTIASCSQDGR	2	100.0%	1																									
				DVAWAPSIGLPTSTIASCSQDGR	3	94.5%	1																									
				FASGGCDNLIK	2	99.9%	2																									
				NGGQILIADLR	2	96.8%	1																									
				VFIWTCDDASSNTWSPK	2	100.0%	1																									
IPI00375380	PSMD13	isoform 2 of 26S proteasome non-ATPase regulatory subunit 13	100.0%	26.5	7	7	8	3	8,968,457	8,989,002	9,467,563	10,062,115	663,389	274,685	726,855	221,288	16.5	6.8	17.2	4.9	1.0	1	1.1	0.6	1.1	0.2	1.1	0.6	1.1	0.02	1.1	0.5
IPI00549672	PSMD13	HSPC027	100.0%	26.5	7	7	8	3	8,968,457	8,989,002	9,467,563	10,062,115	663,389	274,685	726,855	221,288	16.5	6.8	17.2	4.9	1.0	1	1.1	0.6	1.1	0.2	1.1	0.6	1.1	0.02	1.1	0.5
IPI01011099	PSMD13	cDNA FLJ53046, highly similar to 26S proteasome non-ATPase regulatory subunit 1	100.0%	32.2	7	7	8	3	8,968,457	8,989,002	9,467,563	10,062,115	663,389	274,685	726,855	221,288	16.5	6.8	17.2	4.9	1.0	1	1.1	0.6	1.1	0.2	1.1	0.6	1.1	0.02	1.1	0.5
				ETIEDVEEMLNNLPGVTSVHSR	3	99.9%	1																									
				FLGCVDIKDLPVSEQQER	3	96.0%	1																									
				ITVNEVELLVMK	2	100.0%	2																									
				LNIGDLQVTK	2	93.1%	1																									
				QWLIDTLYAFNSGNVER	2	100.0%	1																									
				VLDLQQIK	2	98.1%	1																									
				YYQTIGNHASYYK	2	99.8%	1																									
IPI00375391	EIF6	eukaryotic translation initiation factor 6 isoform c	100.0%	23.0	3	4	5	1	6,583,274	7,037,595	6,354,395	7,574,480	526,912	523,807	630,991	291,849	17.9	16.6	22.2	8.6	1.1	0.6	-1.0	0.8	1.2	0.1	-1.1	0.4	1.1	0.4	1.2	0.1
				ASFENNCEIGCFAK	2	100.0%	1																									
				LNEAQPSTIATSMR	2	100.0%	1																									
				TSIEDQDELSSLLQVPLVAGTVNR	2	100.0%	2																									
				TSIEDQDELSSLLQVPLVAGTVNR	3	99.9%	1																									
IPI00375441	FUBP1	isoform 1 of Far upstream element-binding protein 1	100.0%	24.1	13	13	15	5	15,125,618	15,419,459	14,998,914	17,260,150	978,076	518,869	780,573	601,069	14.5	7.5	11.6	7.8	1.0	0.8	-1.0	0.9	1.1	0.1	-1.0	0.7	1.1	0.05	1.2	0.05
IPI00641948	FUBP1	Uncharacterized protein	100.0%	23.3	13	13	15	5	15,125,618	15,419,459	14,998,914	17,260,150	978,076	518,869	780,573	601,069	14.5	7.5	11.6	7.8	1.0	0.8	-1.0	0.9	1.1	0.1	-1.0	0.7	1.1	0.05	1.2	0.05
IPI00644386	FUBP1	Uncharacterized protein	100.0%	23.7	13	13	15	5	15,125,618	15,419,459	14,998,914	17,260,150	978,076	518,869	780,573	601,069	14.5	7.5	11.6	7.8	1.0	0.8	-1.0	0.9	1.1	0.1	-1.0	0.7	1.1	0.05	1.2	0.05
IPI00853059	FUBP1	Uncharacterized protein	100.0%	23.7	13	13	15	5	15,125,618	15,419,459	14,998,914	17,260,150	978,076	518,869	780,573	601,069	14.5	7.5	11.6	7.8	1.0	0.8	-1.0	0.9	1.1	0.1	-1.0	0.7	1.1	0.05	1.2	0.05
IPI00983652	FUBP1	cDNA FLJ61021, highly similar to Far upstream element-binding protein 1	100.0%	24.6	13	13	15	5	15,125,618	15,419,459	14,998,914	17,260,150	978,076	518,869	780,573	601,069	14.5	7.5	11.6	7.8	1.0	0.8	-1.0	0.9	1.1	0.1	-1.0	0.7	1.1	0.05	1.2	0.05
				FAVGIVIGR	2	99.8%	1																									
				GTPQQIDYAR	2	99.8%	1																									
				IAQITGPPDR	2	81.2%	1																									
				IGGDAGTSLNSNDYGYGGQK	2	100.0%	1																									
				IGGNEGIDVPIPR	2	100.0%	2																									
				IQIAPDSGGLPER	2	99.9%	2																									
				MVMIQDGPQNTGADKPLR	3	100.0%	1																									
				NPPPNADPNMK	2	85.6%	1																									
				RLLDQIVEK	2	86.8%	1																									
				SCMLTGTPESVQSAK	2	100.0%	1																									
				SVMTEEYKVPDGMVGFIIGR	3	100.0%	1																									
				TGLIIGK	2	99.3%	1																									
				VPDGMVGFIIGR	2	97.8%	1																									
IPI00375462	SREK1	isoform 2 of Splicing regulatory glutamine/lysine-rich protein 1	99.4%	5.6	2	2	3	2	1,377,272	1,124,466	1,640,333	1,635,736	84,126	217,191	130,117	150,698	13.7	43.2	17.7	20.6	-1.2	0.3	1.2	0.1	1.2	0.2	1.5	0.08	1.5	0.09	-1.0	1
IPI01010042	SREK1	cDNA FLJ34439 fis, clone HLUNG2001146, highly similar to Splicing factor, arginine	99.4%	6.8	2	2	3	2	1,377,272	1,124,466	1,640,333	1,635,736	84,126	217,191	130,117	150,698	13.7	43.2	17.7	20.6	-1.2	0.3	1.2	0.1	1.2	0.2	1.5	0.08	1.5	0.09	-1.0	1
				TLFSFLGEIEELR	2	99.4%	2																									
				TVYVGNLNSQTTTADQLLEFFK	2	97.7%	1																									
IPI00375496	JMJD6	isoform 2 of Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6	90.4%	3.5	1	1	1	5	630,538	712,388	636,808	707,430	76,885	103,689	67,701	23,665	27.3	32.6	23.8	7.5	1.1	0.5	1.0	1	1.1	0.4	-1.1	0.6	-1.0	1	1.1	0.4
IPI00550958	JMJD6	isoform 1 of Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6	90.4%	3.2	1	1	1	5	630,538	712,388	636,808	707,430	76,885	103,689	67,701	23,665	27.3	32.6	23.8	7.5	1.1	0.5	1.0	1	1.1	0.4	-1.1	0.6	-1.0	1	1.1	0.4
IPI00604598	JMJD6	isoform 3 of Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6	90.4%	3.1	1	1	1	5	630,538	712,388	636,808	707,430	76,885	103,689	67,701	23,665	27.3	32.6	23.8	7.5	1.1	0.5	1.0	1	1.1	0.4	-1.1	0.6	-1.0	1	1.1	0.4
IPI00896458	JMJD6	Phosphatidylserine receptor transcript variant 2	90.4%	3.6	1	1	1	5	630,538	712,388	636,808	707,430	76,885	103,689	67,701	23,665	27.3	32.6	23.8	7.5	1.1	0.5	1.0	1	1.1	0.4	-1.1	0.6	-1.0	1	1.1	0.4
IPI01015282	JMJD6	Phosphatidylserine receptor, isoform CRA_d	90.4%	3.9	1	1	1	5	630,538	712,388	636,808	707,430	76,885	103,689	67,701	23,665	27.3	32.6	23.8	7.5	1.1	0.5	1.0	1	1.1	0.4	-1.1	0.6	-1.0	1	1.1	0.4
				FFTDDLFQYAGEK	2	90.4%	1																									
IPI00375498	TTN	titin isoform novex-1	99.8%	0.3	6	6	6	3	1,793,092	1,841,862	1,954,208	2,062,054	101,679	110,780	115,217	70,267	12.7	13.5	13.2	7.6	1.0	0.8	1.1	0.3	1.1	0.06	1.1	0.5	1.1	0.1	1.1	0.4
IPI00375499	TTN	titin isoform novex-2	99.8%	0.3	6	6	6	3	1,793,092	1,841,862	1,954,208	2,062,054	101,679	110,780	115,217	70,267	12.7	13.5	13.2	7.6	1.0	0.8	1.1	0.3	1.1	0.06	1.1	0.5	1.1	0.1	1.1	0.4
IPI00985334	TTN	isoform 3 of Titin	99.8%	0.3	6	6	6	3	1,793,092	1,841,862	1,954,208	2,062,054	101,679	110,780	115,217	70,267	12.7	13.5	13.2	7.6	1.0	0.8	1.1	0.3	1.1	0.06	1.1	0.5	1.1	0.1	1.1	0.4
				AEDLSATVTDVVEGQEYSFR	3	97.1%	1																									
				ITQFLKAEASKEIAK	2	84.0%	1																									
				MPDDDGGDR	1	92.2%	1																									
				STVTIVDSKR	2	89.8%	1																									
				VNTEDHQGEYVCEALNDSGK	3	87.7%	1																									
				YLISTEEVSYFNVQSR	3	85.6%	1																									
IPI00375631	ISG15	Ubiquitin-like protein ISG15	99.4%	17.6	2	2	2	1	8,968,410	8,611,830	8,424,720	9,712,320	768,377	260,489	544,518	727,182	19.2	6.8	14.5	16.7	-1.0	0.7	-1.1	0.6	1.1	0.5	-1.0	0.8	1.1	0.2	1.2	0.2
				IGVHAFQQR	2	92.5%	1																									
				VPLASQGLGPGSTVLLVVDK	2	99.4%	1																									
IPI00376005	EIF5A	isoform 2 of Eukaryotic translation initiation factor 5A-1	100.0%	46.7	8	10	15	2	43,558,996	44,432,684	47,450,405	50,266,938	3,545,999	2,820,115	4,033,275	1,740,124	18.2	14.2	19.0	7.7	1.0	0.9	1.1	0.5	1.2	0.1	1.1	0.6	1.1	0.1	1.1	0.5
IPI00411704	EIF5A	isoform 1 of Eukaryotic translation initiation factor 5A-1	100.0%	55.8	8	10	15	2	43,558,996	44,432,684	47,450,405	50,266,938	3,545,999	2,820,115	4,033,275	1,740,124	18.2	14.2	19.0	7.7	1.0	0.9	1.1	0.5	1.2	0.1	1.1	0.6	1.1	0.1	1.1	0.5
				EDLRLPEGDLGKEIEQK	3	100.0%	2																									
				IVEMSTSK	1	98.3%	1																									
				IVEMSTSK	2	100.0%	1																									
				KYEDICPSTHNMDVPNIK	3	100.0%	1																									
				NDFQLIGIQDGYLSLLQDSGEVR	2	100.0%	2																									
				NDFQLIGIQDGYLSLLQDSGEVR	3	100.0%	1																									
				NGFVVLK	2	100.0%	3																									
				RNDFQLIGIQDGYLSLLQDSGEVR	3	100.0%	1																									
				VHLVGIDIFTGK	2	100.0%	2																									
				YEDICPSTHNMDVPNIK	3	99.9%	1																									
IPI00376164	TMSB4XP2	Similar to Thymosin beta-4	100.0%	27.3	1	1	2	1	544,489	544,530	576,759	596,157	49,161	42,391	55,712	47,395	20.2	17.4	21.6	17.8	1.0	1	1.1	0.7	1.1	0.5	1.1	0.7	1.1	0.4	1.0	0.8
				TETQEKNPLPSK	2	100.0%	2																									
IPI00376199	IRF2BP2	isoform 1 of Interferon regulatory factor 2-binding protein 2	99.3%	2.6	1	1	1	2	640,989	628,115	644,628	895,706	101,559	128,785	171,165	126,001	35.4	45.9	59.4	31.5	-1.0	0.9	1.0	1	1.4	0.2	1.0	0.9	1.4	0.2	1.4	0.3
IPI00889619	IRF2BP2	isoform 2 of Interferon regulatory factor 2-binding protein 2	99.3%	2.6	1	1	1	2	640,989	628,115	644,628	895,706	101,559	128,785	171,165	126,001	35.4	45.9	59.4	31.5	-1.0	0.9	1.0	1	1.4	0.2	1.0	0.9	1.4	0.2	1.4	0.3
				MPWAMIWDFTEPVCR	2	99.3%	1																									
IPI00376268	ZNF326	isoform 2 of Zinc finger protein 326	98.3%	32.9	1	1	1	1	555,380	598,553	628,227	628,347	37,590	33,754	53,931	72,305	15.1	12.6	19.2	25.7	1.1	0.4	1.1	0.3	1.1	0.4	1.0	0.7	1.0	0.7	1.0	1
				SMDSYLNQSYGMDNHSGGGGGSR	3	98.3%	1																									
IPI00376317	EDC4	isoform 1 of Enhancer of mRNA-decapping protein 4	100.0%	6.4	5	5	5	2	17,349,089	17,331,635	17,229,827	19,597,010	1,098,295	695,366	862,061	723,494	14.2	9.0	11.2	8.3	-1.0	1	-1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.05	1.1	0.07
IPI00641449	EDC4	isoform 2 of Enhancer of mRNA-decapping protein 4	100.0%	7.9	5	5	5	2	17,349,089	17,331,635	17,229,827	19,597,010	1,098,295	695,366	862,061	723,494	14.2	9.0	11.2	8.3	-1.0	1	-1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.05	1.1	0.07
				DHMGSVMAQVR	2	90.9%	1																									
				EQQAAVTSSIMQAMR	2	99.9%	1																									
				GGQLQEQLTQQLSQALSSAVAGR	2	99.5%	1																									
				LGTQEYLQQLESHMK	3	98.7%	1																									
				SLEPMAGQLSNSVATKLTAVEGSMK	3	95.2%	1																									
IPI00376344	MYO1B	isoform 1 of Myosin-Ib	100.0%	2.4	2	2	3	3	1,208,723	1,395,025	1,248,938	1,387,806	148,392	132,461	106,400	88,016	27.5	21.2	19.1	14.2	1.2	0.4	1.0	0.8	1.1	0.3	-1.1	0.4	-1.0	1	1.1	0.3
IPI00414980	MYO1B	isoform 2 of Myosin-Ib	100.0%	2.5	2	2	3	3	1,208,723	1,395,025	1,248,938	1,387,806	148,392	132,461	106,400	88,016	27.5	21.2	19.1	14.2	1.2	0.4	1.0	0.8	1.1	0.3	-1.1	0.4	-1.0	1	1.1	0.3
IPI00795618	MYO1B	Uncharacterized protein	100.0%	2.4	2	2	3	3	1,208,723	1,395,025	1,248,938	1,387,806	148,392	132,461	106,400	88,016	27.5	21.2	19.1	14.2	1.2	0.4	1.0	0.8	1.1	0.3	-1.1	0.4	-1.0	1	1.1	0.3
				LLQSNPVLEAFGNAK	2	100.0%	2																									
				LVMSYVAAVCGK	2	95.7%	1																									
IPI00376379	KRT77	Keratin, type II cytoskeletal 1b	98.0%	4.7	3	3	3	1	37,439,100	41,387,120	38,870,480	45,489,870	2,868,544	2,692,731	2,174,172	1,992,814	17.1	14.6	12.5	9.8	1.1	0.3	1.0	0.7	1.2	0.05	-1.1	0.5	1.1	0.3	1.2	0.06
				LQAEISNVK	2	86.9%	1																									
				QLLEGEESR	2	88.9%	1																									
				SLYNLGGSR	2	98.0%	1																									
IPI00376503	PYCR1	pyrroline-5-carboxylate reductase 1, mitochondrial isoform 2	100.0%	10.8	3	3	5	3	5,399,430	5,601,874	5,527,385	6,095,600	508,769	279,519	375,827	292,792	21.1	11.2	15.2	10.7	1.0	0.7	1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.3	1.1	0.3
IPI00550882	PYCR1	Pyrroline-5-carboxylate reductase	100.0%	9.8	3	3	5	3	5,399,430	5,601,874	5,527,385	6,095,600	508,769	279,519	375,827	292,792	21.1	11.2	15.2	10.7	1.0	0.7	1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.3	1.1	0.3
IPI00941557	PYCR1	Pyrroline-5-carboxylate reductase 1, mitochondrial	100.0%	10.7	3	3	5	3	5,399,430	5,601,874	5,527,385	6,095,600	508,769	279,519	375,827	292,792	21.1	11.2	15.2	10.7	1.0	0.7	1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.3	1.1	0.3
				CMTNTPVVVR	2	86.3%	1																									
				LGAQALLGAAK	2	100.0%	2																									
				SLLINAVEASCIR	2	100.0%	2																									
IPI00376572	LOC391722	calcium-dependent protein kinase 7-like	100.0%	10.9	3	4	6	2	3,523,533	3,592,432	3,319,059	3,963,970	263,626	139,778	192,060	111,421	16.7	8.7	12.9	6.3	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.07	1.2	0.02
IPI00888438	LOC391722	calcium-dependent protein kinase 7-like	100.0%	10.9	3	4	6	2	3,523,533	3,592,432	3,319,059	3,963,970	263,626	139,778	192,060	111,421	16.7	8.7	12.9	6.3	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.07	1.2	0.02
				EAFNMIDQNR	2	100.0%	2																									
				LNGTDPEDVIR	2	100.0%	2																									

				NAFACFDEEATGTIQEDYLR	2	100.0%	1																									
				NAFACFDEEATGTIQEDYLR	3	100.0%	1																									
IPI00376798	RPL11	isoform 1 of 60S ribosomal protein L11	100.0%	20.2	3	3	4	2	8,839,461	8,933,452	8,766,469	10,151,789	815,648	354,952	783,783	536,583	20.6	8.9	20.0	11.8	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.9	1.1	0.09	1.2	0.2
IPI00746438	RPL11	isoform 2 of 60S ribosomal protein L11	100.0%	20.3	3	3	4	2	8,839,461	8,933,452	8,766,469	10,151,789	815,648	354,952	783,783	536,583	20.6	8.9	20.0	11.8	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.9	1.1	0.09	1.2	0.2
				LCLNICVGESGDR	2	99.9%	1																									
				VLEQLTGQTPVFSK	2	99.8%	2																									
				YDGIILPGK	2	100.0%	1																									
IPI00376844	UBE2NL	Putative ubiquitin-conjugating enzyme E2 N-like	100.0%	19.0	3	3	4	1	15,895,995	14,849,770	17,462,065	16,603,585	399,420	656,775	337,069	275,386	5.6	9.9	4.3	3.7	-1.1	0.2	1.1	0.02	1.0	0.2	1.2	0.008	1.1	0.04	-1.1	0.08
				LLAEPVPGIK	2	98.4%	1																									
				TNEAQAIETAR	2	100.0%	2																									
				WSPALQIR	2	99.8%	1																									
IPI00376904	NSFL1C	isoform 4 of NSFL1 cofactor p47	100.0%	28.6	6	6	6	1	9,078,240	9,755,443	9,074,554	11,040,227	710,810	297,406	746,883	431,948	17.5	6.8	18.4	8.8	1.1	0.4	-1.0	1	1.2	0.05	-1.1	0.4	1.1	0.04	1.2	0.05
				ASSSILIDESEPTTNIQIR	2	100.0%	1																									
				EANLLNAVIVQR	2	100.0%	1																									
				LGAAPEEESAYVAGEK	2	99.9%	1																									
				LGAAPEEESAYVAGEKR	3	100.0%	1																									
				SGFSLDNGELR	2	99.9%	1																									
				SYQDPSNAQFLESIR	2	99.5%	1																									
IPI00377187	AKNA	isoform 1 of AT-hook-containing transcription factor	92.3%	0.8	1	1	1	5	684,558	784,602	825,660	854,542	28,636	55,326	68,440	84,835	9.4	15.8	18.5	22.2	1.1	0.1	1.2	0.09	1.2	0.1	1.1	0.7	1.1	0.5	1.0	0.8
IPI00477282	AKNA	isoform 3 of AT-hook-containing transcription factor	92.3%	1.4	1	1	1	5	684,558	784,602	825,660	854,542	28,636	55,326	68,440	84,835	9.4	15.8	18.5	22.2	1.1	0.1	1.2	0.09	1.2	0.1	1.1	0.7	1.1	0.5	1.0	0.8
IPI00657833	AKNA	isoform 2 of AT-hook-containing transcription factor	92.3%	0.9	1	1	1	5	684,558	784,602	825,660	854,542	28,636	55,326	68,440	84,835	9.4	15.8	18.5	22.2	1.1	0.1	1.2	0.09	1.2	0.1	1.1	0.7	1.1	0.5	1.0	0.8
IPI00792192	AKNA	AKNA transcript C1 (Fragment)	92.3%	1.8	1	1	1	5	684,558	784,602	825,660	854,542	28,636	55,326	68,440	84,835	9.4	15.8	18.5	22.2	1.1	0.1	1.2	0.09	1.2	0.1	1.1	0.7	1.1	0.5	1.0	0.8
IPI00847998	AKNA	isoform 7 of AT-hook-containing transcription factor	92.3%	0.9	1	1	1	5	684,558	784,602	825,660	854,542	28,636	55,326	68,440	84,835	9.4	15.8	18.5	22.2	1.1	0.1	1.2	0.09	1.2	0.1	1.1	0.7	1.1	0.5	1.0	0.8
				YAEAENTIDQLR	2	89.5%	1																									
IPI00377214	NLRX1	isoform 2 of NLR family member X1	96.8%	2.4	1	1	1	2	4,377,060	4,798,340	3,975,045	5,444,430	924,236	554,465	679,266	319,326	47.2	25.8	38.2	13.1	1.1	0.7	-1.1	0.7	1.2	0.3	-1.2	0.4	1.1	0.3	1.4	0.09
IPI00465264	NLRX1	isoform 1 of NLR family member X1	96.8%	2.3	1	1	1	2	4,377,060	4,798,340	3,975,045	5,444,430	924,236	554,465	679,266	319,326	47.2	25.8	38.2	13.1	1.1	0.7	-1.1	0.7	1.2	0.3	-1.2	0.4	1.1	0.3	1.4	0.09
				QLQELNVAYNGAGDTAALALAR	2	95.9%	1																									
IPI00382462	RAB18	PNAS-32	99.5%	27.1	1	1	1	2	247,595	259,183	237,410	242,883	23,459	18,352	16,101	11,757	21.2	15.8	15.2	10.8	1.0	0.7	-1.0	0.7	-1.0	0.9	-1.1	0.4	-1.1	0.5	1.0	0.8
IPI00922800	RAB18	cDNA FLJ50154, moderately similar to Ras-related protein Rab-18	99.5%	13.4	1	1	1	2	247,595	259,183	237,410	242,883	23,459	18,352	16,101	11,757	21.2	15.8	15.2	10.8	1.0	0.7	-1.0	0.7	-1.0	0.9	-1.1	0.4	-1.1	0.5	1.0	0.8
				FTDDTFDPELAATIGVDFK	2	99.3%	1																									
IPI00382470	HSP90AA1	isoform 2 of Heat shock protein HSP 90-alpha	100.0%	30.7	25	28	43	2	109,037,440	113,333,113	104,546,845	126,360,818	9,323,216	4,131,919	7,011,889	4,400,665	19.1	8.2	15.0	7.8	1.0	0.7	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.06	1.2	0.03
IPI00784295	HSP90AA1	isoform 1 of Heat shock protein HSP 90-alpha	100.0%	35.8	25	28	43	2	109,037,440	113,333,113	104,546,845	126,360,818	9,323,216	4,131,919	7,011,889	4,400,665	19.1	8.2	15.0	7.8	1.0	0.7	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.06	1.2	0.03
				ADLINNLGTIAK	2	100.0%	2																									
				APFDLFENR	2	100.0%	1																									
				DNSTMGYMAAK	2	100.0%	2																									
				DQVANSAFVER	2	100.0%	2																									
				EDQTEYLEER	2	100.0%	1																									
				EGLELPEDEEEKKK	2	92.9%	1																									
				EKYIDQEELNK	2	99.0%	1																									
				ELHINLIPNKQDR	3	87.4%	1																									
				ELISNSSDALDK	2	100.0%	2																									
				ELISNSSDALDKIR	2	100.0%	2																									
				FYEQFSK	2	99.7%	1																									
				GVVDSEDLPLNISR	2	99.0%	1																									
				HFSVEGQLEFR	2	100.0%	1																									
				HLEINPDHSIIETLR	3	100.0%	2																									
				HSQFIGYPITLFVEK	2	100.0%	2																									
				HSQFIGYPITLFVEK	3	100.0%	1																									
				KHLEINPDHSIIETLR	3	100.0%	1																									
				LVTSPCCIVTSTYGWTANMER	2	100.0%	1																									
				NPDDITNEEYGEFYK	2	100.0%	2																									
				RAPFDLFENR	2	100.0%	2																									
				SLTNDWEDHLAVK	2	100.0%	2																									
				SLTNDWEDHLAVK	3	100.0%	2																									
				VFIMDNCEELIPEYLNFIR	2	100.0%	1																									
				VILHLKEDQTEYLEER	3	100.0%	2																									
				YIDQEELNK	1	100.0%	1																									
				YIDQEELNK	2	100.0%	2																									
				YYTSASGDEMVSLK	2	100.0%	2																									
				YYTSASGDEMVSLKDYCTR	3	100.0%	2																									
IPI00382501	-	Ig heavy chain V-III region DOB	99.0%	18.3	1	1	1	1	4,083,060	3,862,430	4,464,090	4,232,660	355,514	319,167	368,393	381,947	19.5	18.5	18.5	20.2	-1.1	0.7	1.1	0.5	1.0	0.8	1.2	0.3	1.1	0.5	-1.1	0.7
				SLRLSCAASGFNFHEYNMHWLR	3	99.0%	1																									
IPI00382697	FLNB	isoform 3 of Filamin-B	100.0%	24.5	45	49	61	2	44,865,169	46,597,802	43,905,698	51,380,545	4,126,777	1,895,935	2,662,348	1,005,104	20.6	9.1	13.6	4.4	1.0	0.7	-1.0	0.8	1.1	0.2	-1.1	0.4	1.1	0.06	1.2	0.05
IPI00953109	FLNB	isoform 6 of Filamin-B	100.0%	24.8	45	49	61	2	44,865,169	46,597,802	43,905,698	51,380,545	4,126,777	1,895,935	2,662,348	1,005,104	20.6	9.1	13.6	4.4	1.0	0.7	-1.0	0.8	1.1	0.2	-1.1	0.4	1.1	0.06	1.2	0.05
				AAGSGELGVTMK	2	100.0%	1																									
				ADIEMPFDPSK	2	97.7%	1																									
				AGLAPLEVR	2	99.9%	1																									
				AGPGTLSVTIEGPSK	2	100.0%	2																									
				AWGPGLHGGIVGR	2	99.9%	1																									
				CLATGPGIASTVK	2	99.9%	1																									
				DAGEGLLAVQITDQEGKPK	3	100.0%	1																									
				DAGYGGISLAVEGPSK	2	100.0%	2																									
				DGTYAVTYIPDK	2	99.5%	1																									
				DLDIIDNYDYSHTVK	3	99.8%	1																									
				EAGAGGLSIAVEGPSK	2	100.0%	2																									
				EATTDFTVDSRPLTQVGGDHIK	3	100.0%	1																									
				FNGSHVVGSPFK	2	97.1%	1																									
				FNGSHVVGSPFK	3	96.8%	1																									
				GAGIGGLGITVEGPSESK	2	100.0%	2																									
				GAGTGGLGLTVEGPCEAK	2	100.0%	1																									
				GLHVVEVTYDDVPIPNSPFK	3	99.8%	1																									
				IFFAGDTIPK	2	98.6%	1																									
				IGNLQTDLSDGLR	2	100.0%	2																									
				IKVFGPGIEGK	3	99.8%	1																									
				IPYLPITNFNQNWQDGK	2	100.0%	2																									
				IPYLPITNFNQNWQDGK	3	100.0%	1																									
				LIALLEVLSQK	2	100.0%	2																									
				LLGWIQNK	2	98.6%	1																									
				LTVMSLQESGLK	2	100.0%	2																									
				LVSPGSANETSSILVESVTR	2	100.0%	2																									
				MDGTYACSYTPVK	2	100.0%	1																									
				NTVELLVEDKGNQVYR	3	99.9%	1																									
				QMQLENVSVALEFLDRESIK	3	99.2%	1																									
				SGCIVNNLAEFTVDPK	2	100.0%	1																									
				SPFEVQVGPEAGMQK	2	100.0%	2																									
				SPFEVSVDK	2	99.9%	1																									
				TFEMSDFIVDTR	2	100.0%	1																									
				VAVTEGCQPSR	2	100.0%	1																									
				VEVGKDQEFTVDTR	2	99.5%	1																									
				VLFASQEIPASPFR	2	100.0%	1																									
				VLQSFTVDSSK	2	99.9%	1																									
				VNQPASFAIR	2	91.6%	1																									
				VPVKDVVDPSK	3	89.9%	1																									
				VQAQGPGLK	1	97.7%	1																									
				VTASGPGLSSYGVPASLPVDFAIDAR	2	100.0%	2																									
				VTEAEIVPMGK	2	100.0%	1																									
				VTVLFAGQHISK	2	95.5%	1																									
				VTVLFAGQHISK	3	97.6%	1																									
				VVASGPGLEHGK	2	99.9%	1																									
				YGGELVPHFPAR	2	100.0%	1																									
				YGGELVPHFPAR	3	100.0%	1																									
				YGGPNHIVGSPFK	2	100.0%	2																									
				YMIGVTYGGDDIPLSPYR	2	100.0%	1																									
IPI00382703	ACP1	Protein-tyrosine-phosphatase, isoform 3	100.0%	16.4	1	1	1	1	5,482,525	7,126,900	5,815,200	9,545,800	1,524,395	939,540	535,217	714,926	62.2	29.5	20.6	16.8	1.3	0.4	1.1	0.8	1.7	0.04	-1.2	0.3	1.3	0.07	1.6	0.003
				LVTDQNISENWR	2	100.0%	1																									
IPI00382746	GALM	Ibd1 protein (Fragment)	100.0%	15.7	2	2	3	2	2,121,185	2,114,820	2,212,290	2,239,940	306,503	250,467	206,408	234,518	32.3	26.5	20.9	23.4	-1.0	1	1.0	0.8	1.1	0.8	1.0	0.8	1.1	0.7	1.0	0.9
IPI00916994	GALM	16 kDa protein	100.0%	22.2	2	2	3	2	2,121,185	2,114,820	2,212,290	2,239,940	306,503	250,467	206,408	234,518	32.3	26.5	20.9	23.4	-1.0	1	1.0	0.8	1.1	0.8	1.0	0.8	1.1	0.7	1.0	0.9
				ASDVVLGFAELEGYLQK	2	100.0%	1																									
				AVFGELPSGGGTVEK	2	99.3%	2																									
IPI00382844	ACO2	Aconitase (Fragment)	100.0%	2.5	1	1	1	3	521,700	494,307	455,748	506,368	61,024	27,905	23,248	24,516	26.2	12.6	11.4	10.8	-1.1	0.7	-1.1	0.4	-1.0	0.8	-1.1	0.3	1.0	0.8	1.1	0.2
IPI00909879	ACO2	cDNA FLJ50886, highly similar to Aconitate hydratase, mitochondrial	100.0%	3.1	1	1	1	3	521,700	494,307	455,748	506,368	61,024	27,905	23,248	24,516	26.2	12.6	11.4	10.8	-1.1	0.7	-1.1	0.4	-1.0	0.8	-1.1	0.3	1.0	0.8	1.1	0.2
IPI01009581	ACO2	cDNA FLJ60429, highly similar to Aconitate hydratase, mitochondrial	100.0%	3.0	1	1	1	3	521,700	494,307	455,748	506,368	61,024	27,905	23,248	24,516	26.2	12.6	11.4	10.8	-1.1	0.7	-1.1	0.4	-1.0	0.8	-1.1	0.3	1.0	0.8	1.1	0.2
				NAVTQEFGPVPDTAR	2	99.9%	1																									
IPI00382869	FDPS	Farnesyl pyrophosphate synthetase like-4 protein (Fragment)	93.5%	3.5	1	1	1	1	1,749,060	1,755,528	1,716,125	1,978,923	168,987	109,227	177,555	118,610	21.6	13.9	23.1	13.4	1.0	1	-1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.2	1.2	0.3
				QDFVQHFSQIVR	3	93.5%	1																									
IPI00382958	MTAP	MTAP protein	100.0%	22.7	2	2	2	2	10,687,483	10,896,815	9,985,394	12,194,744	1,022,564	363,676	959,561	548,138	21.4	7.5	21.5	10.1	1.0	0.9	-1.1	0.6	1.1	0.2	-1.1	0.4	1.1	0.08	1.2	0.08
IPI00903024	MTAP	16 kDa protein	100.0%	24.5	2	2	2	2	10,687,483	10,896,815	9,985,394	12,194,744	1,022,564	363,676	959,561	548,138	21.4	7.5	21.5	10.1	1.0	0.9	-1.1	0.6	1.1	0.2	-1.1	0.4	1.1	0.08	1.2	0.08
				IGIIGGTGLDDPEILEGR	2	100.0%	1																									
				YVDTPFGKPSDALILGK	3	99.4%	1																									
IPI00383046	CMBL	Carboxymethylenebutenolidase homolog	100.0%	15.1	3	4	4	1	16,200,740	16,111,113	18,223,870	18,631,776	2,361,758	2,201,043	1,998,111	1,235,209	32.6	30.6	24.5	14.8	-1.0	1	1.1	0.5	1.2	0.4	1.1	0.5	1.2	0.3	1.0	0.9
				AVIVIQDIFGWQLPNTR	2	100.0%	1																									
				AVIVIQDIFGWQLPNTR	3	100.0%	1																									
				EVQVEHIK	2	99.8%	1																									
				TFSGQTHGFVHR	2	99.9%	1																									
IPI00383227	CANX	Calnexin (Fragment)	100.0%	9.6	2	2	3	6	1,053,749	1,078,470	1,094,940	1,187,900	115,288	49,468	102,579	63,229	24.5	10.3	21.0	11.9	1.0	0.8	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.5
IPI00477719	CANX	32 kDa protein	100.0%	9.2	2	2	3	6	1,053,749	1,078,470	1,094,940	1,187,900	115,288	49,468	102,579	63,229	24.5	10.3	21.0	11.9	1.0	0.8	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.5
IPI00964541	CANX	Uncharacterized protein	100.0%	18.1	2	2	3	6	1,053,749	1,078,470	1,094,940	1,187,900	115,288	49,468	102,579	63,229	24.5	10.3	21.0	11.9	1.0	0.8	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.5
IPI00964865	CANX	Uncharacterized protein	100.0%	15.5	2	2	3	6	1,053,749	1,078,470	1,094,940	1,187,900	115,288	49,468	102,579	63,229	24.5	10.3	21.0	11.9	1.0	0.8	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.5
IPI00965725	CANX	Uncharacterized protein	100.0%	24.3	2	2	3	6	1,053,749	1,078,470	1,094,940	1,187,900	115,288	49,468	102,579	63,229	24.5	10.3	21.0	11.9	1.0	0.8	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.5
IPI00967621	CANX	Uncharacterized protein	100.0%	19.4	2	2	3	6	1,053,749	1,078,470	1,094,940	1,187,900	115,288	49,468	102,579	63,229	24.5	10.3	21.0	11.9	1.0	0.8	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.2	1.1	0.5
				APVPTGEVYFADSFDR	2	100.0%	2																									
				GTLSGWILSK	2	100.0%	1																									
IPI00383283	KIAA1984	Putative uncharacterized protein pp8875	100.0%	5.8	1	1	2	1	137,114	134,071	166,338	183,635	14,385	5,514	23,505	24,760	23.5	9.2	31.6	30.2	-1.0	0.9	1.2	0.3	1.3	0.1	1.2	0.2	1.4	0.1	1.1	0.6
				FFNIPFLQLQR	2	100.0%	2																									
IPI00383290	LARS	HSPC192	100.0%	6.9	1	1	2	1	818,330	850,095	793,530	996,628	38,066	81,906	93,878	72,752	10.4	21.5	26.5	16.3	1.0	0.7	-1.0	0.8	1.2	0.06	-1.1	0.7	1.2	0.2	1.3	0.1
				VFEVNASNLEK	2	100.0%	2																									
IPI00383971	PSMB5	proteasome subunit beta type-5 isoform 3	100.0%	18.2	2	2	2	1	2,057,936	2,263,166	1,883,439	2,400,634	328,122	169,549	147,297	156,541	35.7	16.8	17.5	14.6	1.1	0.6	-1.1	0.6	1.2	0.4	-1.2	0.1	1.1	0.6	1.3	0.04

				ATAGAYIASQTVK	2	100.0%	1																									
				VIEINPYLLGTMAGGAADCSFWER	2	99.8%	1																									
IPI01011871	-	cDNA FLJ55035, highly similar to Dihydrolipoyllysine-residue succinyltransferase co	100.0%	8.4	1	1	1	2	844,907	947,397	839,397	983,723	61,319	73,015	93,669	34,652	16.2	17.2	25.0	7.9	1.1	0.3	-1.0	1	1.2	0.08	-1.1	0.4	1.0	0.7	1.2	0.2
IPI00384016	DLSTP1;DLST	Full-length cDNA 5-PRIME end of clone CS0DJ009YL13 of T cells (Jurkat cell line)	100.0%	5.0	1	1	1	2	844,907	947,397	839,397	983,723	61,319	73,015	93,669	34,652	16.2	17.2	25.0	7.9	1.1	0.3	-1.0	1	1.2	0.08	-1.1	0.4	1.0	0.7	1.2	0.2
				TPAFAESVTEGDVR	2	100.0%	1																									
IPI00384104	TNKS1BP1	TNKS1BP1 protein (Fragment)	100.0%	9.3	2	2	2	1	5,080,315	5,022,760	5,173,040	5,107,620	242,491	231,817	283,756	253,268	10.7	10.3	12.3	11.1	-1.0	0.9	1.0	0.8	1.0	0.9	1.0	0.7	1.0	0.8	-1.0	0.9
				SSGSEGSSPNWLQALK	2	100.0%	1																									
				VNLFPGLSPSALK	2	99.3%	1																									
IPI00384116	PCK2	isoform 2 of Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	100.0%	6.8	2	2	2	1	6,508,212	5,868,470	6,277,270	6,317,043	339,052	216,852	139,078	151,126	11.7	8.3	5.0	5.4	-1.1	0.2	-1.0	0.5	-1.0	0.6	1.1	0.2	1.1	0.1	1.0	0.9
				GQLGNWMSPADFQR	2	98.2%	1																									
				LGTPVLQALGDGDFVK	2	99.1%	1																									
IPI00384280	PCYOX1	Prenylcysteine oxidase 1	100.0%	13.5	5	5	5	3	6,852,562	7,391,375	6,970,868	7,744,881	529,000	346,167	466,641	263,211	17.3	10.5	15.0	7.6	1.1	0.4	1.0	0.9	1.1	0.2	-1.1	0.5	1.0	0.4	1.1	0.2
IPI00924611	PCYOX1	cDNA, FLJ78912, highly similar to Prenylcysteine oxidase	100.0%	15.9	5	5	5	3	6,852,562	7,391,375	6,970,868	7,744,881	529,000	346,167	466,641	263,211	17.3	10.5	15.0	7.6	1.1	0.4	1.0	0.9	1.1	0.2	-1.1	0.5	1.0	0.4	1.1	0.2
IPI01010177	PCYOX1	cDNA FLJ51879, highly similar to Prenylcysteine oxidase	100.0%	15.9	5	5	5	3	6,852,562	7,391,375	6,970,868	7,744,881	529,000	346,167	466,641	263,211	17.3	10.5	15.0	7.6	1.1	0.4	1.0	0.9	1.1	0.2	-1.1	0.5	1.0	0.4	1.1	0.2
				LVCSGLLQASK	2	99.2%	1																									
				MYEVVYQIGTETR	2	100.0%	1																									
				SDFYDIVLVATPLNR	2	99.1%	1																									
				WNGHTDMIDQDGLYEK	3	96.5%	1																									
				YQSHDYAFSSVEK	3	99.6%	1																									
IPI00384420	PSMD2	P67	100.0%	6.8	3	3	3	1	5,289,180	5,821,160	5,446,444	5,853,874	323,298	151,600	296,260	156,106	13.7	5.8	12.2	6.0	1.1	0.2	1.0	0.7	1.1	0.2	-1.1	0.3	1.0	0.9	1.1	0.3
				SGALLACGIVNSGVR	2	100.0%	1																									
				VGQAVDVVGQAGKPK	3	99.9%	1																									
				YLYSSEDYIK	2	99.5%	1																									
IPI00384458	INTU	isoform 1 of PDZ domain-containing protein 6	96.6%	2.6	1	1	1	1	2,457,870	2,682,580	2,388,340	3,253,310	284,765	180,487	291,975	249,648	25.9	15.0	27.3	17.2	1.1	0.5	-1.0	0.9	1.3	0.07	-1.1	0.4	1.2	0.1	1.4	0.05
				IDERLASSPVPCLSCADWFLTGSR	3	96.6%	1																									
IPI00384489	AP1B1	AP-1 complex subunit beta-1 isoform c	100.0%	15.2	10	10	11	1	6,657,389	6,707,692	6,463,979	7,595,521	576,724	355,259	545,177	160,025	19.4	11.8	18.9	4.7	1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.7	1.1	0.05	1.2	0.1
				AAMIWIVGEYAER	2	100.0%	2																									
				CVSTLLDLIQTK	2	100.0%	1																									
				DCPLNAEAASSK	2	100.0%	1																									
				DIPNENEAQFQIR	2	97.6%	1																									
				FMEMLSK	2	93.5%	1																									
				LAPPLVTLLSAEPELQYVALR	3	100.0%	1																									
				LASQANIAQVLAELKEYATEVDVDFVR	3	100.0%	1																									
				MEPLNNLQVAVK	2	99.8%	1																									
				SQPDMAIMAVNTFVK	2	100.0%	1																									
				YNDPIYVK	2	99.7%	1																									
IPI00384597	PHC2	Polyhomeotic 2 homolog	99.5%	4.4	1	1	1	1	4,172,060	2,860,900	3,461,740	3,425,800	384,307	320,273	98,017	335,736	20.6	25.0	6.3	21.9	-1.5	0.03	-1.2	0.1	-1.2	0.2	1.2	0.1	1.2	0.3	-1.0	0.9
				APAAAPQPRPPPALPPRPR	2	99.1%	1																									
IPI00384624	GART	GARS-AIRS-GART (Fragment)	100.0%	22.8	2	2	2	1	2,810,660	2,861,483	2,739,165	2,872,238	233,045	94,020	96,742	211,472	18.5	7.4	7.9	16.5	1.0	0.8	-1.0	0.8	1.0	0.8	-1.0	0.4	1.0	1	1.0	0.6
				AIAFLQQPR	2	96.8%	1																									
				ESGVDIAAGNMLVK	2	99.4%	1																									
IPI00384626	PTPRF	Protein tyrosine phosphatase, receptor type, F	99.9%	4.3	1	1	1	3	696,758	692,496	771,432	799,238	102,342	31,346	67,864	87,533	32.8	10.1	19.7	24.5	-1.0	1	1.1	0.6	1.1	0.5	1.1	0.3	1.2	0.3	1.0	0.8
IPI00641061	PTPRF	Protein tyrosine phosphatase, receptor type, F	99.9%	4.3	1	1	1	3	696,758	692,496	771,432	799,238	102,342	31,346	67,864	87,533	32.8	10.1	19.7	24.5	-1.0	1	1.1	0.6	1.1	0.5	1.1	0.3	1.2	0.3	1.0	0.8
IPI00655814	PTPRF	Protein tyrosine phosphatase, receptor type, F	99.9%	5.7	1	1	1	3	696,758	692,496	771,432	799,238	102,342	31,346	67,864	87,533	32.8	10.1	19.7	24.5	-1.0	1	1.1	0.6	1.1	0.5	1.1	0.3	1.2	0.3	1.0	0.8
				FEVIEFDDGAGSVLR	2	99.9%	1																									
IPI00908508	-	cDNA FLJ61719, highly similar to quinone oxidoreductase	98.0%	16.5	2	2	2	2	6,640,820	6,606,120	6,920,440	6,893,605	1,097,512	266,106	757,624	317,903	37.0	9.0	24.5	10.3	-1.0	1	1.0	0.8	1.0	0.8	1.0	0.7	1.0	0.5	-1.0	1
IPI00384643	TP53I3	isoform 1 of Quinone oxidoreductase PIG3	98.0%	12.1	2	2	2	2	6,640,820	6,606,120	6,920,440	6,893,605	1,097,512	266,106	757,624	317,903	37.0	9.0	24.5	10.3	-1.0	1	1.0	0.8	1.0	0.8	1.0	0.7	1.0	0.5	-1.0	1
				GAGVNLILDCIGGSYWEK	2	94.1%	1																									
				QMLVNAFTEQILPHFSTEGPQR	3	98.0%	1																									
IPI00384689	PDXDC1	isoform 1 of Pyridoxal-dependent decarboxylase domain-containing protein 1	100.0%	13.2	7	7	7	2	49,239,944	51,013,513	52,921,401	58,287,210	4,820,372	2,994,595	4,003,087	2,042,862	21.9	13.1	16.9	7.8	1.0	0.8	1.1	0.6	1.2	0.1	1.0	0.7	1.1	0.08	1.1	0.3
IPI00645809	PDXDC1	cDNA FLJ53168	100.0%	13.7	7	7	7	2	49,239,944	51,013,513	52,921,401	58,287,210	4,820,372	2,994,595	4,003,087	2,042,862	21.9	13.1	16.9	7.8	1.0	0.8	1.1	0.6	1.2	0.1	1.0	0.7	1.1	0.08	1.1	0.3
				FFQELPGSDPVFK	2	98.8%	1																									
				HDDPALTLVAGLTSNKPTDK	3	100.0%	1																									
				IADPTLAEMGK	2	88.0%	1																									
				LLENMTEVVR	2	99.9%	1																									
				LNELESDLTFK	2	99.9%	1																									
				QIPVVGSVLNWFSPVQALQK	2	99.6%	1																									
				TFNLTAGSLESTEPIYVYK	2	100.0%	1																									
IPI00384697	ALB	isoform 2 of Serum albumin	100.0%	10.3	5	7	11	4	7,082,956	9,724,177	7,481,264	11,851,922	2,131,340	1,455,059	629,847	890,488	67.3	33.5	18.8	16.8	1.4	0.3	1.1	0.9	1.7	0.07	-1.3	0.2	1.2	0.2	1.6	0.004
IPI00878517	ALB	Uncharacterized protein	100.0%	8.7	5	7	11	4	7,082,956	9,724,177	7,481,264	11,851,922	2,131,340	1,455,059	629,847	890,488	67.3	33.5	18.8	16.8	1.4	0.3	1.1	0.9	1.7	0.07	-1.3	0.2	1.2	0.2	1.6	0.004
IPI00953582	ALB	Uncharacterized protein	100.0%	10.3	5	7	11	4	7,082,956	9,724,177	7,481,264	11,851,922	2,131,340	1,455,059	629,847	890,488	67.3	33.5	18.8	16.8	1.4	0.3	1.1	0.9	1.7	0.07	-1.3	0.2	1.2	0.2	1.6	0.004
IPI00965074	ALB	Uncharacterized protein	100.0%	9.4	5	7	11	4	7,082,956	9,724,177	7,481,264	11,851,922	2,131,340	1,455,059	629,847	890,488	67.3	33.5	18.8	16.8	1.4	0.3	1.1	0.9	1.7	0.07	-1.3	0.2	1.2	0.2	1.6	0.004
				CCTESLVNR	2	100.0%	1																									
				KVPQVSTPTLVEVSR	2	100.0%	2																									
				KVPQVSTPTLVEVSR	3	100.0%	2																									
				LVTDLTK	1	99.5%	1																									
				LVTDLTK	2	99.9%	1																									
				VPQVSTPTLVEVSR	2	100.0%	2																									
				YICENQDSISSK	2	100.0%	2																									
IPI00384863	-	HDCMB21P	100.0%	23.7	2	2	3	2	1,933,612	1,995,423	1,770,632	2,167,253	245,149	92,673	111,778	73,545	28.4	10.4	14.1	7.6	1.0	0.8	-1.1	0.6	1.1	0.4	-1.1	0.2	1.1	0.2	1.2	0.02
IPI00910288	-	cDNA FLJ57742	100.0%	17.7	2	2	3	2	1,933,612	1,995,423	1,770,632	2,167,253	245,149	92,673	111,778	73,545	28.4	10.4	14.1	7.6	1.0	0.8	-1.1	0.6	1.1	0.4	-1.1	0.2	1.1	0.2	1.2	0.02
				DLISHDEMFSDIYK	3	100.0%	1																									
				EIADGLCLEVEGK	2	100.0%	2																									
IPI00384973	VCL	isoform 3 of Vinculin	100.0%	11.3	2	2	2	1	3,195,246	3,174,076	2,998,204	3,521,146	285,430	98,215	151,527	181,606	20.0	6.9	11.3	11.5	-1.0	0.9	-1.1	0.6	1.1	0.4	-1.1	0.4	1.1	0.1	1.2	0.06
				MSAEINEIIR	2	99.9%	1																									
				VLQLTSWDEDAWASK	2	100.0%	1																									
IPI00385007	AP1B1	Uncharacterized protein	100.0%	13.3	2	2	2	1	1,021,329	1,051,830	1,000,815	1,106,175	110,793	103,195	46,203	37,443	24.3	21.9	10.3	7.6	1.0	0.8	-1.0	0.9	1.1	0.5	-1.1	0.7	1.1	0.6	1.1	0.1
				DCPLNAEAASSK	2	100.0%	1																									
				MEPLNNLQVAVK	2	99.8%	1																									
IPI00385034	SLC9A3R2	isoform 1 of Na(+)/H(+) exchange regulatory cofactor NHE-RF2	100.0%	10.4	3	3	3	3	3,081,537	3,055,976	2,876,093	3,615,057	330,855	203,631	227,608	275,279	24.0	14.9	17.7	17.0	-1.0	0.9	-1.1	0.6	1.2	0.3	-1.1	0.6	1.2	0.1	1.3	0.07
IPI00398293	SLC9A3R2	isoform 2 of Na(+)/H(+) exchange regulatory cofactor NHE-RF2	100.0%	10.7	3	3	3	3	3,081,537	3,055,976	2,876,093	3,615,057	330,855	203,631	227,608	275,279	24.0	14.9	17.7	17.0	-1.0	0.9	-1.1	0.6	1.2	0.3	-1.1	0.6	1.2	0.1	1.3	0.07
IPI00645815	SLC9A3R2	Na(+)/H(+) exchange regulatory cofactor NHE-RF2 isoform b	100.0%	10.7	3	3	3	3	3,081,537	3,055,976	2,876,093	3,615,057	330,855	203,631	227,608	275,279	24.0	14.9	17.7	17.0	-1.0	0.9	-1.1	0.6	1.2	0.3	-1.1	0.6	1.2	0.1	1.3	0.07
				HAEVVASIK	2	97.5%	1																									
				LIEVNGQNVEGLR	2	100.0%	1																									
				LLVVDQETDEELR	2	99.9%	1																									
IPI00385055	CTNNA2	isoform 1 of Catenin alpha-2	100.0%	6.0	4	4	4	4	1,770,740	1,920,739	1,753,476	2,043,815	152,419	112,260	78,688	66,363	19.3	13.1	10.0	7.3	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.4	1.2	0.02
IPI00743859	CTNNA2	isoform 2 of Catenin alpha-2	100.0%	6.3	4	4	4	4	1,770,740	1,920,739	1,753,476	2,043,815	152,419	112,260	78,688	66,363	19.3	13.1	10.0	7.3	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.4	1.2	0.02
IPI00916487	CTNNA2	isoform 3 of Catenin alpha-2	100.0%	6.6	4	4	4	4	1,770,740	1,920,739	1,753,476	2,043,815	152,419	112,260	78,688	66,363	19.3	13.1	10.0	7.3	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.4	1.2	0.02
IPI00944536	CTNNA2	isoform 5 of Catenin alpha-2	100.0%	6.1	4	4	4	4	1,770,740	1,920,739	1,753,476	2,043,815	152,419	112,260	78,688	66,363	19.3	13.1	10.0	7.3	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.4	1.2	0.02
				IVAECNAVR	2	99.0%	1																									
				LESIISGAALMADSSCTR	2	100.0%	1																									
				TSVQTEDDQLIAGQSAR	2	100.0%	1																									
				WDDSGNDIIVLAK	2	100.0%	1																									
IPI00385082	SMC1A	MSTP142	97.1%	6.8	1	1	1	1	141,195	222,603	178,057	182,140	11,964	23,939	21,816	21,225	19.0	24.1	27.4	26.1	1.6	0.02	1.3	0.2	1.3	0.1	-1.3	0.2	-1.2	0.2	1.0	0.9
				SNLMDAISFVLGEK	2	97.1%	1																									
IPI00385121	BID	isoform 3 of BH3-interacting domain death agonist	100.0%	20.4	1	1	1	2	726,305	697,053	699,805	736,995	58,365	41,882	77,984	31,668	18.0	13.4	24.9	9.6	-1.0	0.7	-1.0	0.8	1.0	0.9	1.0	1	1.1	0.5	1.1	0.7
IPI00978537	BID	BID isoform Si6	100.0%	23.0	1	1	1	2	726,305	697,053	699,805	736,995	58,365	41,882	77,984	31,668	18.0	13.4	24.9	9.6	-1.0	0.7	-1.0	0.8	1.0	0.9	1.0	1	1.1	0.5	1.1	0.7
				ELDALGHELPVLAPQWEGYDELQTDGNR	3	100.0%	1																									
IPI00385156	ISYNA1	Uncharacterized protein	92.5%	2.5	1	1	1	7	322,747	336,391	285,046	414,190	61,771	19,859	51,182	21,886	42.8	13.2	40.2	11.8	1.0	0.8	-1.1	0.7	1.3	0.2	-1.2	0.4	1.2	0.03	1.5	0.05
IPI00478861	ISYNA1	inositol-3-phosphate synthase 1 isoform 2	92.5%	2.6	1	1	1	7	322,747	336,391	285,046	414,190	61,771	19,859	51,182	21,886	42.8	13.2	40.2	11.8	1.0	0.8	-1.1	0.7	1.3	0.2	-1.2	0.4	1.2	0.03	1.5	0.05
IPI00549569	ISYNA1	isoform 1 of Inositol-3-phosphate synthase 1	92.5%	2.3	1	1	1	7	322,747	336,391	285,046	414,190	61,771	19,859	51,182	21,886	42.8	13.2	40.2	11.8	1.0	0.8	-1.1	0.7	1.3	0.2	-1.2	0.4	1.2	0.03	1.5	0.05
IPI00640098	ISYNA1	isoform 2 of Inositol-3-phosphate synthase 1	92.5%	3.0	1	1	1	7	322,747	336,391	285,046	414,190	61,771	19,859	51,182	21,886	42.8	13.2	40.2	11.8	1.0	0.8	-1.1	0.7	1.3	0.2	-1.2	0.4	1.2	0.03	1.5	0.05
IPI00644161	ISYNA1	inositol-3-phosphate synthase 1 isoform 3	92.5%	3.2	1	1	1	7	322,747	336,391	285,046	414,190	61,771	19,859	51,182	21,886	42.8	13.2	40.2	11.8	1.0	0.8	-1.1	0.7	1.3	0.2	-1.2	0.4	1.2	0.03	1.5	0.05
IPI00645069	ISYNA1	52 kDa protein	92.5%	2.7	1	1	1	7	322,747	336,391	285,046	414,190	61,771	19,859	51,182	21,886	42.8	13.2	40.2	11.8	1.0	0.8	-1.1	0.7	1.3	0.2	-1.2	0.4	1.2	0.03	1.5	0.05
IPI01009610	ISYNA1	cDNA FLJ57998, highly similar to Homo sapiens myo-inositol 1-phosphate synthase	92.5%	3.7	1	1	1	7	322,747	336,391	285,046	414,190	61,771	19,859	51,182	21,886	42.8	13.2	40.2	11.8	1.0	0.8	-1.1	0.7	1.3	0.2	-1.2	0.4	1.2	0.03	1.5	0.05
				SVLVDFLIGSGLK	2	92.6%	1																									
IPI00385267	SRPR	Signal recognition particle receptor subunit alpha	99.2%	4.2	2	2	2	2	4,472,685	4,295,680	4,480,670	4,746,525	264,034	388,362	171,337	239,283	13.2	20.2	8.6	11.3	-1.0	0.7	1.0	1	1.1	0.5	1.0	0.7	1.1	0.4	1.1	0.4
IPI00964088	SRPR	signal recognition particle receptor subunit alpha isoform 2	99.2%	4.4	2	2	2	2	4,472,685	4,295,680	4,480,670	4,746,525	264,034	388,362	171,337	239,283	13.2	20.2	8.6	11.3	-1.0	0.7	1.0	1	1.1	0.5	1.0	0.7	1.1	0.4	1.1	0.4
				DAAGIAMEAIAFAR	2	98.5%	1																									
				VMGTFSTVTSTVK	2	99.2%	1																									
IPI00385321	ZMYND8	isoform 2 of Protein kinase C-binding protein 1	99.3%	2.9	1	1	1	10	385,377	408,510	349,802	465,547	45,129	17,583	40,209	24,563	26.2	9.6	25.7	11.8	1.1	0.7	-1.1	0.6	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.04
IPI00741204	ZMYND8	cDNA FLJ56888, highly similar to Protein kinase C-binding protein 1	99.3%	1.5	1	1	1	10	385,377	408,510	349,802	465,547	45,129	17,583	40,209	24,563	26.2	9.6	25.7	11.8	1.1	0.7	-1.1	0.6	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.04
IPI00789719	ZMYND8	isoform 12 of Protein kinase C-binding protein 1	99.3%	1.6	1	1	1	10	385,377	408,510	349,802	465,547	45,129	17,583	40,209	24,563	26.2	9.6	25.7	11.8	1.1	0.7	-1.1	0.6	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.04
IPI00922821	ZMYND8	ZMYND8 protein	99.3%	1.7	1	1	1	10	385,377	408,510	349,802	465,547	45,129	17,583	40,209	24,563	26.2	9.6	25.7	11.8	1.1	0.7	-1.1	0.6	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.04
IPI00941061	ZMYND8	isoform 4 of Protein kinase C-binding protein 1	99.3%	2.4	1	1	1	10	385,377	408,510	349,802	465,547	45,129	17,583	40,209	24,563	26.2	9.6	25.7	11.8	1.1	0.7	-1.1	0.6	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.04
IPI00946867	ZMYND8	isoform 1 of Protein kinase C-binding protein 1	99.3%	1.5	1	1	1	10	385,377	408,510	349,802	465,547	45,129	17,583	40,209	24,563	26.2	9.6	25.7	11.8	1.1	0.7	-1.1	0.6	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.04
IPI01008942	ZMYND8	isoform 3 of Protein kinase C-binding protein 1	99.3%	1.8	1	1	1	10	385,377	408,510	349,802	465,547	45,129	17,583	40,209	24,563	26.2	9.6	25.7	11.8	1.1	0.7	-1.1	0.6	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.04
IPI01008945	ZMYND8	isoform 10 of Protein kinase C-binding protein 1	99.3%	1.5	1	1	1	10	385,377	408,510	349,802	465,547	45,129	17,583	40,209	24,563	26.2	9.6	25.7	11.8	1.1	0.7	-1.1	0.6	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.04
IPI01009867	ZMYND8	RACK7 isoform l	99.3%	1.6	1	1	1	10	385,377	408,510	349,802	465,547	45,129	17,583	40,209	24,563	26.2	9.6	25.7	11.8	1.1	0.7	-1.1	0.6	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.04
IPI01014325	ZMYND8	isoform 14 of Protein kinase C-binding protein 1	99.3%	1.6	1	1	1	10	385,377	408,510	349,802	465,547	45,129	17,583	40,209	24,563	26.2	9.6	25.7	11.8	1.1	0.7	-1.1	0.6	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.04
				ETPSSILLGSNQGSDHSR	2	99.3%	1																									
IPI00385666	NUP54	Putative uncharacterized protein DKFZp434L1613	100.0%	9.0	1	1	2	2	1,454,915	1,566,853	1,543,653	1,679,988	145,880	79,167	63,446	108,636	22.4	11.3	9.2	14.5	1.1	0.5	1.1	0.6	1.2	0.3	-1.0	0.8	1.1	0.4	1.1	0.3
IPI01010440	NUP54	37 kDa protein	100.0%	4.0	1	1	2	2	1,454,915	1,566,853	1,543,653	1,679,988	145,880	79,167	63,446	108,636	22.4	11.3	9.2	14.5	1.1	0.5	1.1	0.6	1.2	0.3	-1.0	0.8	1.1	0.4	1.1	0.3
				LDIISEDISELQK	2	99.9%	2																									
IPI00385761	UNC80	isoform 1 of Protein unc-80 homolog	98.1%	0.4	1	1	1	3	776,053	800,073	741,017	835,167	171,194	58,063	59,212	49,728	49.3	16.2	17.9	13.3	1.0	0.9	-1.0	0.9	1.1	0.8	-1.1	0.5	1.0	0.7	1.1	0.3
IPI00923519	UNC80	isoform 4 of Protein unc-80 homolog	98.1%	0.4	1	1	1	3	776,053	800,073	741,017	835,167	171,194	58,063	59,212	49,728	49.3	16.2	17.9	13.3	1.0	0.9	-1.0	0.9	1.1	0.8	-1.1	0.5	1.0	0.7	1.1	0.3
IPI00923533	UNC80	protein unc-80 homolog isoform 2	98.1%	0.4	1	1	1	3	776,053	800,073	741,017	835,167	171,194	58,063	59,212	49,728	49.3	16.2	17.9	13.3	1.0	0.9	-1.0	0.9	1.1	0.8	-1.1	0.5	1.0	0.7	1.1	0.3
				QVFTRKLEEVGR	2	92.6%	1																									
IPI00385935	-	PRO1252	97.5%	16.2	1	1	1	1	347,965	334,618	387,466	399,276	27,714	19,236	43,541	14,492	17.8	12.9	25.1	8.1	-1.0	0.7	1.1	0.5	1.1	0.1	1.2	0.3	1.2	0.03	1.0	0.8
				CEMSEHPSQTVR	2	97.5%	1																									
IPI00386083	NT5C	isoform 2 of 5'(3')-deoxyribonucleotidase, cytosolic type	100.0%	15.4	1	2	3	2	331,191	289,381	386,624	395,031	31,553	31,892	51,077	30,440	21.3	24.6	29.5	17.2	-1.1	0.4	1.2	0.4	1.2	0.2	1.3	0.1	1.4	0.04	1.0	0.9
IPI00795829	NT5C	9 kDa protein	100.0%	22.2	1	2	3	2	331,191	289,381	386,624	395,031	31,553	31,892	51,077	30,440	21.3	24.6	29.5	17.2	-1.1	0.4	1.2	0.4	1.2	0.2	1.3	0.1	1.4	0.04	1.0	0.9
				VLVDMDGVLADFEAGLLR	2	100.0%	2																									
				VLVDMDGVLADFEAGLLR	3	100.0%	1																									
IPI00386118	SF1	cDNA FLJ54064, highly similar to Splicing factor 1	100.0%	4.9	1	1	1	1	312,293	260,212	317,723	380,367	21,938	31,910	34,675	17,302	15.7	27.4	24.4	10.2	-1.2	0.2	1.0	0.9	1.2	0.04	1.2	0.3	1.5	0.01	1.2	0.1
				VMIPQDEYPEINFVGLLIGPR	3	100.0%	1																									
IPI00386271	SLC25A12	Calcium-binding mitochondrial carrier protein Aralar1	96.9%	3.0	1	1	1	2	1,307,500	1,202,755	1,282,845	1,430,285	151,902	93,776	61,451	122,971	26.0	17.4	10.7	19.2	-1.1	0.6	-1.0	0.9	1.1	0.5	1.1	0.5	1.2	0.2	1.1	0.3
IPI01009336	SLC25A12	cDNA FLJ33752 fis, clone BRCAN2000364, highly similar to Calcium-binding mitoch	96.9%	3.5	1	1	1	2	1,307,500	1,202,755	1,282,845	1,430,285	151,902	93,776	61,451	122,971	26.0	17.4	10.7	19.2	-1.1	0.6	-1.0	0.9	1.1	0.5	1.1	0.5	1.2	0.2	1.1	0.3
				QQSPGLGRPIWLQIAESAYR	2	96.9%	1																									
IPI00386314	CNDP2	FLJ00064 protein (Fragment)	100.0%	23.9	4	4	4	1	3,529,923	3,340,467	3,934,856	3,750,818	271,108	243,616	280,602	172,993	17.2	16.3	16.0	10.3	-1.1	0.6	1.1	0.3	1.1	0.5	1.2	0.1	1.1	0.2	-1.0	0.6
				FCLEGMEESGSEGLDELIFAR	2	100.0%	1																									
				GSTDDKGPVAGWINALEAYQK	3	100.0%	1																									
				LYDDIDFDIEEFAK	2	100.0%	1																									
				TGQEIPVNVR	2	99.6%	1																									
IPI00386354	ARPC4;ARPC4-TTLL	Uncharacterized protein	100.0%	14.1	2	2	4	7	2,884,211	3,521,067	2,856,187	4,322,250	787,950	397,510	197,136	238,465	61.1	25.2	15.4	12.3	1.2	0.5	-1.0	1	1.5	0.1	-1.2	0.2	1.2	0.1	1.5	0.001
IPI00554811	ARPC4;ARPC4-TTLL	Actin-related protein 2/3 complex subunit 4	100.0%	13.1	2	2	4	7	2,884,211	3,521,067	2,856,187	4,322,250	787,950	397,510	197,136	238,465	61.1	25.2	15.4	12.3	1.2	0.5	-1.0	1	1.5	0.1	-1.2	0.2	1.2	0.1	1.5	0.001
IPI00925052	ARPC4;ARPC4-TTLL	actin-related protein 2/3 complex subunit 4 isoform c	100.0%	11.8	2	2	4	7	2,884,211	3,521,067	2,856,187	4,322,250	787,950	397,510	197,136	238,465	61.1	25.2	15.4	12.3	1.2	0.5	-1.0	1	1.5	0.1	-1.2	0.2	1.2	0.1	1.5	0.001

IPI00925334	ARPC4;ARPC4-TTLL	21 kDa protein	100.0%	12.2	2	2	4	7	2,884,211	3,521,067	2,856,187	4,322,250	787,950	397,510	197,136	238,465	61.1	25.2	15.4	12.3	1.2	0.5	-1.0	1	1.5	0.1	-1.2	0.2	1.2	0.1	1.5	0.001
IPI00926232	ARPC4;ARPC4-TTLL	13 kDa protein	100.0%	19.5	2	2	4	7	2,884,211	3,521,067	2,856,187	4,322,250	787,950	397,510	197,136	238,465	61.1	25.2	15.4	12.3	1.2	0.5	-1.0	1	1.5	0.1	-1.2	0.2	1.2	0.1	1.5	0.001
IPI00790262	TTLL3	Uncharacterized protein	100.0%	3.5	2	2	4	7	2,884,211	3,521,067	2,856,187	4,322,250	787,950	397,510	197,136	238,465	61.1	25.2	15.4	12.3	1.2	0.5	-1.0	1	1.5	0.1	-1.2	0.2	1.2	0.1	1.5	0.001
IPI00926054	TTLL3	Protein	100.0%	13.2	2	2	4	7	2,884,211	3,521,067	2,856,187	4,322,250	787,950	397,510	197,136	238,465	61.1	25.2	15.4	12.3	1.2	0.5	-1.0	1	1.5	0.1	-1.2	0.2	1.2	0.1	1.5	0.001
				ELLLQPVTISR	2	100.0%	2																									
				VLIEGSINSVR	2	99.8%	2																									
IPI00386418	MYEF2	isoform 2 of Myelin expression factor 2	97.9%	2.1	1	1	1	3	4,202,473	3,864,187	3,658,013	3,706,847	567,728	576,656	640,797	301,835	30.2	33.4	39.2	18.2	-1.1	0.7	-1.1	0.5	-1.1	0.5	-1.1	0.8	-1.0	0.8	1.0	0.9
IPI00555833	MYEF2	isoform 1 of Myelin expression factor 2	97.9%	2.0	1	1	1	3	4,202,473	3,864,187	3,658,013	3,706,847	567,728	576,656	640,797	301,835	30.2	33.4	39.2	18.2	-1.1	0.7	-1.1	0.5	-1.1	0.5	-1.1	0.8	-1.0	0.8	1.0	0.9
IPI00555987	MYEF2	isoform 3 of Myelin expression factor 2	97.9%	6.4	1	1	1	3	4,202,473	3,864,187	3,658,013	3,706,847	567,728	576,656	640,797	301,835	30.2	33.4	39.2	18.2	-1.1	0.7	-1.1	0.5	-1.1	0.5	-1.1	0.8	-1.0	0.8	1.0	0.9
				GFLSGPMGSGMR	2	97.9%	1																									
IPI00386533	EIF4G1	isoform E of Eukaryotic translation initiation factor 4 gamma 1	100.0%	14.6	14	14	15	2	5,087,074	5,142,976	5,048,946	5,945,700	428,469	143,313	271,756	163,626	18.8	6.2	12.0	6.2	1.0	0.9	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.006	1.2	0.02
IPI01015364	EIF4G1	eukaryotic translation initiation factor 4 gamma 1 isoform 4	100.0%	14.6	14	14	15	2	5,087,074	5,142,976	5,048,946	5,945,700	428,469	143,313	271,756	163,626	18.8	6.2	12.0	6.2	1.0	0.9	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.006	1.2	0.02
				EAVGDLLDAFK	2	100.0%	1																									
				FMLQDVLDLR	2	91.9%	1																									
				GGPGGELPR	2	87.6%	1																									
				HGVESTLER	2	90.6%	1																									
				IHNAENIQPGEQK	2	99.4%	1																									
				ITKPGSIDSNNQLFAPGGR	3	100.0%	1																									
				LQGINCGPDFTPSFANLGR	2	99.8%	1																									
				LTPQMFQQLMK	2	96.0%	1																									
				QVTQLAIDTEER	2	100.0%	2																									
				SDQWKPLNLEEK	3	96.3%	1																									
				TASTPTPPQTGGGLEPQANGETPQVAVIVRPDDR	3	100.0%	1																									
				TPLRPLDPTR	3	83.3%	1																									
				VEYTLGEESEAPGQR	2	93.0%	1																									
				VFDWIEANLSEQQIVSNTLVR	3	97.3%	1																									
IPI00386621	CALM1;CALM3;CALM	Uncharacterized protein	100.0%	32.4	4	6	10	1	26,850,112	27,872,086	28,152,760	31,263,382	2,104,234	1,530,079	2,044,539	701,874	17.5	12.3	16.2	5.0	1.0	0.7	1.0	0.7	1.2	0.1	1.0	0.9	1.1	0.08	1.1	0.2
				DTDSEEEIREAFR	3	95.4%	1																									
				EAFSLFDKDGDGTITTK	2	100.0%	2																									
				EAFSLFDKDGDGTITTK	3	100.0%	1																									
				MKDTDSEEEIREAFR	3	99.7%	2																									
				VFDKDGNGYISAAELR	2	100.0%	2																									
				VFDKDGNGYISAAELR	3	100.0%	2																									
IPI00386751	HDDC2	isoform 2 of HD domain-containing protein 2	99.6%	10.0	1	1	1	2	1,047,305	838,945	924,450	899,095	137,088	102,026	99,952	38,921	29.3	27.2	24.2	9.7	-1.2	0.3	-1.1	0.5	-1.2	0.3	1.1	0.6	1.1	0.6	-1.0	0.8
IPI00872352	HDDC2	isoform 1 of HD domain-containing protein 2	99.6%	8.3	1	1	1	2	1,047,305	838,945	924,450	899,095	137,088	102,026	99,952	38,921	29.3	27.2	24.2	9.7	-1.2	0.3	-1.1	0.5	-1.2	0.3	1.1	0.6	1.1	0.6	-1.0	0.8
				FNHPEIVQLVSELEAER	3	99.6%	1																									
IPI00386755	ERO1L	ERO1-like protein alpha	100.0%	41.5	15	16	18	1	61,604,891	65,736,956	62,699,721	71,017,851	4,827,913	2,251,473	3,234,865	1,449,580	17.5	7.7	11.5	4.6	1.1	0.5	1.0	0.9	1.2	0.1	-1.0	0.5	1.1	0.08	1.1	0.05
				DCAVKPCQSDEVPDGIK	3	100.0%	1																									
				FDGILTEGEGPR	2	100.0%	2																									
				FDGILTEGEGPRR	3	91.0%	1																									
				HDDSSDNFCEADDIQSPEAEYVDLLLNPER	3	100.0%	1																									
				IQDEENKMLLLEILHEIK	3	99.9%	1																									
				IWNVIYEENCFKPQTIK	3	87.3%	1																									
				LGAVDESLSEETQK	2	100.0%	2																									
				LLESDYFR	2	100.0%	1																									
				MLLLEILHEIK	2	100.0%	1																									
				MLLLEILHEIK	3	100.0%	1																									
				NLLQNIH	2	97.1%	1																									
				QEIVSLFNAFGR	2	99.7%	1																									
				RPCPFWNDISQCGR	3	100.0%	1																									
				SFPLHFDENSFFAGDKK	3	99.8%	1																									
				YLLQETWLEK	2	98.9%	1																									
				YSEEANNLIEECEQAER	2	100.0%	1																									
IPI00386803	LASP1	isoform 2 of LIM and SH3 domain protein 1	100.0%	26.6	10	11	14	1	26,982,338	27,896,714	25,209,321	30,458,775	2,202,055	1,050,440	1,105,096	800,011	18.3	8.4	9.8	5.9	1.0	0.7	-1.1	0.5	1.1	0.2	-1.1	0.1	1.1	0.09	1.2	0.005
				GFSVVADTPELQR	2	100.0%	2																									
				IVYPTEK	2	97.7%	1																									
				KPYCNAHYPK	2	99.4%	1																									
				KPYCNAHYPK	3	99.4%	1																									
				LKQQSELQSQVR	3	95.4%	1																									
				MGPSGGEGMEPER	2	99.7%	1																									
				MGPSGGEGMEPERR	2	93.1%	1																									
				QQSELQSQVR	2	100.0%	2																									
				QSFTMVADTPENLR	2	100.0%	1																									
				TQDQISNIK	2	100.0%	2																									
				YHEEFEK	2	89.9%	1																									
IPI00386930	RAP1GAP	isoform 2 of Rap1 GTPase-activating protein 1	97.1%	2.2	1	1	1	5	1,115,914	1,383,984	1,115,158	1,391,936	205,391	228,498	108,442	97,098	41.2	36.9	21.7	15.6	1.2	0.4	-1.0	1	1.2	0.3	-1.2	0.3	1.0	1	1.2	0.09
IPI00843926	RAP1GAP	isoform 1 of Rap1 GTPase-activating protein 1	97.1%	2.3	1	1	1	5	1,115,914	1,383,984	1,115,158	1,391,936	205,391	228,498	108,442	97,098	41.2	36.9	21.7	15.6	1.2	0.4	-1.0	1	1.2	0.3	-1.2	0.3	1.0	1	1.2	0.09
IPI00872409	RAP1GAP	rap1 GTPase-activating protein 1 isoform a	97.1%	2.1	1	1	1	5	1,115,914	1,383,984	1,115,158	1,391,936	205,391	228,498	108,442	97,098	41.2	36.9	21.7	15.6	1.2	0.4	-1.0	1	1.2	0.3	-1.2	0.3	1.0	1	1.2	0.09
IPI00981523	RAP1GAP	Uncharacterized protein	97.1%	2.5	1	1	1	5	1,115,914	1,383,984	1,115,158	1,391,936	205,391	228,498	108,442	97,098	41.2	36.9	21.7	15.6	1.2	0.4	-1.0	1	1.2	0.3	-1.2	0.3	1.0	1	1.2	0.09
IPI01013142	RAP1GAP	isoform 3 of Rap1 GTPase-activating protein 1	97.1%	2.2	1	1	1	5	1,115,914	1,383,984	1,115,158	1,391,936	205,391	228,498	108,442	97,098	41.2	36.9	21.7	15.6	1.2	0.4	-1.0	1	1.2	0.3	-1.2	0.3	1.0	1	1.2	0.09
				SSAIGIENIQEVQEK	2	96.4%	1																									
IPI00387084	RPS21	40S ribosomal protein S21	100.0%	30.0	2	2	4	1	4,549,217	5,630,217	4,568,863	5,799,883	1,105,079	561,503	546,921	363,625	54.3	22.3	26.8	14.0	1.2	0.4	1.0	1	1.3	0.3	-1.2	0.2	1.0	0.8	1.3	0.1
				DHASIQMNVAEVDKVTGR	3	100.0%	2																									
				TYAICGAIR	2	100.0%	2																									
IPI00387159	ING3	isoform 1 of Inhibitor of growth protein 3	99.5%	4.1	1	1	1	2	968,532	1,152,286	1,251,715	1,276,540	128,102	233,460	101,950	147,781	29.6	45.3	18.2	25.9	1.2	0.5	1.3	0.1	1.3	0.2	1.1	0.7	1.1	0.7	1.0	0.9
IPI00927032	ING3	Uncharacterized protein	99.5%	4.2	1	1	1	2	968,532	1,152,286	1,251,715	1,276,540	128,102	233,460	101,950	147,781	29.6	45.3	18.2	25.9	1.2	0.5	1.3	0.1	1.3	0.2	1.1	0.7	1.1	0.7	1.0	0.9
				MELEADNAGITEILERR	2	99.5%	1																									
IPI00394665	ADAR	isoform 1 of Double-stranded RNA-specific adenosine deaminase	96.5%	1.2	1	1	1	4	626,708	665,588	638,093	731,933	66,295	27,091	45,856	87,488	23.7	9.1	16.1	26.7	1.1	0.6	1.0	0.9	1.2	0.4	-1.0	0.6	1.1	0.5	1.1	0.4
IPI00394668	ADAR	isoform 4 of Double-stranded RNA-specific adenosine deaminase	96.5%	1.2	1	1	1	4	626,708	665,588	638,093	731,933	66,295	27,091	45,856	87,488	23.7	9.1	16.1	26.7	1.1	0.6	1.0	0.9	1.2	0.4	-1.0	0.6	1.1	0.5	1.1	0.4
IPI00760588	ADAR	isoform 5 of Double-stranded RNA-specific adenosine deaminase	96.5%	1.6	1	1	1	4	626,708	665,588	638,093	731,933	66,295	27,091	45,856	87,488	23.7	9.1	16.1	26.7	1.1	0.6	1.0	0.9	1.2	0.4	-1.0	0.6	1.1	0.5	1.1	0.4
IPI00978400	ADAR	Uncharacterized protein	96.5%	1.2	1	1	1	4	626,708	665,588	638,093	731,933	66,295	27,091	45,856	87,488	23.7	9.1	16.1	26.7	1.1	0.6	1.0	0.9	1.2	0.4	-1.0	0.6	1.1	0.5	1.1	0.4
				MGFTEVTPVTGASLR	2	96.5%	1																									
IPI00394679	WHSC2	negative elongation factor A	99.5%	2.6	1	1	1	6	492,942	591,615	468,993	515,677	45,162	43,504	21,238	15,695	20.5	16.4	10.1	6.8	1.2	0.2	-1.1	0.6	1.0	0.7	-1.3	0.04	-1.1	0.2	1.1	0.1
IPI00643383	WHSC2	isoform 1 of Negative elongation factor A	99.5%	2.7	1	1	1	6	492,942	591,615	468,993	515,677	45,162	43,504	21,238	15,695	20.5	16.4	10.1	6.8	1.2	0.2	-1.1	0.6	1.0	0.7	-1.3	0.04	-1.1	0.2	1.1	0.1
IPI00926012	WHSC2	Uncharacterized protein	99.5%	4.8	1	1	1	6	492,942	591,615	468,993	515,677	45,162	43,504	21,238	15,695	20.5	16.4	10.1	6.8	1.2	0.2	-1.1	0.6	1.0	0.7	-1.3	0.04	-1.1	0.2	1.1	0.1
IPI00927834	WHSC2	Protein	99.5%	5.7	1	1	1	6	492,942	591,615	468,993	515,677	45,162	43,504	21,238	15,695	20.5	16.4	10.1	6.8	1.2	0.2	-1.1	0.6	1.0	0.7	-1.3	0.04	-1.1	0.2	1.1	0.1
IPI00970857	WHSC2	Uncharacterized protein	99.5%	6.7	1	1	1	6	492,942	591,615	468,993	515,677	45,162	43,504	21,238	15,695	20.5	16.4	10.1	6.8	1.2	0.2	-1.1	0.6	1.0	0.7	-1.3	0.04	-1.1	0.2	1.1	0.1
IPI01011851	WHSC2	cDNA FLJ36721 fis, clone UTERU2011287, highly similar to Negative elongation fac	99.5%	3.6	1	1	1	6	492,942	591,615	468,993	515,677	45,162	43,504	21,238	15,695	20.5	16.4	10.1	6.8	1.2	0.2	-1.1	0.6	1.0	0.7	-1.3	0.04	-1.1	0.2	1.1	0.1
				LLDISELDMVGAGR	2	99.5%	1																									
IPI00394796	TDRD1	isoform 1 of Tudor domain-containing protein 1	98.7%	1.9	1	1	1	3	573,477	797,453	621,053	828,730	28,850	25,633	55,694	68,834	11.3	7.2	20.1	18.6	1.4	0.0004	1.1	0.5	1.4	0.009	-1.3	0.02	1.0	0.7	1.3	0.05
IPI00440758	TDRD1	Uncharacterized protein	98.7%	2.1	1	1	1	3	573,477	797,453	621,053	828,730	28,850	25,633	55,694	68,834	11.3	7.2	20.1	18.6	1.4	0.0004	1.1	0.5	1.4	0.009	-1.3	0.02	1.0	0.7	1.3	0.05
IPI00647142	TDRD1	isoform 3 of Tudor domain-containing protein 1	98.7%	1.9	1	1	1	3	573,477	797,453	621,053	828,730	28,850	25,633	55,694	68,834	11.3	7.2	20.1	18.6	1.4	0.0004	1.1	0.5	1.4	0.009	-1.3	0.02	1.0	0.7	1.3	0.05
				LVENSLSISNPGLFTSLGPPLR	3	98.1%	1																									
IPI00395462	C15orf63	isoform 2 of Huntingtin-interacting protein K	98.0%	11.6	1	1	1	2	425,187	565,081	575,236	590,315	40,512	75,034	60,046	50,260	21.3	29.7	23.3	19.0	1.3	0.1	1.4	0.07	1.4	0.03	1.0	0.9	1.0	0.8	1.0	0.9
IPI00794593	C15orf63	11 kDa protein	98.0%	15.5	1	1	1	2	425,187	565,081	575,236	590,315	40,512	75,034	60,046	50,260	21.3	29.7	23.3	19.0	1.3	0.1	1.4	0.07	1.4	0.03	1.0	0.9	1.0	0.8	1.0	0.9
				EHMGNVVEALIALTN	2	98.0%	1																									
IPI00395627	CACYBP	isoform 1 of Calcyclin-binding protein	100.0%	27.2	6	6	7	3	13,054,354	14,819,960	13,379,727	16,205,340	862,339	706,074	1,262,847	831,332	14.8	10.7	21.1	11.5	1.1	0.2	1.0	0.8	1.2	0.03	-1.1	0.3	1.1	0.2	1.2	0.1
IPI00552308	CACYBP	cDNA FLJ36106 fis, clone TESTI2021531, highly similar to Calcyclin-binding protein	100.0%	30.9	6	6	7	3	13,054,354	14,819,960	13,379,727	16,205,340	862,339	706,074	1,262,847	831,332	14.8	10.7	21.1	11.5	1.1	0.2	1.0	0.8	1.2	0.03	-1.1	0.3	1.1	0.2	1.2	0.1
IPI00977736	CACYBP	calcyclin-binding protein isoform 2	100.0%	33.5	6	6	7	3	13,054,354	14,819,960	13,379,727	16,205,340	862,339	706,074	1,262,847	831,332	14.8	10.7	21.1	11.5	1.1	0.2	1.0	0.8	1.2	0.03	-1.1	0.3	1.1	0.2	1.2	0.1
				ISNYGWDQSDK	2	89.5%	1																									
				ISNYGWDQSDKFVK	3	89.4%	1																									
				KIYEDGDDDMKR	2	99.9%	1																									
				SFDLLVK	2	99.9%	1																									
				SYSMIVNNLLKPISVEGSSK	3	100.0%	1																									
				WDYLTQVEK	2	99.9%	2																									
IPI00395676	UGP2	isoform 2 of UTP--glucose-1-phosphate uridylyltransferase	100.0%	22.9	9	11	14	1	16,591,004	16,806,549	16,188,907	18,627,567	1,023,134	448,693	741,538	575,323	13.8	6.0	10.2	6.9	1.0	0.9	-1.0	0.8	1.1	0.1	-1.0	0.5	1.1	0.04	1.2	0.03
				CEFVMEVTNK	2	87.1%	1																									
				GLPDNISSVLNK	2	99.8%	2																									
				IQRPPEDSIQPYEK	3	99.7%	1																									
				LGSSFTK	2	94.3%	1																									
				LNGGLGTSMGCK	2	86.8%	1																									
				LVEIAQVPK	2	97.2%	1																									
				NENTFLDLTVQQIEHLNK	2	99.8%	1																									
				NENTFLDLTVQQIEHLNK	3	100.0%	2																									
				SFENSLGINVPR	2	100.0%	1																									
				TLDGGLNVIQLETAVGAAIK	2	100.0%	2																									
				TLDGGLNVIQLETAVGAAIK	3	99.7%	1																									
IPI00395694	TNPO3	isoform 2 of Transportin-3	98.7%	2.1	1	1	1	4	956,780	948,138	940,753	913,333	96,536	61,031	87,392	93,179	22.6	14.4	20.8	22.8	-1.0	0.9	-1.0	0.9	-1.0	0.8	-1.0	0.9	-1.0	0.8	-1.0	0.8
IPI00455127	TNPO3	isoform 3 of Transportin-3	98.7%	2.1	1	1	1	4	956,780	948,138	940,753	913,333	96,536	61,031	87,392	93,179	22.6	14.4	20.8	22.8	-1.0	0.9	-1.0	0.9	-1.0	0.8	-1.0	0.9	-1.0	0.8	-1.0	0.8
IPI00944945	TNPO3	transportin-3 isoform 2	98.7%	2.2	1	1	1	4	956,780	948,138	940,753	913,333	96,536	61,031	87,392	93,179	22.6	14.4	20.8	22.8	-1.0	0.9	-1.0	0.9	-1.0	0.8	-1.0	0.9	-1.0	0.8	-1.0	0.8
IPI00946283	TNPO3	Uncharacterized protein	98.7%	2.2	1	1	1	4	956,780	948,138	940,753	913,333	96,536	61,031	87,392	93,179	22.6	14.4	20.8	22.8	-1.0	0.9	-1.0	0.9	-1.0	0.8	-1.0	0.9	-1.0	0.8	-1.0	0.8
				SVDPENNPTLVEVLEGVVR	2	98.7%	1																									
IPI00395771	PPP1R7	isoform 2 of Protein phosphatase 1 regulatory subunit 7	100.0%	18.9	4	4	4	4	7,264,402	6,993,990	8,124,226	9,491,114	997,382	806,298	1,130,632	809,103	30.7	25.8	31.1	19.1	-1.0	0.8	1.1	0.6	1.3	0.1	1.2	0.4	1.4	0.06	1.2	0.4
IPI00893539	PPP1R7	Protein	100.0%	17.9	4	4	4	4	7,264,402	6,993,990	8,124,226	9,491,114	997,382	806,298	1,130,632	809,103	30.7	25.8	31.1	19.1	-1.0	0.8	1.1	0.6	1.3	0.1	1.2	0.4	1.4	0.06	1.2	0.4
IPI00893764	PPP1R7	Uncharacterized protein	100.0%	20.8	4	4	4	4	7,264,402	6,993,990	8,124,226	9,491,114	997,382	806,298	1,130,632	809,103	30.7	25.8	31.1	19.1	-1.0	0.8	1.1	0.6	1.3	0.1	1.2	0.4	1.4	0.06	1.2	0.4
IPI00894184	PPP1R7	Uncharacterized protein	100.0%	21.3	4	4	4	4	7,264,402	6,993,990	8,124,226	9,491,114	997,382	806,298	1,130,632	809,103	30.7	25.8	31.1	19.1	-1.0	0.8	1.1	0.6	1.3	0.1	1.2	0.4	1.4	0.06	1.2	0.4
				ELYLSHNGIEVIEGLENNNK	3	99.9%	1																									
				IEGLQNLVNLR	2	99.8%	1																									
				LQNLDALTNLTVLSMQSNR	2	81.1%	1																									
				LTMLDIASNR	2	99.4%	1																									
IPI00395772	MYH9	isoform 2 of Myosin-9	100.0%	25.6	25	31	40	1	110,341,615	112,768,545	107,703,555	122,124,240	8,553,712	3,939,129	7,651,928	4,869,447	17.3	7.8	15.9	8.9	1.0	0.8	-1.0	0.8	1.1	0.3	-1.0	0.6	1.1	0.2	1.1	0.2
				ALELDSNLYR	2	99.9%	1																									
				ALEQQVEEMK	2	100.0%	1																									
				ALEQQVEEMKTQLEELEDELQATEDAK	3	100.0%	1																									
				ANLQIDQINTDLNLER	2	100.0%	1																									
				ASREEILAQAK	2	99.3%	1																									
				DLEAHIDSANK	2	100.0%	1																									
				DLKITDVIIGFQACCR	3	99.1%	1																									
				DVLLQVDDER	2	92.1%	1																									
				ELEDATETADAMNR	2	100.0%	2																									
				IAQLEEELEEEQGNTELINDR	2	100.0%	1																									
				IAQLEEQLDNETKER	3	99.3%	1																									
				IIGLDQVAGMSETALPGAFK	2	100.0%	1																									
				IIGLDQVAGMSETALPGAFK	3	100.0%	1																									
				IMGIPEEEQMGLLR	2	100.0%	1																									
				KQELEEICHDLEAR	3	99.7%	1																									
				LEEELDDLLVDLDHQR	2	100.0%	2																									

				LEEELDDLLVDLDHQR	3	100.0%	1																									
				LEVNLQAMK	2	99.5%	1																									
				LTEMETLQSQLMAEK	2	100.0%	2																									
				MQQNIQELEEQLEEEESAR	2	100.0%	1																									
				MQQNIQELEEQLEEEESAR	3	100.0%	1																									
				QAQQERDELADEIANSSGK	3	100.0%	1																									
				RGDLPFVVPR	2	100.0%	2																									
				RGDLPFVVPR	3	100.0%	1																									
				SMEAEMIQLQEELAAAER	2	100.0%	2																									
				SMEAEMIQLQEELAAAER	3	100.0%	2																									
				TDLLLEPYNK	2	100.0%	2																									
				VISGVLQLGNIVFK	2	100.0%	2																									
				VSHLLGINVTDFTR	2	100.0%	2																									
				VSHLLGINVTDFTR	3	100.0%	1																									
				YEILTPNSIPK	2	100.0%	1																									
IPI00396004	KRT8P41	cDNA FLJ46111 fis, clone TESTI2034913, moderately similar to Keratin, type II cyto	98.2%	6.1	1	1	1	1	12,923,710	11,962,530	13,953,800	15,460,500	1,724,859	836,370	1,335,432	673,584	29.8	15.6	21.4	9.7	-1.1	0.6	1.1	0.6	1.2	0.2	1.2	0.2	1.3	0.01	1.1	0.3
				SLDMDSIIPEVK	2	98.2%	1																									
IPI00396171	MAP4	isoform 1 of Microtubule-associated protein 4	100.0%	14.6	12	14	15	2	9,061,406	9,198,153	9,104,058	10,122,414	817,822	323,553	458,011	385,333	20.2	7.9	11.3	8.5	1.0	0.9	1.0	1	1.1	0.3	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00880007	MAP4	Microtubule-associated protein	100.0%	7.3	12	14	15	2	9,061,406	9,198,153	9,104,058	10,122,414	817,822	323,553	458,011	385,333	20.2	7.9	11.3	8.5	1.0	0.9	1.0	1	1.1	0.3	-1.0	0.9	1.1	0.1	1.1	0.1
				DFIATLEAEAFDDVVGETVGK	2	100.0%	2																									
				DFIATLEAEAFDDVVGETVGK	3	100.0%	1																									
				DMQPSMESDMALVK	2	99.5%	1																									
				DMSPLSETEMALGK	2	99.4%	1																									
				EAQTLDSQIQETSI	2	95.4%	1																									
				QPAPTTIGGLNK	2	99.1%	1																									
				SVPADLSRPK	2	86.6%	1																									
				TAGPIASAQK	2	99.8%	1																									
				TTTAAAVASTGPSSR	2	99.6%	1																									
				TTTLSGTAPAAGVVPSR	2	100.0%	1																									
				VALSSETEVALAR	2	98.0%	1																									
				VGSLDNVGHLPAGGAVK	2	99.7%	1																									
				VGSLDNVGHLPAGGAVK	3	100.0%	1																									
				WPTETDVSSAK	2	99.7%	1																									
IPI00396314	CNOT10	isoform 3 of CCR4-NOT transcription complex subunit 10	97.6%	1.7	1	1	1	5	422,230	437,272	397,730	443,886	52,521	42,004	47,360	17,050	27.8	21.5	26.6	8.6	1.0	0.8	-1.1	0.7	1.1	0.7	-1.1	0.5	1.0	0.9	1.1	0.4
IPI00790411	CNOT10	cDNA FLJ56488, highly similar to Homo sapiens CCR4-NOT transcription complex,	97.6%	1.5	1	1	1	5	422,230	437,272	397,730	443,886	52,521	42,004	47,360	17,050	27.8	21.5	26.6	8.6	1.0	0.8	-1.1	0.7	1.1	0.7	-1.1	0.5	1.0	0.9	1.1	0.4
IPI00794753	CNOT10	isoform 4 of CCR4-NOT transcription complex subunit 10	97.6%	1.7	1	1	1	5	422,230	437,272	397,730	443,886	52,521	42,004	47,360	17,050	27.8	21.5	26.6	8.6	1.0	0.8	-1.1	0.7	1.1	0.7	-1.1	0.5	1.0	0.9	1.1	0.4
IPI00878368	CNOT10	isoform 2 of CCR4-NOT transcription complex subunit 10	97.6%	1.6	1	1	1	5	422,230	437,272	397,730	443,886	52,521	42,004	47,360	17,050	27.8	21.5	26.6	8.6	1.0	0.8	-1.1	0.7	1.1	0.7	-1.1	0.5	1.0	0.9	1.1	0.4
IPI01014565	CNOT10	isoform 1 of CCR4-NOT transcription complex subunit 10	97.6%	1.6	1	1	1	5	422,230	437,272	397,730	443,886	52,521	42,004	47,360	17,050	27.8	21.5	26.6	8.6	1.0	0.8	-1.1	0.7	1.1	0.7	-1.1	0.5	1.0	0.9	1.1	0.4
				IILNTAVAEFFK	2	97.6%	1																									
IPI00396321	LRRC59	Leucine-rich repeat-containing protein 59	100.0%	14.7	4	4	4	1	31,249,440	32,397,650	32,088,770	38,759,840	2,690,908	1,483,965	3,349,325	2,213,694	19.3	10.2	23.3	12.8	1.0	0.7	1.0	0.8	1.2	0.06	-1.0	0.9	1.2	0.04	1.2	0.1
				ATILDLSCNK	2	96.3%	1																									
				LQQLPADFGR	2	95.7%	1																									
				LVNLQHLDLLNNK	2	97.1%	1																									
				LVTLPVSFAQLK	2	100.0%	1																									
IPI00396370	EIF3B	isoform 1 of Eukaryotic translation initiation factor 3 subunit B	100.0%	21.3	12	13	15	4	16,863,961	17,822,388	17,603,344	19,889,815	1,787,885	565,544	1,412,029	821,510	23.7	7.1	17.9	9.2	1.1	0.6	1.0	0.8	1.2	0.2	-1.0	0.9	1.1	0.07	1.1	0.2
IPI00719752	EIF3B	isoform 2 of Eukaryotic translation initiation factor 3 subunit B	100.0%	19.8	12	13	15	4	16,863,961	17,822,388	17,603,344	19,889,815	1,787,885	565,544	1,412,029	821,510	23.7	7.1	17.9	9.2	1.1	0.6	1.0	0.8	1.2	0.2	-1.0	0.9	1.1	0.07	1.1	0.2
IPI00893431	EIF3B	cDNA FLJ53410, highly similar to Eukaryotic translation initiation factor 3 subunit 9	100.0%	23.4	12	13	15	4	16,863,961	17,822,388	17,603,344	19,889,815	1,787,885	565,544	1,412,029	821,510	23.7	7.1	17.9	9.2	1.1	0.6	1.0	0.8	1.2	0.2	-1.0	0.9	1.1	0.07	1.1	0.2
IPI00985008	EIF3B	Uncharacterized protein	100.0%	19.8	12	13	15	4	16,863,961	17,822,388	17,603,344	19,889,815	1,787,885	565,544	1,412,029	821,510	23.7	7.1	17.9	9.2	1.1	0.6	1.0	0.8	1.2	0.2	-1.0	0.9	1.1	0.07	1.1	0.2
				DFSWSPGGNIIAFWVPEDKDIPAR	3	98.3%	1																									
				DQYSVIFESGDR	2	93.8%	1																									
				GIALWGGEK	2	98.5%	1																									
				GTQGVVTNFEIFR	2	100.0%	2																									
				GYIFLEYASPAHAVDAVK	2	82.4%	1																									
				GYIFLEYASPAHAVDAVK	3	100.0%	1																									
				MAQELYMEQK	2	99.9%	1																									
				MTLDTLSIYETPSMGLLDKK	3	100.0%	1																									
				QQANTIFWSPQGQFVVLAGLR	3	99.9%	1																									
				TSIFWNDVKDPVSIEER	3	100.0%	1																									
				VDNAYWLWTFQGR	2	99.7%	1																									
				VTLMQLPTR	2	99.9%	2																									
				WTETYVR	2	86.1%	1																									
IPI00396378	HNRNPA2B1	isoform B1 of Heterogeneous nuclear ribonucleoproteins A2/B1	100.0%	58.4	17	23	34	1	69,361,194	70,248,837	69,326,786	78,697,349	4,566,665	1,300,237	4,032,375	2,134,344	14.7	4.1	13.0	6.1	1.0	0.9	-1.0	1	1.1	0.1	-1.0	0.8	1.1	0.01	1.1	0.07
				DYFEEYGKIDTIEIITDR	3	100.0%	1																									
				GFGDGYNGYGGGPGGGNFGGSPGYGGGR	2	100.0%	1																									
				GFGFVTFDDHDPVDK	2	100.0%	2																									
				GFGFVTFDDHDPVDK	3	100.0%	1																									
				GFGFVTFDDHDPVDKIVLQK	2	100.0%	1																									
				GFGFVTFDDHDPVDKIVLQK	3	100.0%	2																									
				GFGFVTFSSMAEVDAAMAAR	2	99.4%	1																									
				GGGGNFGPGPGSNFR	2	100.0%	2																									
				GGNFGFGDSR	1	95.5%	1																									
				GGNFGFGDSR	2	99.9%	2																									
				IDTIEIITDR	2	100.0%	1																									
				KLFIGGLSFETTEESLR	3	100.0%	1																									
				LFIGGLSFETTEESLR	2	100.0%	3																									
				LFIGGLSFETTEESLR	3	99.9%	1																									
				LTDCVVMRDPASK	2	100.0%	1																									
				LTDCVVMRDPASKR	3	95.8%	1																									
				NMGGPYGGGNYGPGGSGGSGGYGGR	2	100.0%	2																									
				NMGGPYGGGNYGPGGSGGSGGYGGR	3	99.9%	1																									
				NYYEQWGK	2	99.7%	2																									
				QEMQEVQSSR	2	100.0%	2																									
				TLETVPLER	2	99.7%	2																									
				YHTINGHNAEVR	2	100.0%	1																									
				YHTINGHNAEVR	3	100.0%	2																									
IPI00396399	TGFB1I1	isoform 2 of Transforming growth factor beta-1-induced transcript 1 protein	99.8%	5.4	1	1	1	2	191,459	206,581	231,390	240,451	37,516	38,327	17,157	49,379	43.8	41.5	16.6	45.9	1.1	0.8	1.2	0.4	1.3	0.5	1.1	0.6	1.2	0.6	1.0	0.9
IPI00761017	TGFB1I1	isoform 1 of Transforming growth factor beta-1-induced transcript 1 protein	99.8%	5.2	1	1	1	2	191,459	206,581	231,390	240,451	37,516	38,327	17,157	49,379	43.8	41.5	16.6	45.9	1.1	0.8	1.2	0.4	1.3	0.5	1.1	0.6	1.2	0.6	1.0	0.9
				AWHPEHFVCGGCSTALGGSSFFEK	2	85.5%	1																									
IPI00396435	DHX15	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	100.0%	9.1	6	6	6	2	16,512,734	17,068,271	17,772,756	20,526,238	883,924	955,484	1,102,019	515,152	12.0	12.5	13.9	5.6	1.0	0.7	1.1	0.4	1.2	0.004	1.0	0.6	1.2	0.01	1.2	0.05
IPI01015591	DHX15	cDNA FLJ55635, highly similar to pre-mRNA-splicing factorATP-dependent RNA hel	100.0%	9.2	6	6	6	2	16,512,734	17,068,271	17,772,756	20,526,238	883,924	955,484	1,102,019	515,152	12.0	12.5	13.9	5.6	1.0	0.7	1.1	0.4	1.2	0.004	1.0	0.6	1.2	0.01	1.2	0.05
				EAMNDPLLER	2	99.7%	1																									
				FTDILVR	2	99.6%	1																									
				LGIDDLVHFDFMDPPAPETLMR	3	97.4%	1																									
				TLATDILMGVLK	2	100.0%	1																									
				YGVIILDEAHER	3	97.6%	1																									
				YMTDGMLLR	2	93.2%	1																									
IPI00472724	EEF1A1;EEF1A1P5	Putative elongation factor 1-alpha-like 3	100.0%	47.4	17	23	32	2	94,122,221	95,594,982	96,917,988	109,823,036	8,046,588	3,297,069	9,146,986	3,576,308	19.1	7.7	21.1	7.3	1.0	0.9	1.0	0.8	1.2	0.1	1.0	0.9	1.1	0.02	1.1	0.2
IPI00396485	EEF1A1	Elongation factor 1-alpha 1	100.0%	47.4	17	23	32	2	94,122,221	95,594,982	96,917,988	109,823,036	8,046,588	3,297,069	9,146,986	3,576,308	19.1	7.7	21.1	7.3	1.0	0.9	1.0	0.8	1.2	0.1	1.0	0.9	1.1	0.02	1.1	0.2
				DGNASGTTLLEALDCILPPTRPTDKPLR	3	100.0%	1																									
				EHALLAYTLGVK	2	99.4%	1																									
				EHALLAYTLGVK	3	99.9%	1																									
				EVSTYIK	1	96.3%	1																									
				EVSTYIKK	2	98.6%	1																									
				IGGIGTVPVGR	2	100.0%	3																									
				LPLQDVYK	2	99.9%	1																									
				MDSTEPPYSQK	2	100.0%	1																									
				NMITGTSQADCAVLIVAAGVGEFEAGISK	2	100.0%	2																									
				NMITGTSQADCAVLIVAAGVGEFEAGISK	3	100.0%	1																									
				QLIVGVNK	1	99.2%	1																									
				QLIVGVNK	2	95.0%	2																									
				QTVAVGVIK	1	92.1%	1																									
				QTVAVGVIK	2	100.0%	2																									
				SGDAAIVDMVPGKPMCVESFSDYPPLGR	3	100.0%	1																									
				STTTGHLIYK	2	100.0%	2																									
				THINIVVIGHVDSGK	3	98.4%	1																									
				VETGVLKPGMVVTFAPVNVTTEVK	3	100.0%	1																									
				YEEIVK	1	97.5%	1																									
				YEEIVK	2	93.9%	2																									
				YEEIVKEVSTYIK	2	91.5%	1																									
				YYVTIIDAPGHR	2	100.0%	2																									
				YYVTIIDAPGHR	3	100.0%	2																									
IPI00396967	FHL2	FHL2 isoform 5	93.2%	6.9	2	2	2	2	3,235,723	2,839,005	3,366,356	3,335,914	101,010	169,355	244,427	159,641	7.0	13.3	16.2	10.7	-1.1	0.08	1.0	0.6	1.0	0.6	1.2	0.1	1.2	0.07	-1.0	0.9
IPI00743342	FHL2	Four and a half LIM domains protein 2	93.2%	9.7	2	2	2	2	3,235,723	2,839,005	3,366,356	3,335,914	101,010	169,355	244,427	159,641	7.0	13.3	16.2	10.7	-1.1	0.08	1.0	0.6	1.0	0.6	1.2	0.1	1.2	0.07	-1.0	0.9
				CAGCTNPISGLGGTK	2	90.4%	1																									
				DNQNFCVPCYEK	2	93.2%	1																									
IPI00847956	-	Similar to 40S ribosomal protein S27	99.4%	18.6	1	1	1	6	2,243,467	2,348,367	2,169,120	2,499,865	219,126	141,740	232,409	137,520	21.8	13.5	24.0	12.3	1.0	0.7	-1.0	0.8	1.1	0.4	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00420117	RPS27L	Ribosomal protein S27	99.4%	13.4	1	1	1	6	2,243,467	2,348,367	2,169,120	2,499,865	219,126	141,740	232,409	137,520	21.8	13.5	24.0	12.3	1.0	0.7	-1.0	0.8	1.1	0.4	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00746004	RPS27L	40S ribosomal protein S27-like	99.4%	15.5	1	1	1	6	2,243,467	2,348,367	2,169,120	2,499,865	219,126	141,740	232,409	137,520	21.8	13.5	24.0	12.3	1.0	0.7	-1.0	0.8	1.1	0.4	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00397358	RPS27	Ribosomal protein S27	99.4%	8.8	1	1	1	6	2,243,467	2,348,367	2,169,120	2,499,865	219,126	141,740	232,409	137,520	21.8	13.5	24.0	12.3	1.0	0.7	-1.0	0.8	1.1	0.4	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00514399	RPS27	Uncharacterized protein	99.4%	19.7	1	1	1	6	2,243,467	2,348,367	2,169,120	2,499,865	219,126	141,740	232,409	137,520	21.8	13.5	24.0	12.3	1.0	0.7	-1.0	0.8	1.1	0.4	-1.1	0.5	1.1	0.5	1.2	0.3
IPI01008896	RPS27	40S ribosomal protein S27	99.4%	15.5	1	1	1	6	2,243,467	2,348,367	2,169,120	2,499,865	219,126	141,740	232,409	137,520	21.8	13.5	24.0	12.3	1.0	0.7	-1.0	0.8	1.1	0.4	-1.1	0.5	1.1	0.5	1.2	0.3
				LVQSPNSYFMDVK	2	99.4%	1																									
IPI00397379	EPN2	isoform 1 of Epsin-2	98.8%	2.7	1	1	1	6	329,886	346,208	308,619	417,657	64,076	36,870	34,968	22,333	43.4	23.8	25.3	12.0	1.0	0.8	-1.1	0.8	1.3	0.3	-1.1	0.5	1.2	0.1	1.4	0.03
IPI00397381	EPN2	epsin-2 isoform a	98.8%	2.9	1	1	1	6	329,886	346,208	308,619	417,657	64,076	36,870	34,968	22,333	43.4	23.8	25.3	12.0	1.0	0.8	-1.1	0.8	1.3	0.3	-1.1	0.5	1.2	0.1	1.4	0.03
IPI00790403	EPN2	Uncharacterized protein	98.8%	3.4	1	1	1	6	329,886	346,208	308,619	417,657	64,076	36,870	34,968	22,333	43.4	23.8	25.3	12.0	1.0	0.8	-1.1	0.8	1.3	0.3	-1.1	0.5	1.2	0.1	1.4	0.03
IPI00791739	EPN2	Uncharacterized protein	98.8%	3.5	1	1	1	6	329,886	346,208	308,619	417,657	64,076	36,870	34,968	22,333	43.4	23.8	25.3	12.0	1.0	0.8	-1.1	0.8	1.3	0.3	-1.1	0.5	1.2	0.1	1.4	0.03
IPI00915293	EPN2	isoform 3 of Epsin-2	98.8%	3.1	1	1	1	6	329,886	346,208	308,619	417,657	64,076	36,870	34,968	22,333	43.4	23.8	25.3	12.0	1.0	0.8	-1.1	0.8	1.3	0.3	-1.1	0.5	1.2	0.1	1.4	0.03
IPI00915466	EPN2	69 kDa protein	98.8%	2.7	1	1	1	6	329,886	346,208	308,619	417,657	64,076	36,870	34,968	22,333	43.4	23.8	25.3	12.0	1.0	0.8	-1.1	0.8	1.3	0.3	-1.1	0.5	1.2	0.1	1.4	0.03
				MAQVATGMGSNQITFGR	2	98.8%	1																									
IPI00397519	CLINT1	isoform 2 of Clathrin interactor 1	100.0%	9.3	3	3	4	1	6,306,829	6,645,955	6,379,092	7,318,999	553,202	358,738	528,924	541,874	19.6	12.1	18.5	16.6	1.1	0.6	1.0	0.9	1.2	0.2	-1.0	0.7	1.1	0.3	1.1	0.2
				ATFMYEQFPELMNMLWSR	3	100.0%	1																									
				SQPLQNVSTVLQKPNPLYNQNTDMVQK	3	100.0%	1																									
				YVGVSSDSVGGFR	2	100.0%	2																									
IPI00397526	MYH10	isoform 1 of Myosin-10	100.0%	6.2	9	10	10	3	16,602,259	18,844,646	17,323,986	21,226,097	1,446,674	590,197	1,463,457	545,159	19.5	7.0	18.9	5.7	1.1	0.2	1.0	0.7	1.3	0.03	-1.1	0.4	1.1	0.02	1.2	0.05
IPI00479307	MYH10	isoform 2 of Myosin-10	100.0%	6.1	9	10	10	3	16,602,259	18,844,646	17,323,986	21,226,097	1,446,674	590,197	1,463,457	545,159	19.5	7.0	18.9	5.7	1.1	0.2	1.0	0.7	1.3	0.03	-1.1	0.4	1.1	0.02	1.2	0.05
IPI00790503	MYH10	isoform 3 of Myosin-10	100.0%	6.1	9	10	10	3	16,602,259	18,844,646	17,323,986	21,226,097	1,446,674	590,197	1,463,457	545,159	19.5	7.0	18.9	5.7	1.1	0.2	1.0	0.7	1.3	0.03	-1.1	0.4	1.1	0.02	1.2	0.05
				ADEWLMK	2	99.5%	1																									

				ELEAELEDER	2	87.4%	1																									
				IGQLEEQLEQEAK	2	99.9%	1																									
				KEEELQGALAR	3	89.4%	1																									
				LQNELDNVSTLLEEAEK	3	96.6%	1																									
				NILAEQLQAETELFAEAEEMR	2	100.0%	1																									
				NILAEQLQAETELFAEAEEMR	3	99.3%	1																									
				QLLQANPILESFGNAK	2	86.8%	1																									
				SLEAEILQLQEELASSER	2	98.1%	1																									
				VKPLLQVTR	3	98.4%	1																									
IPI00397609	-	18 kDa protein	100.0%	11.2	2	2	3	2	6,133,783	5,974,020	6,082,673	7,319,500	507,908	319,270	471,119	400,024	18.5	12.0	17.3	12.2	-1.0	0.8	-1.0	0.9	1.2	0.1	1.0	0.9	1.2	0.03	1.2	0.08
IPI00790711	-	17 kDa protein	100.0%	11.9	2	2	3	2	6,133,783	5,974,020	6,082,673	7,319,500	507,908	319,270	471,119	400,024	18.5	12.0	17.3	12.2	-1.0	0.8	-1.0	0.9	1.2	0.1	1.0	0.9	1.2	0.03	1.2	0.08
				IPDWFLNR	2	99.9%	2																									
				VLNTNIDGR	2	99.7%	1																									
IPI00397611	-	24 kDa protein	99.9%	5.2	1	1	1	1	6,352,210	5,997,380	6,111,630	6,114,650	371,930	615,453	402,086	448,048	13.1	23.0	14.7	16.4	-1.1	0.6	-1.0	0.7	-1.0	0.7	1.0	0.9	1.0	0.9	1.0	1
				STESLQANVQR	2	98.4%	1																									
IPI00974423	-	Formin homology 2 domain containing 3 variant	95.5%	1.0	1	1	1	5	241,059	241,718	356,656	329,222	24,526	17,853	54,505	42,464	22.8	16.5	34.2	28.8	1.0	1	1.5	0.09	1.4	0.1	1.5	0.1	1.4	0.09	-1.1	0.7
IPI00397675	FHOD3	isoform 1 of FH1/FH2 domain-containing protein 3	95.5%	1.1	1	1	1	5	241,059	241,718	356,656	329,222	24,526	17,853	54,505	42,464	22.8	16.5	34.2	28.8	1.0	1	1.5	0.09	1.4	0.1	1.5	0.1	1.4	0.09	-1.1	0.7
IPI00843844	FHOD3	isoform 2 of FH1/FH2 domain-containing protein 3	95.5%	1.1	1	1	1	5	241,059	241,718	356,656	329,222	24,526	17,853	54,505	42,464	22.8	16.5	34.2	28.8	1.0	1	1.5	0.09	1.4	0.1	1.5	0.1	1.4	0.09	-1.1	0.7
IPI00903056	FHOD3	cDNA FLJ34580 fis, clone KIDNE2008473, highly similar to Homo sapiens formin ho	95.5%	2.5	1	1	1	5	241,059	241,718	356,656	329,222	24,526	17,853	54,505	42,464	22.8	16.5	34.2	28.8	1.0	1	1.5	0.09	1.4	0.1	1.5	0.1	1.4	0.09	-1.1	0.7
IPI00939843	FHOD3	isoform 3 of FH1/FH2 domain-containing protein 3	95.5%	1.1	1	1	1	5	241,059	241,718	356,656	329,222	24,526	17,853	54,505	42,464	22.8	16.5	34.2	28.8	1.0	1	1.5	0.09	1.4	0.1	1.5	0.1	1.4	0.09	-1.1	0.7
				FHSFLLFMGHPPYAIR	2	95.5%	1																									
IPI00397676	-	30 kDa protein	100.0%	9.0	2	2	3	2	3,558,262	3,818,613	3,513,879	4,361,114	295,181	279,007	118,035	84,029	18.6	16.3	7.5	4.3	1.1	0.5	-1.0	0.9	1.2	0.05	-1.1	0.3	1.1	0.1	1.2	0.0004
IPI00478896	RPL7A	Ribosomal protein L7a	100.0%	12.6	2	2	3	2	3,558,262	3,818,613	3,513,879	4,361,114	295,181	279,007	118,035	84,029	18.6	16.3	7.5	4.3	1.1	0.5	-1.0	0.9	1.2	0.05	-1.1	0.3	1.1	0.1	1.2	0.0004
				AGVNTVTTLVENK	2	100.0%	2																									
				NFGIGQDIQPK	2	99.6%	1																									
IPI00397728	PPP1R12A	isoform 2 of Protein phosphatase 1 regulatory subunit 12A	100.0%	3.6	2	2	2	2	525,001	489,515	544,822	693,982	43,406	39,072	45,275	19,520	18.5	17.9	18.6	6.3	-1.1	0.6	1.0	0.8	1.3	0.008	1.1	0.4	1.4	0.002	1.3	0.02
IPI01015368	PPP1R12A	111 kDa protein	100.0%	3.6	2	2	2	2	525,001	489,515	544,822	693,982	43,406	39,072	45,275	19,520	18.5	17.9	18.6	6.3	-1.1	0.6	1.0	0.8	1.3	0.008	1.1	0.4	1.4	0.002	1.3	0.02
				TGSYGALAEITASK	2	96.0%	1																									
				VGQTAFDVADEDILGYLEELQK	3	100.0%	1																									
IPI00397820	KIF26B	isoform 2 of Kinesin-like protein KIF26B	97.8%	1.0	1	1	1	2	1,465,015	1,711,440	1,668,565	1,729,520	96,335	107,479	152,481	21,554	14.7	14.0	20.4	2.8	1.2	0.1	1.1	0.3	1.2	0.05	-1.0	0.8	1.0	0.9	1.0	0.7
IPI00868928	KIF26B	isoform 1 of Kinesin-like protein KIF26B	97.8%	0.9	1	1	1	2	1,465,015	1,711,440	1,668,565	1,729,520	96,335	107,479	152,481	21,554	14.7	14.0	20.4	2.8	1.2	0.1	1.1	0.3	1.2	0.05	-1.0	0.8	1.0	0.9	1.0	0.7
				AGQSKISAVSRLLLASPR	3	97.8%	1																									
IPI00397904	NUP93	Nuclear pore complex protein Nup93	100.0%	7.9	4	4	4	1	18,924,560	19,985,655	19,269,800	22,139,615	804,796	813,903	1,052,691	656,881	9.5	9.1	12.2	6.6	1.1	0.4	1.0	0.8	1.2	0.01	-1.0	0.6	1.1	0.07	1.1	0.05
				GLDISHISQR	2	96.2%	1																									
				ILHTLLASGEDALDFTQESEPSYISDVGPPGR	3	99.9%	1																									
				NLQEIQQAGER	2	98.6%	1																									
				TLITFAGMIPYR	2	98.4%	1																									
IPI00397949	GPR56	isoform 2 of G-protein coupled receptor 56	90.9%	1.8	1	1	1	5	89,929	95,671	118,471	111,594	11,580	17,329	20,497	14,897	28.8	40.5	38.7	29.9	1.1	0.8	1.3	0.3	1.2	0.3	1.2	0.4	1.2	0.5	-1.1	0.8
IPI00412420	GPR56	isoform 1 of G-protein coupled receptor 56	90.9%	1.7	1	1	1	5	89,929	95,671	118,471	111,594	11,580	17,329	20,497	14,897	28.8	40.5	38.7	29.9	1.1	0.8	1.3	0.3	1.2	0.3	1.2	0.4	1.2	0.5	-1.1	0.8
IPI00442012	GPR56	Uncharacterized protein	90.9%	2.3	1	1	1	5	89,929	95,671	118,471	111,594	11,580	17,329	20,497	14,897	28.8	40.5	38.7	29.9	1.1	0.8	1.3	0.3	1.2	0.3	1.2	0.4	1.2	0.5	-1.1	0.8
IPI00925577	GPR56	G-protein coupled receptor 56 isoform c precursor	90.9%	1.7	1	1	1	5	89,929	95,671	118,471	111,594	11,580	17,329	20,497	14,897	28.8	40.5	38.7	29.9	1.1	0.8	1.3	0.3	1.2	0.3	1.2	0.4	1.2	0.5	-1.1	0.8
IPI01014131	GPR56	57 kDa protein	90.9%	2.3	1	1	1	5	89,929	95,671	118,471	111,594	11,580	17,329	20,497	14,897	28.8	40.5	38.7	29.9	1.1	0.8	1.3	0.3	1.2	0.3	1.2	0.4	1.2	0.5	-1.1	0.8
				LPISSGSTSSSR	2	91.0%	1																									
IPI00398002	PLEC	isoform 3 of Plectin	100.0%	24.7	85	87	98	1	78,275,837	78,961,113	77,790,223	88,383,941	6,422,949	2,720,691	4,963,503	3,108,130	18.4	7.7	14.3	7.9	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.05	1.1	0.1
				AELELELGR	2	99.1%	1																									
				AFCGFEDPR	2	91.4%	1																									
				AGTLSITEFADMLSGNAGGFR	2	100.0%	2																									
				AGVAAPATQVAQVTLQSVQR	2	100.0%	1																									
				AGVAAPATQVAQVTLQSVQR	3	99.4%	1																									
				AGVVGPELHEQLLSAEK	3	92.1%	1																									
				AKLEQLFQDEVAK	2	99.0%	1																									
				APVPASELLASGVLSR	2	100.0%	2																									
				AQLEPVASPAK	2	99.9%	1																									
				AQLMADFQAGR	2	100.0%	1																									
				AQVEQELTTLR	2	100.0%	1																									
				ARQEELYSELQAR	2	99.2%	1																									
				ATTAALLLEAQAATGFLVDPVR	3	100.0%	1																									
				CDNFTSSWR	2	99.9%	1																									
				DDGTGQLLLPLSDAR	2	99.4%	1																									
				DLLPSDMAVALLEAQAGTGHIIDPATSAR	3	97.8%	1																									
				DLSELGSVR	2	97.7%	1																									
				DPYSGSTISLFQAMQK	2	100.0%	1																									
				DSQDAGGFGPEDR	2	95.4%	1																									
				EGLTSIEEVTK	2	100.0%	1																									
				EQELQQTLQQEQSVLDQLR	2	100.0%	1																									
				ESADPLGAWLQDAR	2	100.0%	2																									
				FAEQTLR	2	97.2%	1																									
				FLEGTSCIAGVFVDATK	2	100.0%	1																									
				FLEVQYLTGGLIEPDTPGR	2	100.0%	1																									
				FLEVQYLTGGLIEPDTPGR	3	99.4%	1																									
				FLEVQYLTGGLIEPDTPGRVPLDEALQR	3	100.0%	1																									
				FRELAEEAAR	2	88.2%	1																									
				GANVIAGVWLEEAGQK	2	100.0%	1																									
				GFFDPNTEENLTYLQLMER	2	100.0%	1																									
				GFFDPNTHENLTYLQLLER	3	99.9%	1																									
				GGELVYTDSEAR	2	100.0%	2																									
				GLFDEEMNEILTDPSDDTK	2	100.0%	1																									
				GLHQSIEEFR	2	98.6%	1																									
				GYFDEEMNR	2	100.0%	2																									
				IIITVVEEQEQK	2	100.0%	1																									
				ISYKDALDR	2	98.5%	1																									
				KGLVGPELHDR	3	99.5%	1																									
				LAAEQELIR	2	98.9%	1																									
				LEQLFQDEVAK	2	100.0%	1																									
				LKAEAELLQQQK	2	99.2%	1																									
				LLDAQLATGGIVDPR	2	100.0%	2																									
				LLDAQLSTGGIVDPSK	2	100.0%	2																									
				LLDPEDVDVPQPDEK	2	90.6%	1																									
				LLEAAAQSTK	2	99.9%	2																									
				LLEAQACTGGIIDPSTGERFPVTDAVNK	3	87.1%	1																									
				LLEAQIATGGIIDPVHSHR	3	100.0%	1																									
				LLEAQIATGGVIDPVHSHR	3	99.7%	1																									
				LLLEAQAATGFLLDPVKGER	3	99.9%	1																									
				LQNVQIALDYLR	2	100.0%	1																									
				LREQLQLLEEQHR	3	95.2%	1																									
				LRIEEEIR	3	91.3%	1																									
				LTAEDLFEAR	2	98.5%	1																									
				LTVDEAVR	2	93.3%	1																									
				MGIVGPEFK	2	100.0%	1																									
				MQAVQEATR	2	99.0%	2																									
				MVEGYQGLR	2	80.9%	1																									
				NLVDNITGQR	2	99.8%	1																									
				QITMEELVR	2	91.5%	1																									
				QLLEEELAR	2	98.0%	1																									
				QVEEEILALK	2	97.3%	1																									
				QVQVALETAQR	2	99.9%	1																									
				QYDIDDAIAK	2	99.9%	1																									
				QYINAIKDYELQLVTYK	3	98.2%	1																									
				RASFAEK	2	83.5%	1																									
				RPELEDSTLR	2	99.9%	1																									
				SEEMQTVQQEQLLQETQALQQSFLSEK	3	95.6%	1																									
				SELELTLGK	2	80.0%	1																									
				SIQEELQQLR	2	99.9%	1																									
				SKEQAELEAAR	2	94.1%	1																									
				SLQEEHVAVAQLR	2	99.7%	1																									
				SLVPAAELLESR	2	99.9%	1																									
				SQVEEELFSVR	2	99.9%	1																									
				SQVMDEATALQLR	2	100.0%	2																									
				SYVDPSTDER	2	99.6%	1																									
				TPVEVPVGGFK	2	100.0%	1																									
				TVTIWEIINSEYFTAEQR	2	99.8%	1																									
				VDGAEWGVDLPSVEAQLGSHR	3	100.0%	1																									
				VIDRELYQQLQR	3	95.2%	1																									
				VLADPSDDTK	2	82.7%	1																									
				VPDVQDGELQLR	2	98.3%	1																									
				VPLDVACAR	2	99.8%	1																									
				VPVDVAYQR	2	99.9%	2																									
				VPVDVAYR	2	99.8%	1																									
				VQSGSESVIQEYVDLR	2	100.0%	1																									
				VSAQRLQEAGILSAEELQRLAQGHTTVDELAR	3	99.0%	1																									
				YLQDLLAWVEENQHR	3	100.0%	1																									
IPI00913856	-	Orotidine 5'-phosphate decarboxylase	96.9%	5.6	1	1	1	4	279,309	247,674	248,814	240,125	31,419	22,844	24,718	19,301	25.2	20.6	22.2	18.0	-1.1	0.4	-1.1	0.5	-1.2	0.3	1.0	1	-1.0	0.8	-1.0	0.8
IPI00398067	UMPS	isoform 2 of Uridine 5'-monophosphate synthase	96.9%	5.6	1	1	1	4	279,309	247,674	248,814	240,125	31,419	22,844	24,718	19,301	25.2	20.6	22.2	18.0	-1.1	0.4	-1.1	0.5	-1.2	0.3	1.0	1	-1.0	0.8	-1.0	0.8
IPI00913888	UMPS	Orotidine 5'-phosphate decarboxylase	96.9%	8.3	1	1	1	4	279,309	247,674	248,814	240,125	31,419	22,844	24,718	19,301	25.2	20.6	22.2	18.0	-1.1	0.4	-1.1	0.5	-1.2	0.3	1.0	1	-1.0	0.8	-1.0	0.8
IPI01013339	UMPS	Uridine monophosphate synthetase isoform F	96.9%	4.4	1	1	1	4	279,309	247,674	248,814	240,125	31,419	22,844	24,718	19,301	25.2	20.6	22.2	18.0	-1.1	0.4	-1.1	0.5	-1.2	0.3	1.0	1	-1.0	0.8	-1.0	0.8
				ELLQLADALGPSICMLK	2	96.9%	1																									
IPI00398129	-	Similar to 3-hydroxybutyrate dehydrogenase type 2	99.2%	5.0	1	1	1	2	1,785,860	1,930,198	1,704,458	2,150,580	146,672	88,970	174,732	154,155	18.4	10.3	22.9	16.0	1.1	0.4	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.3	1.3	0.09
IPI00968138	NHEDC2	Uncharacterized protein	99.2%	10.7	1	1	1	2	1,785,860	1,930,198	1,704,458	2,150,580	146,672	88,970	174,732	154,155	18.4	10.3	22.9	16.0	1.1	0.4	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.3	1.3	0.09
				SVAADFIQQGIR	2	99.2%	1																									
IPI00398162	NRAP	isoform 2 of Nebulin-related-anchoring protein	93.8%	0.5	1	1	1	4	270,003	308,915	320,280	338,505	31,790	28,896	18,364	31,605	26.3	20.9	12.8	20.9	1.1	0.4	1.2	0.2	1.3	0.2	1.0	0.7	1.1	0.5	1.1	0.6
IPI00478974	NRAP	isoform 3 of Nebulin-related-anchoring protein	93.8%	0.5	1	1	1	4	270,003	308,915	320,280	338,505	31,790	28,896	18,364	31,605	26.3	20.9	12.8	20.9	1.1	0.4	1.2	0.2	1.3	0.2	1.0	0.7	1.1	0.5	1.1	0.6
IPI00745227	NRAP	isoform 1 of Nebulin-related-anchoring protein	93.8%	0.5	1	1	1	4	270,003	308,915	320,280	338,505	31,790	28,896	18,364	31,605	26.3	20.9	12.8	20.9	1.1	0.4	1.2	0.2	1.3	0.2	1.0	0.7	1.1	0.5	1.1	0.6
IPI00786896	NRAP	isoform 4 of Nebulin-related-anchoring protein	93.8%	0.5	1	1	1	4	270,003	308,915	320,280	338,505	31,790	28,896	18,364	31,605	26.3	20.9	12.8	20.9	1.1	0.4	1.2	0.2	1.3	0.2	1.0	0.7	1.1	0.5	1.1	0.6
				AGELISEK	1	81.2%	1																									
IPI00398728	RP1L1	isoform 1 of Retinitis pigmentosa 1-like 1 protein	94.9%	1.1	2	2	2	1	8,503,020	8,358,163	8,348,590	9,673,048	724,084	411,718	837,806	798,765	19.0	11.0	22.4	18.5	-1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	1	1.2	0.2	1.2	0.3
				RSSASQGAGSR	2	93.3%	1																									
				RSSSCGSTGSSHQSTAR	2	91.3%	1																									

IPI00398735	CNN2	calponin-2 isoform b	100.0%	15.2	3	3	3	1	4,478,037	4,134,340	4,743,797	4,597,990	92,575	180,864	110,355	267,861	4.6	9.8	5.2	13.0	-1.1	0.1	1.1	0.1	1.0	0.7	1.1	0.02	1.1	0.2	-1.0	0.6
				CASQVGMTAPGTR	2	99.1%	1																									
				GPSYGLSAEVK	2	98.6%	1																									
				TWIEGLTGLSIGPDFQK	2	100.0%	1																									
IPI00398758	ECI1	isoform 2 of Enoyl-CoA delta isomerase 1, mitochondrial	99.9%	12.6	3	3	4	1	5,923,645	6,448,485	5,809,690	6,437,495	397,713	356,056	482,748	400,486	15.0	12.4	18.6	13.9	1.1	0.4	-1.0	0.9	1.1	0.4	-1.1	0.3	-1.0	1	1.1	0.3
				DADVQNFVSFISK	2	99.5%	2																									
				SLQMYLER	2	98.5%	1																									
				VLVEPDAGAGVAVMK	2	99.8%	1																									
IPI00398772	PRDM10	isoform 6 of PR domain zinc finger protein 10	100.0%	1.8	1	2	4	1	3,040,565	3,032,535	2,874,770	3,344,290	150,314	102,542	199,672	149,757	11.1	7.6	15.5	10.0	-1.0	1	-1.1	0.5	1.1	0.2	-1.1	0.5	1.1	0.1	1.2	0.1
				SVTELNGDIITNTMTLGDIVFK	2	100.0%	2																									
				SVTELNGDIITNTMTLGDIVFK	3	100.0%	2																									
IPI00398780	GPX1	glutathione peroxidase 1 isoform 2	100.0%	24.5	2	2	2	1	3,172,110	3,358,175	3,041,620	3,658,770	385,841	206,970	175,083	136,529	27.2	13.8	12.9	8.3	1.1	0.7	-1.0	0.8	1.2	0.3	-1.1	0.3	1.1	0.3	1.2	0.02
				DYTQMNELQR	2	99.6%	1																									
				PLAGGEPVSLGSLR	2	99.7%	1																									
IPI00398845	MAGED1	isoform 2 of Melanoma-associated antigen D1	96.1%	2.0	1	1	1	1	5,773,100	6,932,040	5,894,910	6,772,840	589,672	416,987	316,455	258,470	22.8	13.5	12.0	8.5	1.2	0.1	1.0	0.9	1.2	0.2	-1.2	0.08	-1.0	0.8	1.1	0.06
				MDCGAGLLGFQNPDACR	3	96.1%	1																									
IPI00398922	PPP1R14B	Protein phosphatase 1 regulatory subunit 14B	100.0%	6.5	1	1	1	1	170,373	150,778	191,961	241,346	15,909	16,108	35,329	24,829	20.9	23.9	41.2	23.0	-1.1	0.4	1.1	0.6	1.4	0.04	1.3	0.3	1.6	0.02	1.3	0.3
				LNLEEWILEQLTR	3	99.1%	1																									
IPI00399077	-	32 kDa protein	100.0%	9.6	2	2	4	1	2,371,880	2,418,575	2,286,485	2,762,491	231,732	113,521	174,411	98,415	21.9	10.5	17.1	8.0	1.0	0.9	-1.0	0.8	1.2	0.2	-1.1	0.5	1.1	0.05	1.2	0.04
				AIVAIENPADVSVISSR	2	100.0%	2																									
				YVDIAIPCNNK	2	100.0%	2																									
IPI00399089	MESDC2	LDLR chaperone MESD	99.9%	12.0	2	2	2	1	4,885,660	4,812,350	4,919,160	5,951,890	554,275	246,012	442,157	266,643	25.4	11.4	20.1	10.0	-1.0	0.9	1.0	1	1.2	0.1	1.0	0.8	1.2	0.01	1.2	0.08
				DGSYAWEIKDFLVGQDR	3	99.9%	1																									
				IDPSKPESILK	2	90.2%	1																									
IPI00399318	COPE	coatomer subunit epsilon isoform b	100.0%	19.8	3	3	4	1	8,425,655	8,615,110	9,646,803	10,226,295	909,372	430,143	912,157	363,413	24.1	11.2	21.1	8.0	1.0	0.9	1.1	0.4	1.2	0.1	1.1	0.3	1.2	0.02	1.1	0.6
				FGVVLDEIKPSSAPELQAVR	3	100.0%	1																									
				LQDAYYIFQEMADK	2	100.0%	2																									
				NAFYIGSYQQCINEAQR	3	99.2%	1																									
IPI00399319	COPE	coatomer subunit epsilon isoform c	100.0%	14.5	2	2	2	1	7,389,922	7,436,857	8,599,473	8,892,495	750,466	382,339	845,471	329,279	22.7	11.5	22.0	8.3	1.0	1	1.2	0.3	1.2	0.1	1.2	0.2	1.2	0.02	1.0	0.8
				FGVVLDEIKPSSAPELQAVR	3	100.0%	1																									
				NAFYIGSYQQCINEAQR	3	99.2%	1																									
IPI00400834	MED13L	Mediator of RNA polymerase II transcription subunit 13-like	100.0%	2.0	2	2	2	1	15,575,350	16,381,200	13,959,640	17,514,100	2,432,358	1,412,356	1,666,993	1,149,157	34.9	19.3	26.7	14.7	1.1	0.8	-1.1	0.6	1.1	0.5	-1.2	0.3	1.1	0.6	1.3	0.1
				IPDACLFRPSWAIPPK	3	97.3%	1																									
				RYNFGGHGDCGPIISAPAQDDPILLSFIR	3	98.6%	1																									
IPI00401259	-	Putative coiled-coil-helix-coiled-coil-helix domain-containing protein CHCHD2P9, mit	100.0%	27.2	2	2	2	1	1,486,979	1,595,416	1,434,878	1,697,739	110,405	136,585	111,422	122,233	16.6	19.1	17.4	16.1	1.1	0.6	-1.0	0.7	1.1	0.2	-1.1	0.4	1.1	0.6	1.2	0.2
				AAPRPAPVAQPPAAAPPSAVGSSAAAPR	3	100.0%	1																									
				QFLECAQNQGDIK	2	95.3%	1																									
IPI00401264	ERP44	Endoplasmic reticulum resident protein 44	100.0%	10.3	4	4	4	1	20,526,350	19,776,040	19,131,110	21,863,200	1,767,428	840,603	1,297,983	1,033,802	19.3	9.5	15.2	10.6	-1.0	0.7	-1.1	0.5	1.1	0.5	-1.0	0.7	1.1	0.2	1.1	0.1
				DLAEITTLDR	2	100.0%	1																									
				HMYVFGDFKDVLIPGK	3	99.9%	1																									
				NGMMMK	2	91.3%	1																									
				QFVFDLHSGK	3	99.9%	1																									
IPI00401773	VPS37C	Vacuolar protein sorting-associated protein 37C	97.1%	5.4	1	1	1	2	168,139	177,253	211,359	242,311	33,530	26,772	30,774	14,235	44.6	33.8	32.6	13.1	1.1	0.8	1.3	0.4	1.4	0.08	1.2	0.4	1.4	0.06	1.1	0.4
IPI01011695	VPS37C	cDNA FLJ61465, highly similar to Homo sapiens vacuolar protein sorting 37C (VPS3	97.1%	5.9	1	1	1	2	168,139	177,253	211,359	242,311	33,530	26,772	30,774	14,235	44.6	33.8	32.6	13.1	1.1	0.8	1.3	0.4	1.4	0.08	1.2	0.4	1.4	0.06	1.1	0.4
				FLEGEVPLETFLENFSSMR	2	97.1%	1																									
IPI00402061	NXF4	cDNA FLJ42710 fis, clone BRAMY3007609, moderately similar to Homo sapiens nu	94.7%	4.2	1	1	1	1	4,978,680	5,268,190	5,706,270	7,028,800	645,817	575,687	942,421	403,344	29.0	24.4	36.9	12.8	1.1	0.7	1.1	0.5	1.4	0.03	1.1	0.7	1.3	0.04	1.2	0.2
				NFPELLSLNLCDNK	2	94.7%	1																									
IPI00402185	SYNCRIP	heterogeneous nuclear ribonucleoprotein Q isoform 2	100.0%	20.0	8	8	13	1	5,433,691	5,481,683	5,090,203	6,000,655	438,677	178,363	250,049	268,855	18.1	7.3	11.0	10.0	1.0	0.9	-1.1	0.5	1.1	0.3	-1.1	0.2	1.1	0.1	1.2	0.04
				AGPIWDLR	2	98.7%	1																									
				DLFEDELVPLFEK	2	100.0%	2																									
				LMMDPLTGLNR	2	99.9%	2																									
				LYNNHEIR	2	99.9%	1																									
				NLANTVTEEILEK	2	100.0%	2																									
				TGYTLDVTTGQR	2	100.0%	2																									
				TKEQILEEFSK	2	83.1%	1																									
				VTEGLTDVILYHQPDDK	3	100.0%	2																									
IPI00402391	HNRNPUL1	isoform 3 of Heterogeneous nuclear ribonucleoprotein U-like protein 1	100.0%	19.2	9	9	9	1	7,713,036	7,632,848	7,737,486	8,718,264	632,405	373,637	539,692	259,858	18.3	11.0	15.6	6.7	-1.0	0.9	1.0	1	1.1	0.2	1.0	0.9	1.1	0.04	1.1	0.1
				AEPYCSVLPGFTFIQHLPLSER	3	97.4%	1																									
				EALGGQALYPHVLVK	2	99.9%	1																									
				NCAVEFNFGQR	2	100.0%	1																									
				NYILDQTNVYGSAQR	2	99.9%	1																									
				QGAPTSFLPPEASQLKPDR	3	97.9%	1																									
				QNQFYDTQVIKQENESGYER	3	100.0%	1																									
				RPLEMEQQQAYRPEMK	3	82.3%	1																									
				WDVLIQQATQCLNR	2	100.0%	1																									
				YNILGTNAIMDK	2	99.7%	1																									
IPI00409590	LMO7	isoform 1 of LIM domain only protein 7	100.0%	10.5	12	12	15	2	5,777,671	5,663,581	5,900,481	6,549,381	652,142	415,320	376,575	278,285	25.2	16.4	14.3	9.5	-1.0	0.9	1.0	0.9	1.1	0.3	1.0	0.7	1.2	0.1	1.1	0.2
IPI00552510	LMO7	Uncharacterized protein	100.0%	12.7	12	12	15	2	5,777,671	5,663,581	5,900,481	6,549,381	652,142	415,320	376,575	278,285	25.2	16.4	14.3	9.5	-1.0	0.9	1.0	0.9	1.1	0.3	1.0	0.7	1.2	0.1	1.1	0.2
				EPSLATWEATWSEGSK	2	100.0%	1																									
				FSYNDSKEWEEAMAK	3	98.4%	1																									
				GAAMIIESLGLCYHLHCFK	2	90.3%	1																									
				ISINQTPGK	2	99.3%	2																									
				KWEQQLQEEQEQKR	3	92.3%	1																									
				NPSSSVPPPSAGSVK	2	98.4%	1																									
				QQILQEMR	2	97.2%	1																									
				SMSDVSAEDVQNLR	2	100.0%	2																									
				TEEASSGFLPGDR	2	99.7%	1																									
				TPNNVVSTPAPSPDASQLASSLSSQK	3	100.0%	1																									
				TSTTGVATTQSPTPR	2	100.0%	1																									
				WIDATSGIYNSEK	2	100.0%	2																									
IPI00409591	LMO7	isoform 2 of LIM domain only protein 7	100.0%	9.5	11	11	14	2	5,031,399	4,975,466	5,050,878	5,772,136	634,870	402,770	381,153	241,250	28.2	18.1	16.9	9.4	-1.0	0.9	1.0	1	1.1	0.3	1.0	0.9	1.2	0.1	1.1	0.1
IPI00409593	LMO7	isoform 4 of LIM domain only protein 7	100.0%	9.8	11	11	14	2	5,031,399	4,975,466	5,050,878	5,772,136	634,870	402,770	381,153	241,250	28.2	18.1	16.9	9.4	-1.0	0.9	1.0	1	1.1	0.3	1.0	0.9	1.2	0.1	1.1	0.1
				EPSLATWEATWSEGSK	2	100.0%	1																									
				FSYNDSKEWEEAMAK	3	98.4%	1																									
				ISINQTPGK	2	99.3%	2																									
				KWEQQLQEEQEQKR	3	92.3%	1																									
				NPSSSVPPPSAGSVK	2	98.4%	1																									
				QQILQEMR	2	97.2%	1																									
				SMSDVSAEDVQNLR	2	100.0%	2																									
				TEEASSGFLPGDR	2	99.7%	1																									
				TPNNVVSTPAPSPDASQLASSLSSQK	3	100.0%	1																									
				TSTTGVATTQSPTPR	2	100.0%	1																									
				WIDATSGIYNSEK	2	100.0%	2																									
IPI00409640	LSR	isoform 1 of Lipolysis-stimulated lipoprotein receptor	98.3%	2.3	1	1	1	4	905,958	922,488	883,903	985,158	94,580	58,714	73,376	32,444	23.3	14.2	18.6	7.4	1.0	0.9	-1.0	0.9	1.1	0.5	-1.0	0.7	1.1	0.4	1.1	0.2
IPI00409641	LSR	lipolysis-stimulated lipoprotein receptor isoform 3	98.3%	2.6	1	1	1	4	905,958	922,488	883,903	985,158	94,580	58,714	73,376	32,444	23.3	14.2	18.6	7.4	1.0	0.9	-1.0	0.9	1.1	0.5	-1.0	0.7	1.1	0.4	1.1	0.2
IPI00641640	LSR	lipolysis-stimulated lipoprotein receptor isoform 1	98.3%	2.4	1	1	1	4	905,958	922,488	883,903	985,158	94,580	58,714	73,376	32,444	23.3	14.2	18.6	7.4	1.0	0.9	-1.0	0.9	1.1	0.5	-1.0	0.7	1.1	0.4	1.1	0.2
IPI00908558	LSR	cDNA FLJ55699, highly similar to Homo sapiens liver-specific bHLH-Zip transcriptio	98.3%	3.0	1	1	1	4	905,958	922,488	883,903	985,158	94,580	58,714	73,376	32,444	23.3	14.2	18.6	7.4	1.0	0.9	-1.0	0.9	1.1	0.5	-1.0	0.7	1.1	0.4	1.1	0.2
				SSSAGGQGSYVPLLR	2	98.3%	1																									
IPI00909004	-	cDNA FLJ56541, highly similar to Ubiquilin-2	100.0%	4.9	2	3	3	3	3,242,594	3,222,327	2,996,933	3,382,094	234,833	124,653	172,618	171,246	16.2	8.7	12.9	11.3	-1.0	0.9	-1.1	0.4	1.0	0.6	-1.1	0.3	1.0	0.5	1.1	0.2
IPI00409659	UBQLN2	Ubiquilin-2	100.0%	4.0	2	3	3	3	3,242,594	3,222,327	2,996,933	3,382,094	234,833	124,653	172,618	171,246	16.2	8.7	12.9	11.3	-1.0	0.9	-1.1	0.4	1.0	0.6	-1.1	0.3	1.0	0.5	1.1	0.2
IPI00908495	UBQLN2	cDNA FLJ60127, highly similar to Ubiquilin-2	100.0%	5.1	2	3	3	3	3,242,594	3,222,327	2,996,933	3,382,094	234,833	124,653	172,618	171,246	16.2	8.7	12.9	11.3	-1.0	0.9	-1.1	0.4	1.0	0.6	-1.1	0.3	1.0	0.5	1.1	0.2
				NPAMMQEMMR	2	100.0%	1																									
				QLIMANPQMQQLIQR	2	100.0%	1																									
				QLIMANPQMQQLIQR	3	100.0%	1																									
IPI00409671	DDX42	isoform 1 of ATP-dependent RNA helicase DDX42	99.5%	3.8	2	2	2	3	5,726,751	5,842,903	5,896,883	6,666,106	406,476	191,934	514,208	213,841	15.9	7.4	19.5	7.2	1.0	0.8	1.0	0.8	1.2	0.08	1.0	0.9	1.1	0.02	1.1	0.2
IPI00829889	DDX42	isoform 2 of ATP-dependent RNA helicase DDX42	99.5%	4.4	2	2	2	3	5,726,751	5,842,903	5,896,883	6,666,106	406,476	191,934	514,208	213,841	15.9	7.4	19.5	7.2	1.0	0.8	1.0	0.8	1.2	0.08	1.0	0.9	1.1	0.02	1.1	0.2
IPI01011129	DDX42	cDNA FLJ38453 fis, clone FEBRA2019663, highly similar to Homo sapiens DEAD (A	99.5%	5.8	2	2	2	3	5,726,751	5,842,903	5,896,883	6,666,106	406,476	191,934	514,208	213,841	15.9	7.4	19.5	7.2	1.0	0.8	1.0	0.8	1.2	0.08	1.0	0.9	1.1	0.02	1.1	0.2
				ELLDLAMQNAWFR	2	99.5%	1																									
				FGKAYNLRSVAVYGGGSMWEQAK	2	97.5%	1																									
IPI00409750	OTUB1	isoform 2 of Ubiquitin thioesterase OTUB1	100.0%	6.0	2	2	2	2	3,209,127	3,174,132	3,276,512	3,691,295	235,795	140,440	238,986	191,945	16.4	9.9	16.3	11.6	-1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.06	1.1	0.2
IPI01011145	OTUB1	19 kDa protein	100.0%	11.2	2	2	2	2	3,209,127	3,174,132	3,276,512	3,691,295	235,795	140,440	238,986	191,945	16.4	9.9	16.3	11.6	-1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.06	1.1	0.2
				FFEHFIEGGR	3	99.6%	1																									
				LLTSGYLQR	2	99.9%	1																									
IPI00409767	CNGB3	isoform 2 of Cyclic nucleotide-gated cation channel beta-3	90.8%	2.6	1	1	1	2	2,035,680	2,327,140	2,297,755	2,479,900	242,677	32,644	481,730	83,153	26.7	3.1	46.9	7.5	1.1	0.3	1.1	0.6	1.2	0.1	-1.0	1	1.1	0.1	1.1	0.7
IPI00746960	CNGB3	isoform 1 of Cyclic nucleotide-gated cation channel beta-3	90.8%	2.6	1	1	1	2	2,035,680	2,327,140	2,297,755	2,479,900	242,677	32,644	481,730	83,153	26.7	3.1	46.9	7.5	1.1	0.3	1.1	0.6	1.2	0.1	-1.0	1	1.1	0.1	1.1	0.7
				SLKTKSTPVTSEEPHTNIQDK	3	90.8%	1																									
IPI00410096	IFT172	isoform 1 of Intraflagellar transport protein 172 homolog	90.9%	0.7	1	1	1	4	1,278,828	1,181,260	1,216,643	1,248,135	57,292	48,114	52,335	20,325	10.0	9.1	9.6	3.6	-1.1	0.2	-1.1	0.4	-1.0	0.6	1.0	0.6	1.1	0.2	1.0	0.6
IPI00889747	IFT172	isoform 2 of Intraflagellar transport protein 172 homolog	90.9%	0.8	1	1	1	4	1,278,828	1,181,260	1,216,643	1,248,135	57,292	48,114	52,335	20,325	10.0	9.1	9.6	3.6	-1.1	0.2	-1.1	0.4	-1.0	0.6	1.0	0.6	1.1	0.2	1.0	0.6
IPI00893338	IFT172	IFT172 protein	90.9%	2.3	1	1	1	4	1,278,828	1,181,260	1,216,643	1,248,135	57,292	48,114	52,335	20,325	10.0	9.1	9.6	3.6	-1.1	0.2	-1.1	0.4	-1.0	0.6	1.0	0.6	1.1	0.2	1.0	0.6
IPI00902932	IFT172	cDNA FLJ31264 fis, clone KIDNE2006014, highly similar to Homo sapiens selective	90.9%	2.4	1	1	1	4	1,278,828	1,181,260	1,216,643	1,248,135	57,292	48,114	52,335	20,325	10.0	9.1	9.6	3.6	-1.1	0.2	-1.1	0.4	-1.0	0.6	1.0	0.6	1.1	0.2	1.0	0.6
				EGHMLQTFDYSR	3	90.9%	1																									
IPI00410110	DHX40	isoform 1 of Probable ATP-dependent RNA helicase DHX40	90.4%	3.6	1	1	1	5	316,200	260,572	316,003	245,278	15,005	24,668	42,644	24,402	10.6	21.2	30.2	22.3	-1.2	0.09	-1.0	1	-1.3	0.04	1.2	0.3	-1.1	0.7	-1.3	0.2
IPI00789290	DHX40	Uncharacterized protein	90.4%	3.8	1	1	1	5	316,200	260,572	316,003	245,278	15,005	24,668	42,644	24,402	10.6	21.2	30.2	22.3	-1.2	0.09	-1.0	1	-1.3	0.04	1.2	0.3	-1.1	0.7	-1.3	0.2
IPI00797226	DHX40	isoform 3 of Probable ATP-dependent RNA helicase DHX40	90.4%	3.9	1	1	1	5	316,200	260,572	316,003	245,278	15,005	24,668	42,644	24,402	10.6	21.2	30.2	22.3	-1.2	0.09	-1.0	1	-1.3	0.04	1.2	0.3	-1.1	0.7	-1.3	0.2
IPI00952676	DHX40	Uncharacterized protein	90.4%	3.9	1	1	1	5	316,200	260,572	316,003	245,278	15,005	24,668	42,644	24,402	10.6	21.2	30.2	22.3	-1.2	0.09	-1.0	1	-1.3	0.04	1.2	0.3	-1.1	0.7	-1.3	0.2
IPI01010408	DHX40	isoform 2 of Probable ATP-dependent RNA helicase DHX40	90.4%	3.8	1	1	1	5	316,200	260,572	316,003	245,278	15,005	24,668	42,644	24,402	10.6	21.2	30.2	22.3	-1.2	0.09	-1.0	1	-1.3	0.04	1.2	0.3	-1.1	0.7	-1.3	0.2
				DFWNQCMPDHVIPEIKRTSLTSVVLTLK	3	90.4%	1																									
IPI00410128	PPP1CA	serine/threonine-protein phosphatase PP1-alpha catalytic subunit isoform 2	94.8%	7.7	1	1	1	1	231,785	229,840	226,137	241,162	15,355	10,381	29,241	26,208	14.8	10.1	28.9	24.3	-1.0	0.9	-1.0	0.9	1.0	0.8	-1.0	0.9	1.0	0.7	1.1	0.7
				LFEYGGFPPESNYLFLGDYVDR	2	90.7%	1																									
IPI00410214	BPNT1	isoform 1 of 3'(2'),5'-bisphosphate nucleotidase 1	100.0%	14.3	3	3	3	4	1,848,532	2,138,393	2,422,978	2,393,620	172,973	114,663	394,829	243,865	20.9	12.0	36.4	22.8	1.2	0.2	1.3	0.2	1.3	0.1	1.1	0.5	1.1	0.4	-1.0	1
IPI00410215	BPNT1	isoform 2 of 3'(2'),5'-bisphosphate nucleotidase 1	100.0%	13.5	3	3	3	4	1,848,532	2,138,393	2,422,978	2,393,620	172,973	114,663	394,829	243,865	20.9	12.0	36.4	22.8	1.2	0.2	1.3	0.2	1.3	0.1	1.1	0.5	1.1	0.4	-1.0	1
IPI00910437	BPNT1	cDNA FLJ52417, highly similar to 3'(2'),5'-bisphosphate nucleotidase 1	100.0%	16.2	3	3	3	4	1,848,532	2,138,393	2,422,978	2,393,620	172,973	114,663	394,829	243,865	20.9	12.0	36.4	22.8	1.2	0.2	1.3	0.2	1.3	0.1	1.1	0.5	1.1	0.4	-1.0	1
IPI00953320	BPNT1	Uncharacterized protein	100.0%	13.6	3	3	3	4	1,848,532	2,138,393	2,422,978	2,393,620	172,973	114,663	394,829	243,865	20.9	12.0	36.4	22.8	1.2	0.2	1.3	0.2	1.3	0.1	1.1	0.5	1.1	0.4	-1.0	1
				LAQMSICSSLAR	2	100.0%	1																									
				LVTDCVAAMNPDAVLR	2	98.9%	1																									
				TIWGVLGLGAFGFQLK	2	100.0%	1																									
IPI00410244	ZP1	Zona pellucida sperm-binding protein 1	99.4%	4.4	1	1	1	2	1,466,820	1,296,510	1,507,714	1,799,070	252,490	221,597	265,532	151,084	38.5	38.2	39.4	18.8	-1.1	0.6	1.0	0.9	1.2	0.3	1.2	0.6	1.4	0.1	1.2	0.4
IPI01013255	ZP1	Protein	99.4%	70.0	1	1	1	2	1,466,820	1,296,510	1,507,714	1,799,070	252,490	221,597	265,532	151,084	38.5	38.2	39.4	18.8	-1.1	0.6	1.0	0.9	1.2	0.3	1.2	0.6	1.4	0.1	1.2	0.4
				FDVNNCSICYHWVTSRPQEPAVFSADYR	3	99.4%	1																									
IPI00410298	MGC50722	Hypothetical MGC50722	99.1%	1.2	2	2	2	2	8,093,805	7,561,595	7,472,550	8,218,810	415,345	178,110	357,788	406,821	11.5	5.3	10.7	11.1	-1.1	0.3	-1.1	0.3	1.0	0.8	-1.0	0.8	1.1	0.2	1.1	0.2
IPI01010389	MGC50722	MGC50722 protein (Fragment)	99.1%	1.1	2	2	2	2	8,093,805	7,561,595	7,472,550	8,218,810	415,345	178,110	357,788	406,821	11.5	5.3	10.7	11.1	-1.1	0.3	-1.1	0.3	1.0	0.8	-1.0	0.8	1.1	0.2	1.1	0.2
				SLLGPPPVLR	2	87.9%	1																									
				SLLGPPPVLRR	2	92.8%	1																									
IPI00909229	-	cDNA FLJ51308	99.4%	11.5	1	1	1	3	678,617	853,393	774,631	886,467	121,993	50,239	93,991	53,911	40.2	13.2	27.1	13.6	1.3	0.2	1.1	0.6	1.3	0.2	-1.1	0.5	1.0	0.7	1.1	0.3
IPI00410324	LSM12	isoform 1 of Protein LSM12 homolog	99.4%	6.7	1	1	1	3	678,617	853,393	774,631	886,467	121,993	50,239	93,991	53,911	40.2	13.2	27.1	13.6	1.3	0.2	1.1	0.6	1.3	0.2	-1.1	0.5	1.0	0.7	1.1	0.3
IPI00867714	LSM12	isoform 2 of Protein LSM12 homolog	99.4%	6.6	1	1	1	3	678,617	853,393	774,631	886,467	121,993	50,239	93,991	53,911	40.2	13.2	27.1	13.6	1.3	0.2	1.1	0.6	1.3	0.2	-1.1	0.5	1.0	0.7	1.1	0.3
				LQGEVVAFDYQSK	2	99.4%	1																									

IPI00410693	SERBP1	SERPINE1 mRNA binding protein 1, isoform CRA_d	100.0%	20.0	5	5	6	2	4,069,215	4,166,499	4,011,732	4,385,854	266,444	64,135	200,501	135,276	14.6	3.4	11.2	6.9	1.0	0.7	-1.0	0.9	1.1	0.3	-1.0	0.5	1.1	0.2	1.1	0.2
IPI00470497	SERBP1	isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein	100.0%	23.1	5	5	6	2	4,069,215	4,166,499	4,011,732	4,385,854	266,444	64,135	200,501	135,276	14.6	3.4	11.2	6.9	1.0	0.7	-1.0	0.9	1.1	0.3	-1.0	0.5	1.1	0.2	1.1	0.2
				EAGGGGVGGPGAKSAAQAAAQTNSNAAGK	3	83.5%	1																									
				EETQPPVALKK	2	99.5%	1																									
				FDQLFDDESDPFEVLK	2	100.0%	2																									
				KPANDITSQLEINFGDLGR	3	99.1%	1																									
				SSASAPDVDDPEAFPALA	2	99.4%	1																									
IPI00410714	HBA1;HBA2	Hemoglobin subunit alpha	100.0%	28.2	3	4	4	1	24,264,920	23,575,375	24,353,115	29,026,685	2,106,098	1,211,625	1,055,027	1,284,365	19.4	11.5	9.7	9.9	-1.0	0.8	1.0	1	1.2	0.09	1.0	0.6	1.2	0.01	1.2	0.02
				LRVDPVNFK	3	98.3%	1																									
				TYFPHFDLSHGSAQVK	3	100.0%	1																									
				VGAHAGEYGAEALER	2	100.0%	1																									
				VGAHAGEYGAEALER	3	99.6%	1																									
IPI00411387	ACSL5	cDNA FLJ52792, highly similar to Long-chain-fatty-acid--CoA ligase 5	100.0%	6.9	2	2	2	1	3,083,220	3,034,948	2,964,503	3,494,280	233,614	157,720	217,845	158,885	16.9	11.6	16.4	10.2	-1.0	0.9	-1.0	0.7	1.1	0.2	-1.0	0.8	1.2	0.07	1.2	0.09
				SSLVGVVVPDTDVLPSFAAK	2	100.0%	1																									
				TQIDSLYEHIQD	2	100.0%	1																									
IPI00411639	62;SNORA6;RPSAP1	Laminin receptor-like protein LAMRL5	100.0%	26.8	5	6	10	1	8,112,608	8,653,241	8,429,394	9,746,644	676,542	277,208	602,836	230,602	18.7	7.2	16.0	5.3	1.1	0.5	1.0	0.7	1.2	0.07	-1.0	0.7	1.1	0.02	1.2	0.1
				AIVAIENPADVSVISSR	2	100.0%	2																									
				FAAATGATPIAGR	2	100.0%	2																									
				FLAAGTHLGGTNLDFQMEQYIYK	3	100.0%	1																									
				FTPGTFTNQIQAAFR	2	100.0%	2																									
				KSDGIYIINLK	2	99.9%	2																									
				KSDGIYIINLK	3	99.3%	1																									
IPI00411680	PCMT1	isoform 1 of Protein-L-isoaspartate(D-aspartate) O-methyltransferase	100.0%	35.7	7	7	7	3	12,778,588	14,205,860	12,844,821	14,471,835	905,854	948,534	616,630	369,589	15.9	14.9	10.7	5.7	1.1	0.3	1.0	1	1.1	0.1	-1.1	0.3	1.0	0.8	1.1	0.05
IPI00828189	PCMT1	Uncharacterized protein	100.0%	28.3	7	7	7	3	12,778,588	14,205,860	12,844,821	14,471,835	905,854	948,534	616,630	369,589	15.9	14.9	10.7	5.7	1.1	0.3	1.0	1	1.1	0.1	-1.1	0.3	1.0	0.8	1.1	0.05
IPI00947458	PCMT1	protein-L-isoaspartate(D-aspartate) O-methyltransferase	100.0%	28.4	7	7	7	3	12,778,588	14,205,860	12,844,821	14,471,835	905,854	948,534	616,630	369,589	15.9	14.9	10.7	5.7	1.1	0.3	1.0	1	1.1	0.1	-1.1	0.3	1.0	0.8	1.1	0.05
				ELVDDSVNNVR	2	99.9%	1																									
				KDDPTLLSSGR	2	99.8%	1																									
				LILPVGPAGGNQMLEQYDK	2	99.9%	1																									
				LILPVGPAGGNQMLEQYDKLQDGSIK	3	94.8%	1																									
				SGGASHSELIHNLR	3	97.6%	1																									
				VFEVMLATDR	2	96.8%	1																									
				VQLVVGDGR	2	99.9%	1																									
IPI00411706	ESD	S-formylglutathione hydrolase	100.0%	12.4	2	2	2	1	2,551,563	2,465,392	2,869,612	2,667,739	120,919	287,168	153,037	285,029	10.6	26.1	11.9	23.9	-1.0	0.8	1.1	0.1	1.0	0.7	1.2	0.2	1.1	0.6	-1.1	0.6
				AFSGYLGTDQSK	2	98.0%	1																									
				MYSYVTEELPQLINANFPVDPQR	2	99.6%	1																									
IPI00411765	SFN	isoform 2 of 14-3-3 protein sigma	100.0%	19.4	4	5	6	1	25,111,975	25,521,515	21,742,120	28,011,830	2,961,196	1,408,940	1,803,321	792,410	26.4	12.3	18.6	6.3	1.0	0.9	-1.2	0.4	1.1	0.4	-1.2	0.1	1.1	0.2	1.3	0.01
				SAYQEAMDISK	2	100.0%	1																									
				SAYQEAMDISKK	2	100.0%	2																									
				SAYQEAMDISKK	3	99.9%	1																									
				TTFDEAMADLHTLSEDSYK	3	100.0%	1																									
				YLAEVATGDDK	2	100.0%	1																									
IPI00411937	RD86;SNORD110;N	Nucleolar protein 56	93.8%	2.2	1	1	1	3	541,993	499,146	475,999	522,773	61,939	36,392	43,093	37,947	25.6	16.3	20.2	16.2	-1.1	0.6	-1.1	0.4	-1.0	0.8	-1.0	0.7	1.0	0.7	1.1	0.4
IPI00642697	RD86;SNORD110;N	Uncharacterized protein	93.8%	5.8	1	1	1	3	541,993	499,146	475,999	522,773	61,939	36,392	43,093	37,947	25.6	16.3	20.2	16.2	-1.1	0.6	-1.1	0.4	-1.0	0.8	-1.0	0.7	1.0	0.7	1.1	0.4
IPI00984526	RD86;SNORD110;N	Protein	93.8%	5.2	1	1	1	3	541,993	499,146	475,999	522,773	61,939	36,392	43,093	37,947	25.6	16.3	20.2	16.2	-1.1	0.6	-1.1	0.4	-1.0	0.8	-1.0	0.7	1.0	0.7	1.1	0.4
				YPASTVQILGAEK	2	93.8%	1																									
IPI00412153	10-Sep	Uncharacterized protein	100.0%	6.6	1	1	1	1	1,066,829	903,294	1,036,426	1,092,224	99,961	49,994	63,121	13,610	21.0	12.4	13.6	2.8	-1.2	0.2	-1.0	0.8	1.0	0.8	1.1	0.1	1.2	0.02	1.1	0.4
				VNAAMNGQLPFAVVGSMDEVK	2	98.5%	1																									
IPI00412216	VPS13C	vacuolar protein sorting-associated protein 13C isoform 2B	99.6%	1.2	2	2	2	4	14,443,905	16,353,540	16,540,760	18,741,268	3,679,812	2,050,517	2,320,774	1,334,010	57.0	28.0	31.4	15.9	1.1	0.7	1.1	0.6	1.3	0.3	1.0	1	1.1	0.4	1.1	0.4
IPI00465428	VPS13C	isoform 1 of Vacuolar protein sorting-associated protein 13C	99.6%	1.2	2	2	2	4	14,443,905	16,353,540	16,540,760	18,741,268	3,679,812	2,050,517	2,320,774	1,334,010	57.0	28.0	31.4	15.9	1.1	0.7	1.1	0.6	1.3	0.3	1.0	1	1.1	0.4	1.1	0.4
IPI00604778	VPS13C	vacuolar protein sorting-associated protein 13C isoform 1B	99.6%	1.2	2	2	2	4	14,443,905	16,353,540	16,540,760	18,741,268	3,679,812	2,050,517	2,320,774	1,334,010	57.0	28.0	31.4	15.9	1.1	0.7	1.1	0.6	1.3	0.3	1.0	1	1.1	0.4	1.1	0.4
IPI00797358	VPS13C	isoform 3 of Vacuolar protein sorting-associated protein 13C	99.6%	1.2	2	2	2	4	14,443,905	16,353,540	16,540,760	18,741,268	3,679,812	2,050,517	2,320,774	1,334,010	57.0	28.0	31.4	15.9	1.1	0.7	1.1	0.6	1.3	0.3	1.0	1	1.1	0.4	1.1	0.4
				KAAEVPNEELINLLLK	2	97.1%	1																									
				LGIWGGNVALDNLQIKENALSELDVPFK	3	84.5%	1																									
IPI00412272	SH3BGRL2	SH3 domain-binding glutamic acid-rich-like protein 2	99.9%	12.2	1	1	1	1	4,882,210	6,062,450	4,691,480	6,121,330	441,906	784,848	308,938	563,766	20.2	29.0	14.7	20.6	1.2	0.2	-1.0	0.7	1.3	0.1	-1.3	0.2	1.0	1	1.3	0.06
				VFIASSSGFVAIK	2	99.8%	1																									
IPI00412408	BRCA2	Breast cancer type 2 susceptibility protein	96.9%	1.2	3	3	3	1	25,195,070	26,436,910	26,897,520	29,510,280	2,101,658	657,776	2,729,031	466,288	18.7	5.6	22.7	3.5	1.0	0.6	1.1	0.6	1.2	0.1	1.0	0.9	1.1	0.005	1.1	0.4
				DLVYVLAEENK	2	96.9%	1																									
				NNDYMNKWAGLLGPISNHSFGGSFRTASNK	3	89.0%	1																									
				WAGLLGPISNHSFGGSFR	2	96.3%	1																									
IPI00412492	PLXND1	isoform 1 of Plexin-D1	97.9%	1.5	1	1	1	2	1,085,045	1,058,905	1,065,910	1,238,405	85,366	68,141	133,182	61,084	17.6	14.4	27.9	11.0	-1.0	0.8	-1.0	0.9	1.1	0.2	1.0	1	1.2	0.09	1.2	0.3
IPI00472139	PLXND1	isoform 2 of Plexin-D1	97.9%	1.6	1	1	1	2	1,085,045	1,058,905	1,065,910	1,238,405	85,366	68,141	133,182	61,084	17.6	14.4	27.9	11.0	-1.0	0.8	-1.0	0.9	1.1	0.2	1.0	1	1.2	0.09	1.2	0.3
				VLNSTLITCPSPGALSNASAPVDFFINGR	3	97.9%	1																									
IPI00412497	DYNLRB1	Dynein, light chain, roadblock-type 1	99.9%	23.0	2	2	2	2	4,885,515	4,856,190	4,614,465	5,363,498	585,662	288,341	421,742	304,976	26.8	13.3	20.4	12.7	-1.0	1	-1.1	0.7	1.1	0.5	-1.1	0.6	1.1	0.3	1.2	0.2
IPI00643583	DYNLRB1	isoform 1 of Dynein light chain roadblock-type 1	99.9%	35.4	2	2	2	2	4,885,515	4,856,190	4,614,465	5,363,498	585,662	288,341	421,742	304,976	26.8	13.3	20.4	12.7	-1.0	1	-1.1	0.7	1.1	0.5	-1.1	0.6	1.1	0.3	1.2	0.2
				DIDPQNDLTFLR	2	99.8%	1																									
				KNEIMVAPDKDYFLIVIQNPTE	3	98.6%	1																									
IPI00412498	NAPRT1	Uncharacterized protein	100.0%	11.2	3	3	3	3	1,359,036	1,131,661	1,225,038	1,294,152	94,529	54,765	66,427	74,994	15.6	10.8	12.1	13.0	-1.2	0.07	-1.1	0.3	-1.1	0.6	1.1	0.3	1.1	0.1	1.1	0.5
IPI00879716	NAPRT1	isoform 2 of Nicotinate phosphoribosyltransferase	100.0%	9.7	3	3	3	3	1,359,036	1,131,661	1,225,038	1,294,152	94,529	54,765	66,427	74,994	15.6	10.8	12.1	13.0	-1.2	0.07	-1.1	0.3	-1.1	0.6	1.1	0.3	1.1	0.1	1.1	0.5
IPI00952992	NAPRT1	Uncharacterized protein	100.0%	9.4	3	3	3	3	1,359,036	1,131,661	1,225,038	1,294,152	94,529	54,765	66,427	74,994	15.6	10.8	12.1	13.0	-1.2	0.07	-1.1	0.3	-1.1	0.6	1.1	0.3	1.1	0.1	1.1	0.5
				ALDCSEVTVR	2	99.4%	1																									
				LLGSDGSPLMDMLQLAEEPVPQAGQELR	3	99.6%	1																									
				PLLTDLYQATMALGYWR	2	87.6%	1																									
IPI00412525	RAP1B;RAP1BL	Ras-related protein Rap-1b-like protein	100.0%	6.5	1	1	1	3	82,182	109,178	101,179	110,400	3,782	9,700	14,042	10,867	10.3	19.9	31.0	22.0	1.3	0.05	1.2	0.3	1.3	0.06	-1.1	0.7	1.0	0.9	1.1	0.6
IPI00745127	RAP1B	cDNA, FLJ79442, highly similar to Ras-related protein Rap-1b	100.0%	10.2	1	1	1	3	82,182	109,178	101,179	110,400	3,782	9,700	14,042	10,867	10.3	19.9	31.0	22.0	1.3	0.05	1.2	0.3	1.3	0.06	-1.1	0.7	1.0	0.9	1.1	0.6
IPI01012426	RAP1B	12 kDa protein	100.0%	11.7	1	1	1	3	82,182	109,178	101,179	110,400	3,782	9,700	14,042	10,867	10.3	19.9	31.0	22.0	1.3	0.05	1.2	0.3	1.3	0.06	-1.1	0.7	1.0	0.9	1.1	0.6
				INVNEIFYDLVR	2	100.0%	1																									
IPI00412545	NDUFA5	Putative uncharacterized protein DKFZp781K1356	99.5%	43.1	3	3	3	3	2,951,056	2,929,837	3,077,647	3,347,457	285,674	157,497	299,745	106,776	21.7	12.0	21.8	7.1	-1.0	0.9	1.0	0.8	1.1	0.2	1.1	0.7	1.1	0.06	1.1	0.4
IPI00554681	NDUFA5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	99.5%	43.1	3	3	3	3	2,951,056	2,929,837	3,077,647	3,347,457	285,674	157,497	299,745	106,776	21.7	12.0	21.8	7.1	-1.0	0.9	1.0	0.8	1.1	0.2	1.1	0.7	1.1	0.06	1.1	0.4
IPI00946670	NDUFA5	Protein	99.5%	44.6	3	3	3	3	2,951,056	2,929,837	3,077,647	3,347,457	285,674	157,497	299,745	106,776	21.7	12.0	21.8	7.1	-1.0	0.9	1.0	0.8	1.1	0.2	1.1	0.7	1.1	0.06	1.1	0.4
				KLEDQLQGGQLEEVILQAEHELNLAR	3	99.5%	1																									
				LWEPLVEEPPADQWK	2	99.0%	1																									
				YTEQITNEK	2	95.5%	1																									
IPI00412579	RPL10A	60S ribosomal protein L10a	99.4%	6.0	1	1	1	1	5,173,990	6,071,670	4,806,080	6,306,400	575,515	477,022	427,992	150,067	24.9	17.6	19.9	5.3	1.2	0.3	-1.1	0.6	1.2	0.1	-1.3	0.08	1.0	0.7	1.3	0.02
				KYDAFLASESLIK	2	99.4%	1																									
IPI00412601	DYNC1I2	Uncharacterized protein	99.6%	13.9	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
IPI00915884	DYNC1I2	Uncharacterized protein	99.6%	18.9	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
IPI00916160	DYNC1I2	Uncharacterized protein	99.6%	23.2	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
IPI00916278	DYNC1I2	Uncharacterized protein	99.6%	31.8	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
IPI00917075	DYNC1I2	Uncharacterized protein	99.6%	25.6	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
IPI00917180	DYNC1I2	Uncharacterized protein	99.6%	16.4	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
IPI00917325	DYNC1I2	Uncharacterized protein	99.6%	18.7	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
IPI00917564	DYNC1I2	Uncharacterized protein	99.6%	25.2	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
IPI00917685	DYNC1I2	Uncharacterized protein	99.6%	19.0	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
IPI00917785	DYNC1I2	Uncharacterized protein	99.6%	20.2	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
IPI00917978	DYNC1I2	CDNA: FLJ22921 fis, clone KAT06711	99.6%	11.5	2	2	2	11	258,023	304,579	344,238	354,562	12,173	23,459	43,796	40,511	10.6	17.2	28.5	25.6	1.2	0.1	1.3	0.1	1.4	0.07	1.1	0.4	1.2	0.3	1.0	0.9
				EAVAPVQEESDLEK	2	99.4%	1																									
				SVSTPSEAGSQDSGDGAVGSR	2	99.6%	1																									
IPI00412714	SERBP1	isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein	100.0%	24.0	5	5	6	2	4,069,215	4,166,499	4,011,732	4,385,854	266,444	64,135	200,501	135,276	14.6	3.4	11.2	6.9	1.0	0.7	-1.0	0.9	1.1	0.3	-1.0	0.5	1.1	0.2	1.1	0.2
IPI00470498	SERBP1	isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein	100.0%	23.7	5	5	6	2	4,069,215	4,166,499	4,011,732	4,385,854	266,444	64,135	200,501	135,276	14.6	3.4	11.2	6.9	1.0	0.7	-1.0	0.9	1.1	0.3	-1.0	0.5	1.1	0.2	1.1	0.2
				EAGGGGVGGPGAKSAAQAAAQTNSNAAGK	3	83.5%	1																									
				EETQPPVALKK	2	99.5%	1																									
				FDQLFDDESDPFEVLK	2	100.0%	2																									
				KPANDITSQLEINFGDLGR	3	99.1%	1																									
				SSASAPDVDDPEAFPALA	2	99.4%	1																									
IPI00412737	WARS	tryptophanyl-tRNA synthetase, cytoplasmic isoform b	100.0%	21.9	6	6	6	1	8,370,595	8,878,215	8,769,360	10,020,990	490,466	577,747	649,009	463,931	13.1	14.6	16.6	10.4	1.1	0.5	1.0	0.6	1.2	0.04	-1.0	0.9	1.1	0.2	1.1	0.2
				ALIEVLQPLIAEHQAR	2	99.1%	1																									
				DIIACGFDINK	2	95.1%	1																									
				DLTLDQAYSYAVENAK	2	100.0%	1																									
				DMNQVLDAYENK	2	99.9%	1																									
				ISFPAIQAAPSFSNSFPQIFR	3	100.0%	1																									
				TFIFSDLDYMGMSSGFYK	2	99.5%	1																									
IPI00412771	CD2AP	CD2-associated protein	100.0%	18.5	10	10	10	1	166,560,600	170,054,390	157,149,060	183,298,040	########	7,624,292	9,172,949	6,313,266	13.6	10.0	13.1	7.7	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.05
				APAPKPELIAAEK	3	95.0%	1																									
				EGEIIHLISK	2	99.5%	1																									
				ETGEAGWWRGELNGK	2	97.8%	1																									
				HGNVASLVQR	2	99.9%	1																									
				INGEVSSISSK	2	99.9%	1																									
				LGLFPSNFVK	2	99.2%	1																									
				LQEEGWLEGELNGR	2	100.0%	1																									
				SNLEMEIEK	2	96.6%	1																									
				SVDFDSLTVR	2	99.8%	1																									
				VLFEYIPQNEDELELK	2	99.9%	1																									
IPI00412788	GLTSCR2	53 kDa protein	91.4%	3.8	1	1	1	1	6,024,430	6,420,090	6,630,220	6,971,020	444,132	318,471	240,959	217,542	16.5	11.1	8.1	7.0	1.1	0.5	1.1	0.3	1.2	0.09	1.0	0.6	1.1	0.2	1.1	0.3
				SCSGCAGSPGGPEAGGAR	2	91.4%	1																									
IPI00412880	CARM1	isoform 1 of Histone-arginine methyltransferase CARM1	90.5%	2.2	1	1	1	3	965,083	987,317	931,743	1,049,550	97,485	51,021	52,772	57,952	22.6	11.6	12.7	12.4	1.0	0.8	-1.0	0.8	1.1	0.5	-1.1	0.5	1.1	0.4	1.1	0.2
IPI00514607	CARM1	isoform 2 of Histone-arginine methyltransferase CARM1	90.5%	3.4	1	1	1	3	965,083	987,317	931,743	1,049,550	97,485	51,021	52,772	57,952	22.6	11.6	12.7	12.4	1.0	0.8	-1.0	0.8	1.1	0.5	-1.1	0.5	1.1	0.4	1.1	0.2
IPI00639957	CARM1	isoform 3 of Histone-arginine methyltransferase CARM1	90.5%	2.1	1	1	1	3	965,083	987,317	931,743	1,049,550	97,485	51,021	52,772	57,952	22.6	11.6	12.7	12.4	1.0	0.8	-1.0	0.8	1.1	0.5	-1.1	0.5	1.1	0.4	1.1	0.2
				LLTIGDANGEIQR	2	90.5%	1																									
IPI00412987	GMFB	Glia maturation factor, beta	99.6%	7.1	1	1	2	2	1,680,795	1,719,870	1,715,580	1,831,685	70,207	84,354	178,417	131,899	9.3	11.0	23.3	16.1	1.0	0.7	1.0	0.9	1.1	0.3	-1.0	1	1.1	0.5	1.1	0.6
IPI00978910	GMFB	Glia maturation factor beta	99.6%	7.8	1	1	2	2	1,680,795	1,719,870	1,715,580	1,831,685	70,207	84,354	178,417	131,899	9.3	11.0	23.3	16.1	1.0	0.7	1.0	0.9	1.1	0.3	-1.0	1	1.1	0.5	1.1	0.6
				NTEDLTEEWLR	2	99.6%	2																									
IPI00413108	62;SNORA6;RPSAP1	33 kDa protein	100.0%	38.3	10	11	16	3	16,800,172	17,918,305	17,169,064	20,005,476	1,295,238	606,011	1,242,549	673,167	17.2	7.6	16.2	7.5	1.1	0.5	1.0	0.8	1.2	0.06	-1.0	0.6	1.1	0.05	1.2	0.08
IPI00553164	62;SNORA6;RPSAP1	40S ribosomal protein SA	100.0%	39.0	10	11	16	3	16,800,172	17,918,305	17,169,064	20,005,476	1,295,238	606,011	1,242,549	673,167	17.2	7.6	16.2	7.5	1.1	0.5	1.0	0.8	1.2	0.06	-1.0	0.6	1.1	0.05	1.2	0.08
IPI00927101	62;SNORA6;RPSAP1	Uncharacterized protein	100.0%	43.6	10	11	16	3	16,800,172	17,918,305	17,169,064	20,005,476	1,295,238	606,011	1,242,549	673,167	17.2	7.6	16.2	7.5	1.1	0.5	1.0	0.8	1.2	0.06	-1.0	0.6	1.1	0.05	1.2	0.08
				AIVAIENPADVSVISSR	2	100.0%	2																									
				FAAATGATPIAGR	2	100.0%	2																									
				FLAAGTHLGGTNLDFQMEQYIYK	3	100.0%	1																									
				FTPGTFTNQIQAAFR	2	100.0%	2																									
				FTPGTFTNQIQAAFREPR	3	97.3%	1																									
				GAHSVGLMWWMLAR	2	99.9%	1																									
				KSDGIYIINLK	2	99.9%	2																									
				KSDGIYIINLK	3	99.3%	1																									
				LLVVTDPR	2	99.9%	1																									
				SDGIYIINLK	2	99.9%	1																									
				YVDIAIPCNNK	2	100.0%	2																									
IPI00413140	DNM1	isoform 1 of Dynamin-1	100.0%	5.7	4	4	4	5	5,403,646	5,646,811	5,239,902	6,217,331	580,515	152,028	398,480	303,872	24.0	6.0	17.0	10.9	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.4	1.1	0.1	1.2	0.09
IPI00657691	DNM1	isoform 5 of Dynamin-1	100.0%	5.8	4	4	4	5	5,403,646	5,646,811	5,239,902	6,217,331	580,515	152,028	398,480	303,872	24.0	6.0	17.0	10.9	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.4	1.1	0.1	1.2	0.09

IPI00816287	DNM1	isoform 3 of Dynamin-1	100.0%	5.8	4	4	4	5	5,403,646	5,646,811	5,239,902	6,217,331	580,515	152,028	398,480	303,872	24.0	6.0	17.0	10.9	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.4	1.1	0.1	1.2	0.09
IPI00887273	DNM1	isoform 2 of Dynamin-1	100.0%	5.7	4	4	4	5	5,403,646	5,646,811	5,239,902	6,217,331	580,515	152,028	398,480	303,872	24.0	6.0	17.0	10.9	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.4	1.1	0.1	1.2	0.09
IPI00888758	DNM1	isoform 4 of Dynamin-1	100.0%	5.7	4	4	4	5	5,403,646	5,646,811	5,239,902	6,217,331	580,515	152,028	398,480	303,872	24.0	6.0	17.0	10.9	1.0	0.7	-1.0	0.8	1.2	0.2	-1.1	0.4	1.1	0.1	1.2	0.09
				NLVDSYMAIVNK	2	88.0%	1																									
				SSVLENFVGR	2	99.9%	1																									
				TSGNQDEILVIR	2	97.8%	1																									
				VPVGDQPPDIEFQIR	2	99.9%	1																									
IPI00413160	TRIOBP	isoform 2 of TRIO and F-actin-binding protein	91.2%	0.4	1	1	1	4	1,199,743	1,357,243	1,281,395	1,388,863	140,322	73,261	109,447	108,698	26.2	12.1	19.1	17.5	1.1	0.3	1.1	0.7	1.2	0.3	-1.1	0.6	1.0	0.8	1.1	0.5
IPI00736522	TRIOBP	isoform 3 of TRIO and F-actin-binding protein	91.2%	0.4	1	1	1	4	1,199,743	1,357,243	1,281,395	1,388,863	140,322	73,261	109,447	108,698	26.2	12.1	19.1	17.5	1.1	0.3	1.1	0.7	1.2	0.3	-1.1	0.6	1.0	0.8	1.1	0.5
IPI00741684	TRIOBP	isoform 4 of TRIO and F-actin-binding protein	91.2%	0.5	1	1	1	4	1,199,743	1,357,243	1,281,395	1,388,863	140,322	73,261	109,447	108,698	26.2	12.1	19.1	17.5	1.1	0.3	1.1	0.7	1.2	0.3	-1.1	0.6	1.0	0.8	1.1	0.5
IPI00952918	TRIOBP	Uncharacterized protein	91.2%	0.6	1	1	1	4	1,199,743	1,357,243	1,281,395	1,388,863	140,322	73,261	109,447	108,698	26.2	12.1	19.1	17.5	1.1	0.3	1.1	0.7	1.2	0.3	-1.1	0.6	1.0	0.8	1.1	0.5
				ASSTQQETSR	2	87.8%	1																									
IPI00413214	KPNA5	importin subunit alpha-6	98.4%	6.1	2	2	3	4	870,453	927,860	846,248	1,074,305	68,519	72,490	70,046	86,484	17.6	17.5	18.5	18.0	1.1	0.6	-1.0	0.8	1.2	0.1	-1.1	0.4	1.2	0.2	1.3	0.07
IPI00747764	KPNA6	cDNA FLJ53229, highly similar to Importin alpha-7 subunit	98.4%	6.1	2	2	3	4	870,453	927,860	846,248	1,074,305	68,519	72,490	70,046	86,484	17.6	17.5	18.5	18.0	1.1	0.6	-1.0	0.8	1.2	0.1	-1.1	0.4	1.2	0.2	1.3	0.07
IPI01012685	KPNA6	60 kDa protein	98.4%	6.2	2	2	3	4	870,453	927,860	846,248	1,074,305	68,519	72,490	70,046	86,484	17.6	17.5	18.5	18.0	1.1	0.6	-1.0	0.8	1.2	0.1	-1.1	0.4	1.2	0.2	1.3	0.07
IPI01015268	KPNA6	Importin subunit alpha-7	98.4%	6.2	2	2	3	4	870,453	927,860	846,248	1,074,305	68,519	72,490	70,046	86,484	17.6	17.5	18.5	18.0	1.1	0.6	-1.0	0.8	1.2	0.1	-1.1	0.4	1.2	0.2	1.3	0.07
				EAAWAITNATSGGTPEQIR	2	98.0%	1																									
				IVQVALNGLENILR	2	98.4%	2																									
IPI00413344	CFL2	Cofilin-2	100.0%	30.1	4	4	6	1	4,758,820	4,372,560	5,712,239	5,339,487	340,555	459,930	334,053	401,762	16.0	23.5	13.1	16.8	-1.1	0.5	1.2	0.08	1.1	0.3	1.3	0.05	1.2	0.2	-1.1	0.5
				KEDLVFIFWAPESAPLK	3	100.0%	2																									
				MIYASSK	1	100.0%	1																									
				QILVGDIGDTVEDPYTSFVK	2	99.6%	1																									
				VFNDMK	1	100.0%	2																									
IPI00413451	SERPINB6	Serpin B6	100.0%	46.0	13	16	21	1	119,543,517	120,642,580	111,005,320	131,273,762	8,462,920	4,216,425	5,824,768	5,564,622	15.8	7.8	11.7	9.5	1.0	0.9	-1.1	0.4	1.1	0.3	-1.1	0.2	1.1	0.2	1.2	0.04
				ADFSGMSQTDLSLSK	2	100.0%	2																									
				ELNMIIMLPDETTDLR	2	100.0%	1																									
				FKLEESYDMESVLR	2	93.2%	1																									
				FYQAEMEELDFISAVEK	2	100.0%	2																									
				FYQAEMEELDFISAVEK	3	100.0%	1																									
				GNTAAQMAQILSFNK	2	100.0%	2																									
				GNWDEQFDKENTEER	3	100.0%	1																									
				HINTWVAEK	2	99.4%	1																									
				IAELLSPGSVDPLTR	2	100.0%	2																									
				LDMMDEEEVEVSLPR	2	100.0%	1																									
				LVLVNAVYFR	2	99.4%	1																									
				SCDFLSSFR	2	99.9%	1																									
				SGGGGDIHQGFQSLLTEVNK	2	99.8%	1																									
				SGGGGDIHQGFQSLLTEVNK	3	100.0%	1																									
				TYIGEIFTQILVLPYVGK	2	100.0%	2																									
				TYIGEIFTQILVLPYVGK	3	99.5%	1																									
IPI00413587	BID	isoform 1 of BH3-interacting domain death agonist	100.0%	28.7	3	3	3	2	1,754,863	1,687,152	1,612,547	1,819,639	113,456	47,498	149,607	83,063	14.5	6.3	20.8	10.2	-1.0	0.6	-1.1	0.5	1.0	0.7	-1.0	0.7	1.1	0.2	1.1	0.3
IPI00420084	BID	isoform 2 of BH3-interacting domain death agonist	100.0%	23.2	3	3	3	2	1,754,863	1,687,152	1,612,547	1,819,639	113,456	47,498	149,607	83,063	14.5	6.3	20.8	10.2	-1.0	0.6	-1.1	0.5	1.0	0.7	-1.0	0.7	1.1	0.2	1.1	0.3
				DLATALEQLLQAYPR	3	100.0%	1																									
				ELDALGHELPVLAPQWEGYDELQTDGNR	3	100.0%	1																									
				IEADSESQEDIIR	2	99.9%	1																									
IPI00413611	TOP1	DNA topoisomerase 1	92.1%	1.7	1	1	1	1	1,786,140	1,469,210	1,573,217	1,694,510	141,988	55,034	89,250	128,538	17.8	8.4	12.7	17.0	-1.2	0.09	-1.1	0.2	-1.1	0.6	1.1	0.4	1.2	0.1	1.1	0.5
				TYNASITLQQQLK	2	92.1%	1																									
IPI00413778	FKBP1A	FKBP1A protein	100.0%	22.1	2	2	3	2	8,624,905	8,058,660	7,979,670	9,243,545	613,476	521,573	575,824	324,425	15.9	14.5	16.1	7.9	-1.1	0.5	-1.1	0.5	1.1	0.4	-1.0	0.9	1.1	0.09	1.2	0.09
IPI00647507	FKBP1A	FK506 binding protein 1A, 12kDa	100.0%	31.1	2	2	3	2	8,624,905	8,058,660	7,979,670	9,243,545	613,476	521,573	575,824	324,425	15.9	14.5	16.1	7.9	-1.1	0.5	-1.1	0.5	1.1	0.4	-1.0	0.9	1.1	0.09	1.2	0.09
				GWEEGVAQMSVGQR	2	100.0%	2																									
				RGQTCVVHYTGMLEDGKK	3	99.6%	1																									
IPI00414037	C9orf93	C9orf93 protein	99.7%	1.9	2	2	2	1	11,226,450	11,092,990	10,870,010	13,212,750	705,839	767,348	747,844	651,441	14.1	15.5	15.4	11.0	-1.0	0.9	-1.0	0.7	1.2	0.07	-1.0	0.8	1.2	0.07	1.2	0.05
				ASQAEAVADLEIIK	3	95.4%	1																									
				ENASLQSIGSR	2	98.4%	1																									
IPI00414101	TOP2A	isoform 2 of DNA topoisomerase 2-alpha	95.2%	0.8	1	1	1	6	945,060	797,737	943,800	967,503	33,313	8,895	60,632	60,520	7.9	2.5	14.4	14.0	-1.2	0.01	-1.0	1	1.0	0.8	1.2	0.07	1.2	0.05	1.0	0.8
IPI00478232	TOP2A	DNA topoisomerase 2	95.2%	0.8	1	1	1	6	945,060	797,737	943,800	967,503	33,313	8,895	60,632	60,520	7.9	2.5	14.4	14.0	-1.2	0.01	-1.0	1	1.0	0.8	1.2	0.07	1.2	0.05	1.0	0.8
IPI00879004	TOP2A	isoform 4 of DNA topoisomerase 2-alpha	95.2%	0.7	1	1	1	6	945,060	797,737	943,800	967,503	33,313	8,895	60,632	60,520	7.9	2.5	14.4	14.0	-1.2	0.01	-1.0	1	1.0	0.8	1.2	0.07	1.2	0.05	1.0	0.8
IPI00953043	TOP2A	DNA topoisomerase 2	95.2%	0.7	1	1	1	6	945,060	797,737	943,800	967,503	33,313	8,895	60,632	60,520	7.9	2.5	14.4	14.0	-1.2	0.01	-1.0	1	1.0	0.8	1.2	0.07	1.2	0.05	1.0	0.8
IPI00953508	TOP2A	DNA topoisomerase 2	95.2%	0.8	1	1	1	6	945,060	797,737	943,800	967,503	33,313	8,895	60,632	60,520	7.9	2.5	14.4	14.0	-1.2	0.01	-1.0	1	1.0	0.8	1.2	0.07	1.2	0.05	1.0	0.8
IPI01011132	TOP2A	isoform 1 of DNA topoisomerase 2-alpha	95.2%	0.8	1	1	1	6	945,060	797,737	943,800	967,503	33,313	8,895	60,632	60,520	7.9	2.5	14.4	14.0	-1.2	0.01	-1.0	1	1.0	0.8	1.2	0.07	1.2	0.05	1.0	0.8
				TLAVSGLGVVGR	2	95.2%	1																									
IPI00414127	RANBP1	Ran-specific GTPase-activating protein	100.0%	42.8	6	6	8	3	6,754,656	6,612,395	6,367,158	7,052,351	361,707	238,311	426,962	115,148	12.0	8.1	15.0	3.7	-1.0	0.8	-1.1	0.5	1.0	0.5	-1.0	0.6	1.1	0.1	1.1	0.2
IPI00878075	RANBP1	23 kDa protein	100.0%	43.0	6	6	8	3	6,754,656	6,612,395	6,367,158	7,052,351	361,707	238,311	426,962	115,148	12.0	8.1	15.0	3.7	-1.0	0.8	-1.1	0.5	1.0	0.5	-1.0	0.6	1.1	0.1	1.1	0.2
IPI00878611	RANBP1	Uncharacterized protein	100.0%	34.7	6	6	8	3	6,754,656	6,612,395	6,367,158	7,052,351	361,707	238,311	426,962	115,148	12.0	8.1	15.0	3.7	-1.0	0.8	-1.1	0.5	1.0	0.5	-1.0	0.6	1.1	0.1	1.1	0.2
				AWVWNTHADFADECPKPELLAIR	3	100.0%	1																									
				FASENDLPEWK	2	100.0%	2																									
				FLNAENAQK	2	99.9%	2																									
				ICANHYITPMMELKPNAGSDR	3	98.6%	1																									
				TLEEDEEELFK	2	100.0%	1																									
				VAEKLEALSVK	2	94.5%	1																									
IPI00414197	WDR26	isoform 1 of WD repeat-containing protein 26	94.4%	3.0	1	1	1	2	1,064,625	951,865	944,210	975,545	72,621	36,872	54,148	42,922	15.3	8.7	12.8	9.8	-1.1	0.2	-1.1	0.2	-1.1	0.3	-1.0	0.9	1.0	0.7	1.0	0.7
IPI00645819	WDR26	isoform 2 of WD repeat-containing protein 26	94.4%	3.1	1	1	1	2	1,064,625	951,865	944,210	975,545	72,621	36,872	54,148	42,922	15.3	8.7	12.8	9.8	-1.1	0.2	-1.1	0.2	-1.1	0.3	-1.0	0.9	1.0	0.7	1.0	0.7
				GQFYQCDLDGNLLDSWEGVR	3	94.4%	1																									
IPI00414264	SRI	cDNA FLJ60640, highly similar to Sorcin	100.0%	35.6	7	7	8	1	19,699,401	20,617,462	21,775,063	23,912,201	1,331,013	536,284	968,510	883,874	15.1	5.8	10.0	8.3	1.0	0.5	1.1	0.2	1.2	0.03	1.1	0.3	1.2	0.01	1.1	0.1
				DMSGTMGFNEFK	2	98.9%	1																									
				ITFDDYIACCVK	2	100.0%	2																									
				LMVSMLDR	2	99.9%	1																									
				LMVSMLDRDMSGTMGFNEFK	3	99.9%	1																									
				LSPQAVNSIAK	2	99.9%	1																									
				QHFISFDTDR	3	99.8%	1																									
				SGTVDPQELQK	2	99.7%	1																									
IPI00414315	EPS8L2	isoform 1 of Epidermal growth factor receptor kinase substrate 8-like protein 2	100.0%	13.2	7	7	7	1	16,500,770	18,035,955	17,475,165	20,275,686	1,900,464	1,006,793	980,334	956,897	25.8	12.5	12.5	10.6	1.1	0.5	1.1	0.7	1.2	0.1	-1.0	0.7	1.1	0.1	1.2	0.08
				EPQVPLYVPK	3	97.8%	1																									
				IWTQEMLLQVNDQSLR	3	95.5%	1																									
				LLDIESQEELEDFPLPTVQR	3	100.0%	1																									
				SEAITSVDDAIR	2	99.7%	1																									
				SQPVSQPLTYESGPDEVR	2	99.6%	1																									
				SQTVLNQLR	2	86.6%	1																									
				VYSQLTMQK	2	97.3%	1																									
IPI00414320	ANXA11	cDNA FLJ55482, highly similar to Annexin A11	100.0%	17.5	7	7	10	3	20,243,827	20,445,740	20,407,813	24,064,430	2,265,016	995,337	1,750,938	1,295,669	25.0	10.9	19.2	12.0	1.0	0.9	1.0	1	1.2	0.2	-1.0	1	1.2	0.06	1.2	0.1
IPI00909703	ANXA11	Uncharacterized protein	100.0%	25.7	7	7	10	3	20,243,827	20,445,740	20,407,813	24,064,430	2,265,016	995,337	1,750,938	1,295,669	25.0	10.9	19.2	12.0	1.0	0.9	1.0	1	1.2	0.2	-1.0	1	1.2	0.06	1.2	0.1
IPI01010055	ANXA11	cDNA FLJ58379, highly similar to Annexin A11	100.0%	22.5	7	7	10	3	20,243,827	20,445,740	20,407,813	24,064,430	2,265,016	995,337	1,750,938	1,295,669	25.0	10.9	19.2	12.0	1.0	0.9	1.0	1	1.2	0.2	-1.0	1	1.2	0.06	1.2	0.1
				EMSGDLEEGMLAVVK	2	100.0%	1																									
				GFGTDEQAIIDCLGSR	2	100.0%	1																									
				GVGTDEACLIEILASR	2	100.0%	3																									
				LLISLSQGNRDESTNVDMSLAQR	3	100.0%	1																									
				SETDLLDIR	2	85.8%	1																									
				SLYHDISGDTSGDYRK	3	100.0%	2																									
				TPVLFDIYEIK	2	100.0%	1																									
IPI00414367	NHSL1	isoform 2 of NHS-like protein 1	96.3%	0.6	1	1	1	2	4,753,595	5,101,610	5,182,030	5,365,030	393,570	464,641	528,743	236,712	18.5	20.4	22.8	9.9	1.1	0.6	1.1	0.5	1.1	0.2	1.0	0.9	1.1	0.6	1.0	0.8
IPI00455733	NHSL1	isoform 1 of NHS-like protein 1	96.3%	0.6	1	1	1	2	4,753,595	5,101,610	5,182,030	5,365,030	393,570	464,641	528,743	236,712	18.5	20.4	22.8	9.9	1.1	0.6	1.1	0.5	1.1	0.2	1.0	0.9	1.1	0.6	1.0	0.8
				RDSDDDHSR	2	86.5%	1																									
IPI00414384	HSDL2	isoform 1 of Hydroxysteroid dehydrogenase-like protein 2	99.6%	8.9	2	2	2	1	5,095,600	5,294,650	6,351,510	5,596,755	250,401	512,634	653,041	294,037	11.0	21.7	23.0	11.8	1.0	0.7	1.2	0.1	1.1	0.2	1.2	0.2	1.1	0.6	-1.1	0.3
				LLGTIYTAAEEIEAVGGK	2	99.6%	1																									
				VAHILNISPPLNLNPVWFK	3	95.8%	1																									
IPI00414434	SRRT	Arsenite-resistance protein ARS2	100.0%	11.5	2	2	2	1	1,013,448	1,047,364	964,225	1,128,018	131,570	78,256	58,746	56,253	29.0	16.7	13.6	11.2	1.0	0.8	-1.1	0.7	1.1	0.4	-1.1	0.4	1.1	0.4	1.2	0.08
				EVAFFNNFLTDAK	2	100.0%	1																									
				FVTSNTQELGKDK	2	99.2%	1																									
IPI00414554	ARPC5L	Actin-related protein 2/3 complex subunit 5-like protein	99.5%	8.5	1	1	2	1	5,251,840	5,696,740	5,307,800	6,086,770	275,733	255,660	358,659	352,737	11.7	10.0	15.1	13.0	1.1	0.3	1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.4	1.1	0.2
				SSEIEQAVQSLDR	2	99.5%	2																									
IPI00414612	HKDC1	isoform 1 of Putative hexokinase HKDC1	96.8%	1.1	1	1	1	3	274,971	326,651	285,103	283,533	22,649	28,807	23,816	32,387	18.4	19.7	18.7	25.5	1.2	0.2	1.0	0.8	1.0	0.8	-1.1	0.3	-1.2	0.3	-1.0	1
IPI00855827	HKDC1	isoform 2 of Putative hexokinase HKDC1	96.8%	1.2	1	1	1	3	274,971	326,651	285,103	283,533	22,649	28,807	23,816	32,387	18.4	19.7	18.7	25.5	1.2	0.2	1.0	0.8	1.0	0.8	-1.1	0.3	-1.2	0.3	-1.0	1
IPI00856069	HKDC1	isoform 3 of Putative hexokinase HKDC1	96.8%	1.4	1	1	1	3	274,971	326,651	285,103	283,533	22,649	28,807	23,816	32,387	18.4	19.7	18.7	25.5	1.2	0.2	1.0	0.8	1.0	0.8	-1.1	0.3	-1.2	0.3	-1.0	1
				GVQDTDVVSR	2	96.8%	1																									
IPI00414676	HSP90AB1	Heat shock protein HSP 90-beta	100.0%	46.6	32	38	54	1	305,752,030	304,269,035	291,271,740	343,004,230	########	########	########	########	17.1	8.5	15.0	6.6	-1.0	1	-1.0	0.6	1.1	0.2	-1.0	0.6	1.1	0.04	1.2	0.05
				ADLINNLGTIAK	2	100.0%	2																									
				ALLFIPR	2	99.7%	1																									
				DNSTMGYMMAK	2	99.9%	1																									
				EDQTEYLEER	2	100.0%	1																									
				EGLELPEDEEEKKK	2	92.9%	1																									
				EKYIDQEELNK	2	99.0%	1																									
				EQVANSAFVER	2	100.0%	2																									
				FYEAFSK	2	99.7%	1																									
				GFEVVYMTEPIDEYCVQQLK	2	99.8%	2																									
				GVVDSEDLPLNISR	2	99.0%	1																									
				HFSVEGQLEFR	2	100.0%	1																									
				HLEINPDHPIVETLR	3	100.0%	2																									
				HSQFIGYPITLY	2	99.3%	1																									
				IDIIPNPQER	2	100.0%	2																									
				KHLEINPDHPIVETLR	3	100.0%	1																									
				LGIHEDSTNR	1	100.0%	1																									
				LGIHEDSTNR	2	99.9%	1																									
				LSELLR	2	82.8%	1																									
				LVSSPCCIVTSTYGWTANMER	2	100.0%	1																									
				NPDDITQEEYGEFYK	2	100.0%	2																									
				NPDDITQEEYGEFYK	3	99.9%	1																									
				RAPFDLFENK	2	99.9%	2																									
				RAPFDLFENKK	3	98.4%	1																									
				RLSELLR	2	99.6%	1																									
				SIYYITGESK	2	100.0%	2																									
				SLTNDWEDHLAVK	2	100.0%	2																									
				SLTNDWEDHLAVK	3	100.0%	2																									
				SLVSVTK	1	90.2%	1																									
				TLTLVDTGIGMTK	2	98.8%	3																									
				VFIMDSCDELIPEYLNFIR	2	100.0%	2																									
				VFIMDSCDELIPEYLNFIR	3	100.0%	1																									
				VILHLKEDQTEYLEER	3	100.0%	2																									

				VVVITK	1	99.3%	1																									
				YESLTDPSKLDSGK	2	100.0%	1																									
				YHTSQSGDEMTSLSEYVSR	2	100.0%	2																									
				YHTSQSGDEMTSLSEYVSR	3	100.0%	1																									
				YIDQEELNK	1	100.0%	1																									
				YIDQEELNK	2	100.0%	2																									
IPI00414696	HNRNPA2B1	isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	100.0%	57.8	16	22	32	1	61,414,394	60,886,387	61,055,536	68,733,999	3,930,569	1,150,680	3,341,741	1,886,854	14.3	4.2	12.2	6.1	-1.0	0.9	-1.0	0.9	1.1	0.1	1.0	1	1.1	0.007	1.1	0.08
				DYFEEYGKIDTIEIITDR	3	100.0%	1																									
				GFGDGYNGYGGGPGGGNFGGSPGYGGGR	2	100.0%	1																									
				GFGFVTFDDHDPVDK	2	100.0%	2																									
				GFGFVTFDDHDPVDK	3	100.0%	1																									
				GFGFVTFDDHDPVDKIVLQK	2	100.0%	1																									
				GFGFVTFDDHDPVDKIVLQK	3	100.0%	2																									
				GFGFVTFSSMAEVDAAMAAR	2	99.4%	1																									
				GGGGNFGPGPGSNFR	2	100.0%	2																									
				GGNFGFGDSR	1	95.5%	1																									
				GGNFGFGDSR	2	99.9%	2																									
				IDTIEIITDR	2	100.0%	1																									
				KLFIGGLSFETTEESLR	3	100.0%	1																									
				LFIGGLSFETTEESLR	2	100.0%	3																									
				LFIGGLSFETTEESLR	3	99.9%	1																									
				LTDCVVMRDPASK	2	100.0%	1																									
				LTDCVVMRDPASKR	3	95.8%	1																									
				NMGGPYGGGNYGPGGSGGSGGYGGR	2	100.0%	2																									
				NMGGPYGGGNYGPGGSGGSGGYGGR	3	99.9%	1																									
				NYYEQWGK	2	99.7%	2																									
				QEMQEVQSSR	2	100.0%	2																									
				YHTINGHNAEVR	2	100.0%	1																									
				YHTINGHNAEVR	3	100.0%	2																									
IPI00414717	GLG1	isoform 2 of Golgi apparatus protein 1	100.0%	5.6	5	5	5	3	5,600,284	6,447,143	5,446,365	7,012,983	693,023	402,263	576,753	325,734	27.7	14.0	23.7	10.4	1.2	0.3	-1.0	0.9	1.3	0.1	-1.2	0.2	1.1	0.3	1.3	0.05
IPI00641153	GLG1	isoform 1 of Golgi apparatus protein 1	100.0%	5.7	5	5	5	3	5,600,284	6,447,143	5,446,365	7,012,983	693,023	402,263	576,753	325,734	27.7	14.0	23.7	10.4	1.2	0.3	-1.0	0.9	1.3	0.1	-1.2	0.2	1.1	0.3	1.3	0.05
IPI00923461	GLG1	Golgi apparatus protein 1 isoform 2	100.0%	5.6	5	5	5	3	5,600,284	6,447,143	5,446,365	7,012,983	693,023	402,263	576,753	325,734	27.7	14.0	23.7	10.4	1.2	0.3	-1.0	0.9	1.3	0.1	-1.2	0.2	1.1	0.3	1.3	0.05
				ADIFVDPVLHTACALDIK	2	99.4%	1																									
				FCENTQAGEGR	2	97.9%	1																									
				IIIQESALDYR	2	99.9%	1																									
				LQETEMMDPELDYTLMR	2	100.0%	1																									
				LSSDCEDQIR	2	97.9%	1																									
IPI00414836	OSTF1	Osteoclast-stimulating factor 1	100.0%	11.2	2	2	3	1	7,542,973	7,239,439	7,038,093	8,228,127	312,272	407,208	473,112	340,115	9.3	12.6	15.0	9.2	-1.0	0.6	-1.1	0.4	1.1	0.2	-1.0	0.8	1.1	0.1	1.2	0.08
				GYADIVQLLLAK	2	100.0%	2																									
				LGDTALHAAAWK	2	82.7%	1																									
IPI00855775	-	Ribonuclease T2	99.8%	5.2	1	1	1	7	504,970	489,744	530,541	449,747	61,541	22,796	78,794	50,198	27.3	10.4	33.2	25.0	-1.0	0.8	1.1	0.8	-1.1	0.5	1.1	0.6	-1.1	0.5	-1.2	0.4
IPI00964180	-	Protein	99.8%	8.7	1	1	1	7	504,970	489,744	530,541	449,747	61,541	22,796	78,794	50,198	27.3	10.4	33.2	25.0	-1.0	0.8	1.1	0.8	-1.1	0.5	1.1	0.6	-1.1	0.5	-1.2	0.4
IPI00414896	RNASET2	isoform 1 of Ribonuclease T2	99.8%	6.3	1	1	1	7	504,970	489,744	530,541	449,747	61,541	22,796	78,794	50,198	27.3	10.4	33.2	25.0	-1.0	0.8	1.1	0.8	-1.1	0.5	1.1	0.6	-1.1	0.5	-1.2	0.4
IPI00939604	RNASET2	Uncharacterized protein	99.8%	5.2	1	1	1	7	504,970	489,744	530,541	449,747	61,541	22,796	78,794	50,198	27.3	10.4	33.2	25.0	-1.0	0.8	1.1	0.8	-1.1	0.5	1.1	0.6	-1.1	0.5	-1.2	0.4
IPI00964721	RNASET2	Uncharacterized protein	99.8%	7.3	1	1	1	7	504,970	489,744	530,541	449,747	61,541	22,796	78,794	50,198	27.3	10.4	33.2	25.0	-1.0	0.8	1.1	0.8	-1.1	0.5	1.1	0.6	-1.1	0.5	-1.2	0.4
IPI00965425	RNASET2	35 kDa protein	99.8%	5.2	1	1	1	7	504,970	489,744	530,541	449,747	61,541	22,796	78,794	50,198	27.3	10.4	33.2	25.0	-1.0	0.8	1.1	0.8	-1.1	0.5	1.1	0.6	-1.1	0.5	-1.2	0.4
IPI00967269	RNASET2	Uncharacterized protein	99.8%	6.3	1	1	1	7	504,970	489,744	530,541	449,747	61,541	22,796	78,794	50,198	27.3	10.4	33.2	25.0	-1.0	0.8	1.1	0.8	-1.1	0.5	1.1	0.6	-1.1	0.5	-1.2	0.4
				HGTCAAQVDALNSQKK	3	99.7%	1																									
IPI00414909	NAGA	Alpha-N-acetylgalactosaminidase	99.5%	2.7	1	1	2	3	1,820,643	1,786,653	1,834,533	2,107,340	139,839	143,232	147,587	37,414	17.2	17.9	18.0	4.0	-1.0	0.9	1.0	0.9	1.2	0.1	1.0	0.8	1.2	0.09	1.1	0.1
IPI00917198	NAGA	N-acetylgalactosaminidase, alpha-	99.5%	5.2	1	1	2	3	1,820,643	1,786,653	1,834,533	2,107,340	139,839	143,232	147,587	37,414	17.2	17.9	18.0	4.0	-1.0	0.9	1.0	0.9	1.2	0.1	1.0	0.8	1.2	0.09	1.1	0.1
IPI00917374	NAGA	N-acetylgalactosaminidase, alpha- (Fragment)	99.5%	4.3	1	1	2	3	1,820,643	1,786,653	1,834,533	2,107,340	139,839	143,232	147,587	37,414	17.2	17.9	18.0	4.0	-1.0	0.9	1.0	0.9	1.2	0.1	1.0	0.8	1.2	0.09	1.1	0.1
				INQDPLGIQGR	2	99.5%	2																									
IPI00418169	ANXA2	isoform 2 of Annexin A2	100.0%	76.8	35	51	75	2	220,316,001	222,371,921	233,646,675	256,959,968	########	7,950,965	########	4,830,812	18.5	8.0	21.5	4.2	1.0	0.9	1.1	0.7	1.2	0.1	1.1	0.7	1.2	0.006	1.1	0.4
IPI00455315	ANXA2	isoform 1 of Annexin A2	100.0%	80.8	35	51	75	2	220,316,001	222,371,921	233,646,675	256,959,968	########	7,950,965	########	4,830,812	18.5	8.0	21.5	4.2	1.0	0.9	1.1	0.7	1.2	0.1	1.1	0.7	1.2	0.006	1.1	0.4
				AEDGSVIDYELIDQDAR	2	100.0%	2																									
				AEDGSVIDYELIDQDAR	3	100.0%	1																									
				AEDGSVIDYELIDQDARDLYDAGVK	3	99.9%	1																									
				ALLYLCGGDD	1	100.0%	2																									
				AYTNFDAER	2	100.0%	1																									
				AYTNFDAERDALNIETAIK	2	100.0%	2																									
				AYTNFDAERDALNIETAIK	3	100.0%	2																									
				DALNIETAIK	2	100.0%	2																									
				DLYDAGVK	1	100.0%	2																									
				DLYDAGVKR	2	98.4%	1																									
				ELASALK	1	99.4%	1																									
				EVKGDLENAFLNLVQCIQNKPLYFADR	3	100.0%	1																									
				GDLENAFLNLVQCIQNKPLYFADR	2	100.0%	2																									
				GDLENAFLNLVQCIQNKPLYFADR	3	100.0%	1																									
				GLGTDEDSLIEIICSR	2	100.0%	2																									
				GLGTDEDSLIEIICSR	3	100.0%	1																									
				GVDEVTIVNILTNR	2	100.0%	2																									
				GVDEVTIVNILTNR	3	99.9%	1																									
				KLMVALAK	2	99.9%	1																									
				LMVALAK	1	94.2%	1																									
				LMVALAK	2	99.8%	2																									
				LSLEGDHSTPPSAYGSVK	2	100.0%	2																									
				LSLEGDHSTPPSAYGSVK	3	100.0%	1																									
				LYDSMK	1	98.7%	2																									
				QDIAFAYQR	2	100.0%	2																									
				RAEDGSVIDYELIDQDAR	2	100.0%	2																									
				RAEDGSVIDYELIDQDAR	3	100.0%	2																									
				SALSGHLETVILGLLK	2	100.0%	2																									
				SALSGHLETVILGLLK	3	100.0%	2																									
				SALSGHLETVILGLLKTPAQYDASELK	3	99.7%	1																									
				SDTSGDFRK	2	100.0%	2																									
				SEVDMLK	1	98.6%	1																									
				SEVDMLK	2	96.9%	1																									
				SLYYYIQQDTK	2	100.0%	2																									
				SLYYYIQQDTKGDYQK	2	100.0%	1																									
				SLYYYIQQDTKGDYQK	3	99.9%	1																									
				SVPHLQK	1	86.5%	1																									
				SYSPYDMLESIR	2	100.0%	2																									
				SYSPYDMLESIRK	2	100.0%	1																									
				SYSPYDMLESIRK	3	92.2%	1																									
				TDLEKDIISDTSGDFR	2	99.3%	1																									
				TDLEKDIISDTSGDFR	3	100.0%	1																									
				TDLEKDIISDTSGDFRK	2	100.0%	2																									
				TDLEKDIISDTSGDFRK	3	100.0%	2																									
				TKGVDEVTIVNILTNR	2	97.7%	1																									
				TKGVDEVTIVNILTNR	3	100.0%	1																									
				TNQELQEINR	1	99.2%	1																									
				TNQELQEINR	2	100.0%	2																									
				TPAQYDASELK	1	99.0%	1																									
				VYKEMYK	2	87.8%	1																									
				WISIMTER	2	100.0%	2																									
IPI00418240	NEBL	nebulette isoform 2	100.0%	5.2	1	1	1	3	273,362	287,915	329,578	277,580	48,216	15,581	36,121	19,375	39.4	12.1	24.5	15.6	1.1	0.8	1.2	0.4	1.0	0.9	1.1	0.3	-1.0	0.7	-1.2	0.2
IPI00910364	NEBL	cDNA FLJ53769, highly similar to Homo sapiens nebulette (NEBL), transcript variant	100.0%	5.9	1	1	1	3	273,362	287,915	329,578	277,580	48,216	15,581	36,121	19,375	39.4	12.1	24.5	15.6	1.1	0.8	1.2	0.4	1.0	0.9	1.1	0.3	-1.0	0.7	-1.2	0.2
IPI00956362	NEBL	nebulette isoform 3	100.0%	6.3	1	1	1	3	273,362	287,915	329,578	277,580	48,216	15,581	36,121	19,375	39.4	12.1	24.5	15.6	1.1	0.8	1.2	0.4	1.0	0.9	1.1	0.3	-1.0	0.7	-1.2	0.2
				QSFTTVADTPENLR	2	99.9%	1																									
IPI00418262	ALDOC	Fructose-bisphosphate aldolase	100.0%	32.6	10	15	21	1	101,154,498	99,865,187	94,580,083	111,248,460	7,608,242	2,998,410	5,795,039	2,887,127	16.8	6.7	13.7	5.8	-1.0	0.9	-1.1	0.5	1.1	0.3	-1.1	0.4	1.1	0.03	1.2	0.03
				AEVNGLAAQGK	2	100.0%	1																									
				DGADFAK	1	99.2%	1																									
				DGADFAK	2	88.2%	1																									
				DNAGAATEEFIKR	2	100.0%	2																									
				DNAGAATEEFIKR	3	100.0%	1																									
				GVVPLAGTDGETTTQGLDGLSER	2	100.0%	3																									
				GVVPLAGTDGETTTQGLDGLSER	3	100.0%	1																									
				QVLFSADDR	2	99.5%	1																									
				TPSALAILENANVLAR	2	100.0%	2																									
				TPSALAILENANVLAR	3	100.0%	1																									
				VDKGVVPLAGTDGETTTQGLDGLSER	3	100.0%	2																									
				YASICQQNGIVPIVEPEILPDGDHDLKR	3	100.0%	2																									
				YEGSGEDGGAAAQSLYIANHAY	2	100.0%	1																									
				YTPEEIAMATVTALR	2	100.0%	1																									
				YTPEEIAMATVTALR	3	100.0%	1																									
IPI00418336	INTS3	isoform 2 of Integrator complex subunit 3	92.6%	1.8	1	1	1	4	2,926,373	2,940,240	2,990,638	3,440,470	334,610	157,032	198,346	163,942	25.6	11.9	14.8	10.7	1.0	1	1.0	0.9	1.2	0.2	1.0	0.8	1.2	0.06	1.2	0.1
IPI00477093	INTS3	isoform 3 of Integrator complex subunit 3	92.6%	2.1	1	1	1	4	2,926,373	2,940,240	2,990,638	3,440,470	334,610	157,032	198,346	163,942	25.6	11.9	14.8	10.7	1.0	1	1.0	0.9	1.2	0.2	1.0	0.8	1.2	0.06	1.2	0.1
IPI00645811	INTS3	isoform 4 of Integrator complex subunit 3	92.6%	3.4	1	1	1	4	2,926,373	2,940,240	2,990,638	3,440,470	334,610	157,032	198,346	163,942	25.6	11.9	14.8	10.7	1.0	1	1.0	0.9	1.2	0.2	1.0	0.8	1.2	0.06	1.2	0.1
IPI00792312	INTS3	isoform 1 of Integrator complex subunit 3	92.6%	1.8	1	1	1	4	2,926,373	2,940,240	2,990,638	3,440,470	334,610	157,032	198,346	163,942	25.6	11.9	14.8	10.7	1.0	1	1.0	0.9	1.2	0.2	1.0	0.8	1.2	0.06	1.2	0.1
				LLCHLTPSIYTEFPDETLR	3	92.6%	1																									
IPI00418408	CYP2D6	Cytochrome P450	99.4%	2.5	2	2	2	8	2,232,881	2,149,046	2,025,275	2,429,511	266,945	161,525	172,367	84,900	26.7	16.8	19.0	7.8	-1.0	0.8	-1.1	0.5	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.07
IPI00456699	CYP2D6	Cytochrome P450 2D6	99.4%	2.6	2	2	2	8	2,232,881	2,149,046	2,025,275	2,429,511	266,945	161,525	172,367	84,900	26.7	16.8	19.0	7.8	-1.0	0.8	-1.1	0.5	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.07
IPI00873166	CYP2D6	56 kDa protein	99.4%	2.6	2	2	2	8	2,232,881	2,149,046	2,025,275	2,429,511	266,945	161,525	172,367	84,900	26.7	16.8	19.0	7.8	-1.0	0.8	-1.1	0.5	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.07
IPI00873251	CYP2D6	Debrisoquine 4-hydroxylase mutant allele variant (Fragment)	99.4%	2.3	2	2	2	8	2,232,881	2,149,046	2,025,275	2,429,511	266,945	161,525	172,367	84,900	26.7	16.8	19.0	7.8	-1.0	0.8	-1.1	0.5	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.07
IPI00943274	CYP2D6	Cytochrome P450 2D6	99.4%	2.6	2	2	2	8	2,232,881	2,149,046	2,025,275	2,429,511	266,945	161,525	172,367	84,900	26.7	16.8	19.0	7.8	-1.0	0.8	-1.1	0.5	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.07
IPI00969560	CYP2D7P1	Cytochrome P450	99.4%	2.6	2	2	2	8	2,232,881	2,149,046	2,025,275	2,429,511	266,945	161,525	172,367	84,900	26.7	16.8	19.0	7.8	-1.0	0.8	-1.1	0.5	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.07
IPI01010620	CYP2D7P1	50 kDa protein	99.4%	2.9	2	2	2	8	2,232,881	2,149,046	2,025,275	2,429,511	266,945	161,525	172,367	84,900	26.7	16.8	19.0	7.8	-1.0	0.8	-1.1	0.5	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.07
IPI01012300	CYP2D7P1	Cytochrome P4502D6	99.4%	3.2	2	2	2	8	2,232,881	2,149,046	2,025,275	2,429,511	266,945	161,525	172,367	84,900	26.7	16.8	19.0	7.8	-1.0	0.8	-1.1	0.5	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.07
				FEYDDPR	2	94.3%	1																									
				NLGLGK	1	89.7%	1																									
IPI00418663	KRT28	Keratin 25D	92.8%	6.0	1	1	1	1	9,017,390	8,033,960	13,221,180	9,727,580	982,588	1,235,330	1,046,443	1,002,982	24.4	34.4	17.7	23.1	-1.1	0.6	1.5	0.02	1.1	0.6	1.6	0.01	1.2	0.3	-1.4	0.04
				KDAEAWFNEKSASLQQQISHDSGAATFAR	3	92.8%	1																									
IPI00418813	RPS27A	Ribosomal protein S27a	100.0%	17.0	3	3	6	2	1,277,264	1,314,633	1,332,432	1,530,477	95,962	35,332	86,262	51,432	16.8	6.0	14.5	7.5	1.0	0.7	1.0	0.7	1.2	0.05	1.0	0.9	1.2	0.009	1.1	0.08
IPI00794205	-	26 kDa protein	100.0%	16.6	3	3	6	2	1,277,264	1,314,633	1,332,432	1,530,477	95,962	35,332	86,262	51,432	16.8	6.0	14.5	7.5	1.0	0.7	1.0	0.7	1.2	0.05	1.0	0.9	1.2	0.009	1.1	0.08
				ESTLHLVLR	2	99.7%	2																									
				IQDKEGIPPDQQR	2	99.9%	2																									
				TITLEVEPSDTIENVK	2	100.0%	2																									

IPI00418941	TSHZ1	isoform 1 of Teashirt homolog 1	100.0%	2.6	2	2	2	2	6,193,060	6,576,230	6,211,875	6,486,180	403,426	387,741	370,886	322,429	14.6	13.2	13.4	11.1	1.1	0.5	1.0	1	1.0	0.6	-1.1	0.5	-1.0	0.9	1.0	0.6
IPI01008913	TSHZ1	isoform 2 of Teashirt homolog 1	100.0%	2.7	2	2	2	2	6,193,060	6,576,230	6,211,875	6,486,180	403,426	387,741	370,886	322,429	14.6	13.2	13.4	11.1	1.1	0.5	1.0	1	1.0	0.6	-1.1	0.5	-1.0	0.9	1.0	0.6
				EKPPVAGDAEK	3	93.1%	1																									
				NKPLVSSVADSVASPLR	3	99.4%	1																									
IPI00419100	FGD6	isoform 1 of FYVE, RhoGEF and PH domain-containing protein 6	99.6%	2.3	2	2	2	2	7,490,065	7,911,745	7,744,920	8,348,950	687,024	397,462	816,893	307,731	20.5	11.2	23.6	8.2	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.4	1.1	0.5
IPI00471914	FGD6	isoform 2 of FYVE, RhoGEF and PH domain-containing protein 6	99.6%	2.4	2	2	2	2	7,490,065	7,911,745	7,744,920	8,348,950	687,024	397,462	816,893	307,731	20.5	11.2	23.6	8.2	1.1	0.6	1.0	0.8	1.1	0.3	-1.0	0.9	1.1	0.4	1.1	0.5
				LGNKSELNMESNSDAQDLVNSQK	3	91.2%	1																									
				QLGKPVIEDR	2	96.1%	1																									
IPI00419194	IAH1	Isoamyl acetate-hydrolyzing esterase 1 homolog	97.5%	6.1	1	1	1	3	272,503	249,409	302,182	320,230	61,348	33,121	44,891	35,118	50.3	29.7	33.2	24.5	-1.1	0.7	1.1	0.7	1.2	0.5	1.2	0.4	1.3	0.2	1.1	0.8
IPI00432867	IAH1	IAH1 protein (Fragment)	97.5%	6.3	1	1	1	3	272,503	249,409	302,182	320,230	61,348	33,121	44,891	35,118	50.3	29.7	33.2	24.5	-1.1	0.7	1.1	0.7	1.2	0.5	1.2	0.4	1.3	0.2	1.1	0.8
IPI00945158	IAH1	cDNA FLJ60023	97.5%	11.1	1	1	1	3	272,503	249,409	302,182	320,230	61,348	33,121	44,891	35,118	50.3	29.7	33.2	24.5	-1.1	0.7	1.1	0.7	1.2	0.5	1.2	0.4	1.3	0.2	1.1	0.8
				GNEFLFSHLWPLIEK	3	97.5%	1																									
IPI00419237	LAP3	isoform 1 of Cytosol aminopeptidase	100.0%	22.2	7	7	7	1	17,719,059	19,183,529	18,120,785	21,370,214	1,187,325	794,038	1,319,341	657,357	15.0	9.3	16.3	6.9	1.1	0.3	1.0	0.8	1.2	0.03	-1.1	0.5	1.1	0.07	1.2	0.06
				FGSRSLSTADMTKGLVLGIYSK	3	93.6%	1																									
				GITFDSGGISIK	2	99.9%	1																									
				GSPNANEPPLVFVGK	2	96.1%	1																									
				LNLPINIIGLAPLCENMPSGK	2	82.1%	1																									
				LYGSGDQEAWQK	2	99.5%	1																									
				QLMETPANEMTPTR	2	100.0%	1																									
				TFYGLHQDFPSVVLVGLGK	3	100.0%	1																									
IPI01011049	-	19 kDa protein	100.0%	35.2	6	7	9	5	5,693,129	5,364,684	5,248,472	5,701,922	769,269	214,272	317,477	169,680	30.2	8.9	13.5	6.7	-1.1	0.7	-1.1	0.6	1.0	1	-1.0	0.8	1.1	0.3	1.1	0.2
IPI01014153	-	18 kDa protein	100.0%	36.1	6	7	9	5	5,693,129	5,364,684	5,248,472	5,701,922	769,269	214,272	317,477	169,680	30.2	8.9	13.5	6.7	-1.1	0.7	-1.1	0.6	1.0	1	-1.0	0.8	1.1	0.3	1.1	0.2
IPI00419258	HMGB1	High mobility group protein B1	100.0%	26.5	6	7	9	5	5,693,129	5,364,684	5,248,472	5,701,922	769,269	214,272	317,477	169,680	30.2	8.9	13.5	6.7	-1.1	0.7	-1.1	0.6	1.0	1	-1.0	0.8	1.1	0.3	1.1	0.2
IPI00644653	HMGB1	cDNA FLJ56337, highly similar to High mobility group protein B1	100.0%	36.1	6	7	9	5	5,693,129	5,364,684	5,248,472	5,701,922	769,269	214,272	317,477	169,680	30.2	8.9	13.5	6.7	-1.1	0.7	-1.1	0.6	1.0	1	-1.0	0.8	1.1	0.3	1.1	0.2
IPI00645948	HMGB1	Uncharacterized protein	100.0%	26.4	6	7	9	5	5,693,129	5,364,684	5,248,472	5,701,922	769,269	214,272	317,477	169,680	30.2	8.9	13.5	6.7	-1.1	0.7	-1.1	0.6	1.0	1	-1.0	0.8	1.1	0.3	1.1	0.2
				GEHPGLSIGDVAK	2	99.4%	1																									
				HPDASVNFSEFSK	2	99.1%	1																									
				IKGEHPGLSIGDVAK	3	100.0%	2																									
				KHPDASVNFSEFSK	3	99.9%	1																									
				LGEMWNNTAADDKQPYEK	2	99.9%	1																									
				LGEMWNNTAADDKQPYEK	3	100.0%	2																									
				TYIPPKGETK	3	98.9%	1																									
IPI00419373	HNRNPA3	isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	100.0%	34.4	12	14	18	4	24,297,509	25,147,253	23,194,897	27,965,713	1,891,010	680,472	1,516,582	823,345	17.4	6.1	14.6	6.6	1.0	0.7	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.03	1.2	0.02
IPI00455134	HNRNPA3	isoform 2 of Heterogeneous nuclear ribonucleoprotein A3	100.0%	36.5	12	14	18	4	24,297,509	25,147,253	23,194,897	27,965,713	1,891,010	680,472	1,516,582	823,345	17.4	6.1	14.6	6.6	1.0	0.7	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.03	1.2	0.02
IPI00927677	HNRNPA3	Uncharacterized protein	100.0%	40.9	12	14	18	4	24,297,509	25,147,253	23,194,897	27,965,713	1,891,010	680,472	1,516,582	823,345	17.4	6.1	14.6	6.6	1.0	0.7	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.03	1.2	0.02
IPI00939124	HNRNPA3	Uncharacterized protein	100.0%	37.8	12	14	18	4	24,297,509	25,147,253	23,194,897	27,965,713	1,891,010	680,472	1,516,582	823,345	17.4	6.1	14.6	6.6	1.0	0.7	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.03	1.2	0.02
				EDSVKPGAHLTVK	2	100.0%	2																									
				GFAFVTFDDHDTVDK	3	99.5%	1																									
				GFAFVTFDDHDTVDKIVVQK	3	87.0%	1																									
				IETIEVMEDR	2	100.0%	2																									
				IFVGGIKEDTEEYNLR	2	100.0%	1																									
				IFVGGIKEDTEEYNLR	3	100.0%	2																									
				KIFVGGIKEDTEEYNLR	3	100.0%	1																									
				LFIGGLSFETTDDSLR	2	99.9%	1																									
				SSGSPYGGGYGSGGGSGGYGSR	2	100.0%	2																									
				WGTLTDCVVMR	2	99.9%	1																									
				WGTLTDCVVMRDPQTK	3	99.7%	1																									
				YGKIETIEVMEDR	2	99.6%	1																									
				YGKIETIEVMEDR	3	99.9%	1																									
				YHTINGHNCEVKK	3	93.2%	1																									
IPI00419531	CPSF2	Cleavage and polyadenylation specificity factor subunit 2	99.6%	1.7	1	2	2	1	1,170,396	1,310,990	1,164,667	1,257,961	71,374	45,283	62,886	69,858	13.6	7.7	12.1	12.4	1.1	0.1	-1.0	1	1.1	0.4	-1.1	0.1	-1.0	0.5	1.1	0.3
				VLELAQLLDQIWR	2	99.6%	1																									
				VLELAQLLDQIWR	3	98.9%	1																									
IPI00419542	LIPE	isoform 2 of Hormone-sensitive lipase	100.0%	11.5	5	5	5	2	21,139,496	21,929,371	23,117,597	23,269,164	2,073,508	1,663,754	1,690,173	1,117,883	21.9	17.0	16.4	10.7	1.0	0.8	1.1	0.5	1.1	0.4	1.1	0.6	1.1	0.5	1.0	0.9
IPI00643204	LIPE	isoform 1 of Hormone-sensitive lipase	100.0%	8.3	5	5	5	2	21,139,496	21,929,371	23,117,597	23,269,164	2,073,508	1,663,754	1,690,173	1,117,883	21.9	17.0	16.4	10.7	1.0	0.8	1.1	0.5	1.1	0.4	1.1	0.6	1.1	0.5	1.0	0.9
				LGASSWLNSFLELSGR	2	99.9%	1																									
				LLGVAHLFDLDPETPANGYR	3	99.4%	1																									
				LLSLMDPLLPLSVLSK	2	100.0%	1																									
				NPFMSPLLAPDSMLK	2	99.4%	1																									
				VPDGIMAAYPATMLQPAASPSR	2	99.5%	1																									
IPI00419585	PPIA	Peptidyl-prolyl cis-trans isomerase A	100.0%	63.6	13	19	26	1	274,859,141	290,170,310	272,252,579	335,502,295	########	########	########	########	25.9	10.1	20.1	8.4	1.1	0.7	-1.0	0.9	1.2	0.1	-1.1	0.5	1.2	0.04	1.2	0.05
				AGPNTNGSQFFICTAK	2	99.7%	1																									
				EGMNIVEAMER	2	98.7%	1																									
				FEDENFILK	2	99.7%	2																									
				HTGPGILSMANAGPNTNGSQFFICTAK	2	100.0%	1																									
				HTGPGILSMANAGPNTNGSQFFICTAK	3	100.0%	2																									
				IIPGFMCQGGDFTR	2	100.0%	2																									
				ITIADCGQLE	1	100.0%	1																									
				ITIADCGQLE	2	99.4%	1																									
				KITIADCGQLE	2	100.0%	2																									
				SIYGEKFEDENFILK	2	100.0%	1																									
				SIYGEKFEDENFILK	3	99.6%	1																									
				TEWLDGK	1	98.8%	1																									
				TEWLDGK	2	100.0%	1																									
				TEWLDGKHVVFGK	2	98.8%	1																									
				TEWLDGKHVVFGK	3	99.4%	1																									
				VKEGMNIVEAMER	2	99.2%	1																									
				VSFELFADK	2	100.0%	2																									
				VSFELFADKVPK	2	100.0%	2																									
				VSFELFADKVPK	3	100.0%	2																									
IPI00419598	EPGN	isoform 1 of Epigen	92.2%	10.4	1	1	1	3	994,853	1,041,963	1,080,407	1,185,900	107,327	44,575	92,891	66,666	24.1	9.6	19.2	12.6	1.0	0.7	1.1	0.6	1.2	0.2	1.0	0.7	1.1	0.1	1.1	0.4
IPI00923513	EPGN	isoform 2 of Epigen	92.2%	12.0	1	1	1	3	994,853	1,041,963	1,080,407	1,185,900	107,327	44,575	92,891	66,666	24.1	9.6	19.2	12.6	1.0	0.7	1.1	0.6	1.2	0.2	1.0	0.7	1.1	0.1	1.1	0.4
IPI00964038	EPGN	Protein	92.2%	12.3	1	1	1	3	994,853	1,041,963	1,080,407	1,185,900	107,327	44,575	92,891	66,666	24.1	9.6	19.2	12.6	1.0	0.7	1.1	0.6	1.2	0.2	1.0	0.7	1.1	0.1	1.1	0.4
				CEHLTLTSYAVDSYEK	2	92.2%	1																									
IPI00419684	PHC2	isoform 2 of Polyhomeotic-like protein 2	93.5%	3.4	1	1	1	5	344,100	333,300	334,196	381,598	14,306	39,770	10,220	25,193	9.3	26.7	6.8	14.8	-1.0	0.8	-1.0	0.6	1.1	0.2	1.0	1	1.1	0.3	1.1	0.1
IPI00443448	PHC2	Uncharacterized protein	93.5%	3.5	1	1	1	5	344,100	333,300	334,196	381,598	14,306	39,770	10,220	25,193	9.3	26.7	6.8	14.8	-1.0	0.8	-1.0	0.6	1.1	0.2	1.0	1	1.1	0.3	1.1	0.1
IPI00647439	PHC2	isoform 4 of Polyhomeotic-like protein 2	93.5%	1.3	1	1	1	5	344,100	333,300	334,196	381,598	14,306	39,770	10,220	25,193	9.3	26.7	6.8	14.8	-1.0	0.8	-1.0	0.6	1.1	0.2	1.0	1	1.1	0.3	1.1	0.1
IPI00876858	PHC2	isoform 5 of Polyhomeotic-like protein 2	93.5%	1.3	1	1	1	5	344,100	333,300	334,196	381,598	14,306	39,770	10,220	25,193	9.3	26.7	6.8	14.8	-1.0	0.8	-1.0	0.6	1.1	0.2	1.0	1	1.1	0.3	1.1	0.1
IPI00943102	PHC2	isoform 1 of Polyhomeotic-like protein 2	93.5%	1.3	1	1	1	5	344,100	333,300	334,196	381,598	14,306	39,770	10,220	25,193	9.3	26.7	6.8	14.8	-1.0	0.8	-1.0	0.6	1.1	0.2	1.0	1	1.1	0.3	1.1	0.1
				WNVEDVYEFIR	2	93.5%	1																									
IPI00419692	PIPSL	Putative PIP5K1A and PSMD4-like protein	100.0%	3.3	2	2	3	2	1,718,035	2,137,788	1,997,405	2,497,428	312,462	160,530	148,634	140,421	40.7	16.8	16.6	12.6	1.2	0.3	1.2	0.4	1.5	0.05	-1.1	0.5	1.2	0.1	1.3	0.04
IPI00853509	PSMD4	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 4	100.0%	13.8	2	2	3	2	1,718,035	2,137,788	1,997,405	2,497,428	312,462	160,530	148,634	140,421	40.7	16.8	16.6	12.6	1.2	0.3	1.2	0.4	1.5	0.05	-1.1	0.5	1.2	0.1	1.3	0.04
				LTAFVNTLNGK	2	99.9%	2																									
				VNVDIINFGEEEVNTEK	2	100.0%	1																									
IPI00419791	RSRC2	isoform 1 of Arginine/serine-rich coiled-coil protein 2	96.6%	2.8	1	1	1	4	1,181,005	1,193,928	1,217,258	1,278,608	69,619	68,486	60,960	35,676	13.2	12.8	11.2	6.2	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.3	1.1	0.4
IPI00848084	RSRC2	isoform 2 of Arginine/serine-rich coiled-coil protein 2	96.6%	3.1	1	1	1	4	1,181,005	1,193,928	1,217,258	1,278,608	69,619	68,486	60,960	35,676	13.2	12.8	11.2	6.2	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.3	1.1	0.4
IPI00872495	RSRC2	Arginine/serine-rich coiled-coil 2 isoform c	96.6%	3.3	1	1	1	4	1,181,005	1,193,928	1,217,258	1,278,608	69,619	68,486	60,960	35,676	13.2	12.8	11.2	6.2	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.3	1.1	0.4
IPI00902855	RSRC2	HSPC314 (Fragment)	96.6%	4.8	1	1	1	4	1,181,005	1,193,928	1,217,258	1,278,608	69,619	68,486	60,960	35,676	13.2	12.8	11.2	6.2	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.3	1.1	0.4
				NTAMDAQEALAR	2	96.6%	1																									
IPI00974509	TNPO1	Uncharacterized protein	100.0%	2.9	1	1	2	3	572,890	636,068	627,022	627,272	45,227	37,507	28,923	16,400	17.7	13.2	10.3	5.9	1.1	0.3	1.1	0.3	1.1	0.3	-1.0	0.9	-1.0	0.8	1.0	1
IPI00419856	TNPO2	transportin-2 isoform 3	100.0%	1.4	1	1	2	3	572,890	636,068	627,022	627,272	45,227	37,507	28,923	16,400	17.7	13.2	10.3	5.9	1.1	0.3	1.1	0.3	1.1	0.3	-1.0	0.9	-1.0	0.8	1.0	1
IPI01010660	TNPO2	TNPO2 variant protein (Fragment)	100.0%	1.1	1	1	2	3	572,890	636,068	627,022	627,272	45,227	37,507	28,923	16,400	17.7	13.2	10.3	5.9	1.1	0.3	1.1	0.3	1.1	0.3	-1.0	0.9	-1.0	0.8	1.0	1
				TLLENTAITIGR	2	100.0%	2																									
IPI00419880	RPS3A;SNORD73A	40S ribosomal protein S3a	100.0%	22.7	5	6	6	3	10,613,239	11,169,855	10,375,861	12,389,128	557,049	436,154	489,324	322,237	11.7	8.7	10.6	5.8	1.1	0.5	-1.0	0.8	1.2	0.02	-1.1	0.3	1.1	0.05	1.2	0.009
IPI00964983	RPS3A;SNORD73A	Uncharacterized protein	100.0%	26.9	5	6	6	3	10,613,239	11,169,855	10,375,861	12,389,128	557,049	436,154	489,324	322,237	11.7	8.7	10.6	5.8	1.1	0.5	-1.0	0.8	1.2	0.02	-1.1	0.3	1.1	0.05	1.2	0.009
IPI00967073	RPS3A;SNORD73A	Uncharacterized protein	100.0%	26.4	5	6	6	3	10,613,239	11,169,855	10,375,861	12,389,128	557,049	436,154	489,324	322,237	11.7	8.7	10.6	5.8	1.1	0.5	-1.0	0.8	1.2	0.02	-1.1	0.3	1.1	0.05	1.2	0.009
				ACQSIYPLHDVFVR	2	99.9%	1																									
				LITEDVQGK	2	96.4%	1																									
				LMELHGEGSSSGK	2	99.6%	1																									
				MMEIMTR	2	88.7%	1																									
				VFEVSLADLQNDEVAFR	2	100.0%	1																									
				VFEVSLADLQNDEVAFR	3	82.8%	1																									
IPI00419979	PAK2;LOC646214	Serine/threonine-protein kinase PAK 2	100.0%	4.4	2	2	2	1	9,014,660	9,436,665	9,248,240	9,614,530	731,407	492,097	456,587	483,516	18.1	11.7	11.0	11.3	1.0	0.6	1.0	0.8	1.1	0.5	-1.0	0.8	1.0	0.8	1.0	0.6
				IISIFSGTEK	2	99.8%	1																									
				SDNVLLGMEGSVK	2	99.6%	1																									
IPI00740142	LOC652147	u5 small nuclear ribonucleoprotein 200 kDa helicase-like, partial	100.0%	2.6	2	2	2	2	1,032,607	819,934	1,131,073	906,712	113,919	157,926	139,027	103,983	24.7	43.1	27.5	25.6	-1.3	0.3	1.1	0.6	-1.1	0.4	1.4	0.2	1.1	0.7	-1.2	0.2
IPI00420014	SNRNP200	isoform 1 of U5 small nuclear ribonucleoprotein 200 kDa helicase	100.0%	2.1	2	2	2	2	1,032,607	819,934	1,131,073	906,712	113,919	157,926	139,027	103,983	24.7	43.1	27.5	25.6	-1.3	0.3	1.1	0.6	-1.1	0.4	1.4	0.2	1.1	0.7	-1.2	0.2
				LIGLSATLPNYEDVATFLR	2	99.5%	1																									
				YAQDEHLITFFVPVFEPLPPQYFIR	3	98.3%	1																									
IPI00420108	DLSTP1;DLST	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydr	100.0%	10.4	3	3	3	1	7,850,397	7,758,587	8,416,087	9,892,983	567,047	626,751	726,796	321,226	16.2	18.1	19.3	7.3	-1.0	0.9	1.1	0.6	1.3	0.01	1.1	0.5	1.3	0.02	1.2	0.1
				ASAFALQEQPVVNAVIDDTTK	2	99.9%	1																									
				NVEAMNFADIER	2	100.0%	1																									
				TPAFAESVTEGDVR	2	100.0%	1																									
IPI00424869	RAP1GDS1	rap1 GTPase-GDP dissociation stimulator 1 isoform 6	91.7%	3.7	1	1	1	9	86,808	96,312	102,436	89,348	14,200	12,266	13,507	4,922	36.6	28.5	29.5	12.3	1.1	0.6	1.2	0.4	1.0	0.9	1.1	0.7	-1.1	0.6	-1.1	0.4
IPI00607591	RAP1GDS1	isoform 1 of Rap1 GTPase-GDP dissociation stimulator 1	91.7%	3.1	1	1	1	9	86,808	96,312	102,436	89,348	14,200	12,266	13,507	4,922	36.6	28.5	29.5	12.3	1.1	0.6	1.2	0.4	1.0	0.9	1.1	0.7	-1.1	0.6	-1.1	0.4
IPI00619924	RAP1GDS1	rap1 GTPase-GDP dissociation stimulator 1 isoform 4	91.7%	3.4	1	1	1	9	86,808	96,312	102,436	89,348	14,200	12,266	13,507	4,922	36.6	28.5	29.5	12.3	1.1	0.6	1.2	0.4	1.0	0.9	1.1	0.7	-1.1	0.6	-1.1	0.4
IPI00855727	RAP1GDS1	rap1 GTPase-GDP dissociation stimulator 1 isoform 2	91.7%	3.1	1	1	1	9	86,808	96,312	102,436	89,348	14,200	12,266	13,507	4,922	36.6	28.5	29.5	12.3	1.1	0.6	1.2	0.4	1.0	0.9	1.1	0.7	-1.1	0.6	-1.1	0.4
IPI00855767	RAP1GDS1	rap1 GTPase-GDP dissociation stimulator 1 isoform 1	91.7%	3.1	1	1	1	9	86,808	96,312	102,436	89,348	14,200	12,266	13,507	4,922	36.6	28.5	29.5	12.3	1.1	0.6	1.2	0.4	1.0	0.9	1.1	0.7	-1.1	0.6	-1.1	0.4
IPI00856100	RAP1GDS1	isoform 2 of Rap1 GTPase-GDP dissociation stimulator 1	91.7%	3.4	1	1	1	9	86,808	96,312	102,436	89,348	14,200	12,266	13,507	4,922	36.6	28.5	29.5	12.3	1.1	0.6	1.2	0.4	1.0	0.9	1.1	0.7	-1.1	0.6	-1.1	0.4
IPI00967154	RAP1GDS1	Uncharacterized protein	91.7%	12.8	1	1	1	9	86,808	96,312	102,436	89,348	14,200	12,266	13,507	4,922	36.6	28.5	29.5	12.3	1.1	0.6	1.2	0.4	1.0	0.9	1.1	0.7	-1.1	0.6	-1.1	0.4
IPI00967796	RAP1GDS1	Uncharacterized protein	91.7%	14.7	1	1	1	9	86,808	96,312	102,436	89,348	14,200	12,266	13,507	4,922	36.6	28.5	29.5	12.3	1.1	0.6	1.2	0.4	1.0	0.9	1.1	0.7	-1.1	0.6	-1.1	0.4
IPI00968047	RAP1GDS1	Uncharacterized protein	91.7%	15.6	1	1	1	9	86,808	96,312	102,436	89,348	14,200	12,266	13,507	4,922	36.6	28.5	29.5	12.3	1.1	0.6	1.2	0.4	1.0	0.9	1.1	0.7	-1.1	0.6	-1.1	0.4
				IPCVDAGLISPLVQLLNSK	2	91.8%	1																									
IPI00425404	KIF21A	isoform 1 of Kinesin-like protein KIF21A	95.9%	1.2	1	1	1	7	295,870	356,973	362,744	375,367	39,840	41,068	43,721	26,478	30.1	25.7	27.0	15.8	1.2	0.3	1.2	0.3	1.3	0.1	1.0	0.9	1.1	0.7	1.0	0.8
IPI00425405	KIF21A	isoform 2 of Kinesin-like protein KIF21A	95.9%	1.2	1	1	1	7	295,870	356,973	362,744	375,367	39,840	41,068	43,721	26,478	30.1	25.7	27.0	15.8	1.2	0.3	1.2	0.3	1.3	0.1	1.0	0.9	1.1	0.7	1.0	0.8
IPI00425407	KIF21A	isoform 3 of Kinesin-like protein KIF21A	95.9%	1.2	1	1	1	7	295,870	356,973	362,744	375,367	39,840	41,068	43,721	26,478	30.1	25.7	27.0	15.8	1.2	0.3	1.2	0.3	1.3	0.1	1.0	0.9	1.1	0.7	1.0	0.8
IPI00425409	KIF21A	isoform 4 of Kinesin-like protein KIF21A	95.9%	1.2	1	1	1	7	295,870	356,973	362,744	375,367	39,840	41,068	43,721	26,478	30.1	25.7	27.0	15.8	1.2	0.3	1.2	0.3	1.3	0.1	1.0	0.9	1.1	0.7	1.0	0.8
IPI00956238	KIF21A	kinesin-like protein KIF21A isoform 3	95.9%	1.2	1	1	1	7	295,870	356,973	362,744	375,367	39,840	41,068	43,721	26,478	30.1	25.7	27.0	15.8	1.2	0.3	1.2	0.3	1.3	0.1	1.0	0.9	1.1	0.7	1.0	0.8
IPI01013038	KIF21A	kinesin-like protein KIF21A isoform 4	95.9%	1.2	1	1	1	7	295,870	356,973	362,744	375,367	39,840	41,068	43,721	26,478	30.1	25.7	27.0	15.8	1.2	0.3	1.2	0.3	1.3	0.1	1.0	0.9	1.1	0.7	1.0	0.8
IPI01013445	KIF21A	187 kDa protein	95.9%	1.2	1	1	1	7	295,870	356,973	362,744	375,367	39,840	41,068	43,721	26,478	30.1	25.7	27.0	15.8	1.2	0.3	1.2	0.3	1.3	0.1	1.0	0.9	1.1	0.7	1.0	0.8
				DQVLQNLGSVESYSEEKAKK	2	93.9%	1																									
IPI00427586	PRKG1	isoform Alpha of cGMP-dependent protein kinase 1	95.4%	1.8	1	1	1	3	2,662,987	3,374,543	2,732,293	2,800,070	492,629	315,082	325,120	151,055	41.4	20.9	26.6	12.1	1.3	0.3	1.0	0.9	1.1	0.8	-1.2	0.2	-1.2	0.1	1.0	0.9
IPI00436355	PRKG1	isoform Beta of cGMP-dependent protein kinase 1	95.4%	1.8	1	1	1	3	2,662,987	3,374,543	2,732,293	2,800,070	492,629	315,082	325,120	151,055	41.4	20.9	26.6	12.1	1.3	0.3	1.0	0.9	1.1	0.8	-1.2	0.2	-1.2	0.1	1.0	0.9
IPI00647138	PRKG1	cDNA FLJ36117 fis, clone TESTI2022400, highly similar to cGMP-dependent protei	95.4%	3.1	1	1	1	3	2,662,987	3,374,543	2,732,293	2,800,070	492,629	315,082	325,120	151,055	41.4	20.9	26.6	12.1	1.3	0.3	1.0	0.9	1.1	0.8	-1.2	0.2	-1.2	0.1	1.0	0.9
				DLKPENLILDHR	3	95.4%	1																									
IPI00429190	RAB11A	cDNA FLJ61136, highly similar to Ras-related protein Rab-11A	100.0%	15.7	4	4	6	4	9,329,557	8,952,453	8,904,402	9,925,443	619,700	316,991	432,027	298,642	14.9	7.9	10.9	6.7	-1.0	0.6	-1.0	0.6	1.1	0.4	-1.0	0.9	1.1	0.06	1.1	0.09
IPI00795676	RAB11A	22 kDa protein	100.0%	20.7	4	4	6	4	9,329,557	8,952,453	8,904,402	9,925,443	619,700	316,991	432,027	298,642	14.9	7.9	10.9	6.7	-1.0	0.6	-1.0	0.6	1.1	0.4	-1.0	0.9	1.1	0.06	1.1	0.09

IPI01012355	RAB11A	18 kDa protein	100.0%	26.5	4	4	6	4	9,329,557	8,952,453	8,904,402	9,925,443	619,700	316,991	432,027	298,642	14.9	7.9	10.9	6.7	-1.0	0.6	-1.0	0.6	1.1	0.4	-1.0	0.9	1.1	0.06	1.1	0.09
IPI00978887	RAB11B	RAB11B protein	100.0%	18.8	4	4	6	4	9,329,557	8,952,453	8,904,402	9,925,443	619,700	316,991	432,027	298,642	14.9	7.9	10.9	6.7	-1.0	0.6	-1.0	0.6	1.1	0.4	-1.0	0.9	1.1	0.06	1.1	0.09
				AQIWDTAGQER	2	100.0%	2																									
				HLTYENVER	2	100.0%	2																									
				STIGVEFATR	2	100.0%	1																									
				VVLIGDSGVGK	2	98.1%	1																									
IPI00429191	ETF1	Eukaryotic peptide chain release factor subunit 1	100.0%	8.0	3	3	4	3	4,903,563	4,661,859	4,559,557	5,566,125	557,003	307,830	503,347	279,304	25.4	14.8	24.7	11.2	-1.1	0.7	-1.1	0.7	1.1	0.3	-1.0	0.9	1.2	0.06	1.2	0.1
IPI00967460	ETF1	cDNA FLJ56175, highly similar to Eukaryotic peptide chain release factor subunit1	100.0%	8.3	3	3	4	3	4,903,563	4,661,859	4,559,557	5,566,125	557,003	307,830	503,347	279,304	25.4	14.8	24.7	11.2	-1.1	0.7	-1.1	0.7	1.1	0.3	-1.0	0.9	1.2	0.06	1.2	0.1
IPI00968296	ETF1	Eukaryotic translation termination factor 1, isoform CRA_b	100.0%	8.7	3	3	4	3	4,903,563	4,661,859	4,559,557	5,566,125	557,003	307,830	503,347	279,304	25.4	14.8	24.7	11.2	-1.1	0.7	-1.1	0.7	1.1	0.3	-1.0	0.9	1.2	0.06	1.2	0.1
				FGATLEIVTDK	2	99.9%	1																									
				LSVLGAITSVQQR	2	99.9%	2																									
				YFDEISQDTGK	2	100.0%	1																									
IPI00429689	PPP2CB	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	100.0%	17.8	4	4	4	1	7,909,593	8,126,538	7,957,560	8,686,502	552,124	275,103	531,731	271,165	15.6	7.6	14.9	7.0	1.0	0.7	1.0	1	1.1	0.2	-1.0	0.8	1.1	0.2	1.1	0.3
				CGNQAAIMELDDTLK	2	99.9%	1																									
				QITQVYGFYDECLR	2	100.0%	1																									
				SPDTNYLFMGDYVDR	2	100.0%	1																									
				YSFLQFDPAPR	2	100.0%	1																									
IPI00430803	C2orf79	Uncharacterized protein C2orf79	99.5%	15.0	1	1	1	1	3,396,690	3,525,040	3,227,250	4,192,480	587,148	188,524	154,108	304,472	38.7	12.0	10.7	16.2	1.0	0.8	-1.1	0.8	1.2	0.3	-1.1	0.3	1.2	0.1	1.3	0.02
				VVLEAPDETTLKELAETLQQK	3	99.5%	1																									
IPI00430812	CNBP	isoform 1 of Cellular nucleic acid-binding protein	98.4%	8.5	1	1	1	6	899,162	909,245	868,763	918,783	32,468	39,804	89,261	27,874	8.1	9.8	23.0	6.8	1.0	0.8	-1.0	0.8	1.0	0.7	-1.0	0.7	1.0	0.8	1.1	0.6
IPI00430813	CNBP	isoform 2 of Cellular nucleic acid-binding protein	98.4%	8.8	1	1	1	6	899,162	909,245	868,763	918,783	32,468	39,804	89,261	27,874	8.1	9.8	23.0	6.8	1.0	0.8	-1.0	0.8	1.0	0.7	-1.0	0.7	1.0	0.8	1.1	0.6
IPI00895806	CNBP	cellular nucleic acid-binding protein isoform 1	98.4%	8.4	1	1	1	6	899,162	909,245	868,763	918,783	32,468	39,804	89,261	27,874	8.1	9.8	23.0	6.8	1.0	0.8	-1.0	0.8	1.0	0.7	-1.0	0.7	1.0	0.8	1.1	0.6
IPI00895852	CNBP	cellular nucleic acid-binding protein isoform 5	98.4%	8.8	1	1	1	6	899,162	909,245	868,763	918,783	32,468	39,804	89,261	27,874	8.1	9.8	23.0	6.8	1.0	0.8	-1.0	0.8	1.0	0.7	-1.0	0.7	1.0	0.8	1.1	0.6
IPI00895911	CNBP	cellular nucleic acid-binding protein isoform 2	98.4%	8.4	1	1	1	6	899,162	909,245	868,763	918,783	32,468	39,804	89,261	27,874	8.1	9.8	23.0	6.8	1.0	0.8	-1.0	0.8	1.0	0.7	-1.0	0.7	1.0	0.8	1.1	0.6
IPI00967344	CNBP	cellular nucleic acid-binding protein isoform 4	98.4%	8.7	1	1	1	6	899,162	909,245	868,763	918,783	32,468	39,804	89,261	27,874	8.1	9.8	23.0	6.8	1.0	0.8	-1.0	0.8	1.0	0.7	-1.0	0.7	1.0	0.8	1.1	0.6
				GFQFVSSSLPDICYR	2	99.4%	1																									
IPI00432026	DDRGK1	DDRGK domain-containing protein 1	100.0%	5.4	1	1	1	1	293,769	243,906	294,557	301,651	16,284	12,999	17,453	26,772	12.4	11.9	13.3	19.9	-1.2	0.04	1.0	1	1.0	0.8	1.2	0.05	1.2	0.09	1.0	0.8
				FIYITPEELAAVANFIR	2	99.8%	1																									
IPI00432363	MACF1	Microtubule-actin cross-linking factor 1, isoform 4	96.1%	0.2	1	1	1	2	1,873,840	1,903,810	1,802,345	1,873,405	308,736	159,858	342,054	254,096	36.8	18.8	42.4	30.3	1.0	0.9	-1.0	0.9	-1.0	1	-1.1	0.8	-1.0	0.9	1.0	0.9
IPI00974507	MACF1	Uncharacterized protein	96.1%	0.2	1	1	1	2	1,873,840	1,903,810	1,802,345	1,873,405	308,736	159,858	342,054	254,096	36.8	18.8	42.4	30.3	1.0	0.9	-1.0	0.9	-1.0	1	-1.1	0.8	-1.0	0.9	1.0	0.9
				ELQDALALISR	3	94.7%	1																									
IPI00433279	SLFN5	isoform 1 of Schlafen family member 5	92.5%	3.6	1	1	1	1	2,890,390	2,632,140	3,424,580	2,690,460	143,284	143,219	70,234	192,100	11.1	12.2	4.6	16.0	-1.1	0.2	1.2	0.01	-1.1	0.4	1.3	0.001	1.0	0.8	-1.3	0.02
				FSGLERNIVFGINPGVAPPAGAYNLLLCLASR	3	89.6%	1																									
IPI00434968	SUMO4	Small ubiquitin-related modifier 4	100.0%	12.6	1	1	2	1	1,209,107	1,143,584	1,041,240	1,293,086	80,901	54,540	57,979	50,887	15.0	10.7	12.5	8.8	-1.1	0.5	-1.2	0.1	1.1	0.4	-1.1	0.2	1.1	0.08	1.2	0.01
				VAGQDGSVVQFK	2	100.0%	2																									
IPI00438229	TRIM28	isoform 1 of Transcription intermediary factor 1-beta	100.0%	22.6	15	17	21	1	58,134,419	59,600,982	56,268,666	66,206,308	3,402,322	2,057,274	3,268,286	1,741,123	13.1	7.7	13.0	5.9	1.0	0.7	-1.0	0.7	1.1	0.07	-1.1	0.4	1.1	0.04	1.2	0.03
				APGPLSK	1	85.1%	1																									
				DHQYQFLEDAVR	2	100.0%	1																									
				DIVENYFMR	2	100.0%	1																									
				FASWALESDNNTALLLSK	2	99.8%	1																									
				FQWDLNAWTK	2	100.0%	1																									
				IVAERPGTNSTGPAPMAPPR	3	100.0%	1																									
				LDLDLTADSQPPVFK	2	100.0%	2																									
				LSPPYSSPQEFAQDVGR	2	100.0%	2																									
				LTEDKADVQSIIGLQR	2	99.9%	1																									
				LTEDKADVQSIIGLQR	3	100.0%	1																									
				MAILQIMK	2	99.2%	1																									
				MIVDPVEPHGEMK	2	100.0%	1																									
				MIVDPVEPHGEMK	3	99.8%	1																									
				MNEAFGDTK	2	99.9%	1																									
				SAEAFGK	1	95.4%	1																									
				SGEGEVSGLMR	2	99.9%	2																									
				VFPGSTTEDYNLIVIER	2	100.0%	2																									
IPI00438230	TRIM28	isoform 2 of Transcription intermediary factor 1-beta	100.0%	20.6	12	13	17	1	38,143,790	39,384,506	37,022,863	44,842,228	1,781,410	1,311,279	2,211,294	1,886,413	10.4	7.4	13.4	9.4	1.0	0.6	-1.0	0.7	1.2	0.03	-1.1	0.4	1.1	0.04	1.2	0.03
				DHQYQFLEDAVR	2	100.0%	1																									
				FQWDLNAWTK	2	100.0%	1																									
				IVAERPGTNSTGPAPMAPPR	3	100.0%	1																									
				LDLDLTADSQPPVFK	2	100.0%	2																									
				LSPPYSSPQEFAQDVGR	2	100.0%	2																									
				LTEDKADVQSIIGLQR	2	99.9%	1																									
				LTEDKADVQSIIGLQR	3	100.0%	1																									
				MAILQIMK	2	99.2%	1																									
				MIVDPVEPHGEMK	2	100.0%	1																									
				MNEAFGDTK	2	99.9%	1																									
				SAEAFGK	1	95.4%	1																									
				SGEGEVSGLMR	2	99.9%	2																									
				VFPGSTTEDYNLIVIER	2	100.0%	2																									
IPI00439194	MBD3	isoform 1 of Methyl-CpG-binding domain protein 3	96.3%	5.2	1	1	1	2	939,135	719,140	880,710	1,004,780	93,389	46,172	129,342	97,660	22.2	14.4	32.8	21.7	-1.3	0.07	-1.1	0.7	1.1	0.6	1.2	0.3	1.4	0.03	1.1	0.5
IPI00439195	MBD3	isoform 2 of Methyl-CpG-binding domain protein 3	96.3%	5.8	1	1	1	2	939,135	719,140	880,710	1,004,780	93,389	46,172	129,342	97,660	22.2	14.4	32.8	21.7	-1.3	0.07	-1.1	0.7	1.1	0.6	1.2	0.3	1.4	0.03	1.1	0.5
				LSGLNAFDIAEELVK	2	96.3%	1																									
IPI00439209	BAX	isoform Delta of Apoptosis regulator BAX	100.0%	8.4	1	1	1	1	550,922	628,640	570,582	765,330	43,100	46,218	51,360	71,884	17.5	16.4	20.1	21.0	1.1	0.3	1.0	0.8	1.4	0.03	-1.1	0.4	1.2	0.1	1.3	0.06
				GGGPTSSEQIMK	2	99.9%	1																									
IPI00439701	LOC284804	hypothetical protein LOC284804	99.0%	7.5	1	1	1	1	3,640,250	4,229,370	4,291,650	5,193,930	342,106	66,002	468,430	46,498	21.0	3.5	24.4	2.0	1.2	0.2	1.2	0.3	1.4	0.01	1.0	0.9	1.2	2.00E-06	1.2	0.1
				SLAGAREGEPALHLPGLAKWGGAAGR	3	94.6%	1																									
IPI00439761	FAM179B	isoform 3 of Protein FAM179B	99.4%	0.7	1	1	1	4	3,290,700	3,121,973	2,766,350	3,641,673	241,688	222,188	219,493	79,889	16.4	15.9	17.7	4.9	-1.1	0.6	-1.2	0.1	1.1	0.2	-1.1	0.3	1.2	0.08	1.3	0.01
IPI00744872	FAM179B	isoform 1 of Protein FAM179B	99.4%	0.4	1	1	1	4	3,290,700	3,121,973	2,766,350	3,641,673	241,688	222,188	219,493	79,889	16.4	15.9	17.7	4.9	-1.1	0.6	-1.2	0.1	1.1	0.2	-1.1	0.3	1.2	0.08	1.3	0.01
IPI00748234	FAM179B	isoform 2 of Protein FAM179B	99.4%	0.7	1	1	1	4	3,290,700	3,121,973	2,766,350	3,641,673	241,688	222,188	219,493	79,889	16.4	15.9	17.7	4.9	-1.1	0.6	-1.2	0.1	1.1	0.2	-1.1	0.3	1.2	0.08	1.3	0.01
IPI01010012	FAM179B	cDNA FLJ52098	99.4%	0.6	1	1	1	4	3,290,700	3,121,973	2,766,350	3,641,673	241,688	222,188	219,493	79,889	16.4	15.9	17.7	4.9	-1.1	0.6	-1.2	0.1	1.1	0.2	-1.1	0.3	1.2	0.08	1.3	0.01
				NLFQNSR	2	97.7%	1																									
IPI00439924	SLC48A1	isoform 1 of Heme transporter HRG1	91.4%	15.8	1	1	1	2	1,747,895	2,082,310	1,505,675	2,139,500	136,295	132,098	217,519	224,280	17.4	14.2	32.3	23.4	1.2	0.1	-1.2	0.4	1.2	0.2	-1.4	0.05	1.0	0.8	1.4	0.08
IPI00910707	SLC48A1	cDNA FLJ57264	91.4%	15.3	1	1	1	2	1,747,895	2,082,310	1,505,675	2,139,500	136,295	132,098	217,519	224,280	17.4	14.2	32.3	23.4	1.2	0.1	-1.2	0.4	1.2	0.2	-1.4	0.05	1.0	0.8	1.4	0.08
				AAYSGISSVAGFSIFLVWTVVYR	2	91.4%	1																									
IPI00439944	ARCN1	ARCN1 protein	100.0%	12.2	2	2	2	1	2,041,366	2,352,348	1,976,013	2,026,318	81,215	309,697	98,469	132,849	8.9	29.4	11.1	14.7	1.2	0.4	-1.0	0.6	-1.0	0.9	-1.2	0.3	-1.2	0.4	1.0	0.8
				NSNILEDLETLR	2	100.0%	1																									
				TFTEMDSHEEK	2	99.9%	1																									
IPI00440493	ATP5A1	ATP synthase subunit alpha, mitochondrial	100.0%	44.7	19	21	30	1	49,398,886	49,854,568	48,754,815	55,473,524	4,652,287	1,563,622	3,506,816	1,841,375	21.1	7.0	16.1	7.4	1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	0.8	1.1	0.05	1.1	0.1
				APGIIPR	2	99.6%	1																									
				AVDSLVPIGR	2	99.9%	1																									
				EIVTNFLAGFEA	2	100.0%	1																									
				EVAAFAQFGSDLDAATQQLLSR	2	100.0%	2																									
				EVAAFAQFGSDLDAATQQLLSR	3	100.0%	2																									
				FENAFLSHVVSQHQALLGTIR	3	100.0%	2																									
				GIRPAINVGLSVSR	2	97.9%	1																									
				GMSLNLEPDNVGVVVFGNDK	2	100.0%	2																									
				GMSLNLEPDNVGVVVFGNDK	3	99.8%	1																									
				GYLDKLEPSK	3	99.9%	1																									
				HALIIYDDLSK	2	100.0%	2																									
				ILGADTSVDLEETGR	2	100.0%	2																									
				LELAQYR	2	87.8%	1																									
				LKEIVTNFLAGFEA	2	100.0%	2																									
				NVQAEEMVEFSSGLK	2	100.0%	1																									
				QGQYSPMAIEEQVAVIYAGVR	2	97.5%	1																									
				RLTDADAMK	2	99.9%	1																									
				TGAIVDVPVGEELLGR	2	100.0%	2																									
				TGTAEMSSILEER	2	100.0%	2																									
				VLSIGDGIAR	2	100.0%	1																									
				VVDALGNAIDGK	2	100.0%	1																									
IPI00440703	GSTK1	isoform 2 of Glutathione S-transferase kappa 1	100.0%	10.6	2	2	3	1	3,570,560	3,441,595	3,381,340	3,905,235	354,920	133,933	264,158	155,417	22.2	8.7	17.5	8.9	-1.0	0.7	-1.1	0.7	1.1	0.4	-1.0	0.8	1.1	0.05	1.2	0.1
				AGMSAEQAQGLLEK	2	100.0%	1																									
				NEDITEPQSILAAAEK	2	100.0%	2																									
IPI00441550	GLB1	isoform 2 of Beta-galactosidase	96.5%	2.8	1	1	1	1	1,061,493	1,152,150	1,001,118	1,186,740	85,039	109,032	48,917	44,088	17.9	21.2	10.9	8.3	1.1	0.5	-1.1	0.6	1.1	0.2	-1.2	0.2	1.0	0.8	1.2	0.02
				AYVAVDGIPQGVLER	2	96.5%	1																									
IPI00442073	CSRP1	Cysteine and glycine-rich protein 1	100.0%	20.2	2	2	2	3	1,948,229	1,904,469	1,956,777	2,064,546	310,101	135,645	118,674	61,074	35.6	15.9	13.6	6.6	-1.0	0.9	1.0	1	1.1	0.7	1.0	0.8	1.1	0.3	1.1	0.4
IPI00976060	CSRP1	Uncharacterized protein	100.0%	25.5	2	2	2	3	1,948,229	1,904,469	1,956,777	2,064,546	310,101	135,645	118,674	61,074	35.6	15.9	13.6	6.6	-1.0	0.9	1.0	1	1.1	0.7	1.0	0.8	1.1	0.3	1.1	0.4
IPI00979856	CSRP1	cDNA FLJ16406 fis, clone UTERU2026142, highly similar to Cysteine and glycine-ri	100.0%	24.4	2	2	2	3	1,948,229	1,904,469	1,956,777	2,064,546	310,101	135,645	118,674	61,074	35.6	15.9	13.6	6.6	-1.0	0.9	1.0	1	1.1	0.7	1.0	0.8	1.1	0.3	1.1	0.4
				GLESTTLADKDGEIYCK	3	98.6%	1																									
				GYGYGQGAGTLSTDKGESLGIK	3	99.9%	1																									
IPI00442135	HDLBP	Uncharacterized protein	100.0%	3.9	2	2	3	1	3,820,015	4,104,615	4,212,543	4,278,120	259,178	273,563	181,981	286,347	15.2	14.9	9.7	15.0	1.1	0.5	1.1	0.3	1.1	0.3	1.0	0.8	1.0	0.7	1.0	0.9
				EIAEEYGGVMVSFPR	2	100.0%	2																									
				TEIVFTGEKEQLAQAVAR	3	100.0%	1																									
IPI00442863	G3BP1	Uncharacterized protein	100.0%	5.5	1	1	2	1	1,079,463	996,200	1,081,783	1,147,310	88,678	41,135	89,331	60,878	18.4	9.2	18.5	11.9	-1.1	0.4	1.0	1	1.1	0.5	1.1	0.4	1.2	0.07	1.1	0.6
				LPNFGFVVFDDSEPVQK	2	100.0%	2																									
IPI00442866	CANX	Uncharacterized protein	100.0%	3.7	1	1	1	3	1,144,240	1,284,463	1,352,760	1,516,086	79,057	81,999	96,690	128,616	15.5	14.3	16.0	19.0	1.1	0.3	1.2	0.1	1.3	0.04	1.1	0.6	1.2	0.2	1.1	0.3
IPI00966032	CANX	Protein	100.0%	6.3	1	1	1	3	1,144,240	1,284,463	1,352,760	1,516,086	79,057	81,999	96,690	128,616	15.5	14.3	16.0	19.0	1.1	0.3	1.2	0.1	1.3	0.04	1.1	0.6	1.2	0.2	1.1	0.3
IPI00967973	CANX	Uncharacterized protein	100.0%	9.2	1	1	1	3	1,144,240	1,284,463	1,352,760	1,516,086	79,057	81,999	96,690	128,616	15.5	14.3	16.0	19.0	1.1	0.3	1.2	0.1	1.3	0.04	1.1	0.6	1.2	0.2	1.1	0.3
				TPELNLDQFHDK	3	100.0%	1																									
IPI00443415	MCC	isoform 2 of Colorectal mutant cancer protein	98.5%	4.2	2	2	2	1	8,256,040	8,961,843	8,215,370	9,436,080	624,591	387,859	735,669	316,483	16.9	9.7	20.0	7.5	1.1	0.4	-1.0	1	1.1	0.1	-1.1	0.4	1.1	0.4	1.1	0.2
				KIDRLQGTTIR	3	87.6%	1																									
				LLTQSPHIGNSVGGSYLELANTLHSAALASLK	3	88.1%	1																									
IPI00443534	-	cDNA FLJ46889 fis, clone UTERU3017995, highly similar to Homo sapiens likely ort	100.0%	8.4	1	1	1	1	5,227,880	5,222,500	5,150,160	6,350,900	374,148	181,384	421,610	235,798	16.0	7.8	18.3	8.3	-1.0	1	-1.0	0.9	1.2	0.03	-1.0	0.9	1.2	0.005	1.2	0.04
				EANLLNAVIVQR	2	100.0%	1																									
IPI00910502	-	cDNA FLJ52834, moderately similar to Cold-inducible RNA-binding protein	100.0%	22.5	2	3	5	5	1,342,331	1,319,712	1,222,117	1,558,540	134,477	40,764	91,115	17,989	22.4	6.9	16.7	2.6	-1.0	0.9	-1.1	0.5	1.2	0.2	-1.1	0.4	1.2	0.0007	1.3	0.02
IPI00443657	CIRBP	Uncharacterized protein	100.0%	23.7	2	3	5	5	1,342,331	1,319,712	1,222,117	1,558,540	134,477	40,764	91,115	17,989	22.4	6.9	16.7	2.6	-1.0	0.9	-1.1	0.5	1.2	0.2	-1.1	0.4	1.2	0.0007	1.3	0.02
IPI00641579	CIRBP	Cold inducible RNA binding protein, isoform CRA_c	100.0%	10.8	2	3	5	5	1,342,331	1,319,712	1,222,117	1,558,540	134,477	40,764	91,115	17,989	22.4	6.9	16.7	2.6	-1.0	0.9	-1.1	0.5	1.2	0.2	-1.1	0.4	1.2	0.0007	1.3	0.02
IPI00646241	CIRBP	18 kDa protein	100.0%	19.1	2	3	5	5	1,342,331	1,319,712	1,222,117	1,558,540	134,477	40,764	91,115	17,989	22.4	6.9	16.7	2.6	-1.0	0.9	-1.1	0.5	1.2	0.2	-1.1	0.4	1.2	0.0007	1.3	0.02
IPI00909097	CIRBP	cDNA FLJ52850, moderately similar to Cold-inducible RNA-binding protein	100.0%	12.2	2	3	5	5	1,342,331	1,319,712	1,222,117	1,558,540	134,477	40,764	91,115	17,989	22.4	6.9	16.7	2.6	-1.0	0.9	-1.1	0.5	1.2	0.2	-1.1	0.4	1.2	0.0007	1.3	0.02
				LFVGGLSFDTNEQSLEQVFSK	2	100.0%	2																									
				LFVGGLSFDTNEQSLEQVFSK	3	100.0%	1																									
				YGQISEVVVVK	2	100.0%	2																									
IPI00443909	CNPY2	isoform 1 of Protein canopy homolog 2	100.0%	37.4	5	6	8	1	16,729,073	17,705,503	17,897,084	19,439,729	1,220,879	1,132,616	1,509,281	279,231	16.3	14.3	18.9	3.2	1.1	0.6	1.1	0.6	1.2	0.09	1.0	0.9	1.1	0.2	1.1	0.4
				ALVDELEWEIAQVDPK	2	100.0%	1																									
				ALVDELEWEIAQVDPK	3	99.3%	1																									
				EYGEQIDPSTHRK	2	91.1%	1																									
				IDSDISGTLK	2	99.0%	1																									
				INPDGSQSVVEVPYAR	2	100.0%	2																									
				NGESSELDLQGIR	2	99.9%	2																									
IPI00444262	NCL	cDNA FLJ45706 fis, clone FEBRA2028457, highly similar to Nucleolin	100.0%	32.8	17	22	33	2	68,217,854	70,011,905	69,022,327	78,214,650	7,177,592	2,914,895	4,553,034	2,886,369	23.5	9.3	14.8	8.3	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.08	1.1	0.1

IPI00604620	NCL	Nucleolin	100.0%	27.9	17	22	33	2	68,217,854	70,011,905	69,022,327	78,214,650	7,177,592	2,914,895	4,553,034	2,886,369	23.5	9.3	14.8	8.3	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.08	1.1	0.1
				ALELTGLK	2	99.7%	1																									
				EAMEDGEIDGNKVTLDWAKPK	3	100.0%	2																									
				EVFEDAAEIR	2	100.0%	2																									
				FGYVDFESAEDLEK	2	100.0%	2																									
				GFGFVDFNSEEDAK	2	100.0%	3																									
				GIAYIEFK	2	97.0%	1																									
				GLSEDTTEETLK	2	100.0%	1																									
				GLSEDTTEETLKESFDGSVR	2	100.0%	2																									
				GLSEDTTEETLKESFDGSVR	3	100.0%	2																									
				GYAFIEFASFEDAK	2	100.0%	2																									
				KFGYVDFESAEDLEK	2	100.0%	1																									
				KFGYVDFESAEDLEK	3	100.0%	1																									
				SISLYYTGEK	2	95.2%	1																									
				TEADAEKTFEEK	2	100.0%	1																									
				TGISDVFAK	2	100.0%	1																									
				TLVLSNLSYSATEETLQEVFEK	2	100.0%	2																									
				TLVLSNLSYSATEETLQEVFEK	3	100.0%	1																									
				VEGTEPTTAFNLFVGNLNFNK	2	100.0%	1																									
				VEGTEPTTAFNLFVGNLNFNK	3	100.0%	1																									
				VFGNEIK	1	98.3%	1																									
				VTQDELKEVFEDAAEIR	2	100.0%	2																									
				VTQDELKEVFEDAAEIR	3	100.0%	2																									
IPI00444452	MOV10	isoform 1 of Putative helicase MOV-10	96.9%	1.5	1	1	1	2	1,958,335	1,748,460	1,761,295	1,945,765	118,246	177,077	107,792	210,696	13.5	22.7	13.7	24.2	-1.1	0.4	-1.1	0.3	-1.0	1	1.0	1	1.1	0.5	1.1	0.5
IPI00646886	MOV10	Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a	96.9%	1.6	1	1	1	2	1,958,335	1,748,460	1,761,295	1,945,765	118,246	177,077	107,792	210,696	13.5	22.7	13.7	24.2	-1.1	0.4	-1.1	0.3	-1.0	1	1.0	1	1.1	0.5	1.1	0.5
				EGEGGLSLQVEPEWR	2	96.9%	1																									
IPI00444788	SH3BP1	cDNA FLJ44925 fis, clone BRAMY3014613, highly similar to Homo sapiens SH3-do	95.9%	1.7	1	1	1	5	9,694,460	9,755,780	8,755,240	10,260,660	759,145	727,285	438,908	399,025	17.5	16.7	11.2	8.7	1.0	1	-1.1	0.3	1.1	0.5	-1.1	0.3	1.1	0.6	1.2	0.03
IPI00445123	SH3BP1	Uncharacterized protein	95.9%	1.9	1	1	1	5	9,694,460	9,755,780	8,755,240	10,260,660	759,145	727,285	438,908	399,025	17.5	16.7	11.2	8.7	1.0	1	-1.1	0.3	1.1	0.5	-1.1	0.3	1.1	0.6	1.2	0.03
IPI00456744	SH3BP1	isoform 1 of SH3 domain-binding protein 1	95.9%	1.4	1	1	1	5	9,694,460	9,755,780	8,755,240	10,260,660	759,145	727,285	438,908	399,025	17.5	16.7	11.2	8.7	1.0	1	-1.1	0.3	1.1	0.5	-1.1	0.3	1.1	0.6	1.2	0.03
IPI00456745	SH3BP1	cDNA FLJ61632, highly similar to SH3 domain-binding protein 1	95.9%	2.0	1	1	1	5	9,694,460	9,755,780	8,755,240	10,260,660	759,145	727,285	438,908	399,025	17.5	16.7	11.2	8.7	1.0	1	-1.1	0.3	1.1	0.5	-1.1	0.3	1.1	0.6	1.2	0.03
IPI01011491	SH3BP1	isoform 2 of SH3 domain-binding protein 1	95.9%	2.2	1	1	1	5	9,694,460	9,755,780	8,755,240	10,260,660	759,145	727,285	438,908	399,025	17.5	16.7	11.2	8.7	1.0	1	-1.1	0.3	1.1	0.5	-1.1	0.3	1.1	0.6	1.2	0.03
				LPPENLSNLR	2	95.9%	1																									
IPI00444873	DNM2	cDNA FLJ40670 fis, clone THYMU2020959, highly similar to Dynamin-2	100.0%	3.7	2	2	3	1	17,002,651	17,055,163	17,530,684	19,813,057	1,750,129	916,448	1,623,469	733,666	23.0	12.0	20.7	8.3	1.0	1	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.05	1.1	0.2
				NLVDSYVAIINK	2	100.0%	1																									
				TIMHLMINNTK	2	100.0%	2																									
IPI00445108	KARS	Uncharacterized protein	100.0%	8.0	3	3	4	1	4,545,053	4,249,627	4,088,501	4,577,110	521,795	137,680	365,253	147,200	25.7	7.2	20.0	7.2	-1.1	0.6	-1.1	0.5	1.0	1	-1.0	0.7	1.1	0.1	1.1	0.2
				LPETNLFETEETRK	3	100.0%	1																									
				MLVVGGIDR	2	98.5%	1																									
				YLDLILNDFVR	2	100.0%	2																									
IPI00445152	C18orf54	isoform 2 of Uncharacterized protein C18orf54	97.0%	3.9	1	1	1	1	2,654,990	3,460,240	2,989,170	3,279,460	321,357	280,963	306,158	201,287	27.1	18.2	22.9	13.7	1.3	0.1	1.1	0.5	1.2	0.1	-1.2	0.3	-1.1	0.6	1.1	0.5
				DDQCSPRHSHQAQGTSRLINK	3	97.0%	1																									
IPI00445412	PPP1R13B	cDNA FLJ43925 fis, clone TESTI4012505, weakly similar to Tumor suppressor p53-	92.5%	2.6	1	1	1	1	3,482,820	3,409,330	4,263,690	3,478,330	262,838	319,045	107,515	191,675	16.9	20.9	5.6	12.3	-1.0	0.9	1.2	0.03	-1.0	1	1.3	0.05	1.0	0.9	-1.2	0.007
				EPEQDGPAAPAGPTSR	3	92.5%	1																									
IPI00445716	GFRA3	isoform 1 of GDNF family receptor alpha-3	96.6%	2.3	1	1	1	2	773,380	849,740	806,615	981,880	63,769	12,103	80,489	39,357	18.4	3.2	22.3	9.0	1.1	0.3	1.0	0.8	1.3	0.02	-1.1	0.6	1.2	0.03	1.2	0.09
IPI00445717	GFRA3	isoform 2 of GDNF family receptor alpha-3	96.6%	2.4	1	1	1	2	773,380	849,740	806,615	981,880	63,769	12,103	80,489	39,357	18.4	3.2	22.3	9.0	1.1	0.3	1.0	0.8	1.3	0.02	-1.1	0.6	1.2	0.03	1.2	0.09
				LCFSDPLCR	2	96.6%	1																									
IPI00446140	CAPN2	cDNA FLJ42761 fis, clone BRAWH3002574, highly similar to Calpain 2, large	100.0%	10.5	1	2	2	1	252,871	229,555	272,396	308,661	21,172	22,312	21,657	12,880	18.7	21.7	17.8	9.3	-1.1	0.5	1.1	0.5	1.2	0.05	1.2	0.2	1.3	0.02	1.1	0.2
				LFAQLAGEDAEISAFELQTILR	2	100.0%	1																									
				LFAQLAGEDAEISAFELQTILR	3	100.0%	1																									
IPI00446294	TOM1L2	isoform 1 of TOM1-like protein 2	99.5%	7.1	2	2	2	2	836,145	849,062	841,323	881,787	93,833	40,465	121,549	51,818	25.1	10.7	32.3	13.1	1.0	0.9	1.0	1	1.1	0.7	-1.0	1	1.0	0.6	1.0	0.8
IPI00921925	TOM1L2	cDNA FLJ60511, highly similar to Mus musculus target of myb1-like 2 (chicken) (Tor	99.5%	7.5	2	2	2	2	836,145	849,062	841,323	881,787	93,833	40,465	121,549	51,818	25.1	10.7	32.3	13.1	1.0	0.9	1.0	1	1.1	0.7	-1.0	1	1.0	0.6	1.0	0.8
				VLALIQAWADAFR	2	99.5%	1																									
				VSNEEVTEELLHVNDDLNNVFLR	3	99.4%	1																									
IPI00446769	BDH2	isoform 2 of 3-hydroxybutyrate dehydrogenase type 2	98.7%	8.7	1	1	1	1	710,260	733,097	810,663	817,280	86,392	67,585	74,017	28,333	27.2	20.6	20.4	7.8	1.0	0.8	1.1	0.4	1.2	0.3	1.1	0.5	1.1	0.3	1.0	0.9
				SGNIINMSSVASSVK	2	98.7%	1																									
IPI00446788	-	cDNA FLJ41103 fis, clone BLADE2005459	96.4%	5.4	1	1	1	1	35,895,000	35,638,900	33,421,500	36,922,800	2,664,663	2,361,864	2,573,192	1,248,095	16.6	14.8	17.2	7.6	-1.0	0.9	-1.1	0.5	1.0	0.7	-1.1	0.5	1.0	0.6	1.1	0.3
				RTSEVGGSRPHR	3	95.3%	1																									
IPI00446834	SULT1A4;SULT1A3	isoform 2 of Sulfotransferase 1A3/1A4	99.5%	25.9	2	2	2	1	2,612,938	2,665,665	2,753,455	2,845,102	96,409	124,001	201,380	207,352	8.3	10.4	16.4	16.3	1.0	0.7	1.1	0.5	1.1	0.3	1.0	0.7	1.1	0.5	1.0	0.8
				VPFLEVNDPGEPSGLETLKDTPPPR	3	99.5%	1																									
				YFAEALGPLQSFQARPDDLLINTYPK	3	94.0%	1																									
IPI00448169	APOA1BP	Apolipoprotein A-I binding protein	100.0%	4.6	1	1	2	2	1,956,046	1,813,136	1,580,154	1,917,864	48,807	157,682	91,947	116,144	5.6	19.5	13.0	13.5	-1.1	0.4	-1.2	0.007	-1.0	0.8	-1.1	0.2	1.1	0.6	1.2	0.05
IPI00514157	APOA1BP	Apolipoprotein A-I binding protein	100.0%	4.9	1	1	2	2	1,956,046	1,813,136	1,580,154	1,917,864	48,807	157,682	91,947	116,144	5.6	19.5	13.0	13.5	-1.1	0.4	-1.2	0.007	-1.0	0.8	-1.1	0.2	1.1	0.6	1.2	0.05
				LFGYEPTIYYPK	2	100.0%	2																									
IPI00448751	KIAA1598	isoform 3 of Shootin-1	100.0%	3.5	2	2	2	5	3,074,634	2,971,084	2,905,189	3,511,050	176,833	195,898	166,955	240,557	12.9	14.7	12.9	15.3	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.1	1.2	0.07
IPI00854700	KIAA1598	isoform 1 of Shootin-1	100.0%	3.7	2	2	2	5	3,074,634	2,971,084	2,905,189	3,511,050	176,833	195,898	166,955	240,557	12.9	14.7	12.9	15.3	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.1	1.2	0.07
IPI00854856	KIAA1598	isoform 4 of Shootin-1	100.0%	4.1	2	2	2	5	3,074,634	2,971,084	2,905,189	3,511,050	176,833	195,898	166,955	240,557	12.9	14.7	12.9	15.3	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.1	1.2	0.07
IPI00921922	KIAA1598	isoform 6 of Shootin-1	100.0%	3.8	2	2	2	5	3,074,634	2,971,084	2,905,189	3,511,050	176,833	195,898	166,955	240,557	12.9	14.7	12.9	15.3	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.1	1.2	0.07
IPI00922178	KIAA1598	isoform 5 of Shootin-1	100.0%	4.0	2	2	2	5	3,074,634	2,971,084	2,905,189	3,511,050	176,833	195,898	166,955	240,557	12.9	14.7	12.9	15.3	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.1	1.2	0.07
				LVEVIEEVNK	2	92.8%	1																									
				SMPVLGSVSSVTK	2	97.3%	1																									
IPI00449049	PARP1	Poly [ADP-ribose] polymerase 1	100.0%	4.5	3	3	3	2	3,177,456	3,293,151	3,608,825	3,625,860	219,523	209,144	256,302	242,896	15.5	14.2	15.9	15.0	1.0	0.7	1.1	0.2	1.1	0.2	1.1	0.4	1.1	0.3	1.0	1
IPI00981395	PARP1	cDNA FLJ53442, highly similar to Poly (ADP-ribose) polymerase 1	100.0%	4.6	3	3	3	2	3,177,456	3,293,151	3,608,825	3,625,860	219,523	209,144	256,302	242,896	15.5	14.2	15.9	15.0	1.0	0.7	1.1	0.2	1.1	0.2	1.1	0.4	1.1	0.3	1.0	1
				MAIMVQSPMFDGK	2	99.9%	1																									
				RKGDEVDGVDEVAK	3	95.6%	1																									
				SLQELFLAHILSPWGAEVK	3	99.0%	1																									
IPI00450235	YBX1	Nuclease sensitive element binding protein-1	100.0%	13.7	4	4	6	1	3,738,072	3,752,444	3,490,447	4,299,231	296,627	223,944	182,057	179,216	17.7	13.3	11.7	9.3	1.0	1	-1.1	0.5	1.2	0.1	-1.1	0.4	1.1	0.09	1.2	0.01
				GAEAANVTGPGGVPVQGSK	2	100.0%	2																									
				NGYGFINR	2	100.0%	1																									
				SVGDGETVEFDVVEGEK	2	100.0%	2																									
				SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK	3	100.0%	1																									
IPI00451429	NIF3L1	NIF3L1 isoform gamma	100.0%	9.5	2	2	2	5	1,360,434	1,246,162	1,245,798	1,381,934	183,881	46,769	53,585	74,765	30.2	8.4	9.6	12.1	-1.1	0.6	-1.1	0.6	1.0	0.9	-1.0	1	1.1	0.2	1.1	0.2
IPI00451430	NIF3L1	NIF3-like protein 1 isoform 3	100.0%	8.4	2	2	2	5	1,360,434	1,246,162	1,245,798	1,381,934	183,881	46,769	53,585	74,765	30.2	8.4	9.6	12.1	-1.1	0.6	-1.1	0.6	1.0	0.9	-1.0	1	1.1	0.2	1.1	0.2
IPI00604624	NIF3L1	isoform 1 of NIF3-like protein 1	100.0%	6.4	2	2	2	5	1,360,434	1,246,162	1,245,798	1,381,934	183,881	46,769	53,585	74,765	30.2	8.4	9.6	12.1	-1.1	0.6	-1.1	0.6	1.0	0.9	-1.0	1	1.1	0.2	1.1	0.2
IPI00873590	NIF3L1	isoform 2 of NIF3-like protein 1	100.0%	6.9	2	2	2	5	1,360,434	1,246,162	1,245,798	1,381,934	183,881	46,769	53,585	74,765	30.2	8.4	9.6	12.1	-1.1	0.6	-1.1	0.6	1.0	0.9	-1.0	1	1.1	0.2	1.1	0.2
IPI00917949	NIF3L1	Uncharacterized protein	100.0%	11.5	2	2	2	5	1,360,434	1,246,162	1,245,798	1,381,934	183,881	46,769	53,585	74,765	30.2	8.4	9.6	12.1	-1.1	0.6	-1.1	0.6	1.0	0.9	-1.0	1	1.1	0.2	1.1	0.2
				ALMQVVDFLSR	2	98.8%	1																									
				VEFNVNYTQDLDK	2	99.5%	1																									
IPI00453473	;HIST1H4C;HIST2H4	Histone H4	100.0%	38.8	3	4	6	1	28,465,380	28,336,910	28,862,580	33,402,310	2,650,916	2,068,721	1,590,239	1,185,855	20.8	16.3	12.3	7.9	-1.0	1	1.0	0.9	1.2	0.1	1.0	0.8	1.2	0.07	1.2	0.05
				DNIQGITKPAIR	2	99.9%	2																									
				DNIQGITKPAIR	3	97.8%	1																									
				ISGLIYEETR	2	100.0%	2																									
				VFLENVIRDAVTYTEHAK	3	100.0%	1																									
IPI00455033	9-Sep	septin-9 isoform e	100.0%	15.2	5	6	10	1	3,818,381	3,786,308	3,809,947	4,207,363	181,411	96,664	280,093	151,046	10.6	5.7	16.4	8.0	-1.0	0.9	-1.0	1	1.1	0.1	1.0	0.9	1.1	0.05	1.1	0.2
				ADTLTLEER	2	100.0%	1																									
				APVDFGYVGIDSILEQMR	2	100.0%	2																									
				APVDFGYVGIDSILEQMR	3	100.0%	1																									
				DITSSIHFEAYR	2	100.0%	2																									
				VPEVPTAPATDAAPK	2	100.0%	2																									
				YLQEEVNINR	2	100.0%	2																									
IPI00455161	MSI2	isoform 3 of RNA-binding protein Musashi homolog 2	100.0%	9.9	1	1	1	2	851,750	685,410	787,725	927,208	136,049	65,312	67,937	87,853	35.7	21.3	19.3	21.2	-1.2	0.3	-1.1	0.7	1.1	0.7	1.1	0.3	1.4	0.06	1.2	0.2
IPI00908857	MSI2	cDNA FLJ52888, highly similar to RNA-binding protein Musashi homolog 2	100.0%	5.6	1	1	1	2	851,750	685,410	787,725	927,208	136,049	65,312	67,937	87,853	35.7	21.3	19.3	21.2	-1.2	0.3	-1.1	0.7	1.1	0.7	1.1	0.3	1.4	0.06	1.2	0.2
				GFGFVTFENEDVVEK	2	100.0%	1																									
IPI00514814	AKR1C1	Aldo-keto reductase family 1, member C1 (Dihydrodiol dehydrogenase 1	100.0%	3.2	1	1	2	3	551,824	567,610	532,282	603,027	52,356	33,880	36,663	36,115	21.2	13.4	15.4	13.4	1.0	0.8	-1.0	0.8	1.1	0.4	-1.1	0.5	1.1	0.5	1.1	0.2
IPI00455167	AKR1C2	Uncharacterized protein	100.0%	3.6	1	1	2	3	551,824	567,610	532,282	603,027	52,356	33,880	36,663	36,115	21.2	13.4	15.4	13.4	1.0	0.8	-1.0	0.8	1.1	0.4	-1.1	0.5	1.1	0.5	1.1	0.2
IPI00975489	LOC100508006	aldo-keto reductase family 1 member C2-like isoform 3	100.0%	4.6	1	1	2	3	551,824	567,610	532,282	603,027	52,356	33,880	36,663	36,115	21.2	13.4	15.4	13.4	1.0	0.8	-1.0	0.8	1.1	0.4	-1.1	0.5	1.1	0.5	1.1	0.2
				TPALIALR	2	99.8%	2																									
IPI00455333	LOC440434	isoform 1 of Puromycin-sensitive aminopeptidase-like protein	100.0%	6.9	2	2	2	4	817,616	782,676	912,862	941,165	76,826	54,949	81,818	50,090	21.0	15.7	20.0	11.9	-1.0	0.7	1.1	0.4	1.2	0.2	1.2	0.2	1.2	0.07	1.0	0.8
IPI00902599	LOC440434	cDNA FLJ58835, highly similar to Puromycin-sensitive aminopeptidase	100.0%	10.2	2	2	2	4	817,616	782,676	912,862	941,165	76,826	54,949	81,818	50,090	21.0	15.7	20.0	11.9	-1.0	0.7	1.1	0.4	1.2	0.2	1.2	0.2	1.2	0.07	1.0	0.8
IPI00982622	LOC440434	Uncharacterized protein	100.0%	7.0	2	2	2	4	817,616	782,676	912,862	941,165	76,826	54,949	81,818	50,090	21.0	15.7	20.0	11.9	-1.0	0.7	1.1	0.4	1.2	0.2	1.2	0.2	1.2	0.07	1.0	0.8
IPI01010691	LOC440434	Uncharacterized protein	100.0%	6.9	2	2	2	4	817,616	782,676	912,862	941,165	76,826	54,949	81,818	50,090	21.0	15.7	20.0	11.9	-1.0	0.7	1.1	0.4	1.2	0.2	1.2	0.2	1.2	0.07	1.0	0.8
				DYFNVPYPLPK	2	100.0%	1																									
				TPVTSTYLVAFVVGEYDFVETR	3	86.5%	1																									
IPI00455806	PEG10	retrotransposon-derived protein PEG10 isoform 4	97.1%	2.2	1	1	1	3	744,850	716,715	662,652	876,512	68,917	45,784	42,387	66,381	20.7	14.3	14.3	16.9	-1.0	0.7	-1.1	0.3	1.2	0.2	-1.1	0.4	1.2	0.08	1.3	0.03
IPI00939120	PEG10	isoform RF1 of Retrotransposon-derived protein PEG10	97.1%	2.8	1	1	1	3	744,850	716,715	662,652	876,512	68,917	45,784	42,387	66,381	20.7	14.3	14.3	16.9	-1.0	0.7	-1.1	0.3	1.2	0.2	-1.1	0.4	1.2	0.08	1.3	0.03
IPI00976858	PEG10	retrotransposon-derived protein PEG10 isoform 6	97.1%	2.5	1	1	1	3	744,850	716,715	662,652	876,512	68,917	45,784	42,387	66,381	20.7	14.3	14.3	16.9	-1.0	0.7	-1.1	0.3	1.2	0.2	-1.1	0.4	1.2	0.08	1.3	0.03
				LTEENTTLR	2	97.1%	1																									
IPI00456359	ATXN2L	isoform 1 of Ataxin-2-like protein	100.0%	1.7	2	2	2	3	5,523,876	5,645,677	5,639,948	6,496,500	697,100	203,757	367,519	272,617	28.2	8.1	14.6	9.4	1.0	0.9	1.0	0.9	1.2	0.2	-1.0	1	1.2	0.04	1.2	0.1
IPI00639962	ATXN2L	114 kDa protein	100.0%	1.7	2	2	2	3	5,523,876	5,645,677	5,639,948	6,496,500	697,100	203,757	367,519	272,617	28.2	8.1	14.6	9.4	1.0	0.9	1.0	0.9	1.2	0.2	-1.0	1	1.2	0.04	1.2	0.1
IPI00642402	ATXN2L	114 kDa protein	100.0%	1.7	2	2	2	3	5,523,876	5,645,677	5,639,948	6,496,500	697,100	203,757	367,519	272,617	28.2	8.1	14.6	9.4	1.0	0.9	1.0	0.9	1.2	0.2	-1.0	1	1.2	0.04	1.2	0.1
				AEGLQVGQDAR	2	100.0%	1																									
				YIPLPQR	2	95.1%	1																									
IPI00456361	ATXN2L	isoform 2 of Ataxin-2-like protein	95.1%	0.7	1	1	1	6	4,203,722	4,323,133	4,268,378	5,105,067	528,942	250,821	354,433	213,714	28.1	13.0	18.6	9.4	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.05	1.2	0.08
IPI00456363	ATXN2L	isoform 3 of Ataxin-2-like protein	95.1%	0.6	1	1	1	6	4,203,722	4,323,133	4,268,378	5,105,067	528,942	250,821	354,433	213,714	28.1	13.0	18.6	9.4	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.05	1.2	0.08
IPI00456365	ATXN2L	isoform 4 of Ataxin-2-like protein	95.1%	0.7	1	1	1	6	4,203,722	4,323,133	4,268,378	5,105,067	528,942	250,821	354,433	213,714	28.1	13.0	18.6	9.4	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.05	1.2	0.08
IPI00456367	ATXN2L	ataxin-2-like protein isoform B	95.1%	0.7	1	1	1	6	4,203,722	4,323,133	4,268,378	5,105,067	528,942	250,821	354,433	213,714	28.1	13.0	18.6	9.4	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.05	1.2	0.08
IPI00456369	ATXN2L	isoform 6 of Ataxin-2-like protein	95.1%	0.7	1	1	1	6	4,203,722	4,323,133	4,268,378	5,105,067	528,942	250,821	354,433	213,714	28.1	13.0	18.6	9.4	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.05	1.2	0.08
IPI00883782	ATXN2L	ataxin-2-like protein isoform E	95.1%	0.7	1	1	1	6	4,203,722	4,323,133	4,268,378	5,105,067	528,942	250,821	354,433	213,714	28.1	13.0	18.6	9.4	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.05	1.2	0.08
				YIPLPQR	2	95.1%	1																									
IPI00456484	PDE4DIP	isoform 3 of Myomegalin	98.7%	1.2	1	1	1	6	450,905	495,953	487,743	595,195	44,085	16,861	26,348	25,508	21.9	7.6	12.1	9.6	1.1	0.4	1.1	0.5	1.3	0.02	-1.0	0.8	1.2	0.01	1.2	0.02
IPI00470939	PDE4DIP	isoform 1 of Myomegalin	98.7%	1.2	1	1	1	6	450,905	495,953	487,743	595,195	44,085	16,861	26,348	25,508	21.9	7.6	12.1	9.6	1.1	0.4	1.1	0.5	1.3	0.02	-1.0	0.8	1.2	0.01	1.2	0.02
IPI00642902	PDE4DIP	isoform 4 of Myomegalin	98.7%	1.1	1	1	1	6	450,905	495,953	487,743	595,195	44,085	16,861	26,348	25,508	21.9	7.6	12.1	9.6	1.1	0.4	1.1	0.5	1.3	0.02	-1.0	0.8	1.2	0.01	1.2	0.02
IPI00741084	PDE4DIP	Uncharacterized protein	98.7%	1.1	1	1	1	6	450,905	495,953	487,743	595,195	44,085	16,861	26,348	25,508	21.9	7.6	12.1	9.6	1.1	0.4	1.1	0.5	1.3	0.02	-1.0	0.8	1.2	0.01	1.2	0.02
IPI00869114	PDE4DIP	isoform 5 of Myomegalin	98.7%	2.0	1	1	1	6	450,905	495,953	487,743	595,195	44,085	16,861	26,348	25,508	21.9	7.6	12.1	9.6	1.1	0.4	1.1	0.5	1.3	0.02	-1.0	0.8	1.2	0.01	1.2	0.02
IPI00977575	PDE4DIP	Uncharacterized protein	98.7%	1.1	1	1	1	6	450,905	495,953	487,743	595,195	44,085	16,861	26,348	25,508	21.9	7.6	12.1	9.6	1.1	0.4	1.1	0.5	1.3	0.02	-1.0	0.8	1.2	0.01	1.2	0.02
				GLKAYSLDACHQIPLSSDLSHLVAEVR	3	94.3%	1																									
IPI00456599	C7orf70	STAT3-interacting protein as a repressor	94.2%	6.2	1	1	1	3	933,183	917,093	819,987	1,042,783	134,597	103,646	69,634	77,203	32.3	25.3	19.0	16.6	-1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.5	1.1	0.4	1.3	0.06
IPI00978410	C7orf70	Uncharacterized protein	94.2%	13.3	1	1	1	3	933,183	917,093	819,987	1,042,783	134,597	103,646	69,634	77,203	32.3	25.3	19.0	16.6	-1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.5	1.1	0.4	1.3	0.06
IPI00982867	C7orf70	Uncharacterized protein	94.2%	14.7	1	1	1	3	933,183	917,093	819,987	1,042,783	134,597	103,646	69,634	77,203	32.3	25.3	19.0	16.6	-1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.5	1.1	0.4	1.3	0.06
				MPEGPWPADAPSWMNK	3	94.2%	1																									
IPI00456635	UNC13D	isoform 3 of Protein unc-13 homolog D	96.1%	0.9	1	1	1	4	1,342,203	1,474,405	1,424,138	1,641,285	157,634	140,732	140,488	183,280	26.3	21.3	22.1	25.0	1.1	0.5	1.1	0.7	1.2	0.3	-1.0	0.8	1.1	0.5	1.2	0.4
IPI00456636	UNC13D	isoform 2 of Protein unc-13 homolog D	96.1%	2.8	1	1	1	4	1,342,203	1,474,405	1,424,138	1,641,285	157,634	140,732	140,488	183,280	26.3	21.3	22.1	25.0	1.1	0.5	1.1	0.7	1.2	0.3	-1.0	0.8	1.1	0.5	1.2	0.4
IPI00790059	UNC13D	cDNA FLJ54883, highly similar to Unc-13 homolog D	96.1%	1.1	1	1	1	4	1,342,203	1,474,405	1,424,138	1,641,285	157,634	140,732	140,488	183,280	26.3	21.3	22.1	25.0	1.1	0.5	1.1	0.7	1.2	0.3	-1.0	0.8	1.1	0.5	1.2	0.4
IPI00940441	UNC13D	isoform 1 of Protein unc-13 homolog D	96.1%	0.9	1	1	1	4	1,342,203	1,474,405	1,424,138	1,641,285	157,634	140,732	140,488	183,280	26.3	21.3	22.1	25.0	1.1	0.5	1.1	0.7	1.2	0.3	-1.0	0.8	1.1	0.5	1.2	0.4
				ELEKPIFCLK	2	96.1%	1																									
IPI00456750	FAM129B	Niban-like protein 1	100.0%	10.9	5	6	6	2	28,636,338	29,084,867	26,445,411	31,101,600	2,417,695	1,884,014	1,660,160	1,086,224	18.9	14.5	14.0	7.8	1.0	0.9	-1.1	0.5	1.1	0.4	-1.1	0.3	1.1	0.4	1.2	0.05
IPI00647286	FAM129B	niban-like protein 1 isoform 1	100.0%	10.7	5	6	6	2	28,636,338	29,084,867	26,445,411	31,101,600	2,417,695	1,884,014	1,660,160	1,086,224	18.9	14.5	14.0	7.8	1.0	0.9	-1.1	0.5	1.1	0.4	-1.1	0.3	1.1	0.4	1.2	0.05
				EQMDNAVYTFETLLHQELGK	3	99.8%	1																									

				EVTDMNLNVINEGGIDK	2	100.0%	1																									
				FQELIFEDFAR	2	100.0%	1																									
				ILTSVDQYLELIGNSLPGTTAK	2	100.0%	1																									
				ILTSVDQYLELIGNSLPGTTAK	3	100.0%	1																									
				TDMDQIITSK	2	99.6%	1																									
IPI00456758	RPL27A	60S ribosomal protein L27a	96.8%	7.4	1	1	1	4	1,673,053	1,494,548	1,504,285	1,425,333	163,595	124,633	120,101	143,886	21.9	18.7	17.9	22.6	-1.1	0.4	-1.1	0.4	-1.2	0.3	1.0	1	-1.0	0.7	-1.1	0.7
IPI00976934	RPL27A	Uncharacterized protein	96.8%	9.7	1	1	1	4	1,673,053	1,494,548	1,504,285	1,425,333	163,595	124,633	120,101	143,886	21.9	18.7	17.9	22.6	-1.1	0.4	-1.1	0.4	-1.2	0.3	1.0	1	-1.0	0.7	-1.1	0.7
IPI00977964	RPL27A	Uncharacterized protein	96.8%	10.2	1	1	1	4	1,673,053	1,494,548	1,504,285	1,425,333	163,595	124,633	120,101	143,886	21.9	18.7	17.9	22.6	-1.1	0.4	-1.1	0.4	-1.2	0.3	1.0	1	-1.0	0.7	-1.1	0.7
IPI00980350	RPL27A	Uncharacterized protein	96.8%	12.1	1	1	1	4	1,673,053	1,494,548	1,504,285	1,425,333	163,595	124,633	120,101	143,886	21.9	18.7	17.9	22.6	-1.1	0.4	-1.1	0.4	-1.2	0.3	1.0	1	-1.0	0.7	-1.1	0.7
				TGAAPIIDVVR	2	96.8%	1																									
IPI00456887	HNRNPUL2	Heterogeneous nuclear ribonucleoprotein U-like protein 2	100.0%	24.1	14	14	14	1	39,864,825	40,743,060	39,715,545	44,262,460	3,153,981	811,019	2,674,429	1,954,196	17.7	4.5	15.1	9.9	1.0	0.8	-1.0	1	1.1	0.3	-1.0	0.7	1.1	0.1	1.1	0.2
				ANFSLPEK	2	86.7%	1																									
				DLLVQQASQCLSK	2	100.0%	1																									
				EEPFFPPPEEFVFIHAVPVEER	3	95.8%	1																									
				EGCTEVSLLR	2	99.8%	1																									
				FPTLWSGAR	2	97.6%	1																									
				GLEEPEMDPK	2	96.8%	1																									
				KEVEGDDVPESIMLEMK	2	99.9%	1																									
				KVVVVVPNEEDWKK	3	100.0%	1																									
				NCVVELNFGQK	2	99.9%	1																									
				NFILDQCNVYNSGQR	2	100.0%	1																									
				NYYGYQGYR	2	95.9%	1																									
				VGWSVDFSRPQLGEDEFSYGFDGR	3	100.0%	1																									
				VTQNLPMKEGCTEVSLLR	3	99.9%	1																									
				YGGQPLFSEK	2	100.0%	1																									
IPI00456969	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	100.0%	8.6	27	27	28	1	166,404,093	169,379,315	163,524,471	187,828,395	########	5,992,707	########	9,558,146	24.6	7.9	18.4	11.4	1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	0.7	1.1	0.1	1.1	0.2
				ALPDMEVVGLNFSSATTPELLLK	2	99.9%	1																									
				ENFIPTIVNFSAEEISDAIR	2	99.3%	1																									
				EVWNTYELDLVNYQNK	2	99.1%	1																									
				FGNPLLVQDVESYDPVLNPVLNR	2	100.0%	1																									
				FNYGFEYLGVQDK	2	99.4%	2																									
				IAFIMDESNVLDSGFLER	2	100.0%	1																									
				INEWLTLVEK	2	99.7%	1																									
				IQGLTVEQAEAVVR	2	100.0%	1																									
				KLVPLLLEDGGEAPAALEAALEEK	3	99.9%	1																									
				LGGSPFGPAGTGK	2	98.7%	1																									
				LKVNFLPEIITLSKEVR	3	88.4%	1																									
				LLAESVTEVEIFGK	2	100.0%	1																									
				LVPLLLEDGGEAPAALEAALEEK	3	89.9%	1																									
				SFEWLSQMR	2	100.0%	1																									
				SPLVMDVLNIQGVQR	2	99.2%	1																									
				TEYLSNADER	2	85.4%	1																									
				TPVIDADKPVSSQLR	3	100.0%	1																									
				VAAPDVVVPTLDTVR	2	92.3%	1																									
				VLLTTQGVDMISK	2	100.0%	1																									
				VPLAIVNK	2	92.4%	1																									
				VQVALEELQDLK	2	100.0%	1																									
				VTDFGDKVEDPTFLNQLQSGVNR	3	100.0%	1																									
				WAIAQLNYADMLK	2	99.1%	1																									
				WTDENIDTVALK	2	99.4%	1																									
				YKEEYAVLISEAQAIK	3	91.4%	1																									
				YPLIIDPSGQATEFIMNEYKDR	3	97.2%	1																									
				YTGEDFDEDLR	2	98.2%	1																									
IPI00457142	LOC100509022	splicing factor U2AF 35 kDa subunit-like	100.0%	10.7	2	3	3	3	8,807,503	8,938,473	7,450,015	9,208,150	924,918	640,357	695,480	416,403	23.5	16.0	20.9	10.1	1.0	0.9	-1.2	0.3	1.0	0.7	-1.2	0.2	1.0	0.7	1.2	0.06
IPI00619914	U2AF1	splicing factor U2AF 35 kDa subunit isoform b	100.0%	10.8	2	3	3	3	8,807,503	8,938,473	7,450,015	9,208,150	924,918	640,357	695,480	416,403	23.5	16.0	20.9	10.1	1.0	0.9	-1.2	0.3	1.0	0.7	-1.2	0.2	1.0	0.7	1.2	0.06
IPI00619942	U2AF1	splicing factor U2AF 35 kDa subunit isoform c	100.0%	15.6	2	3	3	3	8,807,503	8,938,473	7,450,015	9,208,150	924,918	640,357	695,480	416,403	23.5	16.0	20.9	10.1	1.0	0.9	-1.2	0.3	1.0	0.7	-1.2	0.2	1.0	0.7	1.2	0.06
				AVIDLNNR	2	89.5%	1																									
				WFNGQPIHAELSPVTDFR	2	99.5%	1																									
				WFNGQPIHAELSPVTDFR	3	100.0%	1																									
IPI00465028	TPI1P1;TPI1	triosephosphate isomerase isoform 2	100.0%	79.4	20	33	54	2	291,361,192	304,992,155	284,756,797	347,086,396	########	########	########	########	20.8	10.2	19.3	6.6	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.5	1.1	0.04	1.2	0.05
IPI00797270	TPI1P1;TPI1	isoform 1 of Triosephosphate isomerase	100.0%	91.2	20	33	54	2	291,361,192	304,992,155	284,756,797	347,086,396	########	########	########	########	20.8	10.2	19.3	6.6	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.5	1.1	0.04	1.2	0.05
				DCGATWVVLGHSER	2	100.0%	2																									
				DCGATWVVLGHSER	3	100.0%	1																									
				ELASQPDVDGFLVGGASLKPEFVDIINAK	2	100.0%	2																									
				ELASQPDVDGFLVGGASLKPEFVDIINAK	3	100.0%	3																									
				FFVGGNWK	1	100.0%	1																									
				FFVGGNWK	2	100.0%	2																									
				HVFGESDELIGQK	2	100.0%	2																									
				HVFGESDELIGQK	3	100.0%	2																									
				IAVAAQNCYK	1	100.0%	1																									
				IAVAAQNCYK	2	100.0%	2																									
				IIYGGSVTGATCK	2	100.0%	1																									
				KFFVGGNWK	2	89.8%	1																									
				KFFVGGNWK	3	99.3%	1																									
				KQSLGELIGTLNAAK	2	100.0%	2																									
				KQSLGELIGTLNAAK	3	100.0%	1																									
				LDEREAGITEK	3	99.7%	1																									
				QSLGELIGTLNAAK	2	100.0%	2																									
				RHVFGESDELIGQK	2	100.0%	1																									
				SNVSDAVAQSTR	1	100.0%	1																									
				SNVSDAVAQSTR	2	100.0%	2																									
				TATPQQAQEVHEK	3	99.9%	1																									
				VAHALAEGLGVIACIGEK	2	100.0%	2																									
				VAHALAEGLGVIACIGEK	3	99.9%	1																									
				VIADNVK	1	100.0%	1																									
				VIADNVKDWSK	2	100.0%	2																									
				VPADTEVVCAPPTAYIDFAR	2	100.0%	2																									
				VPADTEVVCAPPTAYIDFAR	3	100.0%	2																									
				VTNGAFTGEISPGMIK	2	100.0%	4																									
				VTNGAFTGEISPGMIK	3	100.0%	1																									
				VVFEQTK	1	98.7%	2																									
				VVFEQTK	2	99.9%	2																									
				VVLAYEPVWAIGTGK	2	100.0%	2																									
				VVLAYEPVWAIGTGK	3	100.0%	1																									
IPI00465044	RCC2	Protein RCC2	100.0%	4.0	2	2	2	1	9,792,660	8,668,270	8,582,690	8,999,590	552,103	228,816	245,584	465,883	12.6	5.9	6.4	11.6	-1.1	0.1	-1.1	0.08	-1.1	0.3	-1.0	0.8	1.0	0.5	1.0	0.5
				IEYDCELVPR	2	99.6%	1																									
				VFSWGFGGYGR	2	99.7%	1																									
IPI00465054	THUMPD1	Putative uncharacterized protein DKFZp686C1054	100.0%	5.9	2	2	2	2	10,628,570	10,301,475	10,505,930	10,859,930	312,510	455,702	296,780	373,898	6.6	9.9	6.3	7.7	-1.0	0.6	-1.0	0.8	1.0	0.6	1.0	0.7	1.1	0.4	1.0	0.5
IPI00550243	THUMPD1	THUMP domain-containing protein 1	100.0%	7.4	2	2	2	2	10,628,570	10,301,475	10,505,930	10,859,930	312,510	455,702	296,780	373,898	6.6	9.9	6.3	7.7	-1.0	0.6	-1.0	0.8	1.0	0.6	1.0	0.7	1.1	0.4	1.0	0.5
				FQSVESGANNVVFIR	2	99.9%	1																									
				YAETFLEPWFK	2	100.0%	1																									
IPI00465085	NAPRT1	isoform 1 of Nicotinate phosphoribosyltransferase	100.0%	16.4	5	5	5	2	4,528,786	4,713,505	4,613,424	5,254,469	348,922	358,049	251,826	228,560	17.2	17.0	12.2	9.7	1.0	0.7	1.0	0.8	1.2	0.1	-1.0	0.8	1.1	0.2	1.1	0.1
IPI00880164	NAPRT1	isoform 3 of Nicotinate phosphoribosyltransferase	100.0%	16.8	5	5	5	2	4,528,786	4,713,505	4,613,424	5,254,469	348,922	358,049	251,826	228,560	17.2	17.0	12.2	9.7	1.0	0.7	1.0	0.8	1.2	0.1	-1.0	0.8	1.1	0.2	1.1	0.1
				DAAEFELFFR	2	100.0%	1																									
				DADVQFLASVLPPDTDPAFFEHLR	3	99.9%	1																									
				LDSGDLLQQAQEIR	2	97.5%	1																									
				LLGSDGSPLMDMLQLAEEPVPQAGQELR	3	99.6%	1																									
				SPAQYQVVLSER	2	100.0%	1																									
IPI00465128	BAG6	isoform 1 of Large proline-rich protein BAG6	99.3%	2.2	2	2	2	5	2,896,947	2,622,767	2,476,249	3,023,530	272,449	79,677	123,906	241,327	21.0	6.8	11.2	17.9	-1.1	0.4	-1.2	0.2	1.0	0.7	-1.1	0.3	1.2	0.2	1.2	0.08
IPI00640922	BAG6	isoform 2 of Large proline-rich protein BAG6	99.3%	2.2	2	2	2	5	2,896,947	2,622,767	2,476,249	3,023,530	272,449	79,677	123,906	241,327	21.0	6.8	11.2	17.9	-1.1	0.4	-1.2	0.2	1.0	0.7	-1.1	0.3	1.2	0.2	1.2	0.08
IPI00645431	BAG6	isoform 3 of Large proline-rich protein BAG6	99.3%	2.2	2	2	2	5	2,896,947	2,622,767	2,476,249	3,023,530	272,449	79,677	123,906	241,327	21.0	6.8	11.2	17.9	-1.1	0.4	-1.2	0.2	1.0	0.7	-1.1	0.3	1.2	0.2	1.2	0.08
IPI00894269	BAG6	119 kDa protein	99.3%	2.2	2	2	2	5	2,896,947	2,622,767	2,476,249	3,023,530	272,449	79,677	123,906	241,327	21.0	6.8	11.2	17.9	-1.1	0.4	-1.2	0.2	1.0	0.7	-1.1	0.3	1.2	0.2	1.2	0.08
IPI00894467	BAG6	Uncharacterized protein	99.3%	2.2	2	2	2	5	2,896,947	2,622,767	2,476,249	3,023,530	272,449	79,677	123,906	241,327	21.0	6.8	11.2	17.9	-1.1	0.4	-1.2	0.2	1.0	0.7	-1.1	0.3	1.2	0.2	1.2	0.08
				AGSSESIAAFIQR	2	94.7%	1																									
				DLEAPEVQESYR	2	98.2%	1																									
IPI00465132	COPE	Coatomer subunit epsilon	100.0%	29.9	5	5	6	1	13,205,437	13,906,448	15,599,806	15,849,481	1,262,507	761,698	1,560,430	502,116	21.4	12.3	22.4	7.1	1.1	0.6	1.2	0.3	1.2	0.09	1.1	0.4	1.1	0.07	1.0	0.9
				DSIVAELDREMSR	2	81.0%	1																									
				FGVVLDEIKPSSAPELQAVR	3	100.0%	1																									
				LQDAYYIFQEMADK	2	100.0%	2																									
				NAFYIGSYQQCINEAQR	3	99.2%	1																									
				SVDVTNTTFLLMAASIYLHDQNPDAALR	3	99.2%	1																									
IPI00465135	CACNA1F	isoform 1 of Voltage-dependent L-type calcium channel subunit alpha-1F	97.4%	1.6	1	1	1	2	1,247,325	1,188,030	1,256,215	1,283,700	94,339	41,292	96,444	57,150	16.9	7.8	17.2	10.0	-1.0	0.6	1.0	0.9	1.0	0.8	1.1	0.5	1.1	0.2	1.0	0.8
IPI00937757	CACNA1F	Voltage-gated L-type calcium channel alpha-1 subunit	97.4%	1.6	1	1	1	2	1,247,325	1,188,030	1,256,215	1,283,700	94,339	41,292	96,444	57,150	16.9	7.8	17.2	10.0	-1.0	0.6	1.0	0.9	1.0	0.8	1.1	0.5	1.1	0.2	1.0	0.8
				GYLDWITQAEELDMEDPSADDNLGSMAEEGR	3	97.4%	1																									
IPI00465164	HMGXB3	HMG domain-containing protein 3	92.3%	1.5	1	1	1	1	4,223,090	4,187,100	4,249,150	4,205,860	325,703	280,305	439,553	210,968	17.3	15.0	23.1	11.2	-1.0	0.9	1.0	1	-1.0	1	1.0	0.9	1.0	1	-1.0	0.9
				QTGASVTTVSLPSSSSSPGLDPR	3	92.4%	1																									
IPI00465233	EIF3L	Eukaryotic translation initiation factor 3, subunit E interacting protein	100.0%	7.4	3	3	3	4	1,625,084	1,685,268	1,683,252	1,841,281	175,511	83,026	177,917	80,790	24.2	11.0	23.6	9.8	1.0	0.8	1.0	0.8	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.4
IPI00745266	EIF3L	Eukaryotic translation initiation factor 3 subunit L	100.0%	8.0	3	3	3	4	1,625,084	1,685,268	1,683,252	1,841,281	175,511	83,026	177,917	80,790	24.2	11.0	23.6	9.8	1.0	0.8	1.0	0.8	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.4
IPI00910422	EIF3L	cDNA FLJ52802, highly similar to Eukaryotic translation initiation factor 3subunit 6-i	100.0%	8.7	3	3	3	4	1,625,084	1,685,268	1,683,252	1,841,281	175,511	83,026	177,917	80,790	24.2	11.0	23.6	9.8	1.0	0.8	1.0	0.8	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.4
IPI00910633	EIF3L	cDNA FLJ59381, highly similar to Eukaryotic translation initiation factor 3 subunit 6-i	100.0%	8.5	3	3	3	4	1,625,084	1,685,268	1,683,252	1,841,281	175,511	83,026	177,917	80,790	24.2	11.0	23.6	9.8	1.0	0.8	1.0	0.8	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.4
				GDPQVYEELFSYSCPK	2	99.5%	1																									
				LAGFLDLTEQEFR	2	100.0%	1																									
				VFSDEVQQQAQLSTIR	3	98.9%	1																									
IPI00465248	ENO1	isoform alpha-enolase of Alpha-enolase	100.0%	77.2	35	55	84	1	694,686,531	710,726,148	666,123,670	810,255,836	########	########	########	########	20.7	10.2	18.5	7.2	1.0	0.8	-1.0	0.7	1.2	0.1	-1.1	0.5	1.1	0.04	1.2	0.05
				AAVPSGASTGIYEALELR	2	100.0%	2																									
				AAVPSGASTGIYEALELR	3	100.0%	1																									
				AGYTDKVVIGMDVAASEFFR	2	99.4%	1																									
				DATNVGDEGGFAPNILENK	2	100.0%	3																									
				DATNVGDEGGFAPNILENKEGLELLK	2	100.0%	1																									
				DYPVVSIEDPFDQDDWGAWQK	2	100.0%	2																									
				DYPVVSIEDPFDQDDWGAWQK	3	100.0%	1																									
				FGANAILGVSLAVCK	2	100.0%	1																									
				FTASAGIQVVGDDLTVTNPK	2	100.0%	2																									
				FTASAGIQVVGDDLTVTNPK	3	100.0%	1																									
				FTASAGIQVVGDDLTVTNPKR	2	100.0%	1																									
				FTASAGIQVVGDDLTVTNPKR	3	100.0%	1																									
				GLFRAAVPSGASTGIYEALELR	3	99.9%	1																									

				GNPTVEVDLFTSK	1	99.3%	2																									
				GNPTVEVDLFTSK	2	99.9%	2																									
				HIADLAGNSEVILPVPAFNVINGGSHAGNK	2	100.0%	1																									
				IDKLMIEMDGTENK	2	100.0%	2																									
				IDKLMIEMDGTENK	3	99.5%	1																									
				IEEELGSK	1	93.6%	1																									
				IGAEVYHNLK	2	100.0%	2																									
				IGAEVYHNLK	3	99.9%	1																									
				KLNVTEQEK	2	99.9%	1																									
				KLNVTEQEKIDK	2	100.0%	2																									
				KLNVTEQEKIDK	3	100.0%	1																									
				LAMQEFMILPVGAANFR	2	100.0%	2																									
				LAMQEFMILPVGAANFR	3	100.0%	2																									
				LAQANGWGVMVSHR	2	100.0%	2																									
				LAQANGWGVMVSHR	3	100.0%	3																									
				LMIEMDGTENK	1	99.6%	1																									
				LMIEMDGTENK	2	100.0%	3																									
				LNVTEQEK	2	99.7%	1																									
				LNVTEQEKIDK	2	99.5%	2																									
				LNVTEQEKIDKLMIEMDGTENK	3	98.6%	1																									
				SCNCLLLK	2	99.6%	2																									
				SFIKDYPVVSIEDPFDQDDWGAWQK	2	100.0%	2																									
				SFIKDYPVVSIEDPFDQDDWGAWQK	3	100.0%	1																									
				SGETEDTFIADLVVGLCTGQIK	2	100.0%	2																									
				SGETEDTFIADLVVGLCTGQIK	3	100.0%	1																									
				SGKYDLDFK	2	98.6%	1																									
				SGKYDLDFK	3	100.0%	1																									
				SGKYDLDFKSPDDPSR	2	100.0%	1																									
				SGKYDLDFKSPDDPSR	3	100.0%	1																									
				TIAPALVSK	1	99.3%	1																									
				TIAPALVSK	2	92.3%	1																									
				VNQIGSVTESLQACK	2	98.9%	2																									
				VNQIGSVTESLQACK	3	85.9%	1																									
				VVIGMDVAASEFFR	2	100.0%	3																									
				VVIGMDVAASEFFR	3	100.0%	1																									
				YDLDFKSPDDPSR	2	100.0%	3																									
				YDLDFKSPDDPSR	3	100.0%	1																									
				YGKDATNVGDEGGFAPNILENK	3	100.0%	2																									
				YGKDATNVGDEGGFAPNILENKEGLELLK	3	100.0%	1																									
				YISPDQLADLYK	1	100.0%	1																									
				YISPDQLADLYK	2	100.0%	3																									
				YNQLLR	1	92.0%	1																									
IPI00465256	AK3	GTP:AMP phosphotransferase, mitochondrial	99.6%	6.2	1	1	1	2	808,180	759,552	782,941	841,080	83,534	105,181	105,067	79,420	23.1	31.0	30.0	21.1	-1.1	0.7	-1.0	0.9	1.0	0.8	1.0	0.9	1.1	0.6	1.1	0.7
IPI00478236	AK3	GTP:AMP phosphotransferase, mitochondrial isoform c	99.6%	8.9	1	1	1	2	808,180	759,552	782,941	841,080	83,534	105,181	105,067	79,420	23.1	31.0	30.0	21.1	-1.1	0.7	-1.0	0.9	1.0	0.8	1.0	0.9	1.1	0.6	1.1	0.7
				NLTQYSWLLDGFPR	2	99.6%	1																									
IPI00465294	CDC5L	Cell division cycle 5-like protein	100.0%	9.2	6	6	6	1	29,375,110	32,718,580	31,825,740	34,835,530	3,152,240	1,239,895	2,516,119	890,360	24.0	8.5	17.7	5.7	1.1	0.4	1.1	0.6	1.2	0.2	-1.0	0.8	1.1	0.2	1.1	0.3
				ESDLPSAILQTSGVSEFTK	2	100.0%	1																									
				GVDYNAEIPFEK	2	97.1%	1																									
				ILLGGYQSR	2	80.6%	1																									
				KESDLPSAILQTSGVSEFTKK	3	85.5%	1																									
				QLNDLWDQIEQAHLELR	3	99.9%	1																									
				QVVQTPNTVLSTPFR	2	99.8%	1																									
IPI00465315	CYCS	Cytochrome c	100.0%	56.2	7	9	10	2	23,896,096	24,897,345	24,356,474	28,827,462	2,999,309	831,022	2,702,598	933,589	28.1	7.5	24.8	7.2	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.01	1.2	0.2
IPI00917605	CYCS	Uncharacterized protein	100.0%	58.4	7	9	10	2	23,896,096	24,897,345	24,356,474	28,827,462	2,999,309	831,022	2,702,598	933,589	28.1	7.5	24.8	7.2	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.01	1.2	0.2
				ADLIAYLK	2	82.9%	1																									
				ADLIAYLKK	2	90.8%	1																									
				GIIWGEDTLMEYLENPK	2	100.0%	2																									
				GIIWGEDTLMEYLENPKK	2	99.5%	1																									
				GIIWGEDTLMEYLENPKK	3	80.5%	1																									
				MIFVGIK	2	81.1%	1																									
				TGPNLHGLFGR	2	99.9%	1																									
				TGPNLHGLFGR	3	99.9%	1																									
				TGQAPGYSYTAANK	2	100.0%	1																									
IPI00465319	CHPF	Chondroitin sulfate synthase 2	97.6%	3.0	1	1	1	2	2,377,795	2,114,505	2,558,760	2,329,280	210,523	190,867	160,311	163,352	19.8	20.2	14.0	15.7	-1.1	0.4	1.1	0.5	-1.0	0.9	1.2	0.1	1.1	0.4	-1.1	0.3
IPI00976127	CHPF	chondroitin sulfate synthase 2 isoform 2	97.6%	3.8	1	1	1	2	2,377,795	2,114,505	2,558,760	2,329,280	210,523	190,867	160,311	163,352	19.8	20.2	14.0	15.7	-1.1	0.4	1.1	0.5	-1.0	0.9	1.2	0.1	1.1	0.4	-1.1	0.3
				HPLDTLFLLAGPDTVLTPDFLNR	3	97.6%	1																									
IPI00465361	RPL13	60S ribosomal protein L13	99.9%	11.4	2	2	2	1	10,760,670	10,528,440	10,395,445	10,620,930	596,794	871,551	719,722	598,642	12.4	18.5	15.5	12.6	-1.0	0.8	-1.0	0.7	-1.0	0.9	-1.0	0.9	1.0	0.9	1.0	0.8
				LATQLTGPVMPVR	2	98.4%	1																									
				STESLQANVQR	2	98.4%	1																									
IPI00465363	HIST1H2BA	Histone H2B type 1-A	100.0%	15.8	2	2	3	1	693,983	777,263	723,937	549,226	132,383	113,644	67,568	40,544	42.7	32.7	20.9	16.5	1.1	0.6	1.0	0.8	-1.3	0.3	-1.1	0.7	-1.4	0.1	-1.3	0.06
				LLLPGELAK	1	84.1%	1																									
				QVHPDTGISSK	2	100.0%	2																									
IPI00465431	LGALS3	Galectin-3	100.0%	36.8	9	11	17	1	124,181,863	132,314,600	130,755,768	147,897,150	########	5,640,724	8,233,523	4,349,051	20.6	9.5	14.1	6.6	1.1	0.5	1.1	0.7	1.2	0.1	-1.0	0.9	1.1	0.06	1.1	0.1
				GNDVAFHFNPR	3	100.0%	2																									
				IALDFQR	2	99.3%	2																									
				IQVLVEPDHFK	2	100.0%	2																									
				IQVLVEPDHFK	3	99.4%	2																									
				KLNEISK	2	90.0%	1																									
				LDNNWGR	2	98.7%	1																									
				MLITILGTVKPNANR	3	100.0%	1																									
				QSVFPFESGKPFK	2	100.0%	2																									
				VAVNDAHLLQYNHR	2	100.0%	2																									
				VAVNDAHLLQYNHR	3	100.0%	1																									
				VIVCNTK	2	92.7%	1																									
IPI00465436	CAT	Catalase	100.0%	24.1	10	10	11	1	61,362,200	64,483,220	63,167,500	71,239,750	3,938,645	2,802,357	3,645,176	1,075,319	14.4	9.7	12.9	3.4	1.1	0.5	1.0	0.7	1.2	0.06	-1.0	0.8	1.1	0.07	1.1	0.09
				ADVLTTGAGNPVGDK	2	99.9%	1																									
				ADVLTTGAGNPVGDKLNVITVGPR	3	100.0%	1																									
				AFYVNVLNEEQR	2	100.0%	2																									
				FNTANDDNVTQVR	2	100.0%	1																									
				GPLLVQDVVFTDEMAHFDR	3	100.0%	1																									
				HMNGYGSHTFK	3	99.9%	1																									
				LCENIAGHLK	3	97.4%	1																									
				LGPNYLHIPVNCPYR	3	100.0%	1																									
				LSQEDPDYGIR	2	99.6%	1																									
				LVNANGEAVYCK	2	98.1%	1																									
IPI00465439	ALDOA	Fructose-bisphosphate aldolase A	100.0%	83.5	25	36	50	2	201,902,216	203,845,334	198,426,790	231,818,897	########	########	########	6,705,144	20.0	11.3	15.9	6.5	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.05	1.2	0.06
IPI00796333	ALDOA	45 kDa protein	100.0%	72.7	25	36	50	2	201,902,216	203,845,334	198,426,790	231,818,897	########	########	########	6,705,144	20.0	11.3	15.9	6.5	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.05	1.2	0.06
				AAQEEYVK	2	99.7%	1																									
				AAQEEYVKR	2	100.0%	1																									
				ADDGRPFPQVIK	2	97.7%	1																									
				ADDGRPFPQVIK	3	100.0%	2																									
				ALANSLACQGK	1	100.0%	1																									
				ALANSLACQGK	2	100.0%	2																									
				ALQASALK	1	99.3%	2																									
				ALQASALK	2	99.4%	1																									
				ALSDHHIYLEGTLLKPNMVTPGHACTQK	3	100.0%	1																									
				CPLLKPWALTFSYGR	3	100.0%	1																									
				CQYVTEK	1	97.8%	1																									
				DGADFAK	1	99.2%	1																									
				DGADFAK	2	88.2%	1																									
				ELSDIAHR	1	100.0%	1																									
				FSHEEIAMATVTALR	2	100.0%	2																									
				FSHEEIAMATVTALR	3	100.0%	1																									
				GGVVGIK	1	98.3%	2																									
				GILAADESTGSIAK	1	100.0%	2																									
				GILAADESTGSIAK	2	100.0%	1																									
				GILAADESTGSIAKR	2	100.0%	1																									
				GILAADESTGSIAKR	3	99.9%	1																									
				GVVPLAGTNGETTTQGLDGLSER	2	99.6%	2																									
				IGEHTPSALAIMENANVLAR	2	100.0%	2																									
				IGEHTPSALAIMENANVLAR	3	100.0%	2																									
				KELSDIAHR	2	100.0%	1																									
				QLLLTADDR	2	100.0%	2																									
				RTVPPAVTGITFLSGGQSEEEASINLNAINK	3	99.9%	1																									
				TVPPAVTGITFLSGGQSEEEASINLNAINK	2	100.0%	2																									
				TVPPAVTGITFLSGGQSEEEASINLNAINK	3	100.0%	1																									
				VDKGVVPLAGTNGETTTQGLDGLSER	3	100.0%	1																									
				VLAAVYK	1	99.5%	1																									
				VLAAVYK	2	89.1%	1																									
				VNPCIGGVILFHETLYQK	2	100.0%	1																									
				YASICQQNGIVPIVEPEILPDGDHDLKR	3	100.0%	2																									
				YTPSGQAGAAASESLFVSNHAY	2	100.0%	3																									
				YTPSGQAGAAASESLFVSNHAY	3	100.0%	1																									
IPI00470387	SMARCC2	Putative uncharacterized protein DKFZp313D0632	99.9%	14.3	1	1	1	1	1,865,058	1,896,150	1,849,460	2,071,165	126,055	82,593	130,903	91,702	15.1	9.7	15.8	9.9	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.2	1.1	0.2
				YYEAADTVTQFDNVR	2	99.6%	1																									
IPI00470467	POR	NADPH--cytochrome P450 reductase	94.2%	3.6	1	1	1	7	168,982	172,219	183,476	209,823	24,559	10,543	12,938	12,039	32.5	13.7	15.8	12.8	1.0	0.9	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.05	1.1	0.2
IPI00903331	POR	72 kDa protein	94.2%	3.8	1	1	1	7	168,982	172,219	183,476	209,823	24,559	10,543	12,938	12,039	32.5	13.7	15.8	12.8	1.0	0.9	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.05	1.1	0.2
IPI00908675	POR	cDNA FLJ59656, highly similar to NADPH--cytochrome P450 reductase	94.2%	5.3	1	1	1	7	168,982	172,219	183,476	209,823	24,559	10,543	12,938	12,039	32.5	13.7	15.8	12.8	1.0	0.9	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.05	1.1	0.2
IPI00910178	POR	cDNA FLJ59702, highly similar to NADPH--cytochrome P450 reductase	94.2%	4.2	1	1	1	7	168,982	172,219	183,476	209,823	24,559	10,543	12,938	12,039	32.5	13.7	15.8	12.8	1.0	0.9	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.05	1.1	0.2
IPI00927647	POR	cDNA, FLJ92914, highly similar to Homo sapiens P450 (cytochrome) oxidoreductase	94.2%	3.5	1	1	1	7	168,982	172,219	183,476	209,823	24,559	10,543	12,938	12,039	32.5	13.7	15.8	12.8	1.0	0.9	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.05	1.1	0.2
IPI00973067	POR	Uncharacterized protein	94.2%	5.7	1	1	1	7	168,982	172,219	183,476	209,823	24,559	10,543	12,938	12,039	32.5	13.7	15.8	12.8	1.0	0.9	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.05	1.1	0.2
IPI01010631	POR	cDNA FLJ52316, highly similar to NADPH--cytochrome P450 reductase	94.2%	4.9	1	1	1	7	168,982	172,219	183,476	209,823	24,559	10,543	12,938	12,039	32.5	13.7	15.8	12.8	1.0	0.9	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.05	1.1	0.2
				ATTPVIMVGPGTGVAPFIGFIQER	3	94.2%	1																									
IPI00470528	RPL15	60S ribosomal protein L15	100.0%	20.6	4	5	6	2	7,005,123	8,227,819	8,051,337	8,939,943	615,359	302,758	711,962	105,759	19.6	8.2	19.8	2.7	1.2	0.1	1.1	0.3	1.3	0.03	-1.0	0.8	1.1	0.08	1.1	0.3
IPI00927715	RPL15	Ribosomal protein L15	100.0%	24.1	4	5	6	2	7,005,123	8,227,819	8,051,337	8,939,943	615,359	302,758	711,962	105,759	19.6	8.2	19.8	2.7	1.2	0.1	1.1	0.3	1.3	0.03	-1.0	0.8	1.1	0.08	1.1	0.3
				FFEVILIDPFHK	2	84.1%	1																									
				FFEVILIDPFHK	3	100.0%	1																									

				SLQSVAEER	2	99.4%	1																									
				VLNSYWVGEDSTYK	2	100.0%	2																									
				YIQELWR	2	99.3%	1																									
IPI00470573	ACTR2	actin-related protein 2 isoform a	100.0%	16.8	5	5	6	3	9,780,910	10,254,640	9,781,795	10,402,215	366,506	318,160	363,628	192,333	8.4	6.9	8.3	4.1	1.0	0.4	1.0	1	1.1	0.2	-1.0	0.4	1.0	0.7	1.1	0.2
IPI00909247	ACTR2	cDNA FLJ51655, highly similar to Actin-like protein 2	100.0%	22.0	5	5	6	3	9,780,910	10,254,640	9,781,795	10,402,215	366,506	318,160	363,628	192,333	8.4	6.9	8.3	4.1	1.0	0.4	1.0	1	1.1	0.2	-1.0	0.4	1.0	0.7	1.1	0.2
IPI01014716	ACTR2	39 kDa protein	100.0%	19.8	5	5	6	3	9,780,910	10,254,640	9,781,795	10,402,215	366,506	318,160	363,628	192,333	8.4	6.9	8.3	4.1	1.0	0.4	1.0	1	1.1	0.2	-1.0	0.4	1.0	0.7	1.1	0.2
				GYAFNHSADFETVR	3	100.0%	1																									
				HIVLSGGSTMYPGLPSR	3	85.0%	1																									
				HLWDYTFGPEK	2	100.0%	1																									
				ILLTEPPMNPTK	2	100.0%	2																									
				LCYVGYNIEQEQK	2	100.0%	1																									
IPI00470590	SF3A1	splicing factor 3A subunit 1 isoform 2	100.0%	11.4	5	5	5	1	11,063,136	11,447,696	10,817,637	12,182,135	695,582	333,159	801,759	408,949	14.1	6.5	16.6	7.5	1.0	0.6	-1.0	0.8	1.1	0.2	-1.1	0.5	1.1	0.2	1.1	0.2
				ASKPLPPAPAPDEYLVSPITGEK	3	100.0%	1																									
				EKQSDDEVYAPGLDIESSLK	3	89.8%	1																									
				FNFLNPNDPYHAYYR	3	99.7%	1																									
				TDIFGVEETAIGK	2	98.6%	1																									
				VTWDGHSGSMAR	2	97.3%	1																									
IPI00793698	PYCR1	30 kDa protein	100.0%	4.5	1	1	2	5	595,624	519,474	582,691	671,424	94,613	30,636	64,987	12,588	35.5	13.2	24.9	4.2	-1.1	0.5	-1.0	0.9	1.1	0.5	1.1	0.4	1.3	0.002	1.2	0.2
IPI00922289	PYCR1	cDNA FLJ56284, moderately similar to Pyrroline-5-carboxylate reductase 1	100.0%	5.4	1	1	2	5	595,624	519,474	582,691	671,424	94,613	30,636	64,987	12,588	35.5	13.2	24.9	4.2	-1.1	0.5	-1.0	0.9	1.1	0.5	1.1	0.4	1.3	0.002	1.2	0.2
IPI00470610	PYCR2	Pyrroline-5-carboxylate reductase 2	100.0%	4.1	1	1	2	5	595,624	519,474	582,691	671,424	94,613	30,636	64,987	12,588	35.5	13.2	24.9	4.2	-1.1	0.5	-1.0	0.9	1.1	0.5	1.1	0.4	1.3	0.002	1.2	0.2
IPI00747534	PYCR2	Pyrroline-5-carboxylate reductase	100.0%	4.1	1	1	2	5	595,624	519,474	582,691	671,424	94,613	30,636	64,987	12,588	35.5	13.2	24.9	4.2	-1.1	0.5	-1.0	0.9	1.1	0.5	1.1	0.4	1.3	0.002	1.2	0.2
IPI00908985	PYCR2	cDNA FLJ54750, moderately similar to Pyrroline-5-carboxylate reductase 2	100.0%	3.6	1	1	2	5	595,624	519,474	582,691	671,424	94,613	30,636	64,987	12,588	35.5	13.2	24.9	4.2	-1.1	0.5	-1.0	0.9	1.1	0.5	1.1	0.4	1.3	0.002	1.2	0.2
				SLLINAVEASCIR	2	100.0%	2																									
IPI00470627	SHPRH	Uncharacterized protein	91.0%	1.3	1	1	1	4	3,178,043	3,369,755	2,943,805	3,705,450	255,259	212,224	169,605	152,293	18.0	14.1	12.9	9.2	1.1	0.6	-1.1	0.5	1.2	0.1	-1.1	0.2	1.1	0.2	1.3	0.01
IPI00470931	SHPRH	isoform 2 of E3 ubiquitin-protein ligase SHPRH	91.0%	2.4	1	1	1	4	3,178,043	3,369,755	2,943,805	3,705,450	255,259	212,224	169,605	152,293	18.0	14.1	12.9	9.2	1.1	0.6	-1.1	0.5	1.2	0.1	-1.1	0.2	1.1	0.2	1.3	0.01
IPI00746978	SHPRH	isoform 3 of E3 ubiquitin-protein ligase SHPRH	91.0%	1.3	1	1	1	4	3,178,043	3,369,755	2,943,805	3,705,450	255,259	212,224	169,605	152,293	18.0	14.1	12.9	9.2	1.1	0.6	-1.1	0.5	1.2	0.1	-1.1	0.2	1.1	0.2	1.3	0.01
IPI00845497	SHPRH	isoform 1 of E3 ubiquitin-protein ligase SHPRH	91.0%	1.3	1	1	1	4	3,178,043	3,369,755	2,943,805	3,705,450	255,259	212,224	169,605	152,293	18.0	14.1	12.9	9.2	1.1	0.6	-1.1	0.5	1.2	0.1	-1.1	0.2	1.1	0.2	1.3	0.01
				GHGFSGTFTLGKNYKEEDICDK	3	88.7%	1																									
IPI00470658	NRNPA3;HNRNPA3F	FBRNP	100.0%	8.6	2	2	4	1	2,680,446	2,511,986	2,462,356	2,775,742	125,217	115,100	125,070	128,542	10.5	10.3	11.4	10.4	-1.1	0.4	-1.1	0.3	1.0	0.6	-1.0	0.8	1.1	0.2	1.1	0.1
				EDSVKPGAHLTVK	2	100.0%	2																									
				IETIEVMEDR	2	100.0%	2																									
IPI00470779	TXLNA	Alpha-taxilin	96.2%	6.6	1	1	1	1	1,240,478	1,303,982	1,487,179	1,263,189	313,887	277,501	211,382	199,426	56.6	47.6	31.8	35.3	1.1	0.9	1.2	0.5	1.0	1	1.1	0.6	-1.0	0.9	-1.2	0.5
				SSPGQPEAGPEGAQERPSQAAPAVEAEGPGSSQAPR	3	96.2%	1																									
IPI00470791	ADI1	isoform 2 of 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	99.5%	6.9	1	1	1	2	2,108,160	2,048,175	2,125,240	1,976,235	101,275	63,543	199,163	165,325	10.7	6.9	21.0	18.7	-1.0	0.6	1.0	0.9	-1.1	0.5	1.0	0.7	-1.0	0.7	-1.1	0.6
IPI00651738	ADI1	isoform 1 of 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	99.5%	6.7	1	1	1	2	2,108,160	2,048,175	2,125,240	1,976,235	101,275	63,543	199,163	165,325	10.7	6.9	21.0	18.7	-1.0	0.6	1.0	0.9	-1.1	0.5	1.0	0.7	-1.0	0.7	-1.1	0.6
				NYSWMDIITICK	2	99.5%	1																									
IPI00470805	MDC1	isoform 2 of Mediator of DNA damage checkpoint protein 1	94.6%	0.6	1	1	1	4	854,100	818,065	785,198	946,723	49,102	33,639	53,820	26,202	12.9	9.2	15.3	6.2	-1.0	0.6	-1.1	0.4	1.1	0.1	-1.0	0.6	1.2	0.02	1.2	0.03
IPI00552897	MDC1	isoform 1 of Mediator of DNA damage checkpoint protein 1	94.6%	0.5	1	1	1	4	854,100	818,065	785,198	946,723	49,102	33,639	53,820	26,202	12.9	9.2	15.3	6.2	-1.0	0.6	-1.1	0.4	1.1	0.1	-1.0	0.6	1.2	0.02	1.2	0.03
IPI00641106	MDC1	227 kDa protein	94.6%	0.5	1	1	1	4	854,100	818,065	785,198	946,723	49,102	33,639	53,820	26,202	12.9	9.2	15.3	6.2	-1.0	0.6	-1.1	0.4	1.1	0.1	-1.0	0.6	1.2	0.02	1.2	0.03
IPI00937211	MDC1	cDNA FLJ51571, moderately similar to Mediator of DNA damage checkpoint protein	94.6%	0.7	1	1	1	4	854,100	818,065	785,198	946,723	49,102	33,639	53,820	26,202	12.9	9.2	15.3	6.2	-1.0	0.6	-1.1	0.4	1.1	0.1	-1.0	0.6	1.2	0.02	1.2	0.03
				TPETLVPTAPK	2	80.3%	1																									
IPI00470891	CSDE1	isoform Long of Cold shock domain-containing protein E1	100.0%	3.9	3	3	3	5	4,404,378	4,670,440	4,185,504	4,784,558	192,093	178,654	318,287	249,663	9.8	8.6	17.0	11.7	1.1	0.3	-1.1	0.6	1.1	0.3	-1.1	0.2	1.0	0.7	1.1	0.2
IPI00844264	CSDE1	Putative uncharacterized protein DKFZp779B0247	100.0%	3.7	3	3	3	5	4,404,378	4,670,440	4,185,504	4,784,558	192,093	178,654	318,287	249,663	9.8	8.6	17.0	11.7	1.1	0.3	-1.1	0.6	1.1	0.3	-1.1	0.2	1.0	0.7	1.1	0.2
IPI00873244	CSDE1	isoform Short of Cold shock domain-containing protein E1	100.0%	4.0	3	3	3	5	4,404,378	4,670,440	4,185,504	4,784,558	192,093	178,654	318,287	249,663	9.8	8.6	17.0	11.7	1.1	0.3	-1.1	0.6	1.1	0.3	-1.1	0.2	1.0	0.7	1.1	0.2
IPI00973794	CSDE1	cold shock domain-containing protein E1 isoform 3	100.0%	3.8	3	3	3	5	4,404,378	4,670,440	4,185,504	4,784,558	192,093	178,654	318,287	249,663	9.8	8.6	17.0	11.7	1.1	0.3	-1.1	0.6	1.1	0.3	-1.1	0.2	1.0	0.7	1.1	0.2
IPI00978608	CSDE1	Uncharacterized protein	100.0%	4.6	3	3	3	5	4,404,378	4,670,440	4,185,504	4,784,558	192,093	178,654	318,287	249,663	9.8	8.6	17.0	11.7	1.1	0.3	-1.1	0.6	1.1	0.3	-1.1	0.2	1.0	0.7	1.1	0.2
				GPDNSMGFGAER	2	99.7%	1																									
				NQNDPLPGR	2	97.7%	1																									
				VTLLEGDHVR	2	87.2%	1																									
IPI00983353	PPP2R2A	CDNA FLJ26613 fis, clone MPB05565, highly similar to Serine/threonine protein pho	100.0%	3.1	1	1	2	2	96,384	59,162	75,573	98,261	12,632	6,128	11,800	15,196	29.3	23.2	34.9	34.6	-1.6	0.03	-1.3	0.3	1.0	0.9	1.3	0.3	1.7	0.04	1.3	0.3
IPI00470920	PPP2R2D	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform	100.0%	3.1	1	1	2	2	96,384	59,162	75,573	98,261	12,632	6,128	11,800	15,196	29.3	23.2	34.9	34.6	-1.6	0.03	-1.3	0.3	1.0	0.9	1.3	0.3	1.7	0.04	1.3	0.3
				SFFSEIISSISDVK	2	100.0%	2																									
IPI00471928	ATP5A1	ATP synthase subunit alpha	100.0%	44.5	17	18	26	1	40,820,246	41,264,368	40,349,055	45,929,814	3,791,423	1,105,427	2,983,511	1,574,631	20.8	6.0	16.5	7.7	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.04	1.1	0.1
				APGIIPR	2	99.6%	1																									
				AVDSLVPIGR	2	99.9%	1																									
				EIVTNFLAGFEA	2	100.0%	1																									
				EVAAFAQFGSDLDAATQQLLSR	2	100.0%	2																									
				EVAAFAQFGSDLDAATQQLLSR	3	100.0%	2																									
				FENAFLSHVVSQHQALLGTIR	3	100.0%	2																									
				GIRPAINVGLSVSR	2	97.9%	1																									
				GMSLNLEPDNVGVVVFGNDK	2	100.0%	2																									
				HALIIYDDLSK	2	100.0%	2																									
				ILGADTSVDLEETGR	2	100.0%	2																									
				LELAQYR	2	87.8%	1																									
				LKEIVTNFLAGFEA	2	100.0%	2																									
				NVQAEEMVEFSSGLK	2	100.0%	1																									
				QGQYSPMAIEEQVAVIYAGVR	2	97.5%	1																									
				RLTDADAMK	2	99.9%	1																									
				TGAIVDVPVGEELLGR	2	100.0%	2																									
				VLSIGDGIAR	2	100.0%	1																									
				VVDALGNAIDGK	2	100.0%	1																									
IPI00472003	BID	isoform 4 of BH3-interacting domain death agonist	100.0%	15.2	1	1	1	1	143,163	99,169	115,862	146,319	5,847	6,300	10,539	10,990	9.1	14.2	20.3	16.8	-1.4	0.0009	-1.2	0.05	1.0	0.8	1.2	0.2	1.5	0.006	1.3	0.08
				DLATALEQLLQAYPR	3	100.0%	1																									
IPI00472075	DENND2A	isoform 1 of DENN domain-containing protein 2A	93.6%	2.1	1	1	1	4	1,352,853	1,470,290	1,935,990	1,709,408	352,818	361,358	273,343	261,989	58.3	55.0	31.6	34.3	1.1	0.8	1.4	0.2	1.3	0.4	1.3	0.3	1.2	0.6	-1.1	0.6
IPI00761166	DENND2A	isoform 2 of DENN domain-containing protein 2A	93.6%	2.6	1	1	1	4	1,352,853	1,470,290	1,935,990	1,709,408	352,818	361,358	273,343	261,989	58.3	55.0	31.6	34.3	1.1	0.8	1.4	0.2	1.3	0.4	1.3	0.3	1.2	0.6	-1.1	0.6
IPI00910069	DENND2A	cDNA FLJ54496, highly similar to DENN domain-containing protein 2A	93.6%	3.1	1	1	1	4	1,352,853	1,470,290	1,935,990	1,709,408	352,818	361,358	273,343	261,989	58.3	55.0	31.6	34.3	1.1	0.8	1.4	0.2	1.3	0.4	1.3	0.3	1.2	0.6	-1.1	0.6
IPI00945161	DENND2A	97 kDa protein	93.6%	2.4	1	1	1	4	1,352,853	1,470,290	1,935,990	1,709,408	352,818	361,358	273,343	261,989	58.3	55.0	31.6	34.3	1.1	0.8	1.4	0.2	1.3	0.4	1.3	0.3	1.2	0.6	-1.1	0.6
				GAVNVGGQDPEPGQDLSQPER	2	93.6%	1																									
IPI00472119	-	30 kDa protein	100.0%	20.1	4	4	4	1	7,014,969	7,630,626	6,857,026	8,242,492	544,266	402,057	339,299	249,606	17.4	11.8	11.1	6.8	1.1	0.4	-1.0	0.8	1.2	0.07	-1.1	0.2	1.1	0.2	1.2	0.01
				ACQSIYPLHDVFVR	2	99.9%	1																									
				LITEDVQGK	2	96.4%	1																									
				LMELHGEGSSSGK	2	99.6%	1																									
				VFEVSLADLQNDEVAFR	2	100.0%	1																									
IPI00472164	WASF2	Wiskott-Aldrich syndrome protein family member 2	100.0%	7.0	3	3	3	1	8,715,388	10,125,851	9,430,450	10,001,968	697,825	402,067	420,953	501,960	17.9	8.9	10.0	11.2	1.2	0.1	1.1	0.4	1.1	0.2	-1.1	0.3	-1.0	0.9	1.1	0.4
				DVVGNDVATILSR	2	99.8%	1																									
				FYTDPSYFFDLWK	2	100.0%	1																									
				MGQEFVESK	2	95.2%	1																									
IPI00472981	CTNNBL1	cDNA FLJ53492, highly similar to Beta-catenin-like protein 1	95.9%	2.2	1	1	1	3	669,763	728,570	902,523	865,763	53,930	60,226	110,503	93,512	18.0	18.5	27.4	24.2	1.1	0.5	1.3	0.09	1.3	0.1	1.2	0.2	1.2	0.3	-1.0	0.8
IPI00645320	CTNNBL1	isoform 3 of Beta-catenin-like protein 1	95.9%	3.9	1	1	1	3	669,763	728,570	902,523	865,763	53,930	60,226	110,503	93,512	18.0	18.5	27.4	24.2	1.1	0.5	1.3	0.09	1.3	0.1	1.2	0.2	1.2	0.3	-1.0	0.8
IPI00844214	CTNNBL1	isoform 1 of Beta-catenin-like protein 1	95.9%	2.1	1	1	1	3	669,763	728,570	902,523	865,763	53,930	60,226	110,503	93,512	18.0	18.5	27.4	24.2	1.1	0.5	1.3	0.09	1.3	0.1	1.2	0.2	1.2	0.3	-1.0	0.8
				GEGLQLMNLMLR	2	94.7%	1																									
IPI00473014	DSTN	Destrin	100.0%	34.6	5	5	6	2	5,969,036	6,075,337	5,738,397	6,791,649	388,382	170,051	292,114	275,326	14.6	6.3	11.4	9.1	1.0	0.8	-1.0	0.6	1.1	0.1	-1.1	0.3	1.1	0.06	1.2	0.03
IPI00845388	DSTN	destrin isoform b	100.0%	38.5	5	5	6	2	5,969,036	6,075,337	5,738,397	6,791,649	388,382	170,051	292,114	275,326	14.6	6.3	11.4	9.1	1.0	0.8	-1.0	0.6	1.1	0.1	-1.1	0.3	1.1	0.06	1.2	0.03
				HECQANGPEDLNR	2	97.5%	1																									
				HFVGMLPEK	2	99.9%	1																									
				KEELMFFLWAPELAPLK	3	99.3%	1																									
				MIYASSK	1	100.0%	1																									
				YALYDASFETK	2	100.0%	2																									
IPI00473047	PRKAG1	cDNA FLJ40287 fis, clone TESTI2027909, highly similar to 5'-AMP-ACTIVATED PR	99.6%	5.6	1	1	1	2	136,677	204,937	232,599	243,020	6,506	48,460	64,850	35,468	10.6	52.9	62.3	32.6	1.5	0.2	1.7	0.2	1.8	0.04	1.1	0.7	1.2	0.5	1.0	0.9
IPI00883914	PRKAG1	5'-AMP-activated protein kinase subunit gamma-1 isoform 2	99.6%	7.7	1	1	1	2	136,677	204,937	232,599	243,020	6,506	48,460	64,850	35,468	10.6	52.9	62.3	32.6	1.5	0.2	1.7	0.2	1.8	0.04	1.1	0.7	1.2	0.5	1.0	0.9
				GIVSLSDILQALVLTGGEK	2	99.6%	1																									
IPI00473136	CTNNA1	isoform 2 of Catenin alpha-1	100.0%	13.7	8	8	9	2	6,318,643	6,466,876	6,397,363	7,360,205	542,925	306,154	366,097	205,146	19.2	10.6	12.8	6.2	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.9	1.1	0.04	1.2	0.05
IPI00953077	CTNNA1	Uncharacterized protein	100.0%	13.7	8	8	9	2	6,318,643	6,466,876	6,397,363	7,360,205	542,925	306,154	366,097	205,146	19.2	10.6	12.8	6.2	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.9	1.1	0.04	1.2	0.05
				ALLSAVTR	2	85.8%	1																									
				AVMDHVSDSFLETNVPLLVLIEAAK	3	99.9%	1																									
				IVAECNAVR	2	99.0%	1																									
				LESIISGAALMADSSCTR	2	100.0%	1																									
				LLILADMADVYK	2	100.0%	1																									
				QIIVDPLSFSEER	2	100.0%	2																									
				VLTDAVDDITSIDDFLAVSENHILEDVNK	3	100.0%	1																									
				WDDSGNDIIVLAK	2	100.0%	1																									
IPI00477173	PARP1	Poly (ADP-ribose) polymerase 1	100.0%	12.0	1	1	1	2	970,300	1,067,412	973,792	1,175,682	91,570	47,166	96,998	90,679	21.1	9.9	22.3	17.3	1.1	0.4	1.0	1	1.2	0.1	-1.1	0.4	1.1	0.3	1.2	0.2
IPI00478427	PARP1	Poly (ADP-ribose) polymerase 1	100.0%	8.4	1	1	1	2	970,300	1,067,412	973,792	1,175,682	91,570	47,166	96,998	90,679	21.1	9.9	22.3	17.3	1.1	0.4	1.0	1	1.2	0.1	-1.1	0.4	1.1	0.3	1.2	0.2
				MAIMVQSPMFDGK	2	99.9%	1																									
IPI00477245	LRRCC1	isoform 1 of Leucine-rich repeat and coiled-coil domain-containing protein 1	98.3%	2.1	1	1	1	2	319,737	292,058	365,425	392,253	36,666	46,140	41,368	23,968	25.6	35.3	25.3	13.7	-1.1	0.7	1.1	0.4	1.2	0.1	1.3	0.3	1.3	0.09	1.1	0.6
IPI00893851	LRRCC1	isoform 2 of Leucine-rich repeat and coiled-coil domain-containing protein 1	98.3%	2.2	1	1	1	2	319,737	292,058	365,425	392,253	36,666	46,140	41,368	23,968	25.6	35.3	25.3	13.7	-1.1	0.7	1.1	0.4	1.2	0.1	1.3	0.3	1.3	0.09	1.1	0.6
				LDDQILQLLNETSNSIDNVLEK	2	93.6%	1																									
IPI00477313	HNRNPC	isoform C2 of Heterogeneous nuclear ribonucleoproteins C1/C2	100.0%	36.0	9	10	13	2	15,406,574	15,749,473	14,788,215	17,756,216	1,486,312	730,666	1,076,322	644,984	21.6	10.4	16.3	8.1	1.0	0.8	-1.0	0.7	1.2	0.2	-1.1	0.5	1.1	0.07	1.2	0.05
IPI01013087	HNRNPC	cDNA, FLJ92712, highly similar to Homo sapiens heterogeneous nuclear ribonucleo	100.0%	36.3	9	10	13	2	15,406,574	15,749,473	14,788,215	17,756,216	1,486,312	730,666	1,076,322	644,984	21.6	10.4	16.3	8.1	1.0	0.8	-1.0	0.7	1.2	0.2	-1.1	0.5	1.1	0.07	1.2	0.05
				GFAFVQYVNER	2	100.0%	2																									
				KSDVEAIFSK	2	100.0%	1																									
				LKGDDLQAIKK	2	99.8%	1																									
				MIAGQVLDINLAAEPK	2	100.0%	1																									
				MIAGQVLDINLAAEPK	3	99.1%	1																									
				SAAEMYGSVTEHPSPSPLLSSSFDLDYDFQR	3	100.0%	1																									
				SDVEAIFSK	2	100.0%	1																									
				VDSLLENLEK	2	100.0%	2																									
				VFIGNLNTLVVK	2	100.0%	2																									
				VPPPPPIAR	2	88.7%	1																									
IPI00477505	ANKRD28	isoform 3 of Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subur	92.6%	1.8	1	1	1	5	374,572	381,842	344,140	341,166	36,955	45,043	12,370	30,720	22.1	26.4	8.0	20.1	1.0	0.9	-1.1	0.5	-1.1	0.5	-1.1	0.5	-1.1	0.5	-1.0	0.9
IPI00514769	ANKRD28	isoform 1 of Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subur	92.6%	1.8	1	1	1	5	374,572	381,842	344,140	341,166	36,955	45,043	12,370	30,720	22.1	26.4	8.0	20.1	1.0	0.9	-1.1	0.5	-1.1	0.5	-1.1	0.5	-1.1	0.5	-1.0	0.9
IPI00908701	ANKRD28	cDNA FLJ54784, highly similar to Ankyrin repeat domain-containing protein 28	92.6%	2.6	1	1	1	5	374,572	381,842	344,140	341,166	36,955	45,043	12,370	30,720	22.1	26.4	8.0	20.1	1.0	0.9	-1.1	0.5	-1.1	0.5	-1.1	0.5	-1.1	0.5	-1.0	0.9
IPI00981632	ANKRD28	isoform 2 of Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subur	92.6%	2.1	1	1	1	5	374,572	381,842	344,140	341,166	36,955	45,043	12,370	30,720	22.1	26.4	8.0	20.1	1.0	0.9	-1.1	0.5	-1.1	0.5	-1.1	0.5	-1.1	0.5	-1.0	0.9
IPI01009712	ANKRD28	isoform 4 of Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subur	92.6%	1.8	1	1	1	5	374,572	381,842	344,140	341,166	36,955	45,043	12,370	30,720	22.1	26.4	8.0	20.1	1.0	0.9	-1.1	0.5	-1.1	0.5	-1.1	0.5	-1.1	0.5	-1.0	0.9
				GAVTGHEECVDALLQHGAK	2	92.6%	1																									
IPI00477619	C19orf2	isoform 1 of Unconventional prefoldin RPB5 interactor	95.5%	1.7	1	1	1	3	1,392,180	1,492,003	1,539,050	1,541,187	93,456	95,268	154,751	61,196	15.0	14.3	22.5	8.9	1.1	0.5	1.1	0.4	1.1	0.2	1.0	0.8	1.0	0.7	1.0	1
IPI00743872	C19orf2	unconventional prefoldin RPB5 interactor isoform b	95.5%	1.8	1	1	1	3	1,392,180	1,492,003	1,539,050	1,541,187	93,456	95,268	154,751	61,196	15.0	14.3	22.5	8.9	1.1	0.5	1.1	0.4	1.1	0.2	1.0	0.8	1.0	0.7	1.0	1
IPI00939535	C19orf2	C19orf2 protein	95.5%	1.8	1	1	1	3	1,392,180	1,492,003	1,539,050	1,541,187	93,456	95,268	154,751	61,196	15.0	14.3	22.5	8.9	1.1	0.5	1.1	0.4	1.1	0.2	1.0	0.8	1.0	0.7	1.0	1
				VEFTEDLQK	2	82.3%	1																									
IPI00477856	NMT2	Glycylpeptide N-tetradecanoyltransferase	100.0%	5.0	2	2	2	1	5,316,968	5,786,741	5,277,944	5,969,309	549,636	393,184	395,449	184,999	23.1	15.2	16.8	6.9	1.1	0.5	-1.0	1	1.1	0.3	-1.1	0.4	1.0	0.7	1.1	0.2
				EVLEGIWEPK	2	96.0%	1																									
				GFDVFNALDLMENK	2	100.0%	1																									
IPI00477946	SRSF10	FUSIP1 protein	99.4%	23.2	1	1	1	1	511,530	420,421	566,562	541,877	41,790	44,785	27,616	30,745	18.3	23.8	10.9	12.7	-1.2	0.2	1.1	0.3	1.1	0.6	1.3	0.02	1.3	0.06	-1.0	0.6
				YGPIVDVYVPLDFYTR	2	99.4%	1																									
IPI00478003	A2M	Alpha-2-macroglobulin	100.0%	2.9	3	3	4	2	2,523,997	2,567,638	2,621,482	2,963,572	279,396	171,991	174,813	170,132	24.8	15.0	14.9	12.8	1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.1	1.1	0.2
IPI01010737	A2M	165 kDa protein	100.0%	2.8	3	3	4	2	2,523,997	2,567,638	2,621,482	2,963,572	279,396	171,991	174,813	170,132	24.8	15.0	14.9	12.8	1.0	0.9	1.0	0.8	1.2	0.2	1.0	0.8	1.2	0.1	1.1	0.2
				DMYSFLEDMGLK	2	99.5%	2																									

				LHTEAQIQEEGTVVELTGR	2	96.0%	1																									
				LPPNVVEESAR	2	98.7%	1																									
IPI00478230	RBBP5	cDNA FLJ59722, highly similar to Retinoblastoma-binding protein 5	99.9%	5.2	2	2	2	3	1,730,607	1,795,860	1,795,877	1,974,270	81,437	97,047	57,597	85,974	10.5	12.1	7.2	9.7	1.0	0.6	1.0	0.5	1.1	0.07	1.0	1	1.1	0.2	1.1	0.1
IPI00645975	RBBP5	isoform 2 of Retinoblastoma-binding protein 5	99.9%	6.0	2	2	2	3	1,730,607	1,795,860	1,795,877	1,974,270	81,437	97,047	57,597	85,974	10.5	12.1	7.2	9.7	1.0	0.6	1.0	0.5	1.1	0.07	1.0	1	1.1	0.2	1.1	0.1
IPI00978359	RBBP5	retinoblastoma-binding protein 5 isoform 3	99.9%	7.3	2	2	2	3	1,730,607	1,795,860	1,795,877	1,974,270	81,437	97,047	57,597	85,974	10.5	12.1	7.2	9.7	1.0	0.6	1.0	0.5	1.1	0.07	1.0	1	1.1	0.2	1.1	0.1
				GSCFLINTADRIIRVYDGR	2	99.3%	1																									
				TDSQDLVASFR	2	81.7%	1																									
IPI00478231	RHOA	Transforming protein RhoA	100.0%	26.4	4	4	5	1	7,875,913	8,119,820	7,760,813	9,196,969	736,542	471,832	521,234	442,589	20.9	13.0	15.0	10.8	1.0	0.8	-1.0	0.9	1.2	0.2	-1.0	0.6	1.1	0.1	1.2	0.07
				DQFPEVYVPTVFENYVADIEVDGK	2	94.7%	2																									
				HFCPNVPIILVGNK	2	99.4%	1																									
				HFCPNVPIILVGNKK	3	100.0%	1																									
				IGAFGYMECSAK	2	100.0%	1																									
IPI00478287	-	22 kDa protein	100.0%	5.7	1	1	2	3	852,313	819,343	780,733	939,415	88,994	63,703	47,576	60,334	23.4	17.4	13.6	14.4	-1.0	0.8	-1.1	0.5	1.1	0.4	-1.0	0.6	1.1	0.2	1.2	0.07
IPI00796554	-	18 kDa protein	100.0%	6.9	1	1	2	3	852,313	819,343	780,733	939,415	88,994	63,703	47,576	60,334	23.4	17.4	13.6	14.4	-1.0	0.8	-1.1	0.5	1.1	0.4	-1.0	0.6	1.1	0.2	1.2	0.07
IPI00798077	-	19 kDa protein	100.0%	6.5	1	1	2	3	852,313	819,343	780,733	939,415	88,994	63,703	47,576	60,334	23.4	17.4	13.6	14.4	-1.0	0.8	-1.1	0.5	1.1	0.4	-1.0	0.6	1.1	0.2	1.2	0.07
				DVNFEFPEFQL	2	100.0%	2																									
IPI00478572	COL4A4	Collagen alpha-4(IV) chain	100.0%	2.4	2	2	3	2	2,788,880	2,931,270	3,221,583	3,287,945	241,521	111,204	148,060	174,201	19.4	8.5	10.3	11.9	1.1	0.6	1.2	0.2	1.2	0.1	1.1	0.2	1.1	0.1	1.0	0.8
IPI00944490	COL4A4	164 kDa protein	100.0%	2.4	2	2	3	2	2,788,880	2,931,270	3,221,583	3,287,945	241,521	111,204	148,060	174,201	19.4	8.5	10.3	11.9	1.1	0.6	1.2	0.2	1.2	0.1	1.1	0.2	1.1	0.1	1.0	0.8
				DIPDPGPPGDQGPPGPDGPR	3	99.8%	2																									
				KGPPGPPGSSGPPGPAGATGR	2	99.7%	1																									
IPI00956049	-	cDNA FLJ55466, highly similar to G-rich sequence factor 1	99.5%	3.8	1	1	1	8	367,834	372,848	367,433	412,265	30,316	5,655	23,758	21,535	18.4	3.4	14.5	11.7	1.0	0.9	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00478657	GRSF1	G-rich sequence factor 1	99.5%	3.5	1	1	1	8	367,834	372,848	367,433	412,265	30,316	5,655	23,758	21,535	18.4	3.4	14.5	11.7	1.0	0.9	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00914953	GRSF1	G-rich sequence factor 1 isoform 2	99.5%	5.4	1	1	1	8	367,834	372,848	367,433	412,265	30,316	5,655	23,758	21,535	18.4	3.4	14.5	11.7	1.0	0.9	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00940450	GRSF1	cDNA FLJ42130 fis, clone TESTI2014716, highly similar to G-rich sequence factor 1	99.5%	3.7	1	1	1	8	367,834	372,848	367,433	412,265	30,316	5,655	23,758	21,535	18.4	3.4	14.5	11.7	1.0	0.9	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00965777	GRSF1	51 kDa protein	99.5%	3.8	1	1	1	8	367,834	372,848	367,433	412,265	30,316	5,655	23,758	21,535	18.4	3.4	14.5	11.7	1.0	0.9	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00966011	GRSF1	13 kDa protein	99.5%	14.9	1	1	1	8	367,834	372,848	367,433	412,265	30,316	5,655	23,758	21,535	18.4	3.4	14.5	11.7	1.0	0.9	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00979483	GRSF1	cDNA FLJ55240, highly similar to G-rich sequence factor 1	99.5%	4.3	1	1	1	8	367,834	372,848	367,433	412,265	30,316	5,655	23,758	21,535	18.4	3.4	14.5	11.7	1.0	0.9	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.2
IPI01012720	GRSF1	G-rich RNA sequence binding factor 1 isoform 2	99.5%	4.1	1	1	1	8	367,834	372,848	367,433	412,265	30,316	5,655	23,758	21,535	18.4	3.4	14.5	11.7	1.0	0.9	-1.0	1	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.2
				YVEVYEINNEDVDALMK	2	99.5%	1																									
IPI00479018	SDCBP	isoform 2 of Syntenin-1	100.0%	7.7	1	1	1	3	349,946	339,058	349,746	389,556	24,481	20,864	34,443	19,702	15.6	13.8	22.0	11.3	-1.0	0.7	-1.0	1	1.1	0.2	1.0	0.8	1.1	0.1	1.1	0.3
IPI00910606	SDCBP	Uncharacterized protein	100.0%	8.6	1	1	1	3	349,946	339,058	349,746	389,556	24,481	20,864	34,443	19,702	15.6	13.8	22.0	11.3	-1.0	0.7	-1.0	1	1.1	0.2	1.0	0.8	1.1	0.1	1.1	0.3
IPI00980584	SDCBP	Syntenin isoform 3	100.0%	7.2	1	1	1	3	349,946	339,058	349,746	389,556	24,481	20,864	34,443	19,702	15.6	13.8	22.0	11.3	-1.0	0.7	-1.0	1	1.1	0.2	1.0	0.8	1.1	0.1	1.1	0.3
				SIDNGIFVQLVQANSPASLVGLR	2	98.8%	1																									
IPI00479058	RPS15	40S ribosomal protein S15	99.6%	13.1	1	1	1	1	2,729,090	2,637,680	2,701,100	2,865,900	260,338	197,176	266,370	150,812	21.3	16.7	22.1	11.8	-1.0	0.8	-1.0	0.9	1.1	0.7	1.0	0.9	1.1	0.4	1.1	0.6
				DMIILPEMVGSMVGVYNGK	2	99.6%	1																									
IPI00479145	KRT19	Keratin, type I cytoskeletal 19	100.0%	81.0	35	48	80	1	644,695,657	646,605,130	628,152,071	744,549,846	########	########	########	########	15.3	7.9	16.7	6.8	1.0	1	-1.0	0.8	1.2	0.08	-1.0	0.7	1.2	0.02	1.2	0.06
				AALEDTLAETEAR	1	100.0%	1																									
				AALEDTLAETEAR	2	100.0%	3																									
				ALEAANGELEVK	1	100.0%	1																									
				ALEAANGELEVK	2	100.0%	3																									
				DAEAWFTSR	2	100.0%	1																									
				DKILGATIENSR	2	99.3%	1																									
				DYSHYYTTIQDLR	2	100.0%	2																									
				DYSHYYTTIQDLR	3	100.0%	1																									
				DYSHYYTTIQDLRDK	3	100.0%	2																									
				DYSHYYTTIQDLRDKILGATIENSR	3	100.0%	1																									
				EVAGHTEQLQMSR	3	81.3%	1																									
				FGAQLAHIQALISGIEAQLGDVR	2	100.0%	2																									
				FGAQLAHIQALISGIEAQLGDVR	3	100.0%	2																									
				FGPGVAFR	2	99.9%	2																									
				FVSSSSSGAYGGGYGGVLTASDGLLAGNEK	2	100.0%	2																									
				FVSSSSSGAYGGGYGGVLTASDGLLAGNEK	3	100.0%	1																									
				GQVGGQVSVEVDSAPGTDLAK	2	100.0%	3																									
				ILGATIENSR	1	98.5%	1																									
				ILGATIENSR	2	100.0%	2																									
				ILSDMR	2	99.6%	2																									
				IVLQIDNAR	2	99.9%	3																									
				KDAEAWFTSR	2	93.3%	1																									
				KNHEEEISTLR	3	99.8%	1																									
				LASYLDK	1	97.8%	1																									
				LEQEIATYR	2	100.0%	2																									
				LTMQNLNDR	2	97.8%	2																									
				MSVEADINGLR	2	100.0%	1																									
				MSVEADINGLRR	2	86.8%	1																									
				MSVEADINGLRR	3	97.9%	1																									
				NHEEEISTLR	2	100.0%	2																									
				QSSATSSFGGLGGGSVR	2	100.0%	3																									
				SLLEGQEDHYNNLSASK	2	100.0%	2																									
				SQYEVMAEQNR	2	100.0%	2																									
				SQYEVMAEQNRK	2	100.0%	2																									
				SQYEVMAEQNRK	3	98.4%	1																									
				SRLEQEIATYR	2	100.0%	2																									
				TDLEMQIEGLK	2	99.9%	1																									
				TDLEMQIEGLKEELAYLK	3	100.0%	2																									
				TDLEMQIEGLKEELAYLKK	2	100.0%	1																									
				TDLEMQIEGLKEELAYLKK	3	100.0%	2																									
				TEELNREVAGHTEQLQMSR	2	100.0%	1																									
				TEELNREVAGHTEQLQMSR	3	100.0%	2																									
				TKFETEQALR	2	99.8%	2																									
				TKFETEQALR	3	99.9%	2																									
				TLQGLEIELQSQLSMK	2	100.0%	2																									
				TLQGLEIELQSQLSMK	3	100.0%	1																									
				VLDELTLAR	1	100.0%	1																									
				VLDELTLAR	2	100.0%	2																									
IPI00479185	TPM3	tropomyosin alpha-3 chain isoform 4	100.0%	39.5	10	11	12	1	41,417,946	41,332,350	40,689,794	46,380,039	3,676,614	2,255,973	2,212,089	1,239,954	19.9	12.2	12.2	6.0	-1.0	1	-1.0	0.9	1.1	0.3	-1.0	0.8	1.1	0.09	1.1	0.06
				ALKDEEKMELQEIQLK	3	100.0%	1																									
				EQAEAEVASLNR	2	82.3%	1																									
				IQVLQQQADDAEER	2	100.0%	2																									
				IQVLQQQADDAEERAER	3	98.7%	1																									
				KIQVLQQQADDAEER	3	100.0%	1																									
				KLVIIEGDLER	2	100.0%	1																									
				KLVIIEGDLER	3	99.9%	1																									
				MELQEIQLK	2	86.0%	1																									
				MLDQTLLDLNEM	2	100.0%	1																									
				NVTNNLKSLEAQAEKYSQK	3	99.6%	1																									
				TIDDLEDKLK	2	99.7%	1																									
IPI00479186	PKM2	isoform M2 of Pyruvate kinase isozymes M1/M2	100.0%	69.3	39	52	83	1	619,767,662	631,831,618	603,928,857	703,396,378	########	########	########	########	19.0	9.8	14.8	7.2	1.0	0.8	-1.0	0.8	1.1	0.2	-1.0	0.6	1.1	0.08	1.2	0.06
				AEGSDVANAVLDGADCIMLSGETAK	2	100.0%	2																									
				AEGSDVANAVLDGADCIMLSGETAK	3	100.0%	1																									
				AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	3	100.0%	2																									
				AGKPVICATQMLESMIK	2	100.0%	2																									
				AGKPVICATQMLESMIK	3	100.0%	1																									
				APIIAVTR	1	100.0%	1																									
				APIIAVTR	2	100.0%	2																									
				CCSGAIIVLTK	2	100.0%	2																									
				CDENILWLDYK	2	100.0%	2																									
				DPVQEAWAEDVDLR	2	100.0%	2																									
				FDEILEASDGIMVAR	2	100.0%	1																									
				FGVEQDVDMVFASFIR	2	100.0%	2																									
				FGVEQDVDMVFASFIR	3	100.0%	2																									
				FGVEQDVDMVFASFIRK	3	100.0%	1																									
				GADFLVTEVENGGSLGSK	2	100.0%	3																									
				GADFLVTEVENGGSLGSKK	3	100.0%	2																									
				GDLGIEIPAEK	2	100.0%	2																									
				GDVVIVLTGWRPGSGFTNTMR	3	100.0%	1																									
				GDYPLEAVR	2	100.0%	2																									
				GIFPVLCKDPVQEAWAEDVDLR	2	100.0%	2																									
				GIFPVLCKDPVQEAWAEDVDLR	3	100.0%	2																									
				GSGTAEVELK	2	99.9%	1																									
				GSGTAEVELKK	2	100.0%	2																									
				GVNLPGAAVDLPAVSEKDIQDLK	3	100.0%	1																									
				ITLDNAYMEK	2	100.0%	2																									
				ITLDNAYMEKCDENILWLDYK	3	95.4%	1																									
				IYVDDGLISLQVK	1	100.0%	1																									
				IYVDDGLISLQVK	2	100.0%	3																									
				KGVNLPGAAVDLPAVSEK	2	100.0%	1																									
				KGVNLPGAAVDLPAVSEK	3	100.0%	1																									
				KGVNLPGAAVDLPAVSEKDIQDLK	3	100.0%	2																									
				LAPITSDPTEATAVGAVEASFK	2	100.0%	4																									
				LAPITSDPTEATAVGAVEASFK	3	100.0%	2																									
				LDIDSPPITAR	2	100.0%	2																									
				LNFSHGTHEYHAETIK	3	100.0%	2																									
				MQHLIAR	1	99.1%	1																									
				MQHLIAR	2	98.0%	1																									
				NTGIICTIGPASR	2	100.0%	2																									
				PVICATQMLESMIK	2	99.9%	1																									
				QKGADFLVTEVENGGSLGSK	3	100.0%	2																									
				QKGADFLVTEVENGGSLGSKK	3	99.5%	1																									
				RFDEILEASDGIMVAR	2	100.0%	2																									
				RFDEILEASDGIMVAR	3	100.0%	1																									
				SVETLKEMIK	2	89.1%	1																									
				SVETLKEMIK	3	95.2%	1																									
				TATESFASDPILYR	2	100.0%	1																									
				TATESFASDPILYRPVAVALDTK	2	100.0%	1																									
				TATESFASDPILYRPVAVALDTK	3	100.0%	1																									
				TATESFASDPILYRPVAVALDTKGPEIR	3	100.0%	1																									
				VFLAQK	1	89.3%	1																									

				VNFAMNVGK	1	97.7%	1																									
				VNFAMNVGK	2	100.0%	2																									
IPI00479217	HNRNPU	isoform Short of Heterogeneous nuclear ribonucleoprotein U	100.0%	23.0	15	17	23	3	32,717,463	33,362,472	32,572,222	35,926,015	2,444,186	1,244,528	1,991,252	1,095,878	16.7	8.3	13.7	6.8	1.0	0.8	-1.0	1	1.1	0.3	-1.0	0.7	1.1	0.2	1.1	0.2
IPI00644224	HNRNPU	cDNA FLJ54020, highly similar to Heterogeneous nuclear ribonucleoprotein U	100.0%	23.6	15	17	23	3	32,717,463	33,362,472	32,572,222	35,926,015	2,444,186	1,244,528	1,991,252	1,095,878	16.7	8.3	13.7	6.8	1.0	0.8	-1.0	1	1.1	0.3	-1.0	0.7	1.1	0.2	1.1	0.2
IPI00883857	HNRNPU	isoform Long of Heterogeneous nuclear ribonucleoprotein U	100.0%	22.4	15	17	23	3	32,717,463	33,362,472	32,572,222	35,926,015	2,444,186	1,244,528	1,991,252	1,095,878	16.7	8.3	13.7	6.8	1.0	0.8	-1.0	1	1.1	0.3	-1.0	0.7	1.1	0.2	1.1	0.2
				DCEVVMMIGLPGAGK	2	100.0%	1																									
				DIDIHEVR	2	95.4%	1																									
				DLPEHAVLK	2	98.1%	1																									
				EKPYFPIPEEYTFIQNVPLEDR	3	100.0%	1																									
				FIEIAAR	2	97.2%	1																									
				GYFEYIEENK	2	99.9%	1																									
				GYFEYIEENKYSR	2	100.0%	1																									
				GYFEYIEENKYSR	3	100.0%	1																									
				LLEQYKEESKK	2	99.9%	2																									
				LNTLLQRAPQCLGK	2	96.4%	1																									
				LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	3	100.0%	3																									
				MMVAGFK	2	99.4%	1																									
				NFILDQTNVSAAAQR	2	100.0%	2																									
				NFILDQTNVSAAAQR	3	100.0%	1																									
				NGQDLGVAFK	2	99.6%	2																									
				VSELKEELKK	2	98.9%	1																									
				YNILGTNTIMDK	2	100.0%	2																									
IPI00479262	EIF4G1	eukaryotic translation initiation factor 4 gamma 1 isoform 1	100.0%	13.5	15	15	16	9	5,942,667	6,263,864	5,877,179	6,893,082	519,519	330,204	338,010	159,054	19.6	11.8	12.9	5.2	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00552639	EIF4G1	isoform A of Eukaryotic translation initiation factor 4 gamma 1	100.0%	13.5	15	15	16	9	5,942,667	6,263,864	5,877,179	6,893,082	519,519	330,204	338,010	159,054	19.6	11.8	12.9	5.2	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00759560	EIF4G1	isoform C of Eukaryotic translation initiation factor 4 gamma 1	100.0%	14.3	15	15	16	9	5,942,667	6,263,864	5,877,179	6,893,082	519,519	330,204	338,010	159,054	19.6	11.8	12.9	5.2	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00798400	EIF4G1	isoform D of Eukaryotic translation initiation factor 4 gamma 1	100.0%	15.1	15	15	16	9	5,942,667	6,263,864	5,877,179	6,893,082	519,519	330,204	338,010	159,054	19.6	11.8	12.9	5.2	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00924828	EIF4G1	Uncharacterized protein	100.0%	13.9	15	15	16	9	5,942,667	6,263,864	5,877,179	6,893,082	519,519	330,204	338,010	159,054	19.6	11.8	12.9	5.2	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00927510	EIF4G1	Uncharacterized protein	100.0%	14.3	15	15	16	9	5,942,667	6,263,864	5,877,179	6,893,082	519,519	330,204	338,010	159,054	19.6	11.8	12.9	5.2	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00927765	EIF4G1	Uncharacterized protein	100.0%	15.0	15	15	16	9	5,942,667	6,263,864	5,877,179	6,893,082	519,519	330,204	338,010	159,054	19.6	11.8	12.9	5.2	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00955980	EIF4G1	isoform B of Eukaryotic translation initiation factor 4 gamma 1	100.0%	13.9	15	15	16	9	5,942,667	6,263,864	5,877,179	6,893,082	519,519	330,204	338,010	159,054	19.6	11.8	12.9	5.2	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00956559	EIF4G1	eukaryotic translation initiation factor 4 gamma 1 isoform 6	100.0%	13.5	15	15	16	9	5,942,667	6,263,864	5,877,179	6,893,082	519,519	330,204	338,010	159,054	19.6	11.8	12.9	5.2	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
				DITEEIMSGAR	2	99.8%	1																									
				EAVGDLLDAFK	2	100.0%	1																									
				FMLQDVLDLR	2	91.9%	1																									
				GGPGGELPR	2	87.6%	1																									
				HGVESTLER	2	90.6%	1																									
				IHNAENIQPGEQK	2	99.4%	1																									
				ITKPGSIDSNNQLFAPGGR	3	100.0%	1																									
				LQGINCGPDFTPSFANLGR	2	99.8%	1																									
				LTPQMFQQLMK	2	96.0%	1																									
				QVTQLAIDTEER	2	100.0%	2																									
				SDQWKPLNLEEK	3	96.3%	1																									
				TASTPTPPQTGGGLEPQANGETPQVAVIVRPDDR	3	100.0%	1																									
				TPLRPLDPTR	3	83.3%	1																									
				VEYTLGEESEAPGQR	2	93.0%	1																									
				VFDWIEANLSEQQIVSNTLVR	3	97.3%	1																									
IPI00479281	-	27 kDa protein	100.0%	4.6	1	1	2	2	1,155,995	1,138,460	1,150,080	1,291,968	179,199	51,813	92,859	26,212	34.7	10.2	18.1	4.5	-1.0	0.9	-1.0	1	1.1	0.5	1.0	0.9	1.1	0.03	1.1	0.2
IPI00798353	-	15 kDa protein	100.0%	7.7	1	1	2	2	1,155,995	1,138,460	1,150,080	1,291,968	179,199	51,813	92,859	26,212	34.7	10.2	18.1	4.5	-1.0	0.9	-1.0	1	1.1	0.5	1.0	0.9	1.1	0.03	1.1	0.2
				TYSYLTPDLWK	2	100.0%	2																									
IPI00479306	PSMB5	Proteasome subunit beta type-5	100.0%	28.1	6	6	6	1	15,717,021	14,588,801	15,614,239	17,456,864	664,086	499,034	634,030	749,372	9.5	7.7	9.1	9.6	-1.1	0.2	-1.0	0.9	1.1	0.1	1.1	0.2	1.2	0.01	1.1	0.1
				ATAGAYIASQTVK	2	100.0%	1																									
				HGVIVAADSR	2	98.9%	1																									
				KVIEINPYLLGTMAGGAADCSFWER	3	99.3%	1																									
				RGPGLYYVDSEGNR	3	89.4%	1																									
				VIEINPYLLGTMAGGAADCSFWER	2	99.8%	1																									
				VSSDNVADLHEK	3	99.0%	1																									
IPI00479722	PSME1	Proteasome activator complex subunit 1	100.0%	27.7	5	5	6	1	14,710,345	15,098,600	14,281,005	17,396,400	1,386,068	511,082	1,187,989	318,461	21.1	7.6	18.6	4.1	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.5	1.2	0.005	1.2	0.06
				IEDGNNFGVAVQEK	2	100.0%	2																									
				KISELDAFLKEPALNEANLSNLK	3	100.0%	1																									
				LEGFHTQISK	2	96.9%	1																									
				TENLLGSYFPK	2	100.0%	1																									
				VFELMTSLHTK	2	99.7%	1																									
IPI00479786	KHSRP	isoform 1 of Far upstream element-binding protein 2	100.0%	27.7	16	18	23	2	45,633,841	47,189,535	43,386,344	52,436,099	3,458,996	1,867,354	2,777,612	1,816,549	17.0	8.9	14.3	7.8	1.0	0.7	-1.1	0.6	1.1	0.1	-1.1	0.3	1.1	0.08	1.2	0.03
IPI00855957	KHSRP	isoform 2 of Far upstream element-binding protein 2	100.0%	27.8	16	18	23	2	45,633,841	47,189,535	43,386,344	52,436,099	3,458,996	1,867,354	2,777,612	1,816,549	17.0	8.9	14.3	7.8	1.0	0.7	-1.1	0.6	1.1	0.1	-1.1	0.3	1.1	0.08	1.2	0.03
				AINQQTGAFVEISR	2	100.0%	2																									
				DAFADAVQR	2	98.8%	1																									
				HSVGVVIGR	2	99.3%	1																									
				IAHIMGPPDR	3	98.9%	1																									
				IGGDAATTVNNSTPDFGFGGQK	2	100.0%	1																									
				IGGDAATTVNNSTPDFGFGGQK	3	100.0%	1																									
				IGGDAATTVNNSTPDFGFGGQKR	3	99.9%	1																									
				IGGGIDVPVPR	2	100.0%	2																									
				IGQQPQQPGAPPQQDYTK	2	99.5%	1																									
				IINDLLQSLR	2	100.0%	1																									
				LASQGDSISSQLGPIHPPPR	3	99.9%	1																									
				MILIQDGSQNTNVDKPLR	2	99.9%	1																									
				MILIQDGSQNTNVDKPLR	3	99.9%	1																									
				MMLDDIVSR	2	100.0%	2																									
				SVSLTGAPESVQK	2	100.0%	2																									
				TSMTEEYRVPDGMVGLIIGR	3	100.0%	1																									
				VPDGMVGLIIGR	2	100.0%	1																									
				VQQACEMVMDILR	2	100.0%	2																									
IPI00479877	ALDH9A1	4-trimethylaminobutyraldehyde dehydrogenase	100.0%	11.4	4	4	4	2	22,108,590	22,167,755	20,396,990	24,142,990	1,569,749	891,084	1,181,713	924,637	15.9	9.0	13.0	8.6	1.0	1	-1.1	0.4	1.1	0.3	-1.1	0.3	1.1	0.2	1.2	0.04
IPI00982620	ALDH9A1	cDNA FLJ61765, highly similar to 4-trimethylaminobutyraldehyde dehydrogenase	100.0%	13.9	4	4	4	2	22,108,590	22,167,755	20,396,990	24,142,990	1,569,749	891,084	1,181,713	924,637	15.9	9.0	13.0	8.6	1.0	1	-1.1	0.4	1.1	0.3	-1.1	0.3	1.1	0.2	1.2	0.04
				IGDPLLEDTR	2	98.6%	1																									
				REPLGVCVGIGAWNYPFQIASWK	3	88.6%	1																									
				VLCGGDIYVPEDPK	2	95.2%	1																									
				VSFTGSVPTGMK	2	99.9%	1																									
IPI00479905	NDUFB10	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	100.0%	20.9	3	3	3	1	20,934,180	20,288,730	21,609,555	21,482,660	614,912	578,508	333,940	833,356	6.6	6.4	3.5	8.7	-1.0	0.5	1.0	0.4	1.0	0.6	1.1	0.08	1.1	0.3	-1.0	0.9
				DYKVDQEIINIMQDR	3	96.7%	1																									
				EVEQFTQVAK	2	98.6%	1																									
				YQDLGAYSSAR	2	93.1%	1																									
IPI00479934	SCP2	non-specific lipid-transfer protein isoform 4 proprotein	100.0%	51.4	8	8	10	2	8,268,961	8,040,372	8,383,626	9,596,291	868,695	287,318	606,179	431,818	23.5	8.0	16.2	10.1	-1.0	0.8	1.0	0.9	1.2	0.2	1.0	0.6	1.2	0.02	1.1	0.1
IPI00943320	SCP2	isoform SCP2 of Non-specific lipid-transfer protein	100.0%	50.4	8	8	10	2	8,268,961	8,040,372	8,383,626	9,596,291	868,695	287,318	606,179	431,818	23.5	8.0	16.2	10.1	-1.0	0.8	1.0	0.9	1.2	0.2	1.0	0.6	1.2	0.02	1.1	0.1
				ADCTITMADSDFLALMTGK	2	100.0%	1																									
				EATWVVDVK	2	99.9%	2																									
				IGGIFAFK	2	100.0%	1																									
				KLEEEGEQFVK	2	100.0%	2																									
				KLEEEGEQFVKK	2	100.0%	1																									
				LQNLQLQPGNAK	2	100.0%	1																									
				LQNLQLQPGNAKL	2	99.5%	1																									
				MNPQSAFFQGK	2	99.4%	1																									
IPI00479988	RAB18	RAB18, member RAS oncogene family	99.5%	6.8	1	1	1	2	2,106,862	2,309,550	2,190,990	1,946,212	172,948	184,127	277,972	211,140	18.4	17.8	28.4	24.3	1.1	0.4	1.0	0.8	-1.1	0.6	-1.1	0.7	-1.2	0.2	-1.1	0.5
IPI00921855	RAB18	cDNA FLJ53088, highly similar to Ras-related protein Rab-18	99.5%	6.0	1	1	1	2	2,106,862	2,309,550	2,190,990	1,946,212	172,948	184,127	277,972	211,140	18.4	17.8	28.4	24.3	1.1	0.4	1.0	0.8	-1.1	0.6	-1.1	0.7	-1.2	0.2	-1.1	0.5
				NDIVNMLVGNK	2	97.9%	1																									
IPI00479997	STMN1	Stathmin	100.0%	18.1	2	2	2	5	7,172,480	6,892,820	6,725,020	8,083,460	444,190	311,366	451,985	476,125	13.9	10.1	15.0	13.2	-1.0	0.6	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.07	1.2	0.07
IPI00921996	STMN1	stathmin isoform b	100.0%	15.5	2	2	2	5	7,172,480	6,892,820	6,725,020	8,083,460	444,190	311,366	451,985	476,125	13.9	10.1	15.0	13.2	-1.0	0.6	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.07	1.2	0.07
IPI00642012	STMN1	Stathmin	100.0%	31.4	2	2	2	5	7,172,480	6,892,820	6,725,020	8,083,460	444,190	311,366	451,985	476,125	13.9	10.1	15.0	13.2	-1.0	0.6	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.07	1.2	0.07
IPI00643115	STMN1	Stathmin	100.0%	23.3	2	2	2	5	7,172,480	6,892,820	6,725,020	8,083,460	444,190	311,366	451,985	476,125	13.9	10.1	15.0	13.2	-1.0	0.6	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.07	1.2	0.07
IPI00744618	STMN1	Stathmin (Fragment)	100.0%	20.2	2	2	2	5	7,172,480	6,892,820	6,725,020	8,083,460	444,190	311,366	451,985	476,125	13.9	10.1	15.0	13.2	-1.0	0.6	-1.1	0.5	1.1	0.2	-1.0	0.8	1.2	0.07	1.2	0.07
				ASGQAFELILSPR	2	97.6%	1																									
				SKESVPEFPLSPPK	3	99.9%	1																									
IPI00513685	HEBP2	OTTHUMP00000017297	100.0%	12.9	1	1	1	1	978,925	1,077,250	928,465	1,136,050	35,294	78,241	25,555	31,369	8.1	16.2	6.2	6.2	1.1	0.3	-1.1	0.3	1.2	0.01	-1.2	0.1	1.1	0.5	1.2	0.0009
				APEDAGPQPGSYEIR	2	99.9%	1																									
IPI00513699	SERPINB6	Uncharacterized protein	100.0%	15.6	2	2	4	1	4,563,145	4,648,755	4,309,415	5,086,485	416,334	126,460	280,755	177,857	20.4	6.1	14.6	7.8	1.0	0.9	-1.1	0.6	1.1	0.3	-1.1	0.3	1.1	0.08	1.2	0.05
				ADFSGMSQTDLSLSK	2	100.0%	2																									
				GNTAAQMAQILSFNK	2	100.0%	2																									
IPI00513728	BAG6	HLA-B associated transcript 3	99.3%	2.5	1	1	1	4	1,629,255	1,787,455	1,180,632	1,217,616	185,719	196,133	197,400	187,917	25.5	24.5	37.4	34.5	1.1	0.6	-1.4	0.1	-1.3	0.2	-1.5	0.06	-1.5	0.07	1.0	0.9
IPI00796135	BAG6	Uncharacterized protein	99.3%	4.4	1	1	1	4	1,629,255	1,787,455	1,180,632	1,217,616	185,719	196,133	197,400	187,917	25.5	24.5	37.4	34.5	1.1	0.6	-1.4	0.1	-1.3	0.2	-1.5	0.06	-1.5	0.07	1.0	0.9
IPI00892541	BAG6	HLA-B associated transcript 3	99.3%	1.8	1	1	1	4	1,629,255	1,787,455	1,180,632	1,217,616	185,719	196,133	197,400	187,917	25.5	24.5	37.4	34.5	1.1	0.6	-1.4	0.1	-1.3	0.2	-1.5	0.06	-1.5	0.07	1.0	0.9
IPI00941157	BAG6	Uncharacterized protein	99.3%	3.6	1	1	1	4	1,629,255	1,787,455	1,180,632	1,217,616	185,719	196,133	197,400	187,917	25.5	24.5	37.4	34.5	1.1	0.6	-1.4	0.1	-1.3	0.2	-1.5	0.06	-1.5	0.07	1.0	0.9
				LLGNTFVALSDLR	2	98.6%	1																									
IPI00513881	LYPLA2	Lysophospholipase II	100.0%	31.5	3	3	3	2	5,485,744	5,446,207	5,231,091	6,037,821	676,801	172,306	541,069	184,314	27.6	7.1	23.1	6.8	-1.0	1	-1.0	0.8	1.1	0.5	-1.0	0.7	1.1	0.05	1.2	0.2
IPI00646978	LYPLA2	Uncharacterized protein	100.0%	24.5	3	3	3	2	5,485,744	5,446,207	5,231,091	6,037,821	676,801	172,306	541,069	184,314	27.6	7.1	23.1	6.8	-1.0	1	-1.0	0.8	1.1	0.5	-1.0	0.7	1.1	0.05	1.2	0.2
				DLAILQCHGELDPMVPVR	3	100.0%	1																									
				IPVTLNMK	2	99.6%	1																									
				MVMPSWFDLMGLSPDAPEDEAGIKK	3	100.0%	1																									
IPI00513927	GSTO1	glutathione S-transferase omega-1 isoform 2	100.0%	11.5	2	2	3	1	5,461,492	6,016,140	6,043,670	6,778,948	251,398	345,598	462,957	196,815	10.3	12.9	17.1	6.5	1.1	0.2	1.1	0.3	1.2	0.003	1.0	1	1.1	0.09	1.1	0.2
				GSAPPGPVPEGSIR	2	99.8%	2																									
				LNECVDHTPK	2	99.9%	1																									
IPI00514026	AGRN	Uncharacterized protein	100.0%	14.3	4	4	5	1	10,230,670	10,462,025	9,390,205	11,052,030	1,120,257	467,616	739,102	356,876	24.5	10.0	17.6	7.2	1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.3	1.1	0.3	1.2	0.08
				AAAVSSGFDGAIQLVSLGGR	2	100.0%	2																									
				GPSGLLLYNGQK	2	85.3%	1																									
				SAGDVDTLAFDGR	2	99.9%	1																									
				TEATQGLVLWSGK	2	98.4%	1																									
IPI00514032	CCT3	Chaperonin containing TCP1, subunit 3	100.0%	20.7	3	5	7	2	2,788,901	2,605,393	2,560,646	2,876,289	282,879	121,213	140,693	140,041	22.7	10.4	12.3	10.9	-1.1	0.6	-1.1	0.5	1.0	0.8	-1.0	0.8	1.1	0.2	1.1	0.2
IPI00975528	CCT3	Uncharacterized protein	100.0%	24.4	3	5	7	2	2,788,901	2,605,393	2,560,646	2,876,289	282,879	121,213	140,693	140,041	22.7	10.4	12.3	10.9	-1.1	0.6	-1.1	0.5	1.0	0.8	-1.0	0.8	1.1	0.2	1.1	0.2
				IPGGIIEDSCVLR	2	100.0%	1																									
				ISIPVDISDSDMMLNIINSSITTK	2	100.0%	2																									
				ISIPVDISDSDMMLNIINSSITTK	3	99.9%	1																									
				MLLDPMGGIVMTNDGNAILR	2	100.0%	2																									
				MLLDPMGGIVMTNDGNAILR	3	100.0%	1																									
IPI00514038	CTNNA2	isoform 6 of Catenin alpha-2	100.0%	1.9	1	1	1	2	1,759,975	1,650,250	1,696,258	1,698,492	290,514	102,119	199,290	103,594	36.9	13.8	26.3	13.6	-1.1	0.7	-1.0	0.9	-1.0	0.8	1.0	0.8	1.0	0.7	1.0	1
IPI00944563	CTNNA2	isoform 4 of Catenin alpha-2	100.0%	2.1	1	1	1	2	1,759,975	1,650,250	1,696,258	1,698,492	290,514	102,119	199,290	103,594	36.9	13.8	26.3	13.6	-1.1	0.7	-1.0	0.9	-1.0	0.8	1.0	0.8	1.0	0.7	1.0	1
				AIMAQLPQEEK	2	93.7%	1																									
IPI00514049	CMPK1	Cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	100.0%	13.7	2	3	5	2	9,284,735	9,216,068	9,473,810	10,296,635	762,420	163,374	377,646	411,143	18.4	4.0	8.9	8.9	-1.0	0.9	1.0	0.8	1.1	0.3	1.0	0.5	1.1	0.04	1.1	0.2
IPI00514929	CMPK1	cDNA FLJ52483, highly similar to Homo sapiens cytidylate kinase (CMPK), mRNA	100.0%	13.6	2	3	5	2	9,284,735	9,216,068	9,473,810	10,296,635	762,420	163,374	377,646	411,143	18.4	4.0	8.9	8.9	-1.0	0.9	1.0	0.8	1.1	0.3	1.0	0.5	1.1	0.04	1.1	0.2

				NQDNLQGWNK	2	100.0%	2																									
				YGYTHLSAGELLR	2	100.0%	2																									
				YGYTHLSAGELLR	3	100.0%	1																									
IPI00514127	HDGF	hepatoma-derived growth factor isoform b	100.0%	38.7	6	9	9	3	16,687,010	15,791,580	16,153,732	19,114,208	1,661,126	309,256	997,806	411,714	22.3	4.4	13.8	4.8	-1.1	0.6	-1.0	0.8	1.1	0.2	1.0	0.7	1.2	0.0002	1.2	0.03
IPI00514330	HDGF	hepatoma-derived growth factor isoform c	100.0%	42.5	6	9	9	3	16,687,010	15,791,580	16,153,732	19,114,208	1,661,126	309,256	997,806	411,714	22.3	4.4	13.8	4.8	-1.1	0.6	-1.0	0.8	1.1	0.2	1.0	0.7	1.2	0.0002	1.2	0.03
IPI00643908	HDGF	cDNA FLJ53700, highly similar to Hepatoma-derived growth factor	100.0%	46.1	6	9	9	3	16,687,010	15,791,580	16,153,732	19,114,208	1,661,126	309,256	997,806	411,714	22.3	4.4	13.8	4.8	-1.1	0.6	-1.0	0.8	1.1	0.2	1.0	0.7	1.2	0.0002	1.2	0.03
				DLFPYEESKEK	2	98.3%	1																									
				EAENPEGEEKEAATLEVERPLPMEVEK	3	100.0%	1																									
				GFSEGLWEIENNPTVK	2	100.0%	1																									
				GFSEGLWEIENNPTVK	3	100.0%	1																									
				GPPQEEEEEEDEEEEATKEDAEAPGIR	3	100.0%	1																									
				KGFSEGLWEIENNPTVK	2	100.0%	1																									
				KGFSEGLWEIENNPTVK	3	100.0%	1																									
				YQVFFFGTHETAFLGPK	2	100.0%	1																									
				YQVFFFGTHETAFLGPK	3	99.9%	1																									
IPI00514153	TMTC4	isoform 2 of Transmembrane and TPR repeat-containing protein 4	90.7%	3.9	1	1	1	4	400,270	428,485	457,209	453,603	42,603	60,778	36,615	37,769	23.8	31.7	17.9	18.6	1.1	0.7	1.1	0.3	1.1	0.4	1.1	0.7	1.1	0.7	-1.0	0.9
IPI00646732	TMTC4	isoform 1 of Transmembrane and TPR repeat-containing protein 4	90.7%	3.2	1	1	1	4	400,270	428,485	457,209	453,603	42,603	60,778	36,615	37,769	23.8	31.7	17.9	18.6	1.1	0.7	1.1	0.3	1.1	0.4	1.1	0.7	1.1	0.7	-1.0	0.9
IPI00953037	TMTC4	isoform 3 of Transmembrane and TPR repeat-containing protein 4	90.7%	3.2	1	1	1	4	400,270	428,485	457,209	453,603	42,603	60,778	36,615	37,769	23.8	31.7	17.9	18.6	1.1	0.7	1.1	0.3	1.1	0.4	1.1	0.7	1.1	0.7	-1.0	0.9
IPI00953129	TMTC4	cDNA FLJ55995, weakly similar to Homo sapiens transmembrane and tetratricopept	90.7%	3.8	1	1	1	4	400,270	428,485	457,209	453,603	42,603	60,778	36,615	37,769	23.8	31.7	17.9	18.6	1.1	0.7	1.1	0.3	1.1	0.4	1.1	0.7	1.1	0.7	-1.0	0.9
				EGAHSSTFWVLLSIFLGAVAMLCK	3	90.7%	1																									
IPI00514154	UCHL3	Uncharacterized protein	100.0%	8.8	2	2	3	1	4,218,405	3,985,295	3,659,445	4,921,085	140,565	558,458	341,240	63,856	7.5	31.3	20.9	2.9	-1.1	0.7	-1.2	0.2	1.2	0.002	-1.1	0.6	1.2	0.2	1.3	0.02
				FLEESVSMSPEER	2	100.0%	2																									
				YLENYDAIR	2	100.0%	1																									
IPI00514234	LAD1	Ladinin-1	100.0%	29.8	10	10	12	1	28,337,040	28,588,165	30,449,400	33,168,315	2,032,993	801,357	776,096	1,453,719	16.0	6.3	5.7	9.8	1.0	0.9	1.1	0.4	1.2	0.09	1.1	0.1	1.2	0.02	1.1	0.1
				GLPCTELFVAPVGVASK	2	100.0%	2																									
				GPWALEEESLVGREPEER	3	100.0%	2																									
				IPSKEEEADMSSPTQR	3	99.7%	1																									
				KDWSALSSLAR	2	95.3%	1																									
				LSGVVTSR	2	97.6%	1																									
				NLPSLAKQGASDPPTVASR	2	100.0%	1																									
				NSLSPVQATQKPLVSK	2	99.9%	1																									
				QVVEAAQAPIQER	2	100.0%	1																									
				RATASEQPLAQEPPASGGSPATTK	3	100.0%	1																									
				SLAPGMALGSGR	2	80.5%	1																									
IPI00514267	LYPLA2	Lysophospholipase II	100.0%	32.8	3	3	3	3	2,483,055	2,419,215	2,386,921	2,811,612	274,311	141,309	234,240	203,853	24.7	13.1	21.9	16.2	-1.0	0.8	-1.0	0.8	1.1	0.4	-1.0	0.9	1.2	0.2	1.2	0.2
IPI00514798	LYPLA2	Lysophospholipase II	100.0%	32.4	3	3	3	3	2,483,055	2,419,215	2,386,921	2,811,612	274,311	141,309	234,240	203,853	24.7	13.1	21.9	16.2	-1.0	0.8	-1.0	0.8	1.1	0.4	-1.0	0.9	1.2	0.2	1.2	0.2
IPI00644956	LYPLA2	Lysophospholipase II	100.0%	43.1	3	3	3	3	2,483,055	2,419,215	2,386,921	2,811,612	274,311	141,309	234,240	203,853	24.7	13.1	21.9	16.2	-1.0	0.8	-1.0	0.8	1.1	0.4	-1.0	0.9	1.2	0.2	1.2	0.2
				ETAAVIFLHGLGDTGHSWADALSTIR	3	89.0%	1																									
				IPVTLNMK	2	99.6%	1																									
				MVMPSWFDLMGLSPDAPEDEAGIKK	3	100.0%	1																									
IPI00514310	TSTD1	isoform 4 of Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein	99.1%	8.2	1	1	1	4	1,415,723	1,653,933	1,395,883	2,022,968	107,607	107,086	165,538	97,091	17.0	14.5	26.5	10.7	1.2	0.2	-1.0	0.9	1.4	0.003	-1.2	0.2	1.2	0.03	1.4	0.01
IPI00607735	TSTD1	isoform 2 of Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein	99.1%	13.5	1	1	1	4	1,415,723	1,653,933	1,395,883	2,022,968	107,607	107,086	165,538	97,091	17.0	14.5	26.5	10.7	1.2	0.2	-1.0	0.9	1.4	0.003	-1.2	0.2	1.2	0.03	1.4	0.01
IPI00645501	TSTD1	isoform 3 of Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein	99.1%	9.2	1	1	1	4	1,415,723	1,653,933	1,395,883	2,022,968	107,607	107,086	165,538	97,091	17.0	14.5	26.5	10.7	1.2	0.2	-1.0	0.9	1.4	0.003	-1.2	0.2	1.2	0.03	1.4	0.01
IPI00965497	TSTD1	isoform 1 of Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein	99.1%	8.7	1	1	1	4	1,415,723	1,653,933	1,395,883	2,022,968	107,607	107,086	165,538	97,091	17.0	14.5	26.5	10.7	1.2	0.2	-1.0	0.9	1.4	0.003	-1.2	0.2	1.2	0.03	1.4	0.01
				RGLQATQLAR	2	99.1%	1																									
IPI00514333	ANP32E	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member E	100.0%	21.5	2	2	2	2	2,435,324	2,672,206	2,435,672	2,554,017	292,877	173,472	193,569	221,353	26.9	14.5	17.8	19.4	1.1	0.5	1.0	1	1.0	0.8	-1.1	0.4	-1.0	0.7	1.0	0.7
IPI00910423	ANP32E	Uncharacterized protein	100.0%	19.4	2	2	2	2	2,435,324	2,672,206	2,435,672	2,554,017	292,877	173,472	193,569	221,353	26.9	14.5	17.8	19.4	1.1	0.5	1.0	1	1.0	0.8	-1.1	0.4	-1.0	0.7	1.0	0.7
				CPNLTYLNLSGNK	2	99.9%	1																									
				KLELSDNIISGGLEVLAEK	3	100.0%	1																									
IPI00514385	IARS	Isoleucyl-tRNA synthetase	100.0%	16.2	3	3	3	1	5,821,097	5,635,417	5,181,463	6,372,267	610,345	265,074	534,945	242,187	23.5	10.5	23.1	8.5	-1.0	0.8	-1.1	0.5	1.1	0.4	-1.1	0.5	1.1	0.07	1.2	0.08
				GSELEITLTR	2	99.8%	1																									
				LFLNETQTQEITEDIPVK	2	90.9%	1																									
				TESAVSQMQSVIELGR	2	100.0%	1																									
IPI00514386	AKNAD1	Chromosome 1 open reading frame 62	99.3%	2.5	1	1	1	6	1,510,787	2,089,917	2,108,657	1,958,115	536,193	725,788	313,998	542,841	79.4	77.7	33.3	62.0	1.4	0.5	1.4	0.4	1.3	0.6	1.0	1	-1.1	0.9	-1.1	0.8
IPI00514779	AKNAD1	isoform 1 of Protein AKNAD1	99.3%	2.2	1	1	1	6	1,510,787	2,089,917	2,108,657	1,958,115	536,193	725,788	313,998	542,841	79.4	77.7	33.3	62.0	1.4	0.5	1.4	0.4	1.3	0.6	1.0	1	-1.1	0.9	-1.1	0.8
IPI00644677	AKNAD1	isoform 4 of Protein AKNAD1	99.3%	2.4	1	1	1	6	1,510,787	2,089,917	2,108,657	1,958,115	536,193	725,788	313,998	542,841	79.4	77.7	33.3	62.0	1.4	0.5	1.4	0.4	1.3	0.6	1.0	1	-1.1	0.9	-1.1	0.8
IPI00827519	AKNAD1	isoform 3 of Protein AKNAD1	99.3%	2.8	1	1	1	6	1,510,787	2,089,917	2,108,657	1,958,115	536,193	725,788	313,998	542,841	79.4	77.7	33.3	62.0	1.4	0.5	1.4	0.4	1.3	0.6	1.0	1	-1.1	0.9	-1.1	0.8
IPI00978050	AKNAD1	isoform 2 of Protein AKNAD1	99.3%	4.3	1	1	1	6	1,510,787	2,089,917	2,108,657	1,958,115	536,193	725,788	313,998	542,841	79.4	77.7	33.3	62.0	1.4	0.5	1.4	0.4	1.3	0.6	1.0	1	-1.1	0.9	-1.1	0.8
IPI00982567	AKNAD1	cDNA, FLJ94377	99.3%	3.2	1	1	1	6	1,510,787	2,089,917	2,108,657	1,958,115	536,193	725,788	313,998	542,841	79.4	77.7	33.3	62.0	1.4	0.5	1.4	0.4	1.3	0.6	1.0	1	-1.1	0.9	-1.1	0.8
				AMHSETCGNTAVTIPLGK	2	99.3%	1																									
IPI00514496	RALY	Uncharacterized protein	100.0%	3.8	1	1	2	1	483,655	624,368	631,725	695,878	117,271	92,893	74,580	61,869	54.2	33.3	26.4	19.9	1.3	0.4	1.3	0.3	1.4	0.1	1.0	1	1.1	0.5	1.1	0.5
				LEQIAAEQK	2	98.9%	2																									
IPI00514549	PSMB7	Proteasome (Prosome, macropain) subunit, beta type, 7	91.8%	4.8	1	1	1	2	2,410,687	2,422,917	2,382,543	2,779,533	181,349	187,731	307,063	89,429	16.8	17.3	28.8	7.2	1.0	1	-1.0	0.9	1.2	0.1	-1.0	0.9	1.1	0.1	1.2	0.3
IPI00908513	PSMB7	cDNA FLJ60039, highly similar to Proteasome subunit beta type 7	91.8%	7.0	1	1	1	2	2,410,687	2,422,917	2,382,543	2,779,533	181,349	187,731	307,063	89,429	16.8	17.3	28.8	7.2	1.0	1	-1.0	0.9	1.2	0.1	-1.0	0.9	1.1	0.1	1.2	0.3
				DGIVLGADTR	2	91.8%	1																									
IPI00514737	PIK3C2B	Phosphoinositide-3-kinase, class 2, beta polypeptide	98.1%	10.4	1	1	1	1	3,219,430	3,357,660	3,181,930	3,423,890	469,840	177,426	307,899	288,263	32.6	11.8	21.6	18.8	1.0	0.8	-1.0	0.9	1.1	0.7	-1.1	0.6	1.0	0.8	1.1	0.6
				EPPYPRPAEPALELAGSK	3	98.1%	1																									
IPI00514742	HMGCL	Uncharacterized protein	100.0%	16.9	3	3	3	1	5,789,057	5,841,300	5,664,730	6,505,817	482,622	193,032	367,266	257,959	18.6	7.4	14.5	8.9	1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.7	1.1	0.07	1.1	0.1
				AAQSANISVR	2	99.3%	1																									
				EVVIFGAASELFTK	2	100.0%	1																									
				NINCSIEESFQR	2	99.9%	1																									
IPI00514834	HYI	Hydroxypyruvate isomerase homolog	97.4%	4.4	1	1	1	1	5,870,770	6,116,780	5,788,190	7,282,470	515,475	213,985	353,013	597,648	19.6	7.8	13.6	18.4	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.4	1.2	0.1	1.3	0.06
				LDMIHLMAGR	2	97.4%	1																									
IPI00514853	C9orf86	cDNA FLJ10322 fis, clone NT2RM2000522, weakly similar to SKIN SECRETORY P	100.0%	4.7	2	2	3	1	1,611,024	1,817,181	2,060,531	1,743,045	107,679	52,192	123,732	62,064	15.0	6.4	13.4	8.0	1.1	0.1	1.3	0.03	1.1	0.3	1.1	0.1	-1.0	0.4	-1.2	0.05
				FFNIPFLQLQR	2	100.0%	2																									
				TAADELEAFLGGGAPGGR	2	90.5%	1																									
IPI00514888	C9orf86	putative GTP-binding protein Parf isoform 4	100.0%	8.0	2	2	3	3	1,218,673	1,291,067	1,311,783	1,288,720	88,088	92,778	124,734	105,143	16.2	16.1	21.3	18.2	1.1	0.6	1.1	0.6	1.1	0.6	1.0	0.9	-1.0	1	-1.0	0.9
IPI00827825	C9orf86	isoform 5 of Putative GTP-binding protein Parf	100.0%	9.7	2	2	3	3	1,218,673	1,291,067	1,311,783	1,288,720	88,088	92,778	124,734	105,143	16.2	16.1	21.3	18.2	1.1	0.6	1.1	0.6	1.1	0.6	1.0	0.9	-1.0	1	-1.0	0.9
IPI00827874	C9orf86	isoform 4 of Putative GTP-binding protein Parf	100.0%	9.7	2	2	3	3	1,218,673	1,291,067	1,311,783	1,288,720	88,088	92,778	124,734	105,143	16.2	16.1	21.3	18.2	1.1	0.6	1.1	0.6	1.1	0.6	1.0	0.9	-1.0	1	-1.0	0.9
				LVGSDQAPGR	2	95.5%	1																									
				NIPAGLQSMNQALQR	2	100.0%	2																									
IPI00514894	KPNA6	Uncharacterized protein	95.8%	3.2	1	1	1	1	103,104	106,853	108,341	101,252	8,967	6,897	3,285	3,271	19.5	14.4	6.8	7.2	1.0	0.7	1.1	0.6	-1.0	0.9	1.0	0.9	-1.1	0.5	-1.1	0.2
				IQAVIDSGVCR	2	95.8%	1																									
IPI00514983	HSPH1	cDNA FLJ52364, highly similar to Heat-shock protein 105 kDa	100.0%	9.1	6	7	8	1	4,807,473	5,323,450	5,489,517	5,971,424	477,733	283,041	466,599	137,217	22.2	11.9	19.0	5.1	1.1	0.4	1.1	0.3	1.2	0.07	1.0	0.8	1.1	0.07	1.1	0.4
				AFNDPFIQK	2	97.4%	1																									
				DLLNMYIETEGK	2	100.0%	2																									
				IEVPLYSLLEQTHLK	3	100.0%	1																									
				NAVEEYVYEFR	2	99.6%	1																									
				SQFEELCAELLQK	2	93.7%	1																									
				VVNVELPIEANLVWQLGK	2	100.0%	1																									
				VVNVELPIEANLVWQLGK	3	99.9%	1																									
IPI00515014	GALE	UDP-galactose-4-epimerase	100.0%	6.5	1	1	1	1	1,018,883	1,171,033	1,105,527	1,385,923	125,704	107,128	98,331	90,184	27.6	20.5	19.9	14.6	1.1	0.4	1.1	0.6	1.4	0.05	-1.1	0.7	1.2	0.2	1.3	0.07
				MCEDLWR	2	99.9%	1																									
IPI00549189	THOP1	Thimet oligopeptidase	98.0%	2.2	1	1	1	1	5,711,960	6,490,720	5,884,190	7,028,870	308,078	402,592	486,944	133,061	12.1	13.9	18.5	4.2	1.1	0.2	1.0	0.8	1.2	0.004	-1.1	0.4	1.1	0.3	1.2	0.08
				TSQTVATFLDELAQK	2	96.6%	1																									
IPI00549343	VAMP3;TNFRSF9	Vesicle-associated membrane protein 3	100.0%	16.0	1	1	1	1	8,914,590	9,474,870	9,449,800	10,673,910	665,455	519,985	612,883	268,822	16.7	12.3	14.5	5.6	1.1	0.5	1.1	0.6	1.2	0.04	-1.0	1	1.1	0.07	1.1	0.1
				LQQTQNQVDEVVDIMR	2	100.0%	1																									
IPI00549467	NIT2	Omega-amidase NIT2	100.0%	8.0	3	3	4	1	13,316,768	13,434,808	12,889,313	14,729,158	962,437	522,531	666,532	506,376	16.2	8.7	11.6	7.7	1.0	0.9	-1.0	0.7	1.1	0.2	-1.0	0.5	1.1	0.1	1.1	0.06
				LALIQLQISSIK	2	100.0%	2																									
				RSDLYAVEMK	2	99.8%	1																									
				SDLYAVEMK	2	99.8%	1																									
IPI00549725	PGAM1	Phosphoglycerate mutase 1	100.0%	72.8	16	20	26	1	188,399,003	198,129,288	185,477,030	216,825,935	########	5,996,158	########	4,397,626	18.9	6.8	15.6	4.5	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.04	1.2	0.07
				ALPFWNEEIVPQIK	2	100.0%	2																									
				AMEAVAAQGK	1	100.0%	1																									
				AMEAVAAQGK	2	87.3%	1																									
				DAGYEFDICFTSVQK	2	94.9%	1																									
				FSGWYDADLSPAGHEEAK	2	100.0%	1																									
				FSGWYDADLSPAGHEEAK	3	100.0%	2																									
				FSGWYDADLSPAGHEEAKR	3	100.0%	2																									
				HGESAWNLENR	2	100.0%	2																									
				HLEGLSEEAIMELNLPTGIPIVYELDK	3	99.6%	1																									
				HYGGLTGLNK	2	99.9%	2																									
				HYGGLTGLNKAETAAK	3	99.6%	1																									
				NLKPIKPMQFLGDEETVR	3	100.0%	1																									
				RSYDVPPPPMEPDHPFYSNISK	3	100.0%	1																									
				RVLIAAHGNSLR	3	99.8%	1																									
				SYDVPPPPMEPDHPFYSNISK	2	100.0%	1																									
				SYDVPPPPMEPDHPFYSNISK	3	99.5%	1																									
				VLIAAHGNSLR	2	100.0%	2																									
				VLIAAHGNSLR	3	98.7%	1																									
				YADLTEDQLPSCESLK	2	97.9%	1																									
				YADLTEDQLPSCESLKDTIAR	2	88.3%	1																									
IPI00549730	APIP	Probable methylthioribulose-1-phosphate dehydratase	100.0%	20.3	3	3	3	3	4,369,587	4,451,430	3,943,723	4,756,230	335,031	244,264	349,370	116,188	17.1	12.3	19.8	5.5	1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.3	1.1	0.3	1.2	0.08
IPI00911064	APIP	cDNA FLJ58961, highly similar to APAF1-interacting protein	100.0%	18.9	3	3	3	3	4,369,587	4,451,430	3,943,723	4,756,230	335,031	244,264	349,370	116,188	17.1	12.3	19.8	5.5	1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.3	1.1	0.3	1.2	0.08
IPI00953224	APIP	Uncharacterized protein	100.0%	24.0	3	3	3	3	4,369,587	4,451,430	3,943,723	4,756,230	335,031	244,264	349,370	116,188	17.1	12.3	19.8	5.5	1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.3	1.1	0.3	1.2	0.08
				AAVMATLLFPGR	2	97.3%	1																									
				AKTMCECYDYLFDIAVSMKK	3	96.5%	1																									
				YDDMLVVPIIENTPEEK	2	99.5%	1																									
IPI00550020	PTMS	Parathymosin	100.0%	10.8	1	2	3	3	4,853,586	5,041,847	3,860,252	5,041,774	406,167	258,053	129,162	470,577	18.7	11.4	7.5	20.9	1.0	0.7	-1.3	0.07	1.0	0.8	-1.3	0.003	-1.0	1	1.3	0.06
IPI01009878	PTMS	12 kDa protein	100.0%	10.6	1	2	3	3	4,853,586	5,041,847	3,860,252	5,041,774	406,167	258,053	129,162	470,577	18.7	11.4	7.5	20.9	1.0	0.7	-1.3	0.07	1.0	0.8	-1.3	0.003	-1.0	1	1.3	0.06
IPI01015029	PTMS	6 kDa protein	100.0%	19.3	1	2	3	3	4,853,586	5,041,847	3,860,252	5,041,774	406,167	258,053	129,162	470,577	18.7	11.4	7.5	20.9	1.0	0.7	-1.3	0.07	1.0	0.8	-1.3	0.003	-1.0	1	1.3	0.06
				SVEAAAELSAK	1	100.0%	1																									
				SVEAAAELSAK	2	100.0%	2																									
IPI00550021	DRD43;RPL3;LOC653	60S ribosomal protein L3	100.0%	12.7	4	4	5	2	9,156,151	9,841,472	9,151,479	11,074,454	1,042,355	587,979	612,781	397,398	25.5	13.4	15.0	8.0	1.1	0.6	-1.0	1	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
IPI00651660	DRD43;RPL3;LOC653	60S ribosomal protein L3 isoform b	100.0%	14.4	4	4	5	2	9,156,151	9,841,472	9,151,479	11,074,454	1,042,355	587,979	612,781	397,398	25.5	13.4	15.0	8.0	1.1	0.6	-1.0	1	1.2	0.1	-1.1	0.4	1.1	0.1	1.2	0.03
				AGMTHIVR	2	96.6%	1																									
				HGSLGFLPR	2	100.0%	2																									
				NNASTDYDLSDK	2	100.0%	1																									
				SINPLGGFVHYGEVTNDFVMLK	3	100.0%	1																									
IPI00550069	RNH1	Ribonuclease inhibitor	100.0%	33.6	11	12	13	1	36,494,897	36,630,099	37,132,243	40,571,390	2,804,397	1,540,165	2,230,990	1,124,154	17.2	9.4	13.4	6.2	1.0	1	1.0	0.9	1.1	0.2	1.0	0.9	1.1	0.07	1.1	0.2
				ELCQGLGQPGSVLR	2	100.0%	1																									
				ELSLAGNELGDEGAR	2	100.0%	2																									
				ELTVSNNDINEAGVR	2	100.0%	1																									
				ESLKELSLAGNELGDEGAR	3	99.9%	1																									
				FLLELQISNNR	2	100.0%	1																									
				LDDCGLTEAR	2	100.0%	1																									
				LGDVGMAELCPGLLHPSSR	3	100.0%	1																									

				LLCETLLEPGCQLESLWVK	2	99.6%	1																									
				LLCETLLEPGCQLESLWVK	3	97.4%	1																									
				SNELGDVGVHCVLQGLQTPSCK	3	99.9%	1																									
				VNPALAELNLR	2	100.0%	1																									
				WAELLPLLQQCQVVR	2	100.0%	1																									
IPI00550181	CHMP2B	Charged multivesicular body protein 2b	94.1%	4.7	1	1	1	3	980,690	1,052,080	1,076,000	1,115,150	114,753	108,799	38,782	22,242	26.2	23.1	8.1	4.5	1.1	0.7	1.1	0.5	1.1	0.3	1.0	0.8	1.1	0.6	1.0	0.4
IPI00793098	CHMP2B	cDNA FLJ57117, highly similar to Charged multivesicular body protein 2b	94.1%	5.8	1	1	1	3	980,690	1,052,080	1,076,000	1,115,150	114,753	108,799	38,782	22,242	26.2	23.1	8.1	4.5	1.1	0.7	1.1	0.5	1.1	0.3	1.0	0.8	1.1	0.6	1.0	0.4
IPI00947040	CHMP2B	Uncharacterized protein	94.1%	5.5	1	1	1	3	980,690	1,052,080	1,076,000	1,115,150	114,753	108,799	38,782	22,242	26.2	23.1	8.1	4.5	1.1	0.7	1.1	0.5	1.1	0.3	1.0	0.8	1.1	0.6	1.0	0.4
				TLQTMQNFQK	2	94.1%	1																									
IPI00550212	CYFIP1	isoform 2 of Cytoplasmic FMR1-interacting protein 1	93.2%	1.7	1	1	1	3	409,450	342,861	519,266	380,560	48,752	26,746	78,158	36,942	26.6	17.4	33.7	21.7	-1.2	0.3	1.3	0.3	-1.1	0.6	1.5	0.09	1.1	0.4	-1.4	0.1
IPI00790459	CYFIP1	57 kDa protein	93.2%	2.8	1	1	1	3	409,450	342,861	519,266	380,560	48,752	26,746	78,158	36,942	26.6	17.4	33.7	21.7	-1.2	0.3	1.3	0.3	-1.1	0.6	1.5	0.09	1.1	0.4	-1.4	0.1
IPI00790673	CYFIP1	isoform 3 of Cytoplasmic FMR1-interacting protein 1	93.2%	3.1	1	1	1	3	409,450	342,861	519,266	380,560	48,752	26,746	78,158	36,942	26.6	17.4	33.7	21.7	-1.2	0.3	1.3	0.3	-1.1	0.6	1.5	0.09	1.1	0.4	-1.4	0.1
				FQILNDEIITILDK	2	93.2%	1																									
IPI00550232	XIRP2	xin actin-binding repeat-containing protein 2 isoform 1	99.8%	1.7	3	3	3	3	10,661,823	12,242,497	12,246,737	13,096,513	1,214,550	828,198	1,255,706	595,237	25.5	15.1	22.9	10.2	1.1	0.3	1.1	0.4	1.2	0.1	1.0	1	1.1	0.4	1.1	0.6
IPI00885004	XIRP2	isoform 2 of Xin actin-binding repeat-containing protein 2	99.8%	1.8	3	3	3	3	10,661,823	12,242,497	12,246,737	13,096,513	1,214,550	828,198	1,255,706	595,237	25.5	15.1	22.9	10.2	1.1	0.3	1.1	0.4	1.2	0.1	1.0	1	1.1	0.4	1.1	0.6
IPI01015807	XIRP2	isoform 3 of Xin actin-binding repeat-containing protein 2	99.8%	1.8	3	3	3	3	10,661,823	12,242,497	12,246,737	13,096,513	1,214,550	828,198	1,255,706	595,237	25.5	15.1	22.9	10.2	1.1	0.3	1.1	0.4	1.2	0.1	1.0	1	1.1	0.4	1.1	0.6
				EFEHGPVSEAKSNRR	3	88.9%	1																									
				ILYSDKEMTTPAKQIK	3	95.3%	1																									
				VVKQKVIDAHLDSQTQNFQQTQIQTAESK	3	95.9%	1																									
IPI00550234	ARPC5	isoform 1 of Actin-related protein 2/3 complex subunit 5	100.0%	26.5	3	3	4	1	12,952,155	13,182,305	12,472,090	15,298,650	1,566,879	763,323	1,020,948	548,219	27.1	13.0	18.3	8.0	1.0	0.9	-1.0	0.8	1.2	0.2	-1.1	0.6	1.2	0.05	1.2	0.04
				ALAAGGVGSIVR	2	99.9%	1																									
				AVQSLDKNGVDLLMK	2	99.8%	1																									
				QGNMTAALQAALK	2	100.0%	2																									
IPI00550272	INTS10	Integrator complex subunit 10	93.6%	3.2	1	1	1	2	1,143,570	1,190,945	1,143,720	1,278,110	107,796	100,199	127,493	74,003	21.1	18.8	24.9	13.0	1.0	0.8	1.0	1	1.1	0.3	-1.0	0.8	1.1	0.5	1.1	0.4
IPI00976479	INTS10	Protein	93.6%	9.8	1	1	1	2	1,143,570	1,190,945	1,143,720	1,278,110	107,796	100,199	127,493	74,003	21.1	18.8	24.9	13.0	1.0	0.8	1.0	1	1.1	0.3	-1.0	0.8	1.1	0.5	1.1	0.4
				STQIENQHQGAQDTSDLMSPSKR	3	93.6%	1																									
IPI00550363	TAGLN2	Transgelin-2	100.0%	86.4	20	28	42	2	112,838,102	118,204,455	107,852,827	130,780,617	8,900,632	6,011,297	8,081,474	6,037,888	17.6	11.4	16.8	10.3	1.0	0.6	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.2	1.2	0.05
IPI00647915	TAGLN2	24 kDa protein	100.0%	78.2	20	28	42	2	112,838,102	118,204,455	107,852,827	130,780,617	8,900,632	6,011,297	8,081,474	6,037,888	17.6	11.4	16.8	10.3	1.0	0.6	-1.0	0.7	1.2	0.1	-1.1	0.3	1.1	0.2	1.2	0.05
				DDGLFSGDPNWFPK	2	100.0%	2																									
				DDGLFSGDPNWFPKK	2	100.0%	2																									
				DDGLFSGDPNWFPKK	3	99.9%	1																									
				DGTVLCELINALYPEGQAPVK	2	100.0%	2																									
				DGTVLCELINALYPEGQAPVK	3	99.9%	1																									
				DGTVLCELINALYPEGQAPVKK	2	100.0%	3																									
				DGTVLCELINALYPEGQAPVKK	3	100.0%	3																									
				ENFQNWLK	2	96.4%	1																									
				GASQAGMTGYGMPR	2	100.0%	1																									
				GPAYGLSR	1	97.1%	1																									
				GPAYGLSR	2	99.6%	2																									
				IEKQYDADLEQILIQWITTQCR	3	99.9%	1																									
				IQASTMAFK	1	98.8%	1																									
				IQASTMAFK	2	99.6%	1																									
				KIQASTMAFK	2	98.2%	1																									
				NFSDNQLQEGK	1	100.0%	1																									
				NFSDNQLQEGK	2	100.0%	2																									
				NMACVQR	1	98.5%	2																									
				NVIGLQMGTNR	2	100.0%	1																									
				NVIGLQMGTNRGASQAGMTGYGMPR	3	89.7%	1																									
				QMEQISQFLQAAER	2	100.0%	2																									
				QMEQISQFLQAAER	3	100.0%	1																									
				QYDADLEQILIQWITTQCRK	3	100.0%	1																									
				TLMNLGGLAVAR	2	100.0%	2																									
				TLMNLGGLAVAR	3	100.0%	1																									
				TLMNLGGLAVARDDGLFSGDPNWFPK	3	99.9%	1																									
				YGINTTDIFQTVDLWEGK	3	100.0%	2																									
				YGINTTDIFQTVDLWEGKNMACVQR	3	100.0%	2																									
IPI00550364	PGM2	Phosphoglucomutase-2	99.0%	2.5	1	1	1	2	2,690,850	1,973,080	2,752,345	2,022,460	182,964	211,485	391,379	155,075	15.2	24.0	31.8	17.2	-1.4	0.03	1.0	0.9	-1.3	0.02	1.4	0.1	1.0	0.9	-1.4	0.1
IPI00966505	PGM2	Uncharacterized protein	99.0%	7.7	1	1	1	2	2,690,850	1,973,080	2,752,345	2,022,460	182,964	211,485	391,379	155,075	15.2	24.0	31.8	17.2	-1.4	0.03	1.0	0.9	-1.3	0.02	1.4	0.1	1.0	0.9	-1.4	0.1
				MNDLTIIQTTQGFCR	2	99.0%	1																									
IPI00550523	ATL3	Atlastin-3	99.0%	7.8	2	2	2	2	7,355,528	7,997,575	7,803,360	7,910,585	756,954	381,574	804,026	252,993	23.0	10.7	23.0	7.2	1.1	0.5	1.1	0.7	1.1	0.5	-1.0	0.8	-1.0	0.9	1.0	0.9
IPI01012170	ATL3	18 kDa protein	99.0%	24.9	2	2	2	2	7,355,528	7,997,575	7,803,360	7,910,585	756,954	381,574	804,026	252,993	23.0	10.7	23.0	7.2	1.1	0.5	1.1	0.7	1.1	0.5	-1.0	0.8	-1.0	0.9	1.0	0.9
				ESGHSNWLGDPEEPLTGFSWR	3	92.7%	1																									
				GADDAMESSKPGPVQVVLVQK	3	99.0%	1																									
IPI00550644	TTC38	Tetratricopeptide repeat protein 38	99.8%	10.2	3	3	3	2	4,369,113	4,082,140	5,282,418	4,845,208	546,016	679,395	986,529	446,464	27.9	37.2	41.8	20.6	-1.1	0.8	1.2	0.4	1.1	0.5	1.3	0.3	1.2	0.4	-1.1	0.7
IPI00880058	TTC38	Novel protein	99.8%	18.3	3	3	3	2	4,369,113	4,082,140	5,282,418	4,845,208	546,016	679,395	986,529	446,464	27.9	37.2	41.8	20.6	-1.1	0.8	1.2	0.4	1.1	0.5	1.3	0.3	1.2	0.4	-1.1	0.7
				ACELWEQILQDHPTDMLALK	3	96.2%	1																									
				IYPFWTPDIPLSSYVK	2	84.2%	1																									
				LPLSTTSNEACK	2	99.5%	1																									
IPI00550689	C22orf28	tRNA-splicing ligase RtcB homolog	100.0%	19.2	8	8	9	2	17,252,158	19,611,617	18,960,478	23,968,254	3,247,110	1,378,193	1,844,662	1,019,731	42.1	15.7	21.8	9.5	1.1	0.5	1.1	0.7	1.4	0.1	-1.0	0.8	1.2	0.03	1.3	0.04
IPI00910144	C22orf28	Uncharacterized protein	100.0%	20.3	8	8	9	2	17,252,158	19,611,617	18,960,478	23,968,254	3,247,110	1,378,193	1,844,662	1,019,731	42.1	15.7	21.8	9.5	1.1	0.5	1.1	0.7	1.4	0.1	-1.0	0.8	1.2	0.03	1.3	0.04
				GLPQLGTLGAGNHYAEIQVVDEIFNEYAAK	3	100.0%	1																									
				LADMGIAIR	2	91.1%	1																									
				LMFEELR	2	96.0%	1																									
				NLDFQDVLDK	2	99.7%	1																									
				NLDFQDVLDKLADMGIAIR	3	100.0%	1																									
				SYNDELQFLEK	2	100.0%	2																									
				TNLDESDVQPVK	2	94.8%	1																									
				TNLDESDVQPVKEQLAQAMFDHIPVGVGSK	3	99.9%	1																									
IPI00550746	NUDC	Nuclear migration protein nudC	100.0%	14.8	4	4	6	1	11,691,895	10,760,255	11,184,990	12,880,025	324,525	637,376	1,022,589	619,700	6.2	13.3	20.4	10.8	-1.1	0.2	-1.0	0.7	1.1	0.1	1.0	0.7	1.2	0.04	1.2	0.2
				DMVVDIQR	2	98.8%	1																									
				GQPAIIDGELYNEVK	2	100.0%	2																									
				TDFFIGGEEGMAEK	2	99.8%	1																									
				VEESSWLIEDGK	2	99.9%	2																									
IPI00550821	CPSF7	isoform 1 of Cleavage and polyadenylation specificity factor subunit 7	96.2%	2.3	1	1	1	7	756,629	636,594	633,901	861,031	129,161	41,974	64,840	236,021	38.2	14.7	22.9	61.3	-1.2	0.4	-1.2	0.4	1.1	0.7	-1.0	1	1.4	0.4	1.4	0.4
IPI00719106	CPSF7	isoform 2 of Cleavage and polyadenylation specificity factor subunit 7	96.2%	2.4	1	1	1	7	756,629	636,594	633,901	861,031	129,161	41,974	64,840	236,021	38.2	14.7	22.9	61.3	-1.2	0.4	-1.2	0.4	1.1	0.7	-1.0	1	1.4	0.4	1.4	0.4
IPI00915356	CPSF7	isoform 3 of Cleavage and polyadenylation specificity factor subunit 7	96.2%	2.1	1	1	1	7	756,629	636,594	633,901	861,031	129,161	41,974	64,840	236,021	38.2	14.7	22.9	61.3	-1.2	0.4	-1.2	0.4	1.1	0.7	-1.0	1	1.4	0.4	1.4	0.4
IPI00927669	CPSF7	23 kDa protein	96.2%	5.4	1	1	1	7	756,629	636,594	633,901	861,031	129,161	41,974	64,840	236,021	38.2	14.7	22.9	61.3	-1.2	0.4	-1.2	0.4	1.1	0.7	-1.0	1	1.4	0.4	1.4	0.4
IPI01013082	CPSF7	24 kDa protein	96.2%	5.0	1	1	1	7	756,629	636,594	633,901	861,031	129,161	41,974	64,840	236,021	38.2	14.7	22.9	61.3	-1.2	0.4	-1.2	0.4	1.1	0.7	-1.0	1	1.4	0.4	1.4	0.4
IPI01013482	CPSF7	32 kDa protein	96.2%	3.8	1	1	1	7	756,629	636,594	633,901	861,031	129,161	41,974	64,840	236,021	38.2	14.7	22.9	61.3	-1.2	0.4	-1.2	0.4	1.1	0.7	-1.0	1	1.4	0.4	1.4	0.4
IPI01014911	CPSF7	41 kDa protein	96.2%	2.9	1	1	1	7	756,629	636,594	633,901	861,031	129,161	41,974	64,840	236,021	38.2	14.7	22.9	61.3	-1.2	0.4	-1.2	0.4	1.1	0.7	-1.0	1	1.4	0.4	1.4	0.4
				QNLSQFEAQAR	2	96.2%	1																									
IPI00550894	GNPDA2	isoform 1 of Glucosamine-6-phosphate isomerase 2	98.0%	10.5	2	2	2	3	2,736,413	2,726,948	2,936,677	2,837,349	257,444	154,045	173,447	101,962	21.0	12.6	13.2	8.0	-1.0	1	1.1	0.5	1.0	0.7	1.1	0.4	1.0	0.6	-1.0	0.6
IPI00896466	GNPDA2	isoform 3 of Glucosamine-6-phosphate isomerase 2	98.0%	11.2	2	2	2	3	2,736,413	2,726,948	2,936,677	2,837,349	257,444	154,045	173,447	101,962	21.0	12.6	13.2	8.0	-1.0	1	1.1	0.5	1.0	0.7	1.1	0.4	1.0	0.6	-1.0	0.6
IPI00896510	GNPDA2	isoform 2 of Glucosamine-6-phosphate isomerase 2	98.0%	10.6	2	2	2	3	2,736,413	2,726,948	2,936,677	2,837,349	257,444	154,045	173,447	101,962	21.0	12.6	13.2	8.0	-1.0	1	1.1	0.5	1.0	0.7	1.1	0.4	1.0	0.6	-1.0	0.6
				TFNMDEYVGLPR	2	98.0%	1																									
				YFTLGLPTGSTPLGCYK	2	94.5%	1																									
IPI00550906	CSTF2T	Cleavage stimulation factor subunit 2 tau variant	100.0%	3.9	2	2	2	1	4,878,148	5,591,128	5,144,463	5,885,810	325,754	236,754	397,266	348,295	14.9	9.5	17.3	13.2	1.1	0.1	1.1	0.6	1.2	0.07	-1.1	0.4	1.1	0.5	1.1	0.2
				AMETEVLETR	2	97.6%	1																									
				GGTLLSVTGEVEPR	2	96.1%	1																									
IPI00550917	TWF2	Twinfilin-2	99.2%	4.9	1	1	1	2	46,224,400	48,102,950	50,016,600	55,929,950	4,853,480	2,877,964	4,838,703	2,038,567	23.5	13.4	21.6	8.2	1.0	0.7	1.1	0.6	1.2	0.1	1.0	0.7	1.2	0.06	1.1	0.3
IPI00966182	TWF2	Uncharacterized protein	99.2%	6.7	1	1	1	2	46,224,400	48,102,950	50,016,600	55,929,950	4,853,480	2,877,964	4,838,703	2,038,567	23.5	13.4	21.6	8.2	1.0	0.7	1.1	0.6	1.2	0.1	1.0	0.7	1.2	0.06	1.1	0.3
				AVLPLLDAQQPCYLLYR	2	99.2%	1																									
IPI00551024	DAK	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	100.0%	25.4	9	11	13	1	24,942,098	24,913,495	24,855,892	27,503,027	1,830,359	938,982	1,736,660	748,909	16.4	8.4	15.6	6.1	-1.0	1	-1.0	1	1.1	0.2	-1.0	1	1.1	0.06	1.1	0.2
				AAGDGDCGTTHSR	3	95.7%	1																									
				EGPPPASPAQLLSK	2	99.9%	1																									
				LEQPDPGAVAAAAILR	2	98.2%	1																									
				SPGADLLQVLTK	2	100.0%	2																									
				TMLDSLWAAGQELQAWK	2	100.0%	2																									
				TSLPAWSAAMDAGLEAMQK	2	100.0%	1																									
				TSLPAWSAAMDAGLEAMQK	3	100.0%	1																									
				VAGALAEAGVGLEEIAK	2	100.0%	1																									
				VAPAEPQEAPDSTAAGGSASK	2	99.3%	1																									
				VCSTLLGLEEHLNALDR	2	100.0%	1																									
				VCSTLLGLEEHLNALDR	3	100.0%	1																									
IPI00552072	CCT7	Uncharacterized protein	100.0%	27.5	9	9	10	1	15,614,844	15,403,544	15,223,421	17,367,997	1,083,359	581,067	1,113,589	871,773	15.5	8.4	16.4	11.2	-1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.9	1.1	0.1	1.1	0.2
				ATISNDGATILK	2	99.8%	1																									
				CAMTALSSK	2	99.3%	1																									
				GGAEQFMEETER	2	100.0%	1																									
				INALTAASEAACLIVSVDETIKNPR	3	100.0%	1																									
				QLCDNAGFDATNILNK	2	100.0%	1																									
				SLHDAIMIVR	2	96.7%	1																									
				TFSYAGFEMQPK	2	100.0%	2																									
				VHTVEDYQAIVDAEWNILYDKLEK	3	97.4%	1																									
				VQGGALEDSQLVAGVAFK	2	100.0%	1																									
IPI00552142	CENPI	isoform 1 of Centromere protein I	96.4%	2.5	1	1	1	2	2,150,970	2,141,695	1,826,450	2,145,615	184,559	133,746	138,939	180,507	19.2	14.0	17.0	18.8	-1.0	1	-1.2	0.2	-1.0	1	-1.2	0.1	1.0	1	1.2	0.2
IPI00647405	CENPI	isoform 2 of Centromere protein I	96.4%	2.6	1	1	1	2	2,150,970	2,141,695	1,826,450	2,145,615	184,559	133,746	138,939	180,507	19.2	14.0	17.0	18.8	-1.0	1	-1.2	0.2	-1.0	1	-1.2	0.1	1.0	1	1.2	0.2
				NGLASEEIDILLNIALSGK	2	96.4%	1																									
IPI00552303	ANXA11	Uncharacterized protein	100.0%	7.4	1	1	1	1	771,533	692,843	854,310	758,660	100,714	36,825	75,752	28,761	29.2	11.9	19.8	8.5	-1.1	0.5	1.1	0.5	-1.0	0.9	1.2	0.09	1.1	0.2	-1.1	0.3
				DAQELYAAGENR	2	100.0%	1																									
IPI00552365	EFHD2	Uncharacterized protein	100.0%	28.3	4	5	7	1	8,597,763	9,477,898	8,815,495	9,693,908	635,845	392,543	467,968	346,648	16.5	9.3	11.9	8.0	1.1	0.3	1.0	0.8	1.1	0.2	-1.1	0.3	1.0	0.7	1.1	0.2
				AAAGELQEDSGLCVLAR	2	100.0%	1																									
				DGFIDLMELK	2	100.0%	2																									
				LGAPQTHLGLK	2	98.9%	1																									
				LGAPQTHLGLK	3	100.0%	1																									
				LSEIDVSSEGVK	2	100.0%	2																									
IPI00552426	STK24	Uncharacterized protein	100.0%	11.2	2	2	3	1	1,378,416	1,445,361	1,524,424	1,847,828	231,227	75,625	188,727	78,260	37.5	11.7	27.7	9.5	1.0	0.8	1.1	0.6	1.3	0.1	1.1	0.7	1.3	0.006	1.2	0.2
				ADIWSLGITAIELAR	2	100.0%	2																									
				TSYLTELIDR	2	99.8%	1																									
IPI00552715	CCT3	T-complex protein 1 subunit gamma isoform c	100.0%	15.4	6	7	9	1	12,015,298	12,668,688	12,295,472	14,164,531	1,188,237	385,554	671,470	446,585	22.1	6.8	12.2	7.1	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.6	1.1	0.03	1.2	0.05
				ELGIWEPLAVK	2	100.0%	2																									
				IDDIVSGHK	2	88.4%	1																									
				IPGGIIEDSCVLR	2	100.0%	1																									
				ISIPVDISDSDMMLNIINSSITTK	2	100.0%	2																									
				ISIPVDISDSDMMLNIINSSITTK	3	99.9%	1																									
				NLQDAMQVCR	2	100.0%	1																									
				TAVETAVLLLR	2	100.0%	1																									
IPI00552768	TXN	Thioredoxin, isoform CRA_b	100.0%	67.1	6	7	9	1	31,985,990	35,131,210	34,580,476	37,897,828	2,018,436	1,380,416	2,228,665	1,053,341	14.1	8.8	14.4	6.2	1.1	0.2	1.1	0.4	1.2	0.03	-1.0	0.8	1.1	0.1	1.1	0.2

				CMPTFQFFK	2	100.0%	1																									
				EKLEATINELV	2	99.5%	2																									
				LVVVDFSATWCGPCK	2	100.0%	1																									
				TAFQEALDAAGDK	2	100.0%	2																									
				VGEFSGANK	1	100.0%	1																									
				VGEFSGANK	2	100.0%	1																									
				VGEFSGANKEK	2	99.3%	1																									
IPI00552818	ABLIM1	Actin binding LIM protein 1	99.9%	9.3	1	1	1	2	414,296	383,657	400,428	438,577	37,231	12,374	33,689	11,453	20.1	7.2	18.8	5.8	-1.1	0.5	-1.0	0.8	1.1	0.6	1.0	0.7	1.1	0.01	1.1	0.3
IPI00937791	ABLIM1	Actin binding LIM protein 1	99.9%	9.3	1	1	1	2	414,296	383,657	400,428	438,577	37,231	12,374	33,689	11,453	20.1	7.2	18.8	5.8	-1.1	0.5	-1.0	0.8	1.1	0.6	1.0	0.7	1.1	0.01	1.1	0.3
				VDNEILDYKDLAAIPK	3	100.0%	1																									
IPI00552834	RHOC	Ras homolog gene family, member C	100.0%	25.6	5	5	6	2	6,890,613	6,587,685	7,691,688	6,620,421	327,188	218,391	163,973	208,478	10.6	7.4	4.8	7.0	-1.0	0.5	1.1	0.06	-1.0	0.5	1.2	0.004	1.0	0.9	-1.2	0.004
IPI00643368	RHOC	Ras homolog gene family, member C	100.0%	40.2	5	5	6	2	6,890,613	6,587,685	7,691,688	6,620,421	327,188	218,391	163,973	208,478	10.6	7.4	4.8	7.0	-1.0	0.5	1.1	0.06	-1.0	0.5	1.2	0.004	1.0	0.9	-1.2	0.004
				DQFPEVYVPTVFENYIADIEVDGK	2	100.0%	2																									
				HFCPNVPIILVGNK	2	99.4%	1																									
				HFCPNVPIILVGNKK	3	100.0%	1																									
				KLVIVGDGACGK	2	99.2%	1																									
				LVIVGDGACGK	2	99.9%	1																									
IPI00552937	NHLRC3	NHL repeat-containing protein 3	99.5%	3.5	1	1	2	3	927,030	997,200	963,757	1,087,317	63,493	85,765	75,815	39,352	15.3	19.2	17.6	8.1	1.1	0.5	1.0	0.7	1.2	0.06	-1.0	0.8	1.1	0.4	1.1	0.2
IPI00556271	NHLRC3	NHL repeat-containing protein 3 isoform b	99.5%	4.3	1	1	2	3	927,030	997,200	963,757	1,087,317	63,493	85,765	75,815	39,352	15.3	19.2	17.6	8.1	1.1	0.5	1.0	0.7	1.2	0.06	-1.0	0.8	1.1	0.4	1.1	0.2
IPI01011617	NHLRC3	17 kDa protein	99.5%	7.8	1	1	2	3	927,030	997,200	963,757	1,087,317	63,493	85,765	75,815	39,352	15.3	19.2	17.6	8.1	1.1	0.5	1.0	0.7	1.2	0.06	-1.0	0.8	1.1	0.4	1.1	0.2
				ILVFTEDGYFLR	2	99.5%	2																									
IPI00552938	RBMX	heterogeneous nuclear ribonucleoprotein G isoform 2	100.0%	17.9	3	3	5	1	10,100,710	10,120,210	10,327,017	12,102,715	1,005,760	596,306	824,910	447,897	22.3	13.2	17.9	8.3	1.0	1	1.0	0.9	1.2	0.1	1.0	0.8	1.2	0.03	1.2	0.1
				ALEAVFGK	2	99.9%	1																									
				GFAFVTFESPADAK	2	100.0%	2																									
				LFIGGLNTETNEK	2	100.0%	2																									
IPI00553131	GALE	UDP-glucose 4-epimerase	100.0%	27.6	8	10	11	1	11,587,313	12,249,422	11,834,049	13,783,872	841,151	425,312	472,246	466,763	16.2	7.8	8.9	7.6	1.1	0.5	1.0	0.8	1.2	0.05	-1.0	0.5	1.1	0.04	1.2	0.02
				DYIHVVDLAK	2	93.1%	1																									
				DYIHVVDLAK	3	99.7%	1																									
				EALNVFGNDYDTEDGTGVR	2	100.0%	1																									
				EALNVFGNDYDTEDGTGVRDYIHVVDLAK	3	99.2%	1																									
				FFIEEMIR	2	99.8%	1																									
				IYNLGTGTGYSVLQMVQAMEK	2	100.0%	1																									
				IYNLGTGTGYSVLQMVQAMEK	3	100.0%	1																									
				MCEDLWR	2	99.9%	1																									
				SVEFEEMDILDQGALQR	3	100.0%	1																									
				VNLTGTIQLLEIMK	2	100.0%	2																									
IPI00553151	SMC1A	Structural maintenance of chromosomes 1A	99.9%	10.0	2	2	2	1	4,893,155	5,396,508	4,977,177	6,137,850	498,419	244,994	599,958	191,644	22.8	10.2	27.0	7.0	1.1	0.4	1.0	0.9	1.3	0.07	-1.1	0.5	1.1	0.04	1.2	0.1
				NFLVFQGAVESIAMK	2	99.6%	1																									
				SNLMDAISFVLGEK	2	97.1%	1																									
IPI00553185	CCT3	T-complex protein 1 subunit gamma	100.0%	44.8	16	18	21	2	34,277,859	37,240,970	36,358,771	40,447,730	3,898,539	1,568,334	2,525,700	924,422	25.4	9.4	15.5	5.1	1.1	0.5	1.1	0.7	1.2	0.2	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00977430	CCT3	cDNA, FLJ79286, highly similar to T-complex protein 1 subunit gamma	100.0%	48.8	16	18	21	2	34,277,859	37,240,970	36,358,771	40,447,730	3,898,539	1,568,334	2,525,700	924,422	25.4	9.4	15.5	5.1	1.1	0.5	1.1	0.7	1.2	0.2	-1.0	0.8	1.1	0.1	1.1	0.2
				ALDDMISTLKK	3	99.0%	1																									
				AVAQALEVIPR	2	99.9%	1																									
				EIQVQHPAAK	2	83.0%	1																									
				ELGIWEPLAVK	2	100.0%	2																									
				IDDIVSGHK	2	88.4%	1																									
				ILQMEEEYIQQLCEDIIQLKPDVVITEK	3	100.0%	1																									
				IPGGIIEDSCVLR	2	100.0%	1																									
				ISIPVDISDSDMMLNIINSSITTK	2	100.0%	2																									
				ISIPVDISDSDMMLNIINSSITTK	3	99.9%	1																									
				IVLLDSSLEYK	2	95.4%	1																									
				IVSRPEELREDDVGTGAGLLEIK	3	100.0%	1																									
				MLLDPMGGIVMTNDGNAILR	2	100.0%	2																									
				MLLDPMGGIVMTNDGNAILR	3	100.0%	1																									
				NLQDAMQVCR	2	100.0%	1																									
				NVLLDPQLVPGGGASEMAVAHALTEK	3	99.8%	1																									
				TAVETAVLLLR	2	100.0%	1																									
				TLIQNCGASTIR	2	100.0%	1																									
				WSSLACNIALDAVK	2	100.0%	1																									
IPI00554433	ACTR3B	actin-related protein 3B isoform 2	100.0%	3.2	1	1	2	3	107,108	103,541	98,788	137,825	8,306	5,756	10,024	16,162	17.3	12.4	22.7	26.2	-1.0	0.7	-1.1	0.5	1.3	0.1	-1.0	0.7	1.3	0.1	1.4	0.07
IPI00642069	ACTR3C	Uncharacterized protein	100.0%	5.0	1	1	2	3	107,108	103,541	98,788	137,825	8,306	5,756	10,024	16,162	17.3	12.4	22.7	26.2	-1.0	0.7	-1.1	0.5	1.3	0.1	-1.0	0.7	1.3	0.1	1.4	0.07
IPI00946655	ACTR3C	isoform 1 of Actin-related protein 3C	100.0%	5.2	1	1	2	3	107,108	103,541	98,788	137,825	8,306	5,756	10,024	16,162	17.3	12.4	22.7	26.2	-1.0	0.7	-1.1	0.5	1.3	0.1	-1.0	0.7	1.3	0.1	1.4	0.07
				DITYFIQQLLR	2	100.0%	2																									
IPI00554579	MAP7D2	isoform 2 of MAP7 domain-containing protein 2	99.3%	5.2	2	2	2	5	3,795,638	3,492,722	4,338,886	3,843,656	247,590	169,136	342,006	177,505	14.6	10.8	17.6	10.3	-1.1	0.3	1.1	0.2	1.0	0.9	1.2	0.06	1.1	0.2	-1.1	0.2
IPI00844217	MAP7D2	isoform 1 of MAP7 domain-containing protein 2	99.3%	5.5	2	2	2	5	3,795,638	3,492,722	4,338,886	3,843,656	247,590	169,136	342,006	177,505	14.6	10.8	17.6	10.3	-1.1	0.3	1.1	0.2	1.0	0.9	1.2	0.06	1.1	0.2	-1.1	0.2
IPI00922426	MAP7D2	MAP7 domain-containing protein 2 isoform 3	99.3%	5.8	2	2	2	5	3,795,638	3,492,722	4,338,886	3,843,656	247,590	169,136	342,006	177,505	14.6	10.8	17.6	10.3	-1.1	0.3	1.1	0.2	1.0	0.9	1.2	0.06	1.1	0.2	-1.1	0.2
IPI00942170	MAP7D2	Uncharacterized protein	99.3%	5.8	2	2	2	5	3,795,638	3,492,722	4,338,886	3,843,656	247,590	169,136	342,006	177,505	14.6	10.8	17.6	10.3	-1.1	0.3	1.1	0.2	1.0	0.9	1.2	0.06	1.1	0.2	-1.1	0.2
IPI01012127	MAP7D2	cDNA FLJ45113 fis, clone BRAWH3034743, weakly similar to Mus musculus microtu	99.3%	6.5	2	2	2	5	3,795,638	3,492,722	4,338,886	3,843,656	247,590	169,136	342,006	177,505	14.6	10.8	17.6	10.3	-1.1	0.3	1.1	0.2	1.0	0.9	1.2	0.06	1.1	0.2	-1.1	0.2
				HAAAAGGKAENSAALGKPTAGTTDAGEAAK	3	91.8%	1																									
				KSDVSPQVKK	3	92.0%	1																									
IPI00554590	RAB3GAP2	isoform 1 of Rab3 GTPase-activating protein non-catalytic subunit	96.8%	0.8	1	1	1	1	10,649,020	10,905,430	11,096,420	12,088,420	956,786	605,766	345,344	479,479	20.1	12.4	7.0	8.9	1.0	0.8	1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.2	1.1	0.1
				QALESILASER	2	95.5%	1																									
IPI00554617	TPP1	cDNA FLJ57277, highly similar to Tripeptidyl-peptidase 1	100.0%	15.3	3	3	3	2	5,267,948	5,169,658	5,507,008	6,039,120	245,996	184,834	390,646	465,264	10.4	8.0	15.9	17.2	-1.0	0.8	1.0	0.6	1.1	0.2	1.1	0.5	1.2	0.1	1.1	0.4
IPI00909516	TPP1	cDNA FLJ58558, highly similar to Tripeptidyl-peptidase 1	100.0%	11.9	3	3	3	2	5,267,948	5,169,658	5,507,008	6,039,120	245,996	184,834	390,646	465,264	10.4	8.0	15.9	17.2	-1.0	0.8	1.0	0.6	1.1	0.2	1.1	0.5	1.2	0.1	1.1	0.4
				AYPDVAALSDGYWVVSNR	3	100.0%	1																									
				LYQQHGAGLFDVTR	3	96.2%	1																									
				VPIPWVSGTSASTPVFGGILSLINEHR	3	100.0%	1																									
IPI00554648	KRT8	Keratin, type II cytoskeletal 8	100.0%	58.4	45	72	116	1	670,526,915	676,660,517	641,244,366	743,968,192	########	########	########	########	12.8	8.8	13.6	5.4	1.0	0.9	-1.0	0.6	1.1	0.1	-1.1	0.5	1.1	0.07	1.2	0.04
				AEAESMYQIK	2	100.0%	2																									
				AEAESMYQIKYEELQSLAGK	3	100.0%	1																									
				AQYEDIANR	1	100.0%	1																									
				AQYEDIANR	2	100.0%	2																									
				ASLEAAIADAEQR	2	100.0%	2																									
				ASLEAAIADAEQRGELAIK	2	100.0%	2																									
				ASLEAAIADAEQRGELAIK	3	99.9%	1																									
				ASLEAAIADAEQRGELAIKDANAK	2	94.9%	1																									
				ASLEAAIADAEQRGELAIKDANAK	3	100.0%	1																									
				DGKLVSESSDVLPK	2	99.9%	1																									
				DVDEAYMNK	2	100.0%	2																									
				DVDEAYMNKVELESR	2	100.0%	2																									
				DVDEAYMNKVELESR	3	100.0%	2																									
				DVDEAYMNKVELESRLEGLTDEINFLR	3	100.0%	2																									
				EYQELMNVK	1	99.2%	1																									
				EYQELMNVK	2	99.9%	1																									
				GELAIK	1	96.9%	2																									
				GELAIKDANAK	2	99.8%	1																									
				GELAIKDANAK	3	99.0%	1																									
				ISSSSFSR	1	96.4%	1																									
				ISSSSFSR	2	99.2%	2																									
				KDVDEAYMNKVELESR	3	84.6%	1																									
				KLLEGEESRLESGMQNMSIHTK	3	88.5%	1																									
				LEAELGNMQGLVEDFK	2	100.0%	2																									
				LEAELGNMQGLVEDFKNK	3	100.0%	2																									
				LEGLTDEINFLR	2	100.0%	2																									
				LESGMQNMSIHTK	2	100.0%	2																									
				LESGMQNMSIHTK	3	100.0%	1																									
				LKLEAELGNMQGLVEDFK	2	100.0%	2																									
				LKLEAELGNMQGLVEDFK	3	100.0%	2																									
				LLEGEESR	1	97.8%	1																									
				LLEGEESR	2	100.0%	1																									
				LLEGEESRLESGMQNMSIHTK	3	100.0%	1																									
				LQAEIEGLK	1	100.0%	1																									
				LQAEIEGLK	2	99.8%	2																									
				LQAEIEGLKGQR	2	99.9%	2																									
				LQAEIEGLKGQR	3	96.3%	1																									
				LSELEAALQR	1	88.7%	1																									
				LSELEAALQR	2	100.0%	3																									
				LSELEAALQR	3	97.2%	1																									
				LVSESSDVLPK	1	99.0%	1																									
				LVSESSDVLPK	2	100.0%	2																									
				NKYEDEINKR	2	99.9%	2																									
				QLETLGQEK	1	99.2%	1																									
				QLETLGQEK	2	99.9%	2																									
				QLREYQELMNVK	2	99.1%	2																									
				QLREYQELMNVK	3	84.3%	1																									
				QLYEEEIR	2	99.8%	2																									
				QLYEEEIRELQSQISDTSVVLSMDNSR	3	100.0%	1																									
				RQLETLGQEK	2	100.0%	3																									
				SLDMDSIIAEVK	1	100.0%	2																									
				SLDMDSIIAEVK	2	100.0%	3																									
				SLDMDSIIAEVKAQYEDIANR	3	100.0%	2																									
				SNMDNMFESYINNLR	2	100.0%	2																									
				SNMDNMFESYINNLR	3	100.0%	1																									
				SNMDNMFESYINNLRR	3	99.9%	2																									
				SRAEAESMYQIK	2	100.0%	2																									
				SRAEAESMYQIK	3	99.9%	1																									
				TEISEMNR	1	96.2%	1																									
				TEISEMNR	2	100.0%	2																									
				TEMENEFVLIK	2	100.0%	2																									
				TEMENEFVLIKK	2	100.0%	2																									
				TEMENEFVLIKK	3	100.0%	2																									
				TKTEISEMNR	1	100.0%	1																									
				TKTEISEMNR	2	100.0%	3																									
				TKTEISEMNR	3	99.2%	2																									
				VELESRLEGLTDEINFLR	2	99.7%	1																									
				VELESRLEGLTDEINFLR	3	100.0%	1																									
				WSLLQQQK	1	96.6%	1																									

				WSLLQQQK	2	99.9%	2																									
				YEELQSLAGK	1	100.0%	2																									
				YEELQSLAGK	2	99.9%	2																									
IPI00554711	JUP	Junction plakoglobin	100.0%	31.1	17	18	25	1	96,921,184	100,947,931	98,474,048	109,567,604	7,871,589	3,591,593	6,006,593	1,401,468	18.2	8.0	13.6	2.9	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.07	1.1	0.1
				ALMGSPQLVAAVVR	2	100.0%	2																									
				ATIGLIR	2	97.2%	1																									
				GIMEEDEACGR	2	100.0%	1																									
				HPEAEMAQNSVR	2	99.7%	1																									
				HVAAGTQQPYTDGVR	2	100.0%	1																									
				LAEPSQLLK	2	99.0%	1																									
				LIILANGGPQALVQIMR	2	100.0%	2																									
				LIILANGGPQALVQIMR	3	100.0%	1																									
				LLNDEDPVVVTK	2	100.0%	2																									
				LLNQPNQWPLVK	2	99.9%	2																									
				LVQLLVK	2	96.9%	2																									
				NLALCPANHAPLQEAAVIPR	3	100.0%	1																									
				QEGLESVLK	2	86.0%	1																									
				SAIVHLINYQDDAELATR	3	100.0%	2																									
				TLVTQNSGVEALIHAILR	3	100.0%	1																									
				TMQNTSDLDTAR	2	100.0%	1																									
				VSVELTNSLFK	2	100.0%	2																									
				VTEWQQTYTYDSGIHSGANTCVPSVSSK	3	100.0%	1																									
IPI00554737	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	100.0%	33.8	16	19	21	2	18,400,762	21,535,095	18,903,603	25,087,803	2,708,983	1,320,834	1,603,368	946,913	32.9	13.7	19.0	8.4	1.2	0.3	1.0	0.9	1.4	0.07	-1.1	0.2	1.2	0.06	1.3	0.01
IPI01014074	PPP2R1A	cDNA FLJ53296, highly similar to Serine/threonine-protein phosphatase 2A 65 kDa	100.0%	34.4	16	19	21	2	18,400,762	21,535,095	18,903,603	25,087,803	2,708,983	1,320,834	1,603,368	946,913	32.9	13.7	19.0	8.4	1.2	0.3	1.0	0.9	1.4	0.07	-1.1	0.2	1.2	0.06	1.3	0.01
				DNTIEHLLPLFLAQLK	3	100.0%	1																									
				DNTIEHLLPLFLAQLKDECPEVR	3	100.0%	1																									
				ELVSDANQHVK	2	98.3%	1																									
				ENVIMSQILPCIK	2	100.0%	1																									
				LNIISNLDCVNEVIGIR	2	100.0%	1																									
				LNIISNLDCVNEVIGIR	3	99.8%	1																									
				LSTIALALGVER	2	100.0%	1																									
				LTQDQDVDVK	2	100.0%	2																									
				MAGDPVANVR	2	100.0%	1																									
				NLCSDDTPMVR	2	97.5%	1																									
				QLSQSLLPAIVELAEDAK	3	100.0%	1																									
				QLSQSLLPAIVELAEDAKWR	3	100.0%	1																									
				SALASVIMGLSPILGK	2	95.3%	1																									
				SEIIPMFSNLASDEQDSVR	2	100.0%	2																									
				TDLVPAFQNLMK	2	99.9%	1																									
				VLAMSGDPNYLHR	2	99.9%	1																									
				VLAMSGDPNYLHR	3	99.7%	1																									
				YMVADKFTELQK	2	99.9%	1																									
				YMVADKFTELQK	3	99.8%	1																									
IPI00554742	API5	isoform 2 of Apoptosis inhibitor 5	100.0%	11.3	4	4	5	6	4,019,260	4,581,307	4,111,459	4,871,792	583,808	391,335	568,552	210,436	32.5	19.1	30.9	9.7	1.1	0.4	1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00555572	API5	isoform 1 of Apoptosis inhibitor 5	100.0%	11.2	4	4	5	6	4,019,260	4,581,307	4,111,459	4,871,792	583,808	391,335	568,552	210,436	32.5	19.1	30.9	9.7	1.1	0.4	1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00555743	API5	isoform 3 of Apoptosis inhibitor 5	100.0%	13.2	4	4	5	6	4,019,260	4,581,307	4,111,459	4,871,792	583,808	391,335	568,552	210,436	32.5	19.1	30.9	9.7	1.1	0.4	1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00855856	API5	apoptosis inhibitor 5 isoform a	100.0%	10.9	4	4	5	6	4,019,260	4,581,307	4,111,459	4,871,792	583,808	391,335	568,552	210,436	32.5	19.1	30.9	9.7	1.1	0.4	1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00908668	API5	apoptosis inhibitor 5 isoform c	100.0%	12.7	4	4	5	6	4,019,260	4,581,307	4,111,459	4,871,792	583,808	391,335	568,552	210,436	32.5	19.1	30.9	9.7	1.1	0.4	1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00978005	API5	cDNA FLJ51754, highly similar to Apoptosis inhibitor 5	100.0%	11.1	4	4	5	6	4,019,260	4,581,307	4,111,459	4,871,792	583,808	391,335	568,552	210,436	32.5	19.1	30.9	9.7	1.1	0.4	1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.5	1.2	0.3
				ELPQFATGENLPR	2	99.9%	2																									
				EVEELILTESK	2	94.2%	1																									
				GTLGGLFSQILQGEDIVR	2	100.0%	1																									
				VLEDVTGEEFVLFMK	2	86.3%	1																									
IPI00554777	ASNS	Asparagine synthetase [glutamine-hydrolyzing]	99.9%	6.1	2	2	2	3	1,713,899	1,754,916	1,799,438	1,981,799	112,889	129,408	143,141	92,452	14.7	16.5	17.8	10.4	1.0	0.8	1.0	0.7	1.2	0.1	1.0	0.8	1.1	0.2	1.1	0.3
IPI00925572	ASNS	asparagine synthetase [glutamine-hydrolyzing] isoform b	99.9%	6.3	2	2	2	3	1,713,899	1,754,916	1,799,438	1,981,799	112,889	129,408	143,141	92,452	14.7	16.5	17.8	10.4	1.0	0.8	1.0	0.7	1.2	0.1	1.0	0.8	1.1	0.2	1.1	0.3
IPI00926480	ASNS	46 kDa protein	99.9%	8.5	2	2	2	3	1,713,899	1,754,916	1,799,438	1,981,799	112,889	129,408	143,141	92,452	14.7	16.5	17.8	10.4	1.0	0.8	1.0	0.7	1.2	0.1	1.0	0.8	1.1	0.2	1.1	0.3
				IGCLLSGGLDSSLVAATLLK	2	95.9%	1																									
				LAVVDPLFGMQPIR	2	99.1%	1																									
IPI00554786	TXNRD1	isoform 5 of Thioredoxin reductase 1, cytoplasmic	100.0%	22.4	6	6	6	9	1,968,504	1,980,872	1,934,698	2,258,582	151,842	107,718	111,611	125,071	17.3	12.2	12.9	12.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.2	0.09
IPI00783641	TXNRD1	isoform 3 of Thioredoxin reductase 1, cytoplasmic	100.0%	18.7	6	6	6	9	1,968,504	1,980,872	1,934,698	2,258,582	151,842	107,718	111,611	125,071	17.3	12.2	12.9	12.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.2	0.09
IPI00847482	TXNRD1	isoform 4 of Thioredoxin reductase 1, cytoplasmic	100.0%	20.3	6	6	6	9	1,968,504	1,980,872	1,934,698	2,258,582	151,842	107,718	111,611	125,071	17.3	12.2	12.9	12.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.2	0.09
IPI00871867	TXNRD1	isoform 2 of Thioredoxin reductase 1, cytoplasmic	100.0%	20.6	6	6	6	9	1,968,504	1,980,872	1,934,698	2,258,582	151,842	107,718	111,611	125,071	17.3	12.2	12.9	12.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.2	0.09
IPI00885213	TXNRD1	isoform 6 of Thioredoxin reductase 1, cytoplasmic	100.0%	18.2	6	6	6	9	1,968,504	1,980,872	1,934,698	2,258,582	151,842	107,718	111,611	125,071	17.3	12.2	12.9	12.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.2	0.09
IPI00981495	TXNRD1	Uncharacterized protein	100.0%	18.3	6	6	6	9	1,968,504	1,980,872	1,934,698	2,258,582	151,842	107,718	111,611	125,071	17.3	12.2	12.9	12.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.2	0.09
IPI00983068	TXNRD1	isoform 1 of Thioredoxin reductase 1, cytoplasmic	100.0%	17.3	6	6	6	9	1,968,504	1,980,872	1,934,698	2,258,582	151,842	107,718	111,611	125,071	17.3	12.2	12.9	12.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.2	0.09
IPI00983539	TXNRD1	Uncharacterized protein	100.0%	18.8	6	6	6	9	1,968,504	1,980,872	1,934,698	2,258,582	151,842	107,718	111,611	125,071	17.3	12.2	12.9	12.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.2	0.09
IPI00984188	TXNRD1	cDNA FLJ56075, highly similar to Thioredoxin reductase 1, cytoplasmic	100.0%	20.5	6	6	6	9	1,968,504	1,980,872	1,934,698	2,258,582	151,842	107,718	111,611	125,071	17.3	12.2	12.9	12.4	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.2	0.09
				FGEENIEVYHSYFWPLEWTIPSR	3	98.4%	1																									
				KVVYENAYGQFIGPHR	3	94.1%	1																									
				SYDYDLIIIGGGSGGLAAAK	2	100.0%	1																									
				VMVLDFVTPTPLGTR	2	100.0%	1																									
				VVGFHVLGPNAGEVTQGFAAALK	3	100.0%	1																									
				WGLGGTCVNVGCIPK	2	94.9%	1																									
IPI00554788	KRT18	Keratin, type I cytoskeletal 18	100.0%	67.7	29	38	57	1	401,505,874	416,257,830	390,018,278	464,386,125	########	########	########	########	16.9	8.8	14.8	8.5	1.0	0.7	-1.0	0.8	1.2	0.1	-1.1	0.4	1.1	0.08	1.2	0.04
				AQIFANTVDNAR	2	100.0%	1																									
				AQIFANTVDNARIVLQIDNAR	3	94.5%	1																									
				AQYDELAR	1	98.9%	1																									
				AQYDELAR	2	99.4%	2																									
				ASLENSLR	1	97.5%	1																									
				ASLENSLR	2	100.0%	2																									
				DWSHYFK	2	99.7%	2																									
				ETMQSLNDR	2	100.0%	2																									
				GGMGSGGLATGIAGGLAGMGGIQNEK	3	100.0%	2																									
				GGMGSGGLATGIAGGLAGMGGIQNEKETMQSLNDR	3	100.0%	1																									
				GLQAQIASSGLTVEVDAPK	2	100.0%	2																									
				GLQAQIASSGLTVEVDAPK	3	100.0%	1																									
				IIEDLRAQIFANTVDNAR	3	100.0%	1																									
				IMADIR	1	97.1%	1																									
				IMADIR	2	97.7%	2																									
				IVLQIDNAR	2	99.9%	3																									
				KVIDDTNITR	2	99.8%	1																									
				LASYLDR	2	97.3%	1																									
				LEAEIATYR	2	100.0%	1																									
				LLEDGEDFNLGDALDSSNSMQTIQK	2	100.0%	2																									
				LLEDGEDFNLGDALDSSNSMQTIQK	3	100.0%	1																									
				LQLETEIEALKEELLFMK	2	100.0%	2																									
				LQLETEIEALKEELLFMK	3	100.0%	2																									
				LQLETEIEALKEELLFMKK	3	100.0%	1																									
				PVSSAASVYAGAGGSGSR	2	100.0%	2																									
				QAQEYEALLNIK	2	100.0%	2																									
				QSVENDIHGLR	2	100.0%	2																									
				QSVENDIHGLRK	2	100.0%	1																									
				QSVENDIHGLRK	3	99.6%	1																									
				RLLEDGEDFNLGDALDSSNSMQTIQK	3	100.0%	1																									
				SLGSVQAPSYGAR	2	99.9%	2																									
				STFSTNYR	1	94.2%	1																									
				STFSTNYR	2	99.5%	1																									
				TVQSLEIDLDSMR	2	100.0%	2																									
				VKLEAEIATYR	2	99.9%	1																									
				VKYETELAMR	2	100.0%	2																									
				VKYETELAMR	3	99.5%	1																									
				YALQMEQLNGILLHLESELAQTR	2	100.0%	2																									
IPI00555593	PDLIM5	Enigma homolog (Fragment)	100.0%	4.8	2	2	2	2	3,347,562	3,355,465	3,344,362	3,161,842	94,320	104,779	78,505	70,943	6.3	7.0	5.3	5.0	1.0	1	-1.0	1	-1.1	0.2	-1.0	0.9	-1.1	0.2	-1.1	0.1
IPI00973432	PDLIM5	PRO2489	100.0%	4.4	2	2	2	2	3,347,562	3,355,465	3,344,362	3,161,842	94,320	104,779	78,505	70,943	6.3	7.0	5.3	5.0	1.0	1	-1.0	1	-1.1	0.2	-1.0	0.9	-1.1	0.2	-1.1	0.1
				GPFLVALGK	2	97.6%	1																									
				NTMAYIGFVEEK	2	99.9%	1																									
IPI00555695	DCTN1	Dynactin 1 isoform 1 variant (Fragment)	99.9%	6.5	2	2	2	2	265,180	274,280	268,920	281,945	27,806	22,704	28,638	15,947	23.5	18.5	23.8	12.7	1.0	0.8	1.0	0.9	1.1	0.6	-1.0	0.9	1.0	0.8	1.0	0.7
IPI00917166	DCTN1	Putative uncharacterized protein DKFZp686E0752	99.9%	3.4	2	2	2	2	265,180	274,280	268,920	281,945	27,806	22,704	28,638	15,947	23.5	18.5	23.8	12.7	1.0	0.8	1.0	0.9	1.1	0.6	-1.0	0.9	1.0	0.8	1.0	0.7
				ELTNQQEASVER	2	97.9%	1																									
				VDELTTDLEILKAEIEEK	3	99.4%	1																									
IPI00555744	RPL14	Ribosomal protein L14 variant	100.0%	13.2	2	2	2	1	7,960,850	7,960,550	7,795,707	8,865,313	595,231	403,574	416,752	290,569	16.7	11.3	12.0	7.3	-1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.07
				ALVDGPCTQVR	2	99.8%	1																									
				GTAAAAAAAAAAAAAAK	2	98.2%	1																									
IPI00555749	PSMC5	Proteasome 26S ATPase subunit 5 variant (Fragment)	100.0%	24.6	6	6	7	1	8,588,368	8,532,524	8,890,158	9,612,413	783,954	380,259	523,693	275,770	20.4	10.0	13.2	6.4	-1.0	1	1.0	0.8	1.1	0.3	1.0	0.6	1.1	0.05	1.1	0.3
				FVVDVDKNIDINDVTPNCR	3	99.9%	1																									
				IEELQLIVNDK	2	100.0%	2																									
				IEFPPPNEEAR	2	90.7%	1																									
				LLREELQLLQEQGSYVGEVVR	3	100.0%	1																									
				VPDSTYEMIGGLDK	2	100.0%	1																									
				VSGSELVQK	2	99.1%	1																									
IPI00555853	TCOF1	isoform 5 of Treacle protein	100.0%	1.5	1	1	1	2	273,982	338,416	231,168	353,492	41,322	29,997	13,834	25,948	33.7	19.8	13.4	16.4	1.2	0.2	-1.2	0.4	1.3	0.1	-1.5	0.01	1.0	0.7	1.5	0.003
IPI00909120	TCOF1	cDNA FLJ58017, moderately similar to Treacle protein	100.0%	2.6	1	1	1	2	273,982	338,416	231,168	353,492	41,322	29,997	13,834	25,948	33.7	19.8	13.4	16.4	1.2	0.2	-1.2	0.4	1.3	0.1	-1.5	0.01	1.0	0.7	1.5	0.003
				GSLGQGTAPVLPGK	2	100.0%	1																									
IPI00555941	-	Ribosomal protein S5 variant (Fragment)	100.0%	9.4	1	1	1	1	2,137,790	2,557,210	2,450,415	3,098,460	245,899	235,057	200,384	273,357	25.7	20.6	18.3	19.7	1.2	0.3	1.1	0.4	1.4	0.03	-1.0	0.7	1.2	0.2	1.3	0.09
				LTNSMMMHGR	2	100.0%	1																									
IPI00555956	PSMB4	Proteasome subunit beta type-4	100.0%	24.6	4	4	5	1	21,511,358	19,596,158	19,959,927	22,930,200	2,130,969	874,150	1,415,263	1,457,032	22.2	10.0	15.9	14.2	-1.1	0.4	-1.1	0.6	1.1	0.6	1.0	0.8	1.2	0.09	1.1	0.2
				FEGGVVIAADMLGSYGSLAR	3	100.0%	1																									
				QPVLSQTEAR	2	100.0%	2																									
				TQNPMVTGTSVLGVK	2	99.9%	1																									
				VNNSTMLGASGDYADFQYLK	2	100.0%	1																									
IPI00555991	ITGAV	isoform 2 of Integrin alpha-V	99.9%	3.5	3	3	3	1	2,413,680	2,528,563	2,408,703	2,689,390	267,886	108,289	189,623	100,511	24.8	9.6	17.6	8.4	1.0	0.7	-1.0	1	1.1	0.4	-1.0	0.6	1.1	0.3	1.1	0.2
				AGTQLLAGLR	2	99.5%	1																									
				IYIGDDNPLTLIVK	2	90.9%	1																									
				LTPITIFMEYR	2	91.0%	1																									
IPI00556013	GPI	Glucose phosphate isomerase variant (Fragment)	90.2%	5.6	1	1	1	1	401,192	387,869	366,947	389,082	34,736	37,485	48,796	15,536	19.4	21.6	29.7	8.9	-1.0	0.8	-1.1	0.6	-1.0	0.8	-1.1	0.7	1.0	1	1.1	0.7
				ITLCLHPFSWAMLLLNEGPEGLFPPACSR	3	90.2%	1																									
IPI00556204	EEF1A2	Eukaryotic translation elongation factor 1 alpha 2 variant (Fragment)	100.0%	15.3	3	4	7	1	9,985,156	10,356,039	10,249,818	11,612,680	767,847	408,262	807,399	302,573	17.2	8.8	17.6	5.8	1.0	0.7	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.04	1.1	0.2

				IGGIGTVPVGR	2	100.0%	3																									
				NMITGTSQADCAVLIVAAGVGEFEAGISK	2	100.0%	2																									
				NMITGTSQADCAVLIVAAGVGEFEAGISK	3	100.0%	1																									
				YYITIIDAPGHR	2	98.9%	1																									
IPI00556256	DDX19A	DDX19-like protein variant (Fragment)	100.0%	7.4	2	2	2	4	1,417,448	1,537,776	1,398,665	1,598,847	78,739	53,347	95,621	65,357	12.4	7.8	15.3	9.1	1.1	0.2	-1.0	0.9	1.1	0.1	-1.1	0.2	1.0	0.5	1.1	0.1
IPI01009735	DDX19A	cDNA FLJ52463, highly similar to ATP-dependent RNA helicase DDX19A	100.0%	5.9	2	2	2	4	1,417,448	1,537,776	1,398,665	1,598,847	78,739	53,347	95,621	65,357	12.4	7.8	15.3	9.1	1.1	0.2	-1.0	0.9	1.1	0.1	-1.1	0.2	1.0	0.5	1.1	0.1
IPI01010082	DDX19A	Putative uncharacterized protein DKFZp686C21137	100.0%	6.2	2	2	2	4	1,417,448	1,537,776	1,398,665	1,598,847	78,739	53,347	95,621	65,357	12.4	7.8	15.3	9.1	1.1	0.2	-1.0	0.9	1.1	0.1	-1.1	0.2	1.0	0.5	1.1	0.1
IPI00556368	DDX19B	ATP-dependent RNA helicase DDX19B isoform 3	100.0%	6.2	2	2	2	4	1,417,448	1,537,776	1,398,665	1,598,847	78,739	53,347	95,621	65,357	12.4	7.8	15.3	9.1	1.1	0.2	-1.0	0.9	1.1	0.1	-1.1	0.2	1.0	0.5	1.1	0.1
				LDTDDLDEIEK	2	98.4%	1																									
				LKREEETLDTIK	2	81.9%	1																									
IPI00556291	PSMB1	Proteasome beta 1 subunit variant (Fragment)	95.0%	5.1	1	1	1	1	2,074,065	2,268,855	2,219,375	2,599,855	321,098	89,114	183,190	97,346	34.6	8.8	18.5	8.4	1.1	0.6	1.1	0.7	1.3	0.2	-1.0	0.8	1.1	0.04	1.2	0.1
				LSEGFSIHTR	2	95.0%	1																									
IPI00556364	ILF3	Interleukin enhancer binding factor 3 isoform c variant (Fragment)	100.0%	7.3	2	2	3	1	1,559,371	1,666,770	1,685,241	1,900,471	116,762	91,313	72,426	121,015	16.7	12.3	9.6	14.2	1.1	0.5	1.1	0.4	1.2	0.08	1.0	0.9	1.1	0.2	1.1	0.2
				QQREDITQSAQHALR	3	80.8%	1																									
				VLAGETLSVNDPPDVLDR	2	100.0%	2																									
IPI00556369	SMG1	411 kDa protein	98.6%	0.8	2	2	2	3	2,834,047	2,989,257	2,931,943	3,499,403	297,401	209,274	417,057	59,713	23.5	15.7	31.8	3.8	1.1	0.7	1.0	0.9	1.2	0.09	-1.0	0.9	1.2	0.07	1.2	0.2
IPI00639874	SMG1	isoform 2 of Serine/threonine-protein kinase SMG1	98.6%	0.9	2	2	2	3	2,834,047	2,989,257	2,931,943	3,499,403	297,401	209,274	417,057	59,713	23.5	15.7	31.8	3.8	1.1	0.7	1.0	0.9	1.2	0.09	-1.0	0.9	1.2	0.07	1.2	0.2
IPI00939320	SMG1	isoform 1 of Serine/threonine-protein kinase SMG1	98.6%	0.8	2	2	2	3	2,834,047	2,989,257	2,931,943	3,499,403	297,401	209,274	417,057	59,713	23.5	15.7	31.8	3.8	1.1	0.7	1.0	0.9	1.2	0.09	-1.0	0.9	1.2	0.07	1.2	0.2
				GPPITEAYVTDVLYR	3	92.8%	1																									
				HFSIILNLLGILLKK	2	80.2%	1																									
IPI00556409	EPB49	Uncharacterized protein	99.6%	2.2	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00884361	EPB49	dematin isoform 3	99.6%	3.4	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00975836	EPB49	Uncharacterized protein	99.6%	4.1	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00976515	EPB49	Uncharacterized protein	99.6%	8.0	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00976998	EPB49	Uncharacterized protein	99.6%	5.7	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00979805	EPB49	Uncharacterized protein	99.6%	8.1	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00980444	EPB49	Uncharacterized protein	99.6%	5.7	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00981330	EPB49	Uncharacterized protein	99.6%	3.5	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00983953	EPB49	Uncharacterized protein	99.6%	6.4	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00984478	EPB49	cDNA FLJ59528, highly similar to Dematin	99.6%	3.3	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
IPI00985119	EPB49	Uncharacterized protein	99.6%	3.7	1	1	1	11	243,299	249,445	224,491	252,502	34,858	15,531	14,473	23,093	32.0	13.9	14.4	20.5	1.0	0.9	-1.1	0.6	1.0	0.8	-1.1	0.3	1.0	0.9	1.1	0.3
				SPGIISQASAPR	2	99.6%	1																									
IPI00556437	DNM2	Dynamin 2 isoform 4 variant (Fragment)	100.0%	18.5	6	6	6	1	1,651,963	1,740,904	1,748,361	2,032,299	112,401	70,466	95,613	27,309	15.2	9.1	12.2	3.0	1.1	0.5	1.1	0.5	1.2	0.03	1.0	1	1.2	0.01	1.2	0.04
				ALLQMVQQFGVDFEK	2	100.0%	1																									
				ALLQMVQQFGVDFEKR	3	100.0%	1																									
				ESSLILAVTPANMDLANSDALK	2	100.0%	1																									
				IEGSGDQVDTLELSGGAR	2	100.0%	1																									
				VPVGDQPPDIEYQIK	2	100.0%	1																									
				VYSPHVLNLTLIDLPGITK	3	100.0%	1																									
IPI00556485	RPLP0	RPLP0 protein	100.0%	38.0	6	6	11	1	11,734,587	11,437,775	11,542,952	12,924,765	1,250,847	330,656	808,565	296,311	23.8	6.5	15.7	5.1	-1.0	0.8	-1.0	0.9	1.1	0.4	1.0	0.9	1.1	0.01	1.1	0.2
				AFLADPSAFVAAAPVAAATTAAPAAAAAPAK	2	100.0%	1																									
				AGAIAPCEVTVPAQNTGLGPEK	2	100.0%	2																									
				CFIVGADNVGSK	2	100.0%	2																									
				GHLENNPALEK	2	100.0%	2																									
				GNVGFVFTK	2	100.0%	2																									
				TSFFQALGITTK	2	100.0%	2																									
IPI00556514	RBM14	RNA binding motif protein 14 variant (Fragment)	100.0%	4.9	2	2	3	1	1,592,272	1,421,737	1,628,454	1,878,831	292,326	147,178	167,753	177,046	41.1	23.2	23.0	21.1	-1.1	0.6	1.0	0.9	1.2	0.4	1.1	0.4	1.3	0.08	1.2	0.3
				ASYVAPLTAQPATYR	2	100.0%	1																									
				KGPGLAVQSGDK	2	100.0%	2																									
IPI00556586	RUFY1	isoform 3 of RUN and FYVE domain-containing protein 1	98.3%	3.4	1	1	1	2	4,209,090	5,113,960	3,853,160	5,508,415	451,849	497,035	365,821	393,203	24.0	21.7	21.2	16.0	1.2	0.2	-1.1	0.6	1.3	0.06	-1.3	0.08	1.1	0.6	1.4	0.02
IPI00744637	RUFY1	isoform 1 of RUN and FYVE domain-containing protein 1	98.3%	2.0	1	1	1	2	4,209,090	5,113,960	3,853,160	5,508,415	451,849	497,035	365,821	393,203	24.0	21.7	21.2	16.0	1.2	0.2	-1.1	0.6	1.3	0.06	-1.3	0.08	1.1	0.6	1.4	0.02
				AAEGWSAPILTLAR	2	98.3%	1																									
IPI00556589	-	4 kDa protein	100.0%	45.7	2	2	2	1	6,798,020	6,843,090	6,578,700	7,213,815	493,493	195,534	526,206	86,272	16.2	6.4	17.9	2.7	1.0	0.9	-1.0	0.8	1.1	0.5	-1.0	0.7	1.1	0.1	1.1	0.3
				EGDVLTLLESER	2	100.0%	1																									
				GPVREGDVLTLLESER	3	99.3%	1																									
IPI00556645	FOXK1	isoform 1 of Forkhead box protein K1	98.9%	1.9	1	1	1	2	4,003,315	4,473,180	3,910,015	4,878,450	495,217	233,517	277,242	307,182	27.7	11.7	15.9	14.1	1.1	0.4	-1.0	0.9	1.2	0.2	-1.1	0.2	1.1	0.3	1.2	0.05
IPI01013576	FOXK1	cDNA FLJ55600, highly similar to Homo sapiens forkhead box K1 (FOXK1), mRNA	98.9%	2.4	1	1	1	2	4,003,315	4,473,180	3,910,015	4,878,450	495,217	233,517	277,242	307,182	27.7	11.7	15.9	14.1	1.1	0.4	-1.0	0.9	1.2	0.2	-1.1	0.2	1.1	0.3	1.2	0.05
				HLQLSFQEPHFYLR	3	98.9%	1																									
IPI00604402	PYCRL	Uncharacterized protein	98.5%	4.0	1	1	1	5	1,232,004	1,331,344	1,375,382	1,400,484	220,577	67,303	117,690	166,674	40.0	11.3	19.1	26.6	1.1	0.7	1.1	0.6	1.1	0.6	1.0	0.8	1.1	0.7	1.0	0.9
IPI00646105	PYCRL	pyrroline-5-carboxylate reductase 3	98.5%	3.9	1	1	1	5	1,232,004	1,331,344	1,375,382	1,400,484	220,577	67,303	117,690	166,674	40.0	11.3	19.1	26.6	1.1	0.7	1.1	0.6	1.1	0.6	1.0	0.8	1.1	0.7	1.0	0.9
IPI00794085	PYCRL	14 kDa protein	98.5%	8.1	1	1	1	5	1,232,004	1,331,344	1,375,382	1,400,484	220,577	67,303	117,690	166,674	40.0	11.3	19.1	26.6	1.1	0.7	1.1	0.6	1.1	0.6	1.0	0.8	1.1	0.7	1.0	0.9
IPI00926788	PYCRL	Pyrroline-5-carboxylate reductase	98.5%	4.3	1	1	1	5	1,232,004	1,331,344	1,375,382	1,400,484	220,577	67,303	117,690	166,674	40.0	11.3	19.1	26.6	1.1	0.7	1.1	0.6	1.1	0.6	1.0	0.8	1.1	0.7	1.0	0.9
IPI00926996	PYCRL	4 kDa protein	98.5%	25.0	1	1	1	5	1,232,004	1,331,344	1,375,382	1,400,484	220,577	67,303	117,690	166,674	40.0	11.3	19.1	26.6	1.1	0.7	1.1	0.6	1.1	0.6	1.0	0.8	1.1	0.7	1.0	0.9
				MAGAIAQGLIR	2	98.5%	1																									
IPI00604407	RBM3	Uncharacterized protein	100.0%	55.6	2	2	2	1	21,887,547	23,918,250	21,780,530	27,705,480	1,517,457	490,107	1,212,989	1,638,880	15.5	4.6	12.5	13.2	1.1	0.3	-1.0	1	1.3	0.03	-1.1	0.1	1.2	0.08	1.3	0.02
				GFGFITFTNPEHASVAMR	3	99.9%	1																									
				LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	3	100.0%	1																									
IPI00604431	CAND1	isoform 2 of Cullin-associated NEDD8-dissociated protein 1	100.0%	16.7	12	13	17	1	24,707,717	23,898,032	25,155,816	27,766,532	2,336,814	1,290,852	2,183,115	717,879	21.2	12.1	19.4	5.8	-1.0	0.8	1.0	0.9	1.1	0.3	1.1	0.6	1.2	0.03	1.1	0.3
				ALTLIAGSPLK	2	99.9%	1																									
				DLLDTVLPHLYNETK	2	85.2%	1																									
				DLLDTVLPHLYNETK	3	98.8%	1																									
				EGPAVVGQFIQDVK	2	99.1%	1																									
				HEMLPEFYK	2	100.0%	2																									
				IDLRPVLGEGVPILASFLR	3	100.0%	1																									
				ISGSILNELIGLVR	2	100.0%	2																									
				LGTLSALDILIK	2	100.0%	2																									
				LTLIDPETLLPR	2	100.0%	2																									
				NGEVQNLAVK	2	82.4%	1																									
				QEDVSVQLEALDIMADMLSR	2	100.0%	1																									
				SPLMSEFQSQISSNPELAAIFESIQK	3	99.9%	1																									
				SVILEAFSSPSEEVK	2	94.8%	1																									
IPI00604566	DFFA	isoform DFF35 of DNA fragmentation factor subunit alpha (Fragment)	99.4%	10.5	2	2	2	1	3,902,936	4,042,120	4,327,095	4,213,555	64,970	116,258	193,032	68,542	3.7	6.4	10.0	3.6	1.0	0.3	1.1	0.09	1.1	0.01	1.1	0.2	1.0	0.2	-1.0	0.6
				AAFGEEVDAVDTGISR	2	99.4%	1																									
				QLLQLYLQALEK	2	99.3%	1																									
IPI00604590	ME1;NME1-NME2;NM	Nucleoside diphosphate kinase	100.0%	48.0	11	17	27	2	35,028,540	34,895,583	36,335,242	41,030,462	3,717,558	1,182,607	2,988,279	1,372,077	23.7	7.6	18.4	7.5	-1.0	1	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.01	1.1	0.2
IPI00795292	ME1;NME1-NME2;NM	isoform 3 of Nucleoside diphosphate kinase B	100.0%	52.4	11	17	27	2	35,028,540	34,895,583	36,335,242	41,030,462	3,717,558	1,182,607	2,988,279	1,372,077	23.7	7.6	18.4	7.5	-1.0	1	1.0	0.8	1.2	0.2	1.0	0.7	1.2	0.01	1.1	0.2
				DRPFFAGLVK	2	99.9%	1																									
				DRPFFAGLVK	3	99.9%	1																									
				DRPFFPGLVK	2	99.8%	1																									
				DRPFFPGLVK	3	88.7%	1																									
				EISLWFKPEELVDYK	2	100.0%	2																									
				EISLWFKPEELVDYK	3	99.9%	1																									
				FMQASEDLLK	2	99.6%	2																									
				GDFCIQVGR	2	100.0%	2																									
				GLVGEIIKR	2	99.9%	2																									
				NIIHGSDSVK	1	100.0%	1																									
				TFIAIKPDGVQR	2	100.0%	2																									
				TFIAIKPDGVQR	3	99.7%	1																									
				VMLGETNPADSKPGTIR	2	100.0%	2																									
				VMLGETNPADSKPGTIR	3	100.0%	1																									
				YMHSGPVVAMVWEGLNVVK	3	100.0%	2																									
				YMNSGPVVAMVWEGLNVVK	2	100.0%	3																									
				YMNSGPVVAMVWEGLNVVK	3	100.0%	2																									
IPI00604664	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform 5	100.0%	20.1	11	11	11	6	9,277,383	8,903,039	8,877,970	10,327,706	962,499	356,470	656,326	494,740	23.2	9.0	16.5	10.7	-1.0	0.7	-1.0	0.7	1.1	0.4	-1.0	1	1.2	0.05	1.2	0.1
IPI00925023	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform 4	100.0%	22.2	11	11	11	6	9,277,383	8,903,039	8,877,970	10,327,706	962,499	356,470	656,326	494,740	23.2	9.0	16.5	10.7	-1.0	0.7	-1.0	0.7	1.1	0.4	-1.0	1	1.2	0.05	1.2	0.1
IPI00925853	NDUFS1	cDNA FLJ60586, highly similar to NADH-ubiquinone oxidoreductase 75 kDa subunit	100.0%	24.4	11	11	11	6	9,277,383	8,903,039	8,877,970	10,327,706	962,499	356,470	656,326	494,740	23.2	9.0	16.5	10.7	-1.0	0.7	-1.0	0.7	1.1	0.4	-1.0	1	1.2	0.05	1.2	0.1
IPI00927225	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform 3	100.0%	24.2	11	11	11	6	9,277,383	8,903,039	8,877,970	10,327,706	962,499	356,470	656,326	494,740	23.2	9.0	16.5	10.7	-1.0	0.7	-1.0	0.7	1.1	0.4	-1.0	1	1.2	0.05	1.2	0.1
IPI00927308	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform 2 precurso	100.0%	21.6	11	11	11	6	9,277,383	8,903,039	8,877,970	10,327,706	962,499	356,470	656,326	494,740	23.2	9.0	16.5	10.7	-1.0	0.7	-1.0	0.7	1.1	0.4	-1.0	1	1.2	0.05	1.2	0.1
IPI00940744	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	100.0%	20.5	11	11	11	6	9,277,383	8,903,039	8,877,970	10,327,706	962,499	356,470	656,326	494,740	23.2	9.0	16.5	10.7	-1.0	0.7	-1.0	0.7	1.1	0.4	-1.0	1	1.2	0.05	1.2	0.1
				ALSEIAGMTLPYDTLDQVR	2	99.9%	1																									
				DFYMTDSISR	2	95.7%	1																									
				DVAAIAGGLVDAEALVALK	2	100.0%	1																									
				FASEIAGVDDLGTTGR	2	99.9%	1																									
				FEAPLFNAR	2	99.3%	1																									
				GLLTYTSWEDALSR	2	99.8%	1																									
				GNDMQVGTYIEK	2	80.3%	1																									
				KPMVVLGSSALQR	2	97.4%	1																									
				MTSGVTGDWK	2	94.6%	1																									
				NDGAAILAAVSSIAQK	2	100.0%	1																									
				VAGMLQSFQGK	2	99.6%	1																									
IPI00604756	NRBP1	Nuclear receptor-binding protein	99.7%	3.2	1	1	1	3	785,923	812,923	939,073	982,800	129,686	80,172	88,907	60,828	36.9	22.1	21.2	13.8	1.0	0.9	1.2	0.4	1.3	0.2	1.2	0.3	1.2	0.1	1.0	0.7
IPI00893743	NRBP1	Uncharacterized protein	99.7%	3.1	1	1	1	3	785,923	812,923	939,073	982,800	129,686	80,172	88,907	60,828	36.9	22.1	21.2	13.8	1.0	0.9	1.2	0.4	1.3	0.2	1.2	0.3	1.2	0.1	1.0	0.7
IPI01014543	NRBP1	cDNA FLJ54186, highly similar to Nuclear receptor-binding protein	99.7%	3.3	1	1	1	3	785,923	812,923	939,073	982,800	129,686	80,172	88,907	60,828	36.9	22.1	21.2	13.8	1.0	0.9	1.2	0.4	1.3	0.2	1.2	0.3	1.2	0.1	1.0	0.7
				NMDTSAVLAEIPAGPGR	2	99.6%	1																									
IPI00607563	ASL	argininosuccinate lyase isoform 3	100.0%	14.8	6	6	6	1	7,539,300	7,557,093	6,811,732	8,857,058	957,478	446,054	874,988	528,474	28.4	13.2	28.7	13.3	1.0	1	-1.1	0.6	1.2	0.3	-1.1	0.5	1.2	0.1	1.3	0.08
				FVGAVDPIMEK	2	97.3%	1																									
				HLWEVDVQGSK	2	99.9%	1																									
				NPDSLELIR	2	93.8%	1																									
				QTCSTLSGLLWELIR	2	99.9%	1																									
				SRNDQVVTDLR	2	87.9%	1																									
				SSVDWQIR	2	96.9%	1																									
IPI00607577	SOD2	superoxide dismutase [Mn], mitochondrial isoform B precursor	100.0%	12.0	2	2	3	1	8,006,185	8,543,183	7,682,783	9,224,480	502,030	424,020	266,027	328,786	14.0	11.1	7.7	8.0	1.1	0.4	-1.0	0.6	1.2	0.08	-1.1	0.1	1.1	0.2	1.2	0.007
				AIWNVINWENVTER	2	100.0%	2																									
				NVRPDYLK	2	92.6%	1																									
IPI00607796	HN1L	Uncharacterized protein	100.0%	22.8	2	2	3	1	5,048,794	5,136,640	5,203,714	5,329,800	563,892	270,802	440,769	223,504	25.0	11.8	18.9	9.4	1.0	0.9	1.0	0.8	1.1	0.7	1.0	0.9	1.0	0.6	1.0	0.8
				GSGIFDESTPVQTR	2	100.0%	2																									
				SRSSAGYLWRLSALD	3	91.8%	1																									
IPI00607799	BDH2	isoform 1 of 3-hydroxybutyrate dehydrogenase type 2	99.2%	11.0	2	2	2	2	2,496,120	2,663,294	2,515,121	2,967,860	226,129	98,870	214,552	129,202	20.3	8.3	19.1	9.7	1.1	0.5	1.0	1	1.2	0.1	-1.1	0.5	1.1	0.1	1.2	0.1
IPI00970819	BDH2	isoform 3 of 3-hydroxybutyrate dehydrogenase type 2	99.2%	18.8	2	2	2	2	2,496,120	2,663,294	2,515,121	2,967,860	226,129	98,870	214,552	129,202	20.3	8.3	19.1	9.7	1.1	0.5	1.0	1	1.2	0.1	-1.1	0.5	1.1	0.1	1.2	0.1
				SGNIINMSSVASSVK	2	98.7%	1																									
				SVAADFIQQGIR	2	99.2%	1																									
IPI00607814	XPNPEP1	xaa-Pro aminopeptidase 1 isoform 2	100.0%	12.8	6	6	9	4	12,620,039	12,261,656	11,270,438	13,636,401	705,586	464,806	752,077	560,987	12.5	8.5	14.9	9.2	-1.0	0.7	-1.1	0.2	1.1	0.3	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00645898	XPNPEP1	X-prolyl aminopeptidase (Aminopeptidase P) 1, soluble	100.0%	14.9	6	6	9	4	12,620,039	12,261,656	11,270,438	13,636,401	705,586	464,806	752,077	560,987	12.5	8.5	14.9	9.2	-1.0	0.7	-1.1	0.2	1.1	0.3	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00793375	XPNPEP1	isoform 1 of Xaa-Pro aminopeptidase 1	100.0%	13.2	6	6	9	4	12,620,039	12,261,656	11,270,438	13,636,401	705,586	464,806	752,077	560,987	12.5	8.5	14.9	9.2	-1.0	0.7	-1.1	0.2	1.1	0.3	-1.1	0.3	1.1	0.1	1.2	0.04
IPI01011873	XPNPEP1	xaa-Pro aminopeptidase 1 isoform 1	100.0%	12.3	6	6	9	4	12,620,039	12,261,656	11,270,438	13,636,401	705,586	464,806	752,077	560,987	12.5	8.5	14.9	9.2	-1.0	0.7	-1.1	0.2	1.1	0.3	-1.1	0.3	1.1	0.1	1.2	0.04
				DAVALCELFNWLEK	2	100.0%	1																									
				DTPTQEDWLVSVLPEGSR	2	100.0%	1																									

				GHLLDSFAR	2	99.6%	1																								
				GSLTFEPLTLVPIQTK	2	100.0%	2																								
				IENVVLVVPVK	2	100.0%	2																								
				VGVDPLIIPTDYWK	2	100.0%	2																								
IPI00607818	MYH14	isoform 6 of Myosin-14	100.0%	32.4	46	50	59	2	67,506,856	68,500,228	66,097,902	75,376,746	5,375,277	2,944,215	3,604,644	2,428,486	17.8	9.6	12.2	7.2	1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.6	1.1	0.1	1.1	0.07
IPI00941217	MYH14	isoform 2 of Myosin-14	100.0%	31.8	46	50	59	2	67,506,856	68,500,228	66,097,902	75,376,746	5,375,277	2,944,215	3,604,644	2,428,486	17.8	9.6	12.2	7.2	1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.6	1.1	0.1	1.1	0.07
				AELEALLSSKDDVGK	2	99.9%	1																								
				AELSSLQTAR	2	99.9%	1																								
				AGVLAQLEEER	2	100.0%	2																								
				AMEAEAAGLREQLEEEAAAR	3	100.0%	1																								
				AQAELENVSGALNEAESK	2	100.0%	2																								
				AQAELENVSGALNEAESK	3	96.0%	1																								
				AQVTELEDELTAAEDAK	2	100.0%	2																								
				AQVTELEDELTAAEDAK	3	100.0%	1																								
				DLGEELEALRGELEDTLDSTNAQQELR	3	100.0%	1																								
				DQADFSVLHYAGK	2	97.2%	1																								
				EAQAALAEAQEDLESER	3	99.9%	1																								
				ELEDVTESAESMNR	2	100.0%	2																								
				ELFQETLESLR	2	99.7%	1																								
				ELQTAQAQLSEWR	2	100.0%	1																								
				ELSSTEAQLHDAQELLQEETR	2	100.0%	1																								
				ELSSTEAQLHDAQELLQEETR	3	100.0%	1																								
				EPGVPASVSTVSYGELER	2	100.0%	1																								
				EQEVTELKK	2	99.3%	1																								
				GPSAGGGPGSGTSPQVEWTAR	2	100.0%	1																								
				HEVPPHVYAVTEGAYR	3	100.0%	1																								
				HGQALGELAEQLEQAR	2	100.0%	1																								
				KEEELQAALAR	2	99.9%	2																								
				KQELELVVSELEAR	2	100.0%	1																								
				LALEAEVSELR	2	100.0%	2																								
				LALEAEVSELRAELSSLQTAR	3	98.9%	1																								
				LAQAEEQLEQETR	2	100.0%	2																								
				LELQLQEVQGR	2	99.9%	1																								
				LKYEATIADMEDR	2	99.9%	1																								
				LLGLGVTDFSR	2	100.0%	2																								
				LLLQVESLTTELSAER	2	100.0%	1																								
				LMATLSNTNPSFVR	2	100.0%	1																								
				LQEELAASDR	2	100.0%	1																								
				LQQELDDATMDLEQQR	2	100.0%	1																								
				LQQELDDATMDLEQQR	3	100.0%	1																								
				LQQHIQELEAHLEAEEGAR	3	100.0%	1																								
				MIQALELDPNLYR	2	100.0%	2																								
				MTIAALESK	2	97.2%	1																								
				MVSAVLQFGNIALK	2	100.0%	1																								
				NMDPLNDNVAALLHQSTDR	3	99.8%	1																								
				NTDQATMPDNTAAQK	2	100.0%	1																								
				QAQQDRDEMADEVANGNLSK	3	99.9%	1																								
				QLPIYTEAIVEMYR	2	98.2%	1																								
				RLDGESSELQEQMVEQQQR	3	100.0%	1																								
				RRQEEEAGALEAGEEAR	3	98.9%	1																								
				TSREEIFSQNR	2	88.9%	1																								
				VAQLEEER	2	94.3%	1																								
				VKPLLQVTR	3	98.4%	1																								
				VQELQQQSAR	2	99.8%	1																								
				VTDIIVSFQAAAR	2	99.8%	1																								
				YEILTPNAIPK	2	96.3%	1																								
IPI00607861	H6PD	GDH/6PGL endoplasmic bifunctional protein	96.8%	1.4	1	1	1	1	54,512,900	52,571,300	50,140,400	60,232,500	3,854,739	2,718,921	3,203,679	2,774,537	15.8	11.6	14.3	10.3	-1.0	0.7	-1.1	0.4	1.1	0.3	-1.0	0.6	1.1	0.08	1.2	0.04
				LANDIEATAVR	2	96.8%	1																								
IPI00619903	UGGT1	isoform 2 of UDP-glucose:glycoprotein glucosyltransferase 1	100.0%	14.8	14	14	14	1	23,894,397	24,325,876	24,521,869	27,870,419	2,110,578	777,636	1,767,495	773,487	19.8	7.2	16.1	6.2	1.0	0.9	1.0	0.8	1.2	0.1	1.0	0.9	1.1	0.01	1.1	0.1
				AIWAALQTQTSNAAK	2	100.0%	1																								
				DYLDLTASNNFFVDDYAR	2	100.0%	1																								
				EGETYFDVVAVVDPVTR	2	99.8%	1																								
				EISYENTQISR	2	100.0%	1																								
				FLDMPQSPLFTLNLNTPESWMVESVR	3	97.8%	1																								
				IIGPLEDSELFNQDDFHLLENIILK	3	100.0%	1																								
				ILETTTFFQR	2	98.0%	1																								
				IVPEWQDYDQEIK	2	99.6%	1																								
				LNIQPSEADYAVDIR	2	100.0%	1																								
				TAAVANSMNYLTK	2	90.1%	1																								
				VDALLSAQPK	2	84.6%	1																								
				VEEDVASDLVMK	2	99.8%	1																								
				WFSTPLLLEASEFLAEDSQEK	2	85.7%	1																								
				YNSWPSSLQELLRPTFPGVIR	3	98.5%	1																								
IPI00619958	TPD52	isoform 1 of Tumor protein D52	100.0%	57.6	7	7	7	7	3,259,249	3,379,352	3,317,345	3,693,973	263,733	164,265	273,524	90,122	18.1	10.9	18.4	5.5	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00873344	TPD52	isoform 3 of Tumor protein D52	100.0%	52.0	7	7	7	7	3,259,249	3,379,352	3,317,345	3,693,973	263,733	164,265	273,524	90,122	18.1	10.9	18.4	5.5	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00896474	TPD52	isoform 2 of Tumor protein D52	100.0%	70.1	7	7	7	7	3,259,249	3,379,352	3,317,345	3,693,973	263,733	164,265	273,524	90,122	18.1	10.9	18.4	5.5	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00941154	TPD52	tumor protein D52 isoform 2	100.0%	62.3	7	7	7	7	3,259,249	3,379,352	3,317,345	3,693,973	263,733	164,265	273,524	90,122	18.1	10.9	18.4	5.5	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00977108	TPD52	Prostate leucine zipper isoform 3	100.0%	55.4	7	7	7	7	3,259,249	3,379,352	3,317,345	3,693,973	263,733	164,265	273,524	90,122	18.1	10.9	18.4	5.5	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00978200	TPD52	Prostate leucine zipper variant 2	100.0%	54.2	7	7	7	7	3,259,249	3,379,352	3,317,345	3,693,973	263,733	164,265	273,524	90,122	18.1	10.9	18.4	5.5	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00984852	TPD52	Prostate leucine zipper variant 1	100.0%	52.2	7	7	7	7	3,259,249	3,379,352	3,317,345	3,693,973	263,733	164,265	273,524	90,122	18.1	10.9	18.4	5.5	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.1	1.1	0.2
				ASAAFSSVGSVITK	2	100.0%	1																								
				ELAKVEEEIQTLSQVLAAK	3	100.0%	1																								
				GWQDVTATSAYK	2	99.9%	1																								
				LGINSLQELK	2	100.0%	1																								
				TDPVPEEGEDVAATISATETLSEEEQEELRR	3	100.0%	1																								
				TSETLSQAGQK	2	99.5%	1																								
				VGGTKPAGGDFGEVLNSAANASATTTEPLPEK	3	100.0%	1																								
IPI00639797	HSD17B10	Hydroxysteroid (17-beta) dehydrogenase 10	100.0%	22.5	2	2	2	1	1,243,770	1,331,750	1,268,796	1,425,583	94,984	56,812	88,547	68,547	17.1	9.5	15.6	10.8	1.1	0.4	1.0	0.9	1.1	0.2	-1.0	0.6	1.1	0.3	1.1	0.2
				LVGQGASAVLLDLPNSGGEAQAK	2	100.0%	1																								
				VDVAVNCAGIAVASK	2	100.0%	1																								
IPI00639819	TARDBP	TAR DNA binding protein	100.0%	20.0	4	4	5	2	2,755,549	2,516,051	2,599,412	2,973,008	182,212	121,228	87,097	65,938	14.8	10.8	7.5	5.0	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.6	1.2	0.01	1.1	0.009
IPI00977115	TARDBP	34 kDa protein	100.0%	19.8	4	4	5	2	2,755,549	2,516,051	2,599,412	2,973,008	182,212	121,228	87,097	65,938	14.8	10.8	7.5	5.0	-1.1	0.3	-1.1	0.5	1.1	0.3	1.0	0.6	1.2	0.01	1.1	0.009
				AFAFVTFADDQIAQSLCGEDLIIK	2	100.0%	1																								
				GISVHISNAEPK	2	96.2%	1																								
				MDETDASSAVK	2	99.6%	1																								
				TSDLIVLGLPWK	2	100.0%	2																								
IPI00639912	NASP	Uncharacterized protein	100.0%	18.4	2	3	4	2	322,759	339,551	365,049	434,424	52,200	43,445	65,125	24,786	36.2	28.6	39.9	12.8	1.1	0.8	1.1	0.6	1.3	0.09	1.1	0.8	1.3	0.09	1.2	0.4
IPI01014799	NASP	Nuclear autoantigenic sperm protein (Fragment)	100.0%	18.2	2	3	4	2	322,759	339,551	365,049	434,424	52,200	43,445	65,125	24,786	36.2	28.6	39.9	12.8	1.1	0.8	1.1	0.6	1.3	0.09	1.1	0.8	1.3	0.09	1.2	0.4
				HLVMGDIPAAVNAFQEAASLLGK	3	100.0%	1																								
				SLQENEEEEIGNLELAWDMLDLAK	2	100.0%	2																								
				SLQENEEEEIGNLELAWDMLDLAK	3	99.9%	1																								
IPI00639931	CAP1	isoform 2 of Adenylyl cyclase-associated protein 1	100.0%	6.8	2	2	3	2	932,923	913,571	774,064	994,967	60,349	71,552	38,917	85,553	14.5	17.5	11.2	19.2	-1.0	0.8	-1.2	0.06	1.1	0.6	-1.2	0.1	1.1	0.5	1.3	0.05
IPI01015971	CAP1	46 kDa protein	100.0%	7.6	2	2	3	2	932,923	913,571	774,064	994,967	60,349	71,552	38,917	85,553	14.5	17.5	11.2	19.2	-1.0	0.8	-1.2	0.06	1.1	0.6	-1.2	0.1	1.1	0.5	1.3	0.05
				AYLSIWTELQAYIK	2	100.0%	1																								
				VENQENVSNLVIEDTELK	2	100.0%	2																								
IPI00639945	PRDX4	Protein	100.0%	28.6	5	6	8	2	10,716,482	11,070,234	10,860,636	12,279,314	823,673	573,194	821,631	776,514	17.2	11.6	16.9	14.1	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.2	1.1	0.2
IPI00647280	PRDX4	Uncharacterized protein	100.0%	17.9	5	6	8	2	10,716,482	11,070,234	10,860,636	12,279,314	823,673	573,194	821,631	776,514	17.2	11.6	16.9	14.1	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.2	1.1	0.2
				GLFIIDDK	2	100.0%	2																								
				GLFIIDDKGILR	2	98.7%	1																								
				IPLLSDLTHQISK	2	94.0%	1																								
				IPLLSDLTHQISK	3	93.5%	1																								
				LVQAFQYTDK	2	98.3%	1																								
				QITLNDLPVGR	2	100.0%	2																								
IPI00640006	GDI2	rab GDP dissociation inhibitor beta isoform 2	100.0%	24.0	7	9	14	1	9,168,576	9,542,287	9,465,379	10,637,305	782,950	433,751	808,856	293,956	19.1	10.2	19.1	6.2	1.0	0.7	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.07	1.1	0.2
				FDLGQDVIDFTGHALALYR	2	100.0%	1																								
				FDLGQDVIDFTGHALALYR	3	100.0%	1																								
				FVSISDLLVPK	2	100.0%	2																								
				KFDLGQDVIDFTGHALALYR	3	100.0%	2																								
				NPYYGGESASITPLEDLYK	2	100.0%	1																								
				PALELLEPIEQK	2	98.8%	1																								
				SPYLYPLYGLGELPQGFAR	2	100.0%	2																								
				SPYLYPLYGLGELPQGFAR	3	100.0%	2																								
				TDDYLDQPCYETINR	2	100.0%	2																								
IPI00640051	SEPHS1	selenide, water dikinase 1 isoform 3	97.0%	3.7	1	1	1	2	615,710	688,160	725,628	677,880	72,445	52,307	137,487	47,821	26.3	17.0	42.4	15.8	1.1	0.4	1.2	0.5	1.1	0.5	1.1	0.8	-1.0	0.9	-1.1	0.8
IPI00640517	SEPHS1	Selenophosphate synthetase 1	97.0%	7.2	1	1	1	2	615,710	688,160	725,628	677,880	72,445	52,307	137,487	47,821	26.3	17.0	42.4	15.8	1.1	0.4	1.2	0.5	1.1	0.5	1.1	0.8	-1.0	0.9	-1.1	0.8
				ESFNPESYELDK	2	97.0%	1																								
IPI00640197	TPP2	Tripeptidyl peptidase II	93.5%	1.2	1	1	1	1	1,620,956	1,499,800	1,858,800	1,688,310	233,342	62,121	148,740	110,767	32.2	9.3	17.9	14.7	-1.1	0.6	1.1	0.4	1.0	0.8	1.2	0.06	1.1	0.2	-1.1	0.4
				DVIPVHYYLIPPPTK	2	89.4%	1																								
IPI00640264	TPM3	Tropomyosin 3	100.0%	4.3	1	1	1	1	1,906,017	1,848,717	1,894,640	2,088,667	83,363	48,642	170,647	125,977	9.8	5.9	20.1	13.5	-1.0	0.6	-1.0	1	1.1	0.3	1.0	0.8	1.1	0.1	1.1	0.4
				TIDDLEDKLK	2	99.7%	1																								
IPI00640279	UCHL5	Ubiquitin carboxyl-terminal hydrolase L5	95.9%	11.1	1	1	1	2	332,479	387,087	314,991	369,709	35,900	29,512	29,653	10,819	24.1	17.1	21.1	6.5	1.2	0.3	-1.1	0.7	1.1	0.4	-1.2	0.1	-1.0	0.6	1.2	0.1
IPI00642987	UCHL5	Ubiquitin carboxyl-terminal hydrolase L5	95.9%	9.6	1	1	1	2	332,479	387,087	314,991	369,709	35,900	29,512	29,653	10,819	24.1	17.1	21.1	6.5	1.2	0.3	-1.1	0.7	1.1	0.4	-1.2	0.1	-1.0	0.6	1.2	0.1
				NQMLIEEEVQK	2	95.9%	1																								
IPI00640357	USP14	ubiquitin carboxyl-terminal hydrolase 14 isoform b	100.0%	30.5	10	10	11	1	15,546,052	17,615,065	15,979,443	19,891,435	1,906,574	1,143,193	1,790,578	553,893	27.4	14.5	25.1	6.2	1.1	0.4	1.0	0.9	1.3	0.08	-1.1	0.5	1.1	0.1	1.2	0.09
				AQLFALTGVQPAR	2	99.9%	1																								
				ASGEMASAQYITAALR	2	100.0%	1																								
				EKFEGVELNTDEPPMVFK	3	99.9%	1																								
				FEGVELNTDEPPMVFK	2	100.0%	1																								
				FPLMLDMYELCTPELQEK	2	99.7%	1																								
				GGTLKDDDWGNIK	2	98.6%	1																								
				LEAIEDDSVKETDSSSASAATPSK	3	100.0%	1																								
				LPAYLTIQMVR	2	100.0%	2																								
				RVEIMEEESEQ	2	100.0%	1																								
				SLIDQFFGVEFETTMK	2	100.0%	1																								
IPI00640416	VAPA	19 kDa protein	99.9%	21.1	2	2	2	1	1,295,423	1,529,871	1,526,303	1,625,443	174,074	110,475	135,883	125,407	30.1	16.2	19.9	17.3	1.2	0.3	1.2	0.3	1.3	0.2	-1.0	1	1.1	0.6	1.1	0.6
				FMVQTIFAPPNTSDMEAVWK	2	99.0%	1																								
				VAHSDKPGSTSTASFR	3	87.9%	1																								

IPI00640466	PRDX4	Uncharacterized protein	100.0%	10.2	1	1	1	1	5,394,435	4,598,855	6,300,640	4,758,830	342,573	324,098	423,097	311,957	14.2	15.8	15.0	14.7	-1.2	0.1	1.2	0.1	-1.1	0.2	1.4	0.01	1.0	0.7	-1.3	0.02
				ISKPAPYWEGTAVIDGEFK	3	99.9%	1																									
IPI00640703	XPO5	Exportin-5	96.4%	1.3	1	1	1	1	21,550,600	27,649,900	21,890,800	29,959,100	1,985,054	2,428,004	3,248,079	1,886,115	20.6	19.6	33.2	14.1	1.3	0.09	1.0	0.9	1.4	0.02	-1.3	0.2	1.1	0.5	1.4	0.06
				IFSFLLNTLQENVNK	2	96.4%	1																									
IPI00640741	PRDX1	19 kDa protein	100.0%	60.8	12	12	18	1	57,093,327	56,642,062	55,853,601	62,682,159	3,802,470	2,511,198	2,711,702	2,610,316	14.9	9.9	10.9	9.3	-1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.8	1.1	0.1	1.1	0.1
				ATAVMPDGQFK	2	100.0%	2																									
				DISLSDYK	1	98.4%	1																									
				GLFIIDDK	2	100.0%	2																									
				GLFIIDDKGILR	2	98.7%	1																									
				KQGGLGPMNIPLVSDPK	3	100.0%	1																									
				KQGGLGPMNIPLVSDPKR	3	100.0%	2																									
				LNCQVIGASVDSHFCHLAWVNTPK	3	99.8%	1																									
				LVQAFQFTDK	2	100.0%	2																									
				QGGLGPMNIPLVSDPK	2	100.0%	1																									
				QITVNDLPVGR	2	100.0%	2																									
				RTIAQDYGVLK	2	99.5%	1																									
				TIAQDYGVLK	2	100.0%	2																									
IPI00640779	ARPC5	Actin-related protein 2/3 complex subunit 5	100.0%	20.7	2	2	3	1	3,665,705	3,951,555	3,947,440	4,158,850	376,683	269,496	291,660	384,599	23.0	15.3	16.5	20.7	1.1	0.6	1.1	0.6	1.1	0.4	-1.0	1	1.1	0.7	1.1	0.7
				AVQSLDKNGVDLLMK	2	99.8%	1																									
				QGNMTAALQAALK	2	100.0%	2																									
IPI00910317	DDX39A	cDNA FLJ59857, moderately similar to ATP-dependent RNA helicase DDX39	100.0%	14.8	2	2	2	8	405,191	413,077	405,985	462,662	54,392	24,250	31,325	19,176	30.0	13.1	17.3	9.3	1.0	0.9	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00640787	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	11.8	2	2	2	8	405,191	413,077	405,985	462,662	54,392	24,250	31,325	19,176	30.0	13.1	17.3	9.3	1.0	0.9	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00641325	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	11.8	2	2	2	8	405,191	413,077	405,985	462,662	54,392	24,250	31,325	19,176	30.0	13.1	17.3	9.3	1.0	0.9	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00641926	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	16.2	2	2	2	8	405,191	413,077	405,985	462,662	54,392	24,250	31,325	19,176	30.0	13.1	17.3	9.3	1.0	0.9	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00642880	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	11.2	2	2	2	8	405,191	413,077	405,985	462,662	54,392	24,250	31,325	19,176	30.0	13.1	17.3	9.3	1.0	0.9	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00791495	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	17.6	2	2	2	8	405,191	413,077	405,985	462,662	54,392	24,250	31,325	19,176	30.0	13.1	17.3	9.3	1.0	0.9	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00795722	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	16.7	2	2	2	8	405,191	413,077	405,985	462,662	54,392	24,250	31,325	19,176	30.0	13.1	17.3	9.3	1.0	0.9	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.1	1.1	0.2
IPI00908716	DDX39B;SNORD84	cDNA FLJ53763, highly similar to Spliceosome RNA helicase BAT1	100.0%	15.8	2	2	2	8	405,191	413,077	405,985	462,662	54,392	24,250	31,325	19,176	30.0	13.1	17.3	9.3	1.0	0.9	1.0	1	1.1	0.4	-1.0	0.9	1.1	0.1	1.1	0.2
				DFLLKPELLR	3	90.9%	1																									
				GSYVSIHSSGFR	2	99.7%	1																									
IPI00640938	RALY	RNA binding protein, autoantigenic	99.4%	11.2	1	1	1	2	952,708	902,310	862,170	997,614	84,054	13,397	56,614	18,696	19.7	3.3	14.7	4.2	-1.1	0.6	-1.1	0.4	1.0	0.6	-1.0	0.5	1.1	0.003	1.2	0.07
IPI00641351	RALY	RNA binding protein, autoantigenic	99.4%	5.5	1	1	1	2	952,708	902,310	862,170	997,614	84,054	13,397	56,614	18,696	19.7	3.3	14.7	4.2	-1.1	0.6	-1.1	0.4	1.0	0.6	-1.0	0.5	1.1	0.003	1.2	0.07
				KSDVETIFSK	2	99.0%	1																									
IPI00640965	SAE1	SUMO-activating enzyme subunit 1 isoform b	100.0%	3.7	1	1	2	3	1,016,913	1,044,455	1,008,095	956,430	178,290	152,630	127,842	61,305	39.2	32.7	28.4	14.3	1.0	0.9	-1.0	1	-1.1	0.8	-1.0	0.9	-1.1	0.6	-1.1	0.7
IPI00647006	SAE1	cDNA FLJ14689 fis, clone NT2RP2005204, highly similar to Ubiquitin-like 1-activatin	100.0%	3.7	1	1	2	3	1,016,913	1,044,455	1,008,095	956,430	178,290	152,630	127,842	61,305	39.2	32.7	28.4	14.3	1.0	0.9	-1.0	1	-1.1	0.8	-1.0	0.9	-1.1	0.6	-1.1	0.7
IPI01011453	SAE1	SUMO-activating enzyme subunit 1 isoform c	100.0%	4.1	1	1	2	3	1,016,913	1,044,455	1,008,095	956,430	178,290	152,630	127,842	61,305	39.2	32.7	28.4	14.3	1.0	0.9	-1.0	1	-1.1	0.8	-1.0	0.9	-1.1	0.6	-1.1	0.7
				AQNLNPMVDVK	2	100.0%	2																									
IPI00640981	UBR4	isoform 4 of E3 ubiquitin-protein ligase UBR4	99.6%	0.7	2	2	2	4	1,383,448	1,358,119	1,428,437	1,493,648	96,808	51,066	81,144	68,173	15.7	8.4	12.7	10.2	-1.0	0.8	1.0	0.7	1.1	0.4	1.1	0.5	1.1	0.2	1.0	0.6
IPI00646605	UBR4	isoform 3 of E3 ubiquitin-protein ligase UBR4	99.6%	0.7	2	2	2	4	1,383,448	1,358,119	1,428,437	1,493,648	96,808	51,066	81,144	68,173	15.7	8.4	12.7	10.2	-1.0	0.8	1.0	0.7	1.1	0.4	1.1	0.5	1.1	0.2	1.0	0.6
IPI00746934	UBR4	isoform 2 of E3 ubiquitin-protein ligase UBR4	99.6%	0.7	2	2	2	4	1,383,448	1,358,119	1,428,437	1,493,648	96,808	51,066	81,144	68,173	15.7	8.4	12.7	10.2	-1.0	0.8	1.0	0.7	1.1	0.4	1.1	0.5	1.1	0.2	1.0	0.6
IPI00843999	UBR4	isoform 1 of E3 ubiquitin-protein ligase UBR4	99.6%	0.7	2	2	2	4	1,383,448	1,358,119	1,428,437	1,493,648	96,808	51,066	81,144	68,173	15.7	8.4	12.7	10.2	-1.0	0.8	1.0	0.7	1.1	0.4	1.1	0.5	1.1	0.2	1.0	0.6
				ILGPAESDEFLAR	2	98.5%	1																									
				LEQVSSDEGIGTLAENLLEALR	2	99.0%	1																									
IPI00641040	ESD	28 kDa protein	100.0%	13.8	2	2	2	2	2,551,563	2,465,392	2,869,612	2,667,739	120,919	287,168	153,037	285,029	10.6	26.1	11.9	23.9	-1.0	0.8	1.1	0.1	1.0	0.7	1.2	0.2	1.1	0.6	-1.1	0.6
IPI00645836	ESD	Protein	100.0%	15.2	2	2	2	2	2,551,563	2,465,392	2,869,612	2,667,739	120,919	287,168	153,037	285,029	10.6	26.1	11.9	23.9	-1.0	0.8	1.1	0.1	1.0	0.7	1.2	0.2	1.1	0.6	-1.1	0.6
				AFSGYLGTDQSK	2	98.0%	1																									
				MYSYVTEELPQLINANFPVDPQR	2	99.6%	1																									
IPI00641064	NUDT5	Uncharacterized protein	100.0%	13.3	1	1	2	1	672,162	641,487	622,353	659,615	53,117	39,956	24,826	55,760	17.7	13.9	8.9	18.9	-1.0	0.7	-1.1	0.4	-1.0	0.9	-1.0	0.7	1.0	0.8	1.1	0.6
				QYIISEELISEGK	2	100.0%	2																									
IPI00641123	GALE	UDP-galactose-4-epimerase	100.0%	20.1	3	3	4	2	2,815,869	2,941,362	2,878,027	3,343,227	269,431	123,088	176,093	76,361	21.4	9.4	13.7	5.1	1.0	0.7	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.02	1.2	0.04
IPI00644364	GALE	UDP-galactose-4-epimerase	100.0%	20.0	3	3	4	2	2,815,869	2,941,362	2,878,027	3,343,227	269,431	123,088	176,093	76,361	21.4	9.4	13.7	5.1	1.0	0.7	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.02	1.2	0.04
				FFIEEMIR	2	99.8%	1																									
				SVEFEEMDILDQGALQR	3	100.0%	1																									
				VNLTGTIQLLEIMK	2	100.0%	2																									
IPI00641181	MARCKSL1	MARCKS-related protein	100.0%	25.1	2	2	2	1	5,708,190	5,658,890	6,101,760	6,002,620	287,435	334,552	450,838	435,657	11.3	13.2	16.5	16.2	-1.0	0.9	1.1	0.5	1.1	0.6	1.1	0.5	1.1	0.5	-1.0	0.9
				GDVTAEEAAGASPAK	2	99.3%	1																									
				GEGESPPVNGTDEAAGATGDAIEPAPPSQGAEAK	3	100.0%	1																									
IPI00641244	PRDX1	11 kDa protein	100.0%	21.7	2	2	4	1	13,187,740	13,444,873	12,444,200	14,855,180	746,289	563,977	660,171	685,853	12.7	9.4	11.9	10.3	1.0	0.8	-1.1	0.5	1.1	0.1	-1.1	0.3	1.1	0.2	1.2	0.04
				LVQAFQFTDK	2	100.0%	2																									
				QITVNDLPVGR	2	100.0%	2																									
IPI00641266	CAPN2	calpain-2 catalytic subunit isoform 2	100.0%	19.8	7	9	10	1	7,623,174	7,852,334	8,055,543	8,802,906	735,639	121,139	590,991	170,188	21.6	3.5	16.4	4.3	1.0	0.8	1.1	0.7	1.2	0.2	1.0	0.8	1.1	0.002	1.1	0.3
				DGELLFVHSAEGSEFWSALLEK	3	100.0%	1																									
				FADDQLIIDFDNFVR	2	100.0%	1																									
				FADDQLIIDFDNFVR	3	95.2%	1																									
				GHAYSVTGAEEVESNGSLQK	3	82.0%	1																									
				LEICNLTPDTLTSDTYKK	3	99.9%	1																									
				LFAQLAGEDAEISAFELQTILR	2	100.0%	1																									
				LFAQLAGEDAEISAFELQTILR	3	100.0%	1																									
				NPWGEVEWTGR	2	100.0%	1																									
				NYPNTFWMNPQYLIK	2	100.0%	2																									
IPI00641430	LMO7	Uncharacterized protein	100.0%	13.0	9	9	12	1	4,961,316	5,297,659	4,843,133	5,921,723	631,405	447,837	440,720	179,589	28.5	18.9	20.4	6.8	1.1	0.7	-1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.2	1.2	0.05
				EPSLATWEATWSEGSK	2	100.0%	1																									
				FSYNDSKEWEEAMAK	3	98.4%	1																									
				ISINQTPGK	2	99.3%	2																									
				KWEQQLQEEQEQKR	3	92.3%	1																									
				SMSDVSAEDVQNLR	2	100.0%	2																									
				SWASPVYTEADGTFSR	2	100.0%	1																									
				TEEASSGFLPGDR	2	99.7%	1																									
				TPNNVVSTPAPSPDASQLASSLSSQK	3	100.0%	1																									
				WIDATSGIYNSEK	2	100.0%	2																									
IPI00641498	PDZK1	30 kDa protein	99.9%	8.3	2	2	2	1	3,393,960	3,587,520	3,731,667	3,977,527	150,813	151,810	541,230	155,493	9.9	9.5	32.4	8.7	1.1	0.4	1.1	0.6	1.2	0.03	1.0	0.8	1.1	0.1	1.1	0.7
				IEKDTEGHLVR	3	82.1%	1																									
				QEGQNYGFFLR	2	99.2%	1																									
IPI00641565	CRYZ	Uncharacterized protein	100.0%	18.1	3	3	4	1	13,755,298	14,732,932	15,132,777	17,521,757	1,770,401	837,929	1,452,687	506,463	28.8	12.7	21.5	6.5	1.1	0.6	1.1	0.6	1.3	0.1	1.0	0.8	1.2	0.02	1.2	0.2
				AGESVLVHGASGGVGLAACQIAR	3	100.0%	2																									
				DLSLLSHGGR	2	99.3%	1																									
				VFEFGGPEVLK	2	100.0%	1																									
IPI00641634	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	16.9	4	5	5	4	3,544,423	3,563,674	3,260,463	3,818,509	293,139	186,413	261,249	147,345	18.5	11.7	17.9	8.6	1.0	1	-1.1	0.5	1.1	0.4	-1.1	0.4	1.1	0.3	1.2	0.1
IPI00642800	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	16.5	4	5	5	4	3,544,423	3,563,674	3,260,463	3,818,509	293,139	186,413	261,249	147,345	18.5	11.7	17.9	8.6	1.0	1	-1.1	0.5	1.1	0.4	-1.1	0.4	1.1	0.3	1.2	0.1
IPI00643815	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	13.5	4	5	5	4	3,544,423	3,563,674	3,260,463	3,818,509	293,139	186,413	261,249	147,345	18.5	11.7	17.9	8.6	1.0	1	-1.1	0.5	1.1	0.4	-1.1	0.4	1.1	0.3	1.2	0.1
IPI00796920	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	16.4	4	5	5	4	3,544,423	3,563,674	3,260,463	3,818,509	293,139	186,413	261,249	147,345	18.5	11.7	17.9	8.6	1.0	1	-1.1	0.5	1.1	0.4	-1.1	0.4	1.1	0.3	1.2	0.1
				DFLLKPELLR	2	99.3%	1																									
				DFLLKPELLR	3	90.9%	1																									
				GSYVSIHSSGFR	2	99.7%	1																									
				HFILDECDK	2	99.7%	1																									
				MLEQLDMR	2	100.0%	1																									
IPI00641665	ILF2	12 kDa protein	100.0%	12.2	1	1	1	1	4,992,540	4,893,385	4,921,605	5,093,105	332,734	244,291	364,600	108,214	14.9	11.2	16.6	4.8	-1.0	0.8	-1.0	0.9	1.0	0.8	1.0	1	1.0	0.5	1.0	0.7
				ILPTLEAVAALGNK	2	100.0%	1																									
IPI00641706	TUBB6	46 kDa protein	99.9%	10.8	2	2	2	2	3,452,589	3,450,510	3,668,805	3,748,657	153,151	189,639	124,552	71,106	9.9	12.3	7.6	4.2	-1.0	1	1.1	0.3	1.1	0.1	1.1	0.4	1.1	0.2	1.0	0.6
IPI00908469	TUBB6	cDNA FLJ52712, highly similar to Tubulin beta-6 chain	99.9%	10.5	2	2	2	2	3,452,589	3,450,510	3,668,805	3,748,657	153,151	189,639	124,552	71,106	9.9	12.3	7.6	4.2	-1.0	1	1.1	0.3	1.1	0.1	1.1	0.4	1.1	0.2	1.0	0.6
				FWEVISDEHGIDPAGGYVGDSALQLER	3	99.7%	1																									
				MASTFIGNSTAIQELFK	2	99.5%	1																									
IPI00641829	DDX39B;SNORD84	isoform 2 of Spliceosome RNA helicase DDX39B	100.0%	32.7	12	13	14	2	13,412,360	13,422,404	13,274,177	15,403,674	1,324,268	574,654	833,898	520,370	22.1	9.6	14.1	7.6	1.0	1	-1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.03	1.2	0.06
IPI00848161	DDX39B;SNORD84	isoform 1 of Spliceosome RNA helicase DDX39B	100.0%	33.9	12	13	14	2	13,412,360	13,422,404	13,274,177	15,403,674	1,324,268	574,654	833,898	520,370	22.1	9.6	14.1	7.6	1.0	1	-1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.03	1.2	0.06
				CIALAQLLVEQNFPAIAIHR	3	100.0%	2																									
				DFLLKPELLR	2	99.3%	1																									
				DFLLKPELLR	3	90.9%	1																									
				FMQDPMEIFVDDETK	2	99.8%	1																									
				GLAITFVSDENDAK	2	100.0%	1																									
				GSYVSIHSSGFR	2	99.7%	1																									
				HFILDECDK	2	99.7%	1																									
				ILNDVQDR	2	99.9%	1																									
				ILVATNLFGR	2	98.9%	1																									
				MLEQLDMR	2	100.0%	1																									
				NCPHIVVGTPGR	2	99.8%	1																									
				RDVQEIFR	2	98.1%	1																									
				VNIAFNYDMPEDSDTYLHR	3	100.0%	1																									
IPI00641837	SLC2A1	Uncharacterized protein	100.0%	10.0	2	2	4	2	1,522,293	1,429,513	1,532,768	1,602,665	189,135	89,040	149,938	76,046	27.8	13.9	21.9	10.6	-1.1	0.7	1.0	1	1.1	0.7	1.1	0.6	1.1	0.2	1.0	0.7
IPI01015815	SLC2A1	cDNA FLJ60414, highly similar to Solute carrier family 2, facilitated glucose transpor	100.0%	5.5	2	2	4	2	1,522,293	1,429,513	1,532,768	1,602,665	189,135	89,040	149,938	76,046	27.8	13.9	21.9	10.6	-1.1	0.7	1.0	1	1.1	0.7	1.1	0.6	1.1	0.2	1.0	0.7
				GTADVTHDLQEMKEESR	3	100.0%	2																									
				VTILELFR	2	100.0%	2																									
IPI00641881	CAP1	Adenylyl cyclase-associated protein	100.0%	19.2	3	4	6	7	524,650	607,392	587,452	662,460	45,927	23,169	56,888	37,944	19.6	8.5	21.7	12.8	1.2	0.1	1.1	0.4	1.3	0.05	-1.0	0.8	1.1	0.3	1.1	0.3
IPI00642414	CAP1	Adenylyl cyclase-associated protein	100.0%	22.4	3	4	6	7	524,650	607,392	587,452	662,460	45,927	23,169	56,888	37,944	19.6	8.5	21.7	12.8	1.2	0.1	1.1	0.4	1.3	0.05	-1.0	0.8	1.1	0.3	1.1	0.3
IPI00644109	CAP1	Adenylyl cyclase-associated protein	100.0%	21.7	3	4	6	7	524,650	607,392	587,452	662,460	45,927	23,169	56,888	37,944	19.6	8.5	21.7	12.8	1.2	0.1	1.1	0.4	1.3	0.05	-1.0	0.8	1.1	0.3	1.1	0.3
IPI00644589	CAP1	Adenylyl cyclase-associated protein	100.0%	18.8	3	4	6	7	524,650	607,392	587,452	662,460	45,927	23,169	56,888	37,944	19.6	8.5	21.7	12.8	1.2	0.1	1.1	0.4	1.3	0.05	-1.0	0.8	1.1	0.3	1.1	0.3
IPI00646269	CAP1	Adenylyl cyclase-associated protein	100.0%	22.2	3	4	6	7	524,650	607,392	587,452	662,460	45,927	23,169	56,888	37,944	19.6	8.5	21.7	12.8	1.2	0.1	1.1	0.4	1.3	0.05	-1.0	0.8	1.1	0.3	1.1	0.3
IPI00646869	CAP1	Adenylyl cyclase-associated protein	100.0%	18.1	3	4	6	7	524,650	607,392	587,452	662,460	45,927	23,169	56,888	37,944	19.6	8.5	21.7	12.8	1.2	0.1	1.1	0.4	1.3	0.05	-1.0	0.8	1.1	0.3	1.1	0.3
IPI00647351	CAP1	Adenylyl cyclase-associated protein	100.0%	19.3	3	4	6	7	524,650	607,392	587,452	662,460	45,927	23,169	56,888	37,944	19.6	8.5	21.7	12.8	1.2	0.1	1.1	0.4	1.3	0.05	-1.0	0.8	1.1	0.3	1.1	0.3
				AGAAPYVQAFDSLLAGPVAEYLK	2	100.0%	2																									
				AGAAPYVQAFDSLLAGPVAEYLK	3	99.9%	1																									
				ALLVTASQCQQPAENK	2	100.0%	1																									
				GAAPYVQAFDSLLAGPVAEYLK	2	99.9%	2																									
IPI00641988	LIPE	57 kDa protein	100.0%	13.0	4	4	4	1	3,920,846	3,690,021	3,953,497	4,207,614	214,410	115,949	231,893	169,773	12.2	7.0	13.1	9.0	-1.1	0.4	1.0	0.9	1.1	0.3	1.1	0.3	1.1	0.04	1.1	0.4
				LGASSWLNSFLELSGR	2	99.9%	1																									
				LLSLMDPLLPLSVLSK	2	100.0%	1																									
				NPFMSPLLAPDSMLK	2	99.4%	1																									
				VPDGIMAAYPATMLQPAASPSR	2	99.5%	1																									
IPI00642016	CRYZ	Uncharacterized protein	100.0%	16.5	2	2	3	1	12,809,701	13,691,922	14,163,470	16,356,324	1,742,473	779,325	1,404,451	516,989	30.4	12.7	22.2	7.1	1.1	0.7	1.1	0.6	1.3	0.1	1.0	0.8	1.2	0.02	1.2	0.2
				AGESVLVHGASGGVGLAACQIAR	3	100.0%	2																									
				VFEFGGPEVLK	2	100.0%	1																									
IPI00642048	GMDS	Uncharacterized protein	99.9%	9.9	2	3	3	1	3,833,779	3,791,785	3,782,521	4,557,045	142,134	224,736	385,597	127,957	8.3	13.3	22.8	6.3	-1.0	0.9	-1.0	0.9	1.2	0.005	-1.0	1	1.2	0.02	1.2	0.1
				ISFDLAEYTADVDGVGTLR	2	99.6%	1																									
				ISFDLAEYTADVDGVGTLR	3	99.5%	1																									
				VQEIPQKETTPFYPR	3	87.2%	1																									
IPI00642097	GSPT2	Eukaryotic peptide chain release factor GTP-binding subunit ERF3B	100.0%	7.3	4	4	5	1	7,894,043	7,508,229	7,396,882	8,229,364	533,346	203,167	332,056	360,116	15.1	6.1	10.0	9.8	-1.1	0.5	-1.1	0.5	1.0	0.6	-1.0	0.8	1.1	0.1	1.1	0.1
				GQQLVMMPNK	2	100.0%	1																									
				HFTILDAPGHK	3	99.2%	1																									

				HLIVLINK	2	95.5%	1																									
				PFVPNVHAAEFVPSFLR	3	100.0%	2																									
IPI00642117	GNB1	cDNA FLJ16663 fis, clone THYMU2005759, highly similar to Guanine nucleotide-bin	100.0%	26.3	4	5	8	1	6,681,096	7,126,728	7,355,709	7,687,784	790,378	306,466	666,974	279,140	26.5	9.6	20.3	8.1	1.1	0.6	1.1	0.5	1.2	0.3	1.0	0.8	1.1	0.2	1.0	0.7
				AGVLAGHDNR	2	100.0%	1																									
				LFVSGACDASAK	2	100.0%	2																									
				LLLAGYDDFNCNVWDALK	2	100.0%	2																									
				VSCLGVTDDGMAVATGSWDSFLK	2	100.0%	2																									
				VSCLGVTDDGMAVATGSWDSFLK	3	100.0%	1																									
IPI00642144	ALDH1A1	Aldehyde dehydrogenase 1 family, member A1	100.0%	7.4	1	1	2	1	1,321,928	1,381,743	1,222,893	1,412,308	138,364	125,143	153,061	173,147	23.4	20.3	28.0	27.4	1.0	0.8	-1.1	0.6	1.1	0.7	-1.1	0.4	1.0	0.9	1.2	0.4
				LYSNAYLNDLAGCIK	2	100.0%	2																									
IPI00642197	HUWE1	HECT, UBA and WWE domain containing 1	99.9%	2.4	3	3	3	1	6,460,601	6,814,788	6,225,268	7,927,371	732,440	278,785	505,556	230,770	25.4	9.2	18.2	6.5	1.1	0.7	-1.0	0.8	1.2	0.1	-1.1	0.3	1.2	0.02	1.3	0.02
				LPGGVQNFPQFSALR	2	94.6%	1																									
				QVVNQVWEAADVLIK	2	98.8%	1																									
				SILTLSHEPK	2	97.5%	1																									
IPI00642199	-	14 kDa protein	94.9%	10.7	1	1	1	1	3,981,470	4,159,130	4,454,460	4,787,090	623,843	394,023	147,371	342,062	35.0	21.2	7.4	16.0	1.0	0.8	1.1	0.5	1.2	0.3	1.1	0.5	1.2	0.3	1.1	0.4
				GCIWEMQVDTHSR	3	94.9%	1																									
IPI00642211	RNPEP	Aminopeptidase B	100.0%	17.5	9	10	10	1	34,938,175	35,586,515	35,315,600	39,395,358	3,271,360	1,680,974	2,441,848	1,090,354	20.9	10.6	15.5	6.2	1.0	0.9	1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.09	1.1	0.2
				AEFGPPGPGAGSR	2	93.9%	1																									
				AFFPCFDTPAVK	2	81.3%	1																									
				AIEAVAISPWK	2	100.0%	1																									
				GLSGTAVLDLR	2	97.4%	1																									
				NDHQEDFWK	2	97.3%	1																									
				NDHQEDFWK	3	85.9%	1																									
				TYQLVYFLDK	2	92.5%	1																									
				VDIIPGFEFDR	2	99.9%	1																									
				VGEGPGVCWLAPEQTAGK	2	100.0%	1																									
				VKIEPGVDPDDTYNETPYEK	3	99.8%	1																									
IPI00642213	RALY	RNA binding protein, autoantigenic	100.0%	24.9	4	4	5	1	3,626,613	3,668,686	3,665,006	4,355,154	253,648	189,228	412,531	206,424	15.6	11.5	25.2	10.6	1.0	0.9	1.0	0.9	1.2	0.06	-1.0	1	1.2	0.04	1.2	0.2
				GDGGGAGGGGGGGGSGGGGSGGGGGGGGGS	3	93.2%	1																									
				GYAFVQYSNER	2	99.9%	1																									
				KSDVETIFSK	2	99.0%	1																									
				LEQIAAEQK	2	98.9%	2																									
IPI00642387	EIF1AX	13 kDa protein	100.0%	56.9	4	5	6	1	8,891,011	8,460,865	7,598,640	9,643,565	701,557	371,763	604,350	666,780	17.6	9.8	17.8	15.5	-1.1	0.6	-1.2	0.2	1.1	0.5	-1.1	0.3	1.1	0.2	1.3	0.05
				AYGELPEHAK	2	99.3%	1																									
				AYGELPEHAK	3	84.5%	1																									
				DYQDNKADVILK	2	99.8%	1																									
				INETDTFGPGDDDEIQFDDIGDDDEDIDDI	3	97.6%	1																									
				VWINTSDIILVGLR	2	100.0%	2																									
IPI00642393	SMS	isoform 2 of Spermine synthase	100.0%	10.9	2	3	3	1	6,845,341	5,697,074	5,591,234	6,996,150	946,865	254,809	541,323	450,858	30.9	10.0	21.7	14.4	-1.2	0.3	-1.2	0.3	1.0	0.9	-1.0	0.9	1.2	0.04	1.3	0.08
				HSTLDFMLGAK	2	100.0%	1																									
				YFTQGNCVNLTEALSLYEEQLGR	2	99.6%	1																									
				YFTQGNCVNLTEALSLYEEQLGR	3	99.7%	1																									
IPI00642454	RPL7A;SNORD24	Ribosomal protein L7a	100.0%	8.6	1	1	2	1	1,463,205	1,831,930	1,475,503	2,070,928	167,417	191,990	72,156	79,510	25.6	23.4	10.9	8.6	1.3	0.2	1.0	0.9	1.4	0.01	-1.2	0.1	1.1	0.3	1.4	0.0005
				AGVNTVTTLVENK	2	100.0%	2																									
IPI00642457	APRT	adenine phosphoribosyltransferase isoform b	100.0%	47.8	5	6	11	1	32,569,905	34,144,404	34,060,940	36,108,489	3,367,063	2,534,637	2,346,032	1,322,061	23.1	16.6	15.4	8.2	1.0	0.7	1.0	0.7	1.1	0.4	-1.0	1	1.1	0.5	1.1	0.5
				AAIGLLAR	2	99.0%	2																									
				DISPVLKDPASFR	2	100.0%	2																									
				DISPVLKDPASFR	3	98.0%	1																									
				GFLFGPSLAQELGLGCVLIR	3	100.0%	2																									
				IDYIAGLDSR	2	100.0%	2																									
				SFPDFPTPGVVFR	2	100.0%	2																									
IPI00642494	UPRT	isoform 1 of Uracil phosphoribosyltransferase homolog	90.5%	5.2	1	1	1	3	953,920	1,002,237	965,533	1,069,510	116,159	60,010	98,334	67,662	27.2	13.4	22.8	14.2	1.1	0.7	1.0	0.9	1.1	0.4	-1.0	0.8	1.1	0.5	1.1	0.4
IPI00797517	UPRT	isoform 3 of Uracil phosphoribosyltransferase homolog	90.5%	5.7	1	1	1	3	953,920	1,002,237	965,533	1,069,510	116,159	60,010	98,334	67,662	27.2	13.4	22.8	14.2	1.1	0.7	1.0	0.9	1.1	0.4	-1.0	0.8	1.1	0.5	1.1	0.4
IPI00978934	UPRT	Uncharacterized protein	90.5%	9.3	1	1	1	3	953,920	1,002,237	965,533	1,069,510	116,159	60,010	98,334	67,662	27.2	13.4	22.8	14.2	1.1	0.7	1.0	0.9	1.1	0.4	-1.0	0.8	1.1	0.5	1.1	0.4
				LIRLVVEEGLNQLPYK	2	90.5%	1																									
IPI00642548	PHGDH	Phosphoglycerate dehydrogenase	100.0%	21.6	7	8	11	1	26,827,771	28,029,812	27,461,116	29,443,413	1,737,594	886,643	1,195,962	1,417,797	14.5	7.1	9.7	10.8	1.0	0.6	1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.3
				AGTGVDNVDLEAATR	2	100.0%	2																									
				ALVDHENVISCPHLGASTK	3	100.0%	1																									
				CGEEIAVQFVDMVK	2	100.0%	1																									
				GGIVDEGALLR	2	99.9%	1																									
				NAGNCLSPAVIVGLLK	2	100.0%	2																									
				TQTSDPAMLPTMIGLLAEAGVR	2	100.0%	2																									
				TQTSDPAMLPTMIGLLAEAGVR	3	100.0%	1																									
				VTADVINAAEK	2	91.2%	1																									
IPI00642549	RAD23B	cDNA FLJ56531, highly similar to UV excision repair protein RAD23 homolog B	100.0%	22.1	8	9	10	1	19,344,530	18,997,558	19,363,530	21,416,093	1,227,614	453,475	923,465	866,062	14.2	5.3	10.7	9.0	-1.0	0.8	1.0	1	1.1	0.2	1.0	0.7	1.1	0.04	1.1	0.1
				ASFNNPDR	2	93.1%	1																									
				AVEYLLMGIPGDR	2	99.5%	1																									
				GKDAFPVAGQK	2	98.6%	1																									
				IDIDPEETVK	2	99.8%	1																									
				NFVVVMVTKPK	2	99.8%	1																									
				NQPQFQQMR	2	99.9%	1																									
				QIIQQNPSLLPALLQQIGR	2	100.0%	2																									
				QIIQQNPSLLPALLQQIGR	3	100.0%	1																									
				TLQQQTFK	2	97.2%	1																									
IPI00642560	AKR1C1	Uncharacterized protein	100.0%	19.0	3	3	3	1	2,189,733	2,324,463	2,272,010	2,701,812	150,290	130,932	118,572	129,665	15.4	12.6	11.7	10.7	1.1	0.5	1.0	0.7	1.2	0.03	-1.0	0.8	1.2	0.07	1.2	0.04
				HIDSAHLYNNEEQVGLAIR	3	100.0%	1																									
				LAIEAGFR	2	97.8%	1																									
				QLEMILNKPGLK	3	81.8%	1																									
IPI00642656	CNDP2	14 kDa protein	100.0%	8.1	1	1	1	2	1,343,352	1,457,782	1,261,108	1,660,940	107,457	89,968	115,966	139,080	17.9	13.8	20.6	18.7	1.1	0.4	-1.1	0.6	1.2	0.1	-1.2	0.2	1.1	0.3	1.3	0.06
IPI00643827	CNDP2	15 kDa protein	100.0%	7.6	1	1	1	2	1,343,352	1,457,782	1,261,108	1,660,940	107,457	89,968	115,966	139,080	17.9	13.8	20.6	18.7	1.1	0.4	-1.1	0.6	1.2	0.1	-1.2	0.2	1.1	0.3	1.3	0.06
				MMEVAAADVK	2	100.0%	1																									
IPI00642705	ARID1A	isoform 2 of AT-rich interactive domain-containing protein 1A	95.3%	1.5	1	1	1	2	118,890	118,310	126,632	151,790	27,566	13,462	18,053	12,654	51.9	25.4	31.9	18.6	-1.0	1	1.1	0.8	1.3	0.3	1.1	0.7	1.3	0.1	1.2	0.3
IPI00643722	ARID1A	isoform 1 of AT-rich interactive domain-containing protein 1A	95.3%	1.3	1	1	1	2	118,890	118,310	126,632	151,790	27,566	13,462	18,053	12,654	51.9	25.4	31.9	18.6	-1.0	1	1.1	0.8	1.3	0.3	1.1	0.7	1.3	0.1	1.2	0.3
				ELQDGAESNGGGGGGGAGSGGGPGAEPDLK	2	95.3%	1																									
IPI00642780	MYL12A	13 kDa protein	100.0%	8.7	1	1	2	1	891,081	920,650	836,980	937,178	64,356	30,315	49,058	33,311	16.2	7.4	13.1	8.0	1.0	0.7	-1.1	0.5	1.1	0.5	-1.1	0.2	1.0	0.7	1.1	0.1
				EAFNMIDQNR	2	100.0%	2																									
IPI00642792	CNDP2	19 kDa protein	100.0%	27.2	3	3	3	1	3,008,304	3,035,806	2,980,266	3,547,110	229,275	207,884	247,005	99,564	17.0	15.3	18.5	6.3	1.0	0.9	-1.0	0.9	1.2	0.06	-1.0	0.9	1.2	0.06	1.2	0.07
				GSTDDKGPVAGWINALEAYQK	3	100.0%	1																									
				LPDGSEIPLPPILLGR	2	99.3%	1																									
				MMEVAAADVK	2	100.0%	1																									
IPI00642816	SRP9	Signal recognition particle 9 kDa protein	100.0%	23.3	2	2	2	1	8,662,067	8,725,890	8,968,833	8,980,470	560,571	279,036	497,118	127,182	14.5	7.2	12.4	3.2	1.0	0.9	1.0	0.7	1.0	0.6	1.0	0.7	1.0	0.4	1.0	1
				HSDGNLCVK	2	99.7%	1																									
				VTDDLVCLVYK	2	99.2%	1																									
IPI00929577	ABHD2	Similar to Vesicle-associated membrane protein-associated protein A isoform 2	100.0%	3.9	1	1	1	4	637,377	790,311	746,559	840,384	72,600	91,309	67,352	52,076	25.5	25.8	20.2	13.9	1.2	0.2	1.2	0.3	1.3	0.05	-1.1	0.7	1.1	0.6	1.1	0.3
IPI00642826	VAPA	14 kDa protein	100.0%	9.6	1	1	1	4	637,377	790,311	746,559	840,384	72,600	91,309	67,352	52,076	25.5	25.8	20.2	13.9	1.2	0.2	1.2	0.3	1.3	0.05	-1.1	0.7	1.1	0.6	1.1	0.3
IPI00748221	VAPB	isoform 2 of Vesicle-associated membrane protein-associated protein B/C	100.0%	12.1	1	1	1	4	637,377	790,311	746,559	840,384	72,600	91,309	67,352	52,076	25.5	25.8	20.2	13.9	1.2	0.2	1.2	0.3	1.3	0.05	-1.1	0.7	1.1	0.6	1.1	0.3
IPI00980397	VAPB	Uncharacterized protein	100.0%	16.9	1	1	1	4	637,377	790,311	746,559	840,384	72,600	91,309	67,352	52,076	25.5	25.8	20.2	13.9	1.2	0.2	1.2	0.3	1.3	0.05	-1.1	0.7	1.1	0.6	1.1	0.3
				GPFTDVVTTNLK	2	99.9%	1																									
IPI00642931	SEC23B	Sec23 homolog B	100.0%	18.4	4	4	4	1	8,051,999	8,011,149	8,162,785	9,424,327	616,990	438,254	619,859	322,605	17.1	12.2	17.0	7.7	-1.0	1	1.0	0.9	1.2	0.08	1.0	0.8	1.2	0.03	1.2	0.1
				AVLNPLCQVDYR	2	91.1%	1																									
				IDMNLTDLLGELQRDPWPVTQGK	3	98.9%	1																									
				MVVPLACLLTPLK	2	92.4%	1																									
				PAQPQEHPFASSR	3	97.5%	1																									
IPI00642936	GSTO1	glutathione S-transferase omega-1 isoform 3	100.0%	30.5	6	6	8	1	15,785,765	15,935,410	16,534,707	17,817,303	1,085,552	666,619	1,383,747	293,204	15.4	9.4	18.7	3.7	1.0	0.9	1.0	0.7	1.1	0.1	1.0	0.7	1.1	0.03	1.1	0.4
				EDPTVSALLTSEK	2	99.1%	1																									
				HEVININLK	2	100.0%	2																									
				LNECVDHTPK	2	99.9%	1																									
				MILELFSK	2	91.1%	1																									
				SQNKEDYAGLKEEFR	3	100.0%	1																									
				VPSLVGSFIR	2	100.0%	2																									
IPI00642976	CPNE1	Copine I	100.0%	19.3	3	3	5	7	724,450	909,984	742,271	981,679	52,558	45,022	56,327	113,598	16.2	11.1	17.0	25.9	1.3	0.03	1.0	0.8	1.4	0.07	-1.2	0.05	1.1	0.6	1.3	0.1
IPI00643325	CPNE1	Copine I	100.0%	12.8	3	3	5	7	724,450	909,984	742,271	981,679	52,558	45,022	56,327	113,598	16.2	11.1	17.0	25.9	1.3	0.03	1.0	0.8	1.4	0.07	-1.2	0.05	1.1	0.6	1.3	0.1
IPI00643422	CPNE1	Copine I	100.0%	18.3	3	3	5	7	724,450	909,984	742,271	981,679	52,558	45,022	56,327	113,598	16.2	11.1	17.0	25.9	1.3	0.03	1.0	0.8	1.4	0.07	-1.2	0.05	1.1	0.6	1.3	0.1
IPI00644561	CPNE1	Copine I	100.0%	12.8	3	3	5	7	724,450	909,984	742,271	981,679	52,558	45,022	56,327	113,598	16.2	11.1	17.0	25.9	1.3	0.03	1.0	0.8	1.4	0.07	-1.2	0.05	1.1	0.6	1.3	0.1
IPI00645270	CPNE1	Copine I	100.0%	18.7	3	3	5	7	724,450	909,984	742,271	981,679	52,558	45,022	56,327	113,598	16.2	11.1	17.0	25.9	1.3	0.03	1.0	0.8	1.4	0.07	-1.2	0.05	1.1	0.6	1.3	0.1
IPI00645712	CPNE1	Copine I	100.0%	16.9	3	3	5	7	724,450	909,984	742,271	981,679	52,558	45,022	56,327	113,598	16.2	11.1	17.0	25.9	1.3	0.03	1.0	0.8	1.4	0.07	-1.2	0.05	1.1	0.6	1.3	0.1
IPI00647692	CPNE1	Copine I	100.0%	22.4	3	3	5	7	724,450	909,984	742,271	981,679	52,558	45,022	56,327	113,598	16.2	11.1	17.0	25.9	1.3	0.03	1.0	0.8	1.4	0.07	-1.2	0.05	1.1	0.6	1.3	0.1
				FGIYDIDNK	2	98.5%	1																									
				SDPFLEFFR	2	100.0%	2																									
				SDPLCVLLQDVGGGSWAELGR	2	100.0%	2																									
IPI00643041	RAN;RANP1	GTP-binding nuclear protein Ran	100.0%	31.0	6	7	11	3	12,172,433	12,415,033	11,767,556	13,911,675	1,141,920	608,916	724,204	522,558	21.0	11.0	13.8	8.4	1.0	0.9	-1.0	0.8	1.1	0.2	-1.1	0.5	1.1	0.1	1.2	0.04
IPI00795671	RAN;RANP1	Uncharacterized protein	100.0%	28.8	6	7	11	3	12,172,433	12,415,033	11,767,556	13,911,675	1,141,920	608,916	724,204	522,558	21.0	11.0	13.8	8.4	1.0	0.9	-1.0	0.8	1.1	0.2	-1.1	0.5	1.1	0.1	1.2	0.04
IPI00796462	RAN;RANP1	27 kDa protein	100.0%	28.6	6	7	11	3	12,172,433	12,415,033	11,767,556	13,911,675	1,141,920	608,916	724,204	522,558	21.0	11.0	13.8	8.4	1.0	0.9	-1.0	0.8	1.1	0.2	-1.1	0.5	1.1	0.1	1.2	0.04
				FNVWDTAGQEK	2	100.0%	2																									
				HLTGEFEK	2	99.9%	2																									
				LVLVGDGGTGK	2	96.9%	1																									
				NLQYYDISAK	2	100.0%	2																									
				SNYNFEKPFLWLAR	2	99.8%	1																									
				SNYNFEKPFLWLAR	3	100.0%	1																									
				VCENIPIVLCGNK	2	100.0%	2																									
IPI00643056	CRABP2	Cellular retinoic acid binding protein 2	100.0%	46.3	4	4	5	1	13,383,825	13,959,245	13,349,755	14,793,470	1,215,599	451,498	961,053	723,252	20.3	7.2	16.1	10.9	1.0	0.7	-1.0	1	1.1	0.3	-1.0	0.6	1.1	0.4	1.1	0.3
				SENFEELLK	2	99.9%	2																									
				TTEINFK	2	93.2%	1																									
				VGEEFEEQTVDGR	2	100.0%	1																									
				VLGVNVMLR	2	100.0%	1																									
IPI00643131	KPNA3	Karyopherin alpha 3	98.4%	14.3	1	1	1	1	3,718,250	4,216,930	4,104,575	5,056,600	232,259	115,492	207,206	397,441	14.0	6.1	11.3	17.6	1.1	0.09	1.1	0.2	1.4	0.02	-1.0	0.6	1.2	0.1	1.2	0.07
				DSQVVQVVLDGLK	2	98.4%	1																									
IPI00643152	HSPA1L	cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L	100.0%	11.1	4	4	6	2	6,760,184	6,966,741	6,640,932	7,643,731	374,644	290,395	341,802	359,949	12.4	9.3	11.5	10.5	1.0	0.7	-1.0	0.8	1.1	0.1	-1.0	0.5	1.1	0.2	1.2	0.08
IPI00893099	HSPA1L	Heat shock 70kDa protein 1-like variant	100.0%	12.2	4	4	6	2	6,760,184	6,966,741	6,640,932	7,643,731	374,644	290,395	341,802	359,949	12.4	9.3	11.5	10.5	1.0	0.7	-1.0	0.8	1.1	0.1	-1.0	0.5	1.1	0.2	1.2	0.08
				AFYPEEISSMVLTK	2	100.0%	2																									
				ATAGDTHLGGEDFDNR	2	100.0%	2																									
				GVPQIEVTFDIDANGILNVTAMDKSTGKVNK	3	99.4%	1																									
				MDKAKIHDIVLVGGSTR	3	97.4%	1																									
IPI00643158	TUBB6	43 kDa protein	99.9%	4.5	1	1	1	3	2,021,634	2,046,150	1,988,400	2,389,692	179,651	151,862	196,012	63,742	19.9	16.6	22.0	6.0	1.0	0.9	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.07	1.2	0.1
IPI00646779	TUBB6	TUBB6 protein	99.9%	3.8	1	1	1	3	2,021,634	2,046,150	1,988,400	2,389,692	179,651	151,862	196,012	63,742	19.9	16.6	22.0	6.0	1.0	0.9	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.07	1.2	0.1
IPI01011853	TUBB6	cDNA FLJ35358 fis, clone PUAEN2000497, highly similar to Tubulin beta-6 chain	99.9%	4.6	1	1	1	3	2,021,634	2,046,150	1,988,400	2,389,692	179,651	151,862	196,012	63,742	19.9	16.6	22.0	6.0	1.0	0.9	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.07	1.2	0.1
				MASTFIGNSTAIQELFK	2	99.5%	1																									

IPI00643196	PFKP	cDNA FLJ35278 fis, clone PROST2006579, highly similar to 6-phosphofructokinase	100.0%	7.7	4	4	6	1	18,131,855	19,900,750	17,781,295	21,455,310	2,161,999	784,444	1,476,118	990,559	26.7	8.8	18.6	10.3	1.1	0.5	-1.0	0.9	1.2	0.2	-1.1	0.2	1.1	0.3	1.2	0.07
				ASYDVSDSGQLEHVQPWSV	2	100.0%	2																									
				EIGWTDVGGWTGQGGSILGTK	2	100.0%	2																									
				NVIFQPVAELK	2	100.0%	1																									
				VTILGHVQR	2	99.2%	1																									
IPI00643286	SDR39U1	isoform 2 of Epimerase family protein SDR39U1	93.9%	7.2	1	1	1	1	480,672	408,997	438,939	441,144	117,452	45,001	43,303	44,938	54.6	24.6	22.1	22.8	-1.2	0.6	-1.1	0.8	-1.1	0.8	1.1	0.6	1.1	0.6	1.0	1
				VLVGGGTGFIGTALTQLLNAR	3	93.9%	1																									
IPI00643288	PPA1	Pyrophosphatase (Inorganic) 1	100.0%	20.8	2	2	3	1	4,474,295	4,215,510	4,583,005	4,861,330	507,726	71,966	356,794	89,426	25.4	3.8	17.4	4.1	-1.1	0.6	1.0	0.9	1.1	0.5	1.1	0.4	1.2	0.0005	1.1	0.5
				GYIWNYGAIPQTWEDPGHNDK	3	100.0%	1																									
				VLGILAMIDEGETDWK	2	100.0%	2																									
IPI00643351	YBX1	Protein	100.0%	21.7	5	5	7	1	2,822,817	2,901,016	2,697,464	3,312,638	229,271	128,503	195,025	147,688	18.2	9.9	16.2	10.0	1.0	0.8	-1.0	0.7	1.2	0.1	-1.1	0.4	1.1	0.07	1.2	0.04
				GAEAANVTGPGGVPVQGSK	2	100.0%	2																									
				NDTKEDVFVHQTAIKK	3	100.0%	1																									
				NYQQNYQNSESGEKNEGSESAPEGQAQQR	3	100.0%	1																									
				SVGDGETVEFDVVEGEK	2	100.0%	2																									
				SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK	3	100.0%	1																									
IPI00643370	TPM3	Tropomyosin 3	100.0%	12.7	2	2	2	1	16,764,137	16,418,228	15,672,278	18,510,865	1,752,717	1,549,622	973,770	1,213,221	23.4	21.1	13.9	14.7	-1.0	0.9	-1.1	0.6	1.1	0.4	-1.0	0.7	1.1	0.3	1.2	0.1
				KLVIIEGDLER	2	100.0%	1																									
				MELQEIQLK	2	86.0%	1																									
IPI00643452	SMS	Protein	99.6%	7.4	1	1	1	1	298,537	327,459	379,367	350,780	31,466	23,627	24,850	20,539	23.6	16.1	14.7	13.1	1.1	0.5	1.3	0.08	1.2	0.2	1.2	0.2	1.1	0.5	-1.1	0.4
				QFGNILILSGDVNLAESDLAYTR	2	99.6%	1																									
IPI00643517	PLIN2	Uncharacterized protein	100.0%	14.3	4	4	4	1	10,453,085	9,443,000	10,315,485	11,723,980	935,109	344,037	488,368	159,103	20.0	8.2	10.6	3.0	-1.1	0.4	-1.0	0.9	1.1	0.2	1.1	0.2	1.2	0.0003	1.1	0.04
				DAVTTTVTGAK	2	100.0%	1																									
				DSVASTITGVMDK	2	100.0%	1																									
				EVSDSLLTSSK	2	98.6%	1																									
				LPILNQPSTQIVANAK	2	100.0%	1																									
IPI00643595	ACO1	Aconitase 1, soluble	100.0%	8.3	2	2	3	1	2,098,188	2,015,708	2,285,393	2,361,712	165,538	113,985	199,810	95,881	17.6	12.6	19.6	9.1	-1.0	0.7	1.1	0.5	1.1	0.2	1.1	0.3	1.2	0.05	1.0	0.7
				FVEFFGPGVAQLSIADR	2	100.0%	2																									
				VILQDFTGVPAVVDFAAMR	2	100.0%	1																									
IPI00643842	PGLS	20 kDa protein	100.0%	12.5	2	2	2	1	3,078,670	3,213,459	3,929,085	3,540,365	253,589	297,519	170,169	286,776	18.4	20.7	9.7	18.1	1.0	0.7	1.3	0.02	1.1	0.3	1.2	0.07	1.1	0.5	-1.1	0.3
				AACCLAGAR	2	99.9%	1																									
				FALGLSGGSLVSMLAR	2	100.0%	1																									
IPI00643900	NARS	cDNA FLJ56692, highly similar to Asparaginyl-tRNA synthetase, cytoplasmic	100.0%	2.8	1	1	1	2	3,987,477	3,829,267	3,667,617	4,562,507	233,857	194,961	278,601	261,411	13.1	11.4	17.0	12.8	-1.0	0.6	-1.1	0.4	1.1	0.1	-1.0	0.6	1.2	0.05	1.2	0.05
IPI00646656	NARS	cDNA FLJ52485, highly similar to Asparaginyl-tRNA synthetase, cytoplasmic	100.0%	4.6	1	1	1	2	3,987,477	3,829,267	3,667,617	4,562,507	233,857	194,961	278,601	261,411	13.1	11.4	17.0	12.8	-1.0	0.6	-1.1	0.4	1.1	0.1	-1.0	0.6	1.2	0.05	1.2	0.05
				IGALEGYR	2	99.8%	1																									
IPI00643920	TKT	cDNA FLJ54957, highly similar to Transketolase	100.0%	31.1	16	20	27	3	34,786,502	34,648,170	33,815,371	40,077,604	2,561,944	1,233,593	2,309,665	1,345,784	16.5	8.0	15.3	7.5	-1.0	1	-1.0	0.8	1.2	0.1	-1.0	0.8	1.2	0.02	1.2	0.05
IPI00793119	TKT	cDNA FLJ56274, highly similar to Transketolase	100.0%	34.0	16	20	27	3	34,786,502	34,648,170	33,815,371	40,077,604	2,561,944	1,233,593	2,309,665	1,345,784	16.5	8.0	15.3	7.5	-1.0	1	-1.0	0.8	1.2	0.1	-1.0	0.8	1.2	0.02	1.2	0.05
IPI00942979	TKT	Transketolase	100.0%	31.5	16	20	27	3	34,786,502	34,648,170	33,815,371	40,077,604	2,561,944	1,233,593	2,309,665	1,345,784	16.5	8.0	15.3	7.5	-1.0	1	-1.0	0.8	1.2	0.1	-1.0	0.8	1.2	0.02	1.2	0.05
				AVELAANTK	1	100.0%	1																									
				AVELAANTK	2	100.0%	2																									
				GITGVEDKESWHGKPLPK	3	81.1%	1																									
				IIALDGDTK	2	99.9%	1																									
				ILATPPQEDAPSVDIANIR	2	100.0%	2																									
				ILATPPQEDAPSVDIANIR	3	100.0%	1																									
				ISSDLDGHPVPK	2	100.0%	1																									
				KISSDLDGHPVPK	2	99.8%	1																									
				LGQSDPAPLQHQMDIYQK	3	100.0%	1																									
				MFGIDR	2	99.8%	1																									
				MFGIDRDAIAQAVR	2	99.8%	1																									
				MFGIDRDAIAQAVR	3	100.0%	1																									
				MPSLPSYK	2	100.0%	2																									
				NMAEQIIQEIYSQIQSK	2	100.0%	2																									
				NMAEQIIQEIYSQIQSK	3	100.0%	1																									
				NSTFSEIFKK	2	99.8%	1																									
				SGKPAELLK	2	96.8%	1																									
				SVPTSTVFYPSDGVATEK	2	100.0%	2																									
				TSRPENAIIYNNNEDFQVGQAK	3	100.0%	2																									
				VLDPFTIKPLDR	2	100.0%	2																									
IPI00643994	CAPN5	cDNA FLJ46245 fis, clone TESTI4020596, highly similar to Homo sapiens calpain 5	99.4%	2.1	1	1	1	3	752,842	706,003	877,190	809,567	84,669	98,713	47,613	91,480	25.2	31.3	12.1	25.3	-1.1	0.7	1.2	0.2	1.1	0.7	1.2	0.2	1.1	0.5	-1.1	0.5
IPI00742984	CAPN5	Calpain-5	99.4%	2.2	1	1	1	3	752,842	706,003	877,190	809,567	84,669	98,713	47,613	91,480	25.2	31.3	12.1	25.3	-1.1	0.7	1.2	0.2	1.1	0.7	1.2	0.2	1.1	0.5	-1.1	0.5
IPI00902710	CAPN5	Uncharacterized protein	99.4%	2.1	1	1	1	3	752,842	706,003	877,190	809,567	84,669	98,713	47,613	91,480	25.2	31.3	12.1	25.3	-1.1	0.7	1.2	0.2	1.1	0.7	1.2	0.2	1.1	0.5	-1.1	0.5
				DTFFQNPQYIFEVK	2	99.4%	1																									
IPI00979384	PABPC1	16 kDa protein	100.0%	19.3	2	2	4	5	625,177	591,795	634,887	683,570	53,364	21,758	51,943	41,530	19.1	8.2	18.3	13.6	-1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.5	1.2	0.09	1.1	0.5
IPI00979703	PABPC1	Uncharacterized protein	100.0%	23.7	2	2	4	5	625,177	591,795	634,887	683,570	53,364	21,758	51,943	41,530	19.1	8.2	18.3	13.6	-1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.5	1.2	0.09	1.1	0.5
IPI00983093	PABPC1	Uncharacterized protein	100.0%	25.9	2	2	4	5	625,177	591,795	634,887	683,570	53,364	21,758	51,943	41,530	19.1	8.2	18.3	13.6	-1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.5	1.2	0.09	1.1	0.5
IPI01013146	PABPC1	Uncharacterized protein	100.0%	21.7	2	2	4	5	625,177	591,795	634,887	683,570	53,364	21,758	51,943	41,530	19.1	8.2	18.3	13.6	-1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.5	1.2	0.09	1.1	0.5
IPI00644016	PABPC4	Poly(A) binding protein, cytoplasmic 4	100.0%	21.7	2	2	4	5	625,177	591,795	634,887	683,570	53,364	21,758	51,943	41,530	19.1	8.2	18.3	13.6	-1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.5	1.2	0.09	1.1	0.5
				ALDTMNFDVIK	2	100.0%	2																									
				SLGYAYVNFQQPADAER	2	100.0%	2																									
IPI00644077	ALDH1A1	Aldehyde dehydrogenase 1 family, member A1	100.0%	25.7	3	3	4	2	3,860,544	4,275,799	4,193,149	4,484,011	294,447	258,736	283,594	184,655	17.1	13.5	15.1	9.2	1.1	0.3	1.1	0.4	1.2	0.1	-1.0	0.8	1.0	0.5	1.1	0.4
IPI00644628	ALDH1A1	Aldehyde dehydrogenase 1 family, member A1	100.0%	24.8	3	3	4	2	3,860,544	4,275,799	4,193,149	4,484,011	294,447	258,736	283,594	184,655	17.1	13.5	15.1	9.2	1.1	0.3	1.1	0.4	1.2	0.1	-1.0	0.8	1.0	0.5	1.1	0.4
				IGPALSCGNTVVVKPAEQTPLTALHVASLIK	3	100.0%	1																									
				LLLATMESMNGGK	2	100.0%	1																									
				LYSNAYLNDLAGCIK	2	100.0%	2																									
IPI00644079	HNRNPU	cDNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heterogeneous nuclea	100.0%	9.2	5	5	8	1	11,175,458	12,074,188	11,278,175	12,805,540	1,118,340	699,461	786,444	369,743	22.4	13.0	15.6	6.5	1.1	0.5	1.0	0.9	1.1	0.2	-1.1	0.5	1.1	0.4	1.1	0.1
				EKPYFPIPEEYTFIQNVPLEDR	3	100.0%	1																									
				GYFEYIEENK	2	99.9%	1																									
				NFILDQTNVSAAAQR	2	100.0%	2																									
				NGQDLGVAFK	2	99.6%	2																									
				YNILGTNTIMDK	2	100.0%	2																									
IPI00644108	BUB3	Uncharacterized protein	100.0%	20.9	5	5	6	1	8,759,963	7,988,323	8,588,218	9,161,518	762,745	341,904	329,353	278,647	19.5	9.6	8.6	6.8	-1.1	0.4	-1.0	0.8	1.0	0.6	1.1	0.2	1.1	0.03	1.1	0.2
				LNQPPEDGISSVK	2	99.3%	1																									
				LYDVPANSMR	2	98.9%	1																									
				QGYVLSSIEGR	2	99.8%	1																									
				VAVEYLDPSPEVQK	2	100.0%	2																									
				VYTLSVSGDR	2	99.4%	1																									
IPI00644127	IARS	Isoleucyl-tRNA synthetase, cytoplasmic	100.0%	13.7	13	13	14	1	27,852,335	28,467,242	28,259,458	32,609,165	2,582,252	1,598,064	2,284,631	875,626	20.7	12.6	18.1	6.0	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.9	1.1	0.05	1.2	0.1
				EFEDAFPADFIAEGIDQTR	2	100.0%	1																									
				FGWDCHGLPVEYEIDK	3	89.0%	1																									
				FVDILTNWYVR	2	100.0%	1																									
				GSELEITLTR	2	99.8%	1																									
				LFLNETQTQEITEDIPVK	2	90.9%	1																									
				LQKEEEIEFLYNENTVR	3	89.2%	1																									
				NNDLCYWVPELVR	2	85.9%	1																									
				NVIVNGLVLASDGQK	2	98.8%	1																									
				QLSSEELEQFQK	2	99.7%	2																									
				TESAVSQMQSVIELGR	2	100.0%	1																									
				VENMVDQLLR	2	96.6%	1																									
				WIDFDNDYK	2	89.2%	1																									
				YGADALR	2	91.4%	1																									
IPI00644196	SERPINB5	isoform 2 of Serpin B5	100.0%	21.2	3	3	3	1	6,509,060	6,223,200	7,226,173	7,311,917	439,407	310,533	663,192	369,487	15.1	11.2	20.5	11.3	-1.0	0.6	1.1	0.4	1.1	0.2	1.2	0.2	1.2	0.05	1.0	0.9
				DLTDGHFENILADNSVNDQTK	3	99.8%	1																									
				DVPFGFQTVTSDVNK	2	99.6%	1																									
				SLNLSTEFISSTK	2	100.0%	1																									
IPI00644231	CYFIP1	isoform 1 of Cytoplasmic FMR1-interacting protein 1	100.0%	2.0	2	2	2	2	2,262,408	2,070,185	2,276,607	2,561,323	165,899	162,040	130,225	93,401	16.4	17.5	12.8	8.2	-1.1	0.4	1.0	0.9	1.1	0.2	1.1	0.3	1.2	0.03	1.1	0.1
IPI00903062	CYFIP1	cDNA FLJ43948 fis, clone TESTI4014924, highly similar to Homo sapiens cytoplasm	100.0%	2.0	2	2	2	2	2,262,408	2,070,185	2,276,607	2,561,323	165,899	162,040	130,225	93,401	16.4	17.5	12.8	8.2	-1.1	0.4	1.0	0.9	1.1	0.2	1.1	0.3	1.2	0.03	1.1	0.1
				LCCGLSMFEVILTR	2	95.9%	1																									
				LGTPQQIAIAR	2	86.7%	1																									
IPI00644292	NUDT5	Uncharacterized protein	100.0%	15.6	2	2	4	1	1,116,030	1,134,163	1,094,005	1,205,305	52,398	59,844	49,657	82,625	10.5	11.8	10.2	15.3	1.0	0.8	-1.0	0.8	1.1	0.4	-1.0	0.6	1.1	0.5	1.1	0.3
				EQTADGVAVIPVLQR	2	100.0%	2																									
				QYIISEELISEGK	2	100.0%	2																									
IPI00644301	UTRN	Utrophin	99.7%	1.1	1	1	1	1	1,232,985	1,361,710	1,333,730	1,260,690	94,274	91,765	82,342	119,399	17.1	15.1	13.8	21.2	1.1	0.4	1.1	0.4	1.0	0.9	-1.0	0.8	-1.1	0.5	-1.1	0.6
				QLLEQPESDSR	2	98.4%	1																									
IPI00644339	GALE	UDP-galactose-4-epimerase	100.0%	31.7	6	8	9	1	9,001,647	9,504,399	9,165,389	10,610,192	591,017	379,116	335,661	417,493	14.7	8.9	8.2	8.8	1.1	0.5	1.0	0.8	1.2	0.06	-1.0	0.5	1.1	0.09	1.2	0.03
				DYIHVVDLAK	2	93.1%	1																									
				DYIHVVDLAK	3	99.7%	1																									
				EALNVFGNDYDTEDGTGVR	2	100.0%	1																									
				EALNVFGNDYDTEDGTGVRDYIHVVDLAK	3	99.2%	1																									
				FFIEEMIR	2	99.8%	1																									
				IYNLGTGTGYSVLQMVQAMEK	2	100.0%	1																									
				IYNLGTGTGYSVLQMVQAMEK	3	100.0%	1																									
				VNLTGTIQLLEIMK	2	100.0%	2																									
IPI00644401	KIAA1217	KIAA1217	100.0%	1.5	1	1	1	2	259,124	267,826	284,738	313,624	20,234	24,394	14,726	18,575	17.5	20.4	11.6	13.2	1.0	0.8	1.1	0.3	1.2	0.08	1.1	0.6	1.2	0.2	1.1	0.3
IPI00908793	KIAA1217	cDNA FLJ56199, weakly similar to p130Cas-associated protein	100.0%	2.0	1	1	1	2	259,124	267,826	284,738	313,624	20,234	24,394	14,726	18,575	17.5	20.4	11.6	13.2	1.0	0.8	1.1	0.3	1.2	0.08	1.1	0.6	1.2	0.2	1.1	0.3
				SMVVPGNATIPR	2	100.0%	1																									
IPI00644409	GDA	Uncharacterized protein	100.0%	25.6	6	7	8	3	9,244,073	9,208,427	8,537,944	10,018,305	857,718	250,593	679,370	370,293	20.8	6.1	17.8	8.3	-1.0	1	-1.1	0.5	1.1	0.4	-1.1	0.4	1.1	0.1	1.2	0.09
IPI00873506	GDA	Guanine aminohydrolase	100.0%	22.3	6	7	8	3	9,244,073	9,208,427	8,537,944	10,018,305	857,718	250,593	679,370	370,293	20.8	6.1	17.8	8.3	-1.0	1	-1.1	0.5	1.1	0.4	-1.1	0.4	1.1	0.1	1.2	0.09
IPI00942902	GDA	Guanine deaminase	100.0%	23.1	6	7	8	3	9,244,073	9,208,427	8,537,944	10,018,305	857,718	250,593	679,370	370,293	20.8	6.1	17.8	8.3	-1.0	1	-1.1	0.5	1.1	0.4	-1.1	0.4	1.1	0.1	1.2	0.09
				ASDSPIDLFYGDFFGDISEAVIQK	2	100.0%	1																									
				ASDSPIDLFYGDFFGDISEAVIQK	3	100.0%	1																									
				AVMVSNILLINK	2	97.5%	1																									
				DHLLGVSDSGK	2	98.7%	1																									
				FQNIDFAEEVYTR	2	86.2%	1																									
				IVFLEEASQQEK	2	100.0%	2																									
				LATLGGSQALGLDGEIGNFEVGKEFDAILINPK	3	100.0%	1																									
IPI00644425	RHOC	Ras homolog gene family, member C	100.0%	39.1	3	3	4	2	5,245,376	4,925,910	5,959,203	4,751,501	358,224	216,105	173,998	147,453	15.3	9.8	6.5	6.9	-1.1	0.5	1.1	0.1	-1.1	0.2	1.2	0.006	-1.0	0.5	-1.3	0.0007
IPI00982162	RHOC	Uncharacterized protein	100.0%	54.6	3	3	4	2	5,245,376	4,925,910	5,959,203	4,751,501	358,224	216,105	173,998	147,453	15.3	9.8	6.5	6.9	-1.1	0.5	1.1	0.1	-1.1	0.2	1.2	0.006	-1.0	0.5	-1.3	0.0007
				DQFPEVYVPTVFENYIADIEVDGK	2	100.0%	2																									
				KLVIVGDGACGK	2	99.2%	1																									
				LVIVGDGACGK	2	99.9%	1																									
IPI00644431	DDX39A	ATP-dependent RNA helicase DDX39A isoform 2	100.0%	13.2	6	7	7	2	6,469,519	6,402,347	6,405,972	7,367,179	671,678	338,007	448,637	440,279	23.2	11.8	15.7	13.4	-1.0	0.9	-1.0	0.9	1.1	0.3	1.0	1	1.2	0.1	1.2	0.2
IPI00940237	DDX39A	ATP-dependent RNA helicase DDX39A	100.0%	14.5	6	7	7	2	6,469,519	6,402,347	6,405,972	7,367,179	671,678	338,007	448,637	440,279	23.2	11.8	15.7	13.4	-1.0	0.9	-1.0	0.9	1.1	0.3	1.0	1	1.2	0.1	1.2	0.2
				DFLLKPELLR	2	99.3%	1																									
				DFLLKPELLR	3	90.9%	1																									
				GLAITFVSDENDAK	2	100.0%	1																									
				GSYVSIHSSGFR	2	99.7%	1																									
				ILNDVQDR	2	99.9%	1																									

				ILVATNLFGR	2	98.9%	1																									
				MLEQLDMR	2	100.0%	1																									
IPI00644506	NUP93	cDNA FLJ58756, highly similar to Nuclear pore complex protein Nup93	100.0%	4.6	1	1	1	1	4,303,120	4,786,425	4,799,100	6,033,985	327,255	260,228	656,796	286,945	17.0	12.2	30.6	10.6	1.1	0.3	1.1	0.5	1.4	0.004	1.0	1	1.3	0.01	1.3	0.1
				ILHTLLASGEDALDFTQESEPSYISDVGPPGR	3	99.9%	1																									
IPI00644531	TAGLN2	21 kDa protein	100.0%	84.5	18	26	40	1	108,519,647	113,956,085	104,366,192	126,495,737	8,393,265	5,981,008	7,850,089	5,804,875	17.3	11.7	16.8	10.3	1.1	0.6	-1.0	0.7	1.2	0.1	-1.1	0.4	1.1	0.2	1.2	0.05
				DDGLFSGDPNWFPK	2	100.0%	2																									
				DDGLFSGDPNWFPKK	2	100.0%	2																									
				DDGLFSGDPNWFPKK	3	99.9%	1																									
				DGTVLCELINALYPEGQAPVK	2	100.0%	2																									
				DGTVLCELINALYPEGQAPVK	3	99.9%	1																									
				DGTVLCELINALYPEGQAPVKK	2	100.0%	3																									
				DGTVLCELINALYPEGQAPVKK	3	100.0%	3																									
				ENFQNWLK	2	96.4%	1																									
				GPAYGLSR	1	97.1%	1																									
				GPAYGLSR	2	99.6%	2																									
				IEKQYDADLEQILIQWITTQCR	3	99.9%	1																									
				IQASTMAFK	1	98.8%	1																									
				IQASTMAFK	2	99.6%	1																									
				KIQASTMAFK	2	98.2%	1																									
				NFSDNQLQEGK	1	100.0%	1																									
				NFSDNQLQEGK	2	100.0%	2																									
				NMACVQR	1	98.5%	2																									
				NVIGLQMGTNR	2	100.0%	1																									
				QMEQISQFLQAAER	2	100.0%	2																									
				QMEQISQFLQAAER	3	100.0%	1																									
				QYDADLEQILIQWITTQCRK	3	100.0%	1																									
				TLMNLGGLAVAR	2	100.0%	2																									
				TLMNLGGLAVAR	3	100.0%	1																									
				TLMNLGGLAVARDDGLFSGDPNWFPK	3	99.9%	1																									
				YGINTTDIFQTVDLWEGK	3	100.0%	2																									
				YGINTTDIFQTVDLWEGKNMACVQR	3	100.0%	2																									
IPI00644568	BUB3	Uncharacterized protein	100.0%	26.9	2	2	2	1	1,062,106	1,064,440	1,182,034	1,032,733	67,551	39,489	70,055	83,720	14.2	8.3	13.3	18.1	1.0	1	1.1	0.3	-1.0	0.8	1.1	0.2	-1.0	0.7	-1.1	0.2
				FSPNTSQFLLVSSWDTSVR	2	100.0%	1																									
				MHDLNTDQENLVGTHDAPIR	3	100.0%	1																									
IPI00644697	HEBP2	HEBP2 protein (Fragment)	100.0%	17.3	3	3	3	1	5,895,210	6,171,830	5,773,610	6,918,120	276,403	258,457	477,232	159,946	10.5	9.4	18.5	5.2	1.0	0.5	-1.0	0.8	1.2	0.01	-1.1	0.5	1.1	0.04	1.2	0.07
				APEDAGPQPGSYEIR	2	99.9%	1																									
				NNEVWLIQK	2	99.6%	1																									
				NQEQLLTLASILR	2	100.0%	1																									
IPI00644708	TIAL1	nucleolysin TIAR isoform 2	100.0%	27.0	8	8	9	1	12,940,852	12,715,677	12,410,011	14,297,253	1,166,968	445,601	932,929	544,020	20.2	7.8	16.8	8.5	-1.0	0.9	-1.0	0.7	1.1	0.3	-1.0	0.8	1.1	0.05	1.2	0.1
				DAAAALAAMNGR	2	92.8%	1																									
				DTSNHFHVFVGDLSPEITTEDIK	3	94.8%	1																									
				FEDVVNQSSPK	2	100.0%	1																									
				GYGFVSFYNK	2	83.3%	1																									
				LDAENAIVHMGGQWLGGR	3	100.0%	1																									
				QTFSPFGQIMEIR	2	100.0%	2																									
				SAFAPFGK	2	99.9%	1																									
				VNWATTPSSQK	2	98.8%	1																									
IPI00644712	XRCC6	X-ray repair cross-complementing protein 6	100.0%	16.6	7	8	9	1	8,676,045	8,842,976	8,973,700	9,939,127	987,524	184,340	650,376	152,855	25.5	4.7	16.2	3.4	1.0	0.9	1.0	0.8	1.1	0.3	1.0	0.9	1.1	0.002	1.1	0.2
				DIISIAEDEDLR	2	99.9%	1																									
				IQVTPPGFQLVFLPFADDKR	3	93.8%	1																									
				KQELLEALTK	2	99.8%	1																									
				LGSLVDEFK	2	99.5%	1																									
				NIYVLQELDNPGAK	2	100.0%	1																									
				NLEALALDLMEPEQAVDLTLPK	2	100.0%	2																									
				NLEALALDLMEPEQAVDLTLPK	3	100.0%	1																									
				QIILEKEETEELKR	3	90.2%	1																									
IPI00644764	RBM39	RNA binding motif protein 39	94.2%	5.7	1	1	1	2	458,776	432,965	487,491	409,025	80,172	31,831	41,579	21,550	39.1	16.4	19.1	11.8	-1.1	0.8	1.1	0.8	-1.1	0.6	1.1	0.3	-1.1	0.6	-1.2	0.1
IPI00647282	RBM39	RNA binding motif protein 39	94.2%	4.8	1	1	1	2	458,776	432,965	487,491	409,025	80,172	31,831	41,579	21,550	39.1	16.4	19.1	11.8	-1.1	0.8	1.1	0.8	-1.1	0.6	1.1	0.3	-1.1	0.6	-1.2	0.1
				DLEEFFSTVGK	2	94.2%	1																									
IPI00916274	RBM14-RBM4	Pseudogene candidate	100.0%	10.9	1	1	1	7	246,747	288,052	233,520	294,474	29,084	27,500	28,886	19,517	26.4	21.4	27.7	14.8	1.2	0.3	-1.1	0.8	1.2	0.2	-1.2	0.2	1.0	0.9	1.3	0.1
IPI01009009	RBM14-RBM4	RBM14-RBM4 protein isoform 2	100.0%	13.6	1	1	1	7	246,747	288,052	233,520	294,474	29,084	27,500	28,886	19,517	26.4	21.4	27.7	14.8	1.2	0.3	-1.1	0.8	1.2	0.2	-1.2	0.2	1.0	0.9	1.3	0.1
IPI00644837	RBM14	isoform 2 of RNA-binding protein 14	100.0%	10.3	1	1	1	7	246,747	288,052	233,520	294,474	29,084	27,500	28,886	19,517	26.4	21.4	27.7	14.8	1.2	0.3	-1.1	0.8	1.2	0.2	-1.2	0.2	1.0	0.9	1.3	0.1
IPI00916896	RBM14	14 kDa protein	100.0%	12.4	1	1	1	7	246,747	288,052	233,520	294,474	29,084	27,500	28,886	19,517	26.4	21.4	27.7	14.8	1.2	0.3	-1.1	0.8	1.2	0.2	-1.2	0.2	1.0	0.9	1.3	0.1
IPI00917085	RBM14	Uncharacterized protein	100.0%	10.1	1	1	1	7	246,747	288,052	233,520	294,474	29,084	27,500	28,886	19,517	26.4	21.4	27.7	14.8	1.2	0.3	-1.1	0.8	1.2	0.2	-1.2	0.2	1.0	0.9	1.3	0.1
IPI00969146	RBM14	RNA-binding protein 14 isoform 3	100.0%	13.5	1	1	1	7	246,747	288,052	233,520	294,474	29,084	27,500	28,886	19,517	26.4	21.4	27.7	14.8	1.2	0.3	-1.1	0.8	1.2	0.2	-1.2	0.2	1.0	0.9	1.3	0.1
IPI01012323	RBM14	Uncharacterized protein	100.0%	13.6	1	1	1	7	246,747	288,052	233,520	294,474	29,084	27,500	28,886	19,517	26.4	21.4	27.7	14.8	1.2	0.3	-1.1	0.8	1.2	0.2	-1.2	0.2	1.0	0.9	1.3	0.1
				IFVGNVSAACTSQELR	2	100.0%	1																									
IPI00644848	NONO	Protein	100.0%	15.7	3	3	4	1	2,918,330	2,730,927	2,739,656	3,162,373	264,052	119,692	154,124	112,359	20.2	9.8	12.6	7.9	-1.1	0.5	-1.1	0.6	1.1	0.4	1.0	1	1.2	0.03	1.2	0.06
				EKLEMEMEAAR	2	99.9%	1																									
				FAQPGSFEYEYAMR	2	100.0%	2																									
				RMEELHNQEVQK	3	100.0%	1																									
IPI00644968	-	Similar to Heterogeneous nuclear ribonucleoprotein A1 isoform a	100.0%	18.8	4	5	9	1	2,722,328	2,830,822	2,909,234	3,132,992	206,810	167,304	243,956	97,072	17.0	13.2	18.8	6.9	1.0	0.7	1.1	0.6	1.2	0.1	1.0	0.8	1.1	0.2	1.1	0.4
				EDSQRPGAHLTVK	2	90.2%	1																									
				GFGFVTYATVEEVDAAMNAR	2	100.0%	2																									
				GFGFVTYATVEEVDAAMNAR	3	100.0%	2																									
				LFIGGLSFETTDESLR	2	100.0%	3																									
				WGTLTDCVVMR	2	99.9%	1																									
IPI00644994	FBP1	Fructose-1,6-bisphosphatase 1	100.0%	8.0	1	1	1	1	2,980,550	2,878,135	2,968,715	3,236,010	203,630	247,015	241,959	123,049	15.3	19.2	18.2	8.5	-1.0	0.8	-1.0	1	1.1	0.3	1.0	0.8	1.1	0.2	1.1	0.4
				DFDPAVTEYIQR	2	100.0%	1																									
IPI00645010	NONO	Uncharacterized protein	100.0%	33.1	8	8	10	1	14,988,953	14,845,341	14,069,735	17,052,036	1,548,542	606,360	1,025,519	604,362	23.1	9.1	16.3	7.9	-1.0	0.9	-1.1	0.6	1.1	0.3	-1.1	0.5	1.1	0.03	1.2	0.04
				EKLEMEMEAAR	2	99.9%	1																									
				FACHSASLTVR	3	100.0%	1																									
				FAQPGSFEYEYAMR	2	100.0%	2																									
				LFVGNLPPDITEEEMR	2	100.0%	1																									
				MEELHNQEVQKRK	2	99.0%	1																									
				RMEELHNQEVQK	3	100.0%	1																									
				TLAEIAK	1	98.8%	1																									
				VELDNMPLR	2	100.0%	2																									
IPI00645078	UBA1	Ubiquitin-like modifier-activating enzyme 1	100.0%	40.5	27	36	49	1	173,720,125	176,245,658	179,235,490	199,296,714	########	6,413,566	########	6,417,736	17.8	8.1	16.7	7.2	1.0	0.9	1.0	0.8	1.1	0.1	1.0	0.8	1.1	0.03	1.1	0.2
				AAVATFLQSVQVPEFTPK	2	99.7%	1																									
				AAVATFLQSVQVPEFTPK	3	100.0%	1																									
				AENYDIPSADR	2	100.0%	1																									
				ALPAVQQNNLDEDLIR	2	100.0%	2																									
				DEFEGLFKQPAENVNQYLTDPK	3	99.9%	1																									
				DNPGVVTCLDEAR	2	100.0%	2																									
				FEVQGLQPNGEEMTLK	2	100.0%	1																									
				GNVQVVIPFLTESYSSSQDPPEK	2	100.0%	1																									
				GNVQVVIPFLTESYSSSQDPPEK	3	98.6%	1																									
				HGFESGDFVSFSEVQGMVELNGNQPMEIK	3	100.0%	1																									
				IHVSDQELQSANASVDDSRLEELK	3	100.0%	1																									
				IYDDDFFQNLDGVANALDNVDAR	2	100.0%	2																									
				IYDDDFFQNLDGVANALDNVDAR	3	100.0%	1																									
				KLAYVAAGDLAPINAFIGGLAAQEVMK	3	100.0%	1																									
				LAGTQPLEVLEAVQR	2	100.0%	1																									
				LAGTQPLEVLEAVQR	3	99.7%	1																									
				LAYVAAGDLAPINAFIGGLAAQEVMK	2	100.0%	2																									
				LAYVAAGDLAPINAFIGGLAAQEVMK	3	100.0%	2																									
				LDQPMTEIVSR	2	100.0%	2																									
				LKSDTAAAAVR	2	99.4%	1																									
				LQTSSVLVSGLR	2	100.0%	2																									
				NEEDAAELVALAQAVNAR	2	100.0%	1																									
				NEEDAAELVALAQAVNAR	3	100.0%	2																									
				NFPNAIEHTLQWAR	2	100.0%	2																									
				NGFLNLALPFFGFSEPLAAPR	2	100.0%	2																									
				NGFLNLALPFFGFSEPLAAPR	3	100.0%	1																									
				NGSEADIDEGLYSR	2	100.0%	2																									
				QFLFRPWDVTK	2	99.9%	1																									
				QFLFRPWDVTK	3	88.4%	1																									
				QLYVLGHEAMK	2	99.9%	1																									
				QPAENVNQYLTDPK	2	100.0%	1																									
				SLVASLAEPDFVVTDFAK	2	100.0%	1																									
				SLVASLAEPDFVVTDFAK	3	100.0%	1																									
				VLGPYTFSICDTSNFSDYIR	2	100.0%	1																									
				YDGQVAVFGSDLQEK	2	100.0%	2																									
				YFLVGAGAIGCELLK	2	100.0%	2																									
IPI00645255	GDI2	GDP dissociation inhibitor 2	100.0%	37.6	6	7	10	1	6,137,892	6,705,518	6,601,263	7,464,847	553,434	275,688	286,281	360,196	20.2	9.2	9.7	10.8	1.1	0.4	1.1	0.5	1.2	0.08	-1.0	0.8	1.1	0.1	1.1	0.1
				FDLGQDVIDFTGHALALYR	3	100.0%	1																									
				NPYYGGESASITPLEDLYK	2	100.0%	1																									
				SPYLYPLYGLGELPQGFAR	2	100.0%	2																									
				TDDYLDQPCYETINR	2	100.0%	2																									
				TFEGIDPK	2	99.9%	1																									
				VPSTEAEALASSLMGLFEK	2	100.0%	2																									
				VPSTEAEALASSLMGLFEK	3	100.0%	1																									
IPI00645370	VPS4B	16 kDa protein	94.7%	7.6	1	1	1	1	2,148,225	2,513,450	2,346,500	2,622,215	233,678	89,601	305,811	84,700	24.3	8.0	29.1	7.2	1.2	0.2	1.1	0.6	1.2	0.1	-1.1	0.6	1.0	0.4	1.1	0.4
				WSDVAGLEGAK	2	94.7%	1																									
IPI00645403	KIAA1217	isoform 1 of Sickle tail protein homolog	100.0%	2.2	3	3	3	1	2,889,613	3,156,489	2,816,496	3,295,463	336,137	231,489	104,403	197,186	26.0	16.4	8.3	13.4	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.2	1.0	0.7	1.2	0.06
				GDAPVDKVELSEDSPNSEQDLEK	3	99.5%	1																									
				GPITSYSK	2	86.5%	1																									
				SMVVPGNATIPR	2	100.0%	1																									
IPI00645425	CRYZ	quinone oxidoreductase isoform c	100.0%	26.0	3	3	4	1	1,998,532	2,145,215	2,001,563	2,346,881	172,087	175,806	181,333	69,847	19.3	18.3	20.3	6.7	1.1	0.6	1.0	1	1.2	0.1	-1.1	0.6	1.1	0.3	1.2	0.1
				AGESVLVHGASGGVGLAACQIAR	3	100.0%	2																									
				DLSLLSHGGR	2	99.3%	1																									
				VAEAHENIIHGSGATGK	3	100.0%	1																									
IPI00645646	SLC25A6	17 kDa protein	100.0%	27.9	4	4	6	1	7,715,288	7,875,585	8,189,802	9,015,862	564,679	419,571	550,398	515,773	16.4	11.9	15.0	12.8	1.0	0.8	1.1	0.6	1.2	0.1	1.0	0.7	1.1	0.1	1.1	0.3
				DFLAGGIAAAISK	2	100.0%	2																									
				EQGVLSFWR	2	99.7%	1																									
				LLLQVQHASK	2	95.3%	1																									

				YFPTQALNFAFK	2	100.0%	2																									
IPI00645781	TMEM191B	Conserved hypothetical protein	93.4%	24.0	1	1	1	1	644,423	656,423	735,725	804,374	130,894	132,915	113,227	133,169	45.4	45.3	34.4	37.0	1.0	1	1.1	0.6	1.2	0.4	1.1	0.7	1.2	0.5	1.1	0.7
				RLRVALEPHLGDDAAPPALHAVPAAGAAR	3	93.4%	1																									
IPI00646047	CAPZB	cDNA FLJ43095 fis, clone CORDB2000541, highly similar to F-actin capping protein	100.0%	32.7	7	7	10	2	5,883,631	5,955,357	5,719,216	6,784,303	562,713	245,350	437,841	275,269	21.4	9.2	17.1	9.1	1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.7	1.1	0.05	1.2	0.07
IPI01013714	CAPZB	Capping protein (Actin filament) muscle Z-line, beta	100.0%	41.3	7	7	10	2	5,883,631	5,955,357	5,719,216	6,784,303	562,713	245,350	437,841	275,269	21.4	9.2	17.1	9.1	1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.7	1.1	0.05	1.2	0.07
				DYLLCDYNR	2	100.0%	2																									
				LEVEANNAFDQYR	2	100.0%	1																									
				QMEKDETVSDCSPHIANIGR	3	99.9%	1																									
				RLPPQQIEK	2	99.9%	2																									
				SGSGTMNLGGSLTR	2	100.0%	2																									
				SPWSNKYDPPLEDGAMPSAR	3	100.0%	1																									
				YDPPLEDGAMPSAR	2	98.2%	1																									
IPI00646121	CPNE1	Copine I	100.0%	14.3	4	4	6	1	1,513,728	1,826,694	1,614,401	1,944,049	106,750	74,225	87,124	148,626	15.8	9.1	12.1	17.1	1.2	0.04	1.1	0.5	1.3	0.05	-1.1	0.1	1.1	0.5	1.2	0.09
				FGIYDIDNK	2	98.5%	1																									
				LYGPTNFAPIINHVAR	3	100.0%	1																									
				SDPFLEFFR	2	100.0%	2																									
				SDPLCVLLQDVGGGSWAELGR	2	100.0%	2																									
IPI00646182	ATP1A1	sodium/potassium-transporting ATPase subunit alpha-1 isoform c	100.0%	25.2	19	19	25	2	37,513,298	39,266,141	39,952,491	43,292,918	2,960,922	1,942,340	2,526,532	1,574,365	17.7	11.1	14.1	8.1	1.0	0.6	1.1	0.5	1.2	0.1	1.0	0.8	1.1	0.1	1.1	0.3
IPI00977640	ATP1A1	sodium/potassium-transporting ATPase subunit alpha-1 isoform d	100.0%	26.0	19	19	25	2	37,513,298	39,266,141	39,952,491	43,292,918	2,960,922	1,942,340	2,526,532	1,574,365	17.7	11.1	14.1	8.1	1.0	0.6	1.1	0.5	1.2	0.1	1.0	0.8	1.1	0.1	1.1	0.3
				ADIGVAMGIAGSDVSK	2	100.0%	2																									
				AVAGDASESALLK	2	100.0%	1																									
				AVFQANQENLPILK	2	100.0%	2																									
				DGPNALTPPPTTPEWIK	2	97.7%	1																									
				DMTSEQLDDILK	2	100.0%	1																									
				EQPLDEELKDAFQNAYLELGGLGER	3	100.0%	1																									
				GIVVYTGDR	2	100.0%	1																									
				IAGLCNR	2	95.9%	1																									
				IVEIPFNSTNK	2	99.9%	2																									
				LNIPVSQVNPR	2	99.9%	2																									
				LSLDELHR	2	99.6%	1																									
				MSINAEEVVVGDLVEVK	2	100.0%	1																									
				NPNTSEPQHLLVMK	3	99.9%	1																									
				QAADMILLDDNFASIVTGVEEGR	2	100.0%	2																									
				QGAIVAVTGDGVNDSPALK	2	100.0%	1																									
				SPDFTNENPLETR	2	100.0%	2																									
				VIMVTGDHPITAK	2	99.7%	1																									
				YGTDLSR	2	97.7%	1																									
				YHTEIVFAR	3	82.4%	1																									
IPI00646185	CNDP2	8 kDa protein	100.0%	18.4	1	1	1	1	553,330	617,610	659,978	607,668	34,862	57,278	38,608	30,883	14.1	20.7	13.1	11.4	1.1	0.4	1.2	0.07	1.1	0.3	1.1	0.6	-1.0	0.9	-1.1	0.3
				LYDDIDFDIEEFAK	2	100.0%	1																									
IPI00646304	PPIB	Peptidyl-prolyl cis-trans isomerase B	100.0%	51.4	11	14	21	1	54,436,648	53,745,512	52,751,223	58,218,358	4,450,219	2,958,248	3,220,928	2,371,725	18.3	12.3	13.7	9.1	-1.0	0.9	-1.0	0.8	1.1	0.5	-1.0	0.8	1.1	0.3	1.1	0.2
				DFMIQGGDFTR	2	100.0%	2																									
				DKPLKDVIIADCGK	2	97.9%	1																									
				DKPLKDVIIADCGK	3	99.9%	1																									
				DTNGSQFFITTVK	2	100.0%	2																									
				FPDENFK	2	97.8%	1																									
				HVVFGK	1	97.1%	1																									
				IEVEKPFAIAKE	2	99.2%	2																									
				IEVEKPFAIAKE	3	96.3%	1																									
				IGDEDVGRVIFGLFGK	3	100.0%	1																									
				TAWLDGK	2	99.4%	2																									
				TVDNFVALATGEK	2	100.0%	2																									
				VIKDFMIQGGDFTR	2	100.0%	2																									
				VIKDFMIQGGDFTR	3	100.0%	1																									
				VLEGMEVVR	2	100.0%	2																									
IPI00646366	CEP110	Centrosomal protein 110kDa	95.2%	0.4	1	1	1	3	642,327	866,240	1,062,253	830,717	51,612	59,387	168,821	114,591	18.0	15.3	35.5	30.8	1.3	0.02	1.7	0.07	1.3	0.2	1.2	0.3	-1.0	0.8	-1.3	0.3
IPI00657962	CEP110	isoform 1 of Centriolin	95.2%	0.4	1	1	1	3	642,327	866,240	1,062,253	830,717	51,612	59,387	168,821	114,591	18.0	15.3	35.5	30.8	1.3	0.02	1.7	0.07	1.3	0.2	1.2	0.3	-1.0	0.8	-1.3	0.3
IPI00888387	CEP110	isoform 5 of Centriolin	95.2%	0.4	1	1	1	3	642,327	866,240	1,062,253	830,717	51,612	59,387	168,821	114,591	18.0	15.3	35.5	30.8	1.3	0.02	1.7	0.07	1.3	0.2	1.2	0.3	-1.0	0.8	-1.3	0.3
				QLEEAIQLK	2	93.1%	1																									
IPI00646459	NASP	Nuclear autoantigenic sperm protein	100.0%	14.2	3	4	5	5	1,535,622	1,518,122	1,508,419	1,645,019	77,036	114,494	74,533	86,165	11.2	16.9	11.1	11.7	-1.0	0.9	-1.0	0.8	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.3
IPI00977790	NASP	Uncharacterized protein	100.0%	22.4	3	4	5	5	1,535,622	1,518,122	1,508,419	1,645,019	77,036	114,494	74,533	86,165	11.2	16.9	11.1	11.7	-1.0	0.9	-1.0	0.8	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.3
IPI00977883	NASP	nuclear autoantigenic sperm protein isoform 4	100.0%	8.3	3	4	5	5	1,535,622	1,518,122	1,508,419	1,645,019	77,036	114,494	74,533	86,165	11.2	16.9	11.1	11.7	-1.0	0.9	-1.0	0.8	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.3
IPI00983159	NASP	Protein	100.0%	20.8	3	4	5	5	1,535,622	1,518,122	1,508,419	1,645,019	77,036	114,494	74,533	86,165	11.2	16.9	11.1	11.7	-1.0	0.9	-1.0	0.8	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.3
IPI01015635	NASP	cDNA FLJ53176, highly similar to Nuclear autoantigenic sperm protein	100.0%	8.7	3	4	5	5	1,535,622	1,518,122	1,508,419	1,645,019	77,036	114,494	74,533	86,165	11.2	16.9	11.1	11.7	-1.0	0.9	-1.0	0.8	1.1	0.4	-1.0	0.9	1.1	0.4	1.1	0.3
				LLAETHYQLGLAYGYNSQYDEAVAQFSK	3	100.0%	1																									
				SIEVIENR	2	83.7%	1																									
				SLQENEEEEIGNLELAWDMLDLAK	2	100.0%	2																									
				SLQENEEEEIGNLELAWDMLDLAK	3	99.9%	1																									
IPI00646632	CNDP2	28 kDa protein	100.0%	31.5	5	5	5	1	5,349,955	5,296,239	5,649,671	6,054,110	443,566	366,998	487,304	165,232	18.5	15.5	19.3	6.1	-1.0	0.9	1.1	0.7	1.1	0.2	1.1	0.6	1.1	0.1	1.1	0.5
				FCLEGMEESGSEGLDELIFAR	2	100.0%	1																									
				GSTDDKGPVAGWINALEAYQK	3	100.0%	1																									
				LPDGSEIPLPPILLGR	2	99.3%	1																									
				MMEVAAADVK	2	100.0%	1																									
				TGQEIPVNVR	2	99.6%	1																									
IPI00646689	TXNDC17	Thioredoxin domain-containing protein 17	100.0%	38.2	3	3	3	1	4,535,439	4,807,255	4,671,208	5,083,942	200,953	155,788	318,660	100,547	9.9	7.3	15.3	4.4	1.1	0.3	1.0	0.7	1.1	0.04	-1.0	0.7	1.1	0.2	1.1	0.3
				LVESECLQANLVEMLFSED	2	100.0%	1																									
				SWCPDCVQAEPVVR	2	98.7%	1																									
				YEEVSVSGFEEFHR	3	99.9%	1																									
IPI00646767	NUDC	24 kDa protein	100.0%	6.7	1	1	1	1	3,586,635	3,185,750	3,537,995	3,698,425	149,979	189,871	291,965	225,025	9.4	13.3	18.5	13.6	-1.1	0.1	-1.0	0.9	1.0	0.7	1.1	0.3	1.2	0.1	1.0	0.7
				TDFFIGGEEGMAEK	2	99.8%	1																									
IPI00646841	ZNF577	isoform 2 of Zinc finger protein 577	99.6%	2.4	1	1	1	3	3,954,927	3,835,617	3,892,643	4,045,260	493,085	295,239	252,318	245,573	27.9	17.2	14.5	13.6	-1.0	0.8	-1.0	0.9	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.7
IPI00925509	ZNF577	54 kDa protein	99.6%	2.1	1	1	1	3	3,954,927	3,835,617	3,892,643	4,045,260	493,085	295,239	252,318	245,573	27.9	17.2	14.5	13.6	-1.0	0.8	-1.0	0.9	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.7
IPI00953310	ZNF577	isoform 1 of Zinc finger protein 577	99.6%	2.1	1	1	1	3	3,954,927	3,835,617	3,892,643	4,045,260	493,085	295,239	252,318	245,573	27.9	17.2	14.5	13.6	-1.0	0.8	-1.0	0.9	1.0	0.9	1.0	0.9	1.1	0.6	1.0	0.7
				NATIVMSVRR	2	95.0%	1																									
IPI00646917	NUDT21	Cleavage and polyadenylation specificity factor subunit 5	99.3%	20.7	2	2	2	1	3,558,295	3,688,911	3,676,794	4,397,000	524,264	199,604	347,830	109,982	33.0	12.1	21.2	5.6	1.0	0.8	1.0	0.9	1.2	0.2	-1.0	1	1.2	0.01	1.2	0.1
				LPGGELNPGEDEVEGLKR	3	96.5%	1																									
				LVAAPLFELYDNAPGYGPIISSLPQLLSR	3	99.3%	1																									
IPI00646963	REEP6	Uncharacterized protein	100.0%	10.9	2	2	2	2	8,422,658	8,376,118	7,574,916	9,398,324	868,151	303,947	479,391	497,311	23.1	8.1	14.2	11.8	-1.0	1	-1.1	0.4	1.1	0.4	-1.1	0.2	1.1	0.1	1.2	0.03
IPI00647161	REEP6	Receptor expression-enhancing protein 6	100.0%	12.5	2	2	2	2	8,422,658	8,376,118	7,574,916	9,398,324	868,151	303,947	479,391	497,311	23.1	8.1	14.2	11.8	-1.0	1	-1.1	0.4	1.1	0.4	-1.1	0.2	1.1	0.1	1.2	0.03
				ALDAAAGITR	2	99.5%	1																									
				NLVTEVLGALEAK	2	100.0%	1																									
IPI00647001	ANP32B	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B	100.0%	18.6	2	2	3	1	3,617,977	2,798,910	3,541,088	3,479,880	278,900	179,265	305,277	254,459	17.2	14.3	19.3	16.4	-1.3	0.04	-1.0	0.9	-1.0	0.7	1.3	0.07	1.2	0.06	-1.0	0.9
				LPNLTHLNLSGNK	2	100.0%	1																									
				SLDLFNCEVTNLNDYR	2	100.0%	2																									
IPI00647102	ATP1A2	cDNA FLJ42590 fis, clone BRACE3009708, highly similar to Sodium/potassium-tran	100.0%	2.2	2	2	2	1	7,641,920	8,240,610	7,180,180	8,688,340	462,632	411,227	607,220	353,592	13.5	11.2	18.9	9.1	1.1	0.4	-1.1	0.6	1.1	0.1	-1.1	0.2	1.1	0.4	1.2	0.06
				QGAIVAVTGDGVDDSPALK	2	100.0%	1																									
				QGAIVAVTGDGVDDSPALKK	3	100.0%	1																									
IPI00647118	EIF1AY	Uncharacterized protein	99.9%	7.9	1	1	1	1	4,157,000	4,009,275	3,188,055	4,536,025	501,058	224,435	326,757	465,307	27.0	12.5	22.9	22.9	-1.0	0.8	-1.3	0.1	1.1	0.6	-1.3	0.07	1.1	0.3	1.4	0.05
				AYGELPEHAK	2	99.3%	1																									
IPI00647145	GLG1	79 kDa protein	100.0%	2.2	1	1	1	1	656,332	661,395	631,020	603,175	45,240	77,283	98,658	79,480	15.4	26.1	35.0	29.5	1.0	1	-1.0	0.8	-1.1	0.6	-1.0	0.8	-1.1	0.6	-1.0	0.8
				ALNEACESVIQTACK	2	100.0%	1																									
IPI00878431	-	15 kDa protein	100.0%	10.9	1	1	2	3	1,395,656	1,422,692	1,313,214	1,521,394	98,690	77,186	91,675	52,021	15.8	12.1	15.6	7.7	1.0	0.8	-1.1	0.6	1.1	0.3	-1.1	0.4	1.1	0.3	1.2	0.08
IPI00647168	RPL11	Ribosomal protein L11	100.0%	10.7	1	1	2	3	1,395,656	1,422,692	1,313,214	1,521,394	98,690	77,186	91,675	52,021	15.8	12.1	15.6	7.7	1.0	0.8	-1.1	0.6	1.1	0.3	-1.1	0.4	1.1	0.3	1.2	0.08
IPI00647674	RPL11	Ribosomal protein L11	100.0%	8.1	1	1	2	3	1,395,656	1,422,692	1,313,214	1,521,394	98,690	77,186	91,675	52,021	15.8	12.1	15.6	7.7	1.0	0.8	-1.1	0.6	1.1	0.3	-1.1	0.4	1.1	0.3	1.2	0.08
				VLEQLTGQTPVFSK	2	99.8%	2																									
IPI00647188	HYDIN2;HYDIN	isoform 1 of Hydrocephalus-inducing protein homolog	90.9%	0.4	1	1	1	1	479,338	569,536	623,488	823,775	43,370	46,493	97,891	152,998	20.2	18.3	35.1	41.5	1.2	0.2	1.3	0.2	1.7	0.09	1.1	0.6	1.4	0.2	1.3	0.3
				EGEEAAQEAAVGQNVIGQGR	2	86.3%	1																									
IPI00647217	SKIV2L2	Superkiller viralicidic activity 2-like 2	96.9%	1.3	1	1	1	2	1,848,680	2,132,610	1,708,005	2,283,990	258,913	153,428	161,704	206,748	31.3	16.1	21.2	20.2	1.2	0.4	-1.1	0.7	1.2	0.2	-1.2	0.09	1.1	0.6	1.3	0.06
IPI00964997	SKIV2L2	Protein	96.9%	15.9	1	1	1	2	1,848,680	2,132,610	1,708,005	2,283,990	258,913	153,428	161,704	206,748	31.3	16.1	21.2	20.2	1.2	0.4	-1.1	0.7	1.2	0.2	-1.2	0.09	1.1	0.6	1.3	0.06
				DVDFEGTDEPIFGK	2	96.9%	1																									
IPI00647259	NT5E	NT5E protein	92.6%	5.7	1	1	1	1	2,068,067	2,133,053	2,525,483	2,148,720	101,473	181,650	128,228	73,819	11.0	19.0	11.4	7.7	1.0	0.8	1.2	0.02	1.0	0.5	1.2	0.1	1.0	0.9	-1.2	0.03
				GPLASQISGLYLPYK	2	92.6%	1																									
IPI00647366	CRYZ	quinone oxidoreductase isoform b	100.0%	20.0	3	3	3	1	13,057,770	13,974,265	14,664,696	16,716,333	1,736,835	728,009	1,460,869	540,332	29.7	11.7	22.3	7.2	1.1	0.6	1.1	0.5	1.3	0.1	1.0	0.7	1.2	0.02	1.1	0.2
				EEFQQYAAALQAGMEIGWLKPVIGSQYPLEK	3	99.4%	1																									
				VAEAHENIIHGSGATGK	3	100.0%	1																									
				VFEFGGPEVLK	2	100.0%	1																									
IPI00647380	PSMA7	Uncharacterized protein	100.0%	15.2	2	2	3	1	2,045,143	2,275,167	1,904,960	2,282,960	226,951	172,101	123,845	84,816	24.8	16.9	14.5	8.3	1.1	0.4	-1.1	0.6	1.1	0.4	-1.2	0.1	1.0	1	1.2	0.04
				LTVEDPVTVEYITR	2	100.0%	1																									
				NYTDEAIETDDLTIK	2	100.0%	2																									
IPI00647400	RNPEP	Uncharacterized protein	100.0%	25.0	11	12	12	1	37,176,792	37,149,485	37,206,679	42,094,488	3,842,797	1,534,896	1,857,216	1,040,934	23.1	9.2	11.2	5.5	-1.0	1	1.0	1	1.1	0.3	1.0	1	1.1	0.03	1.1	0.05
				AEFGPPGPGAGSR	2	93.9%	1																									
				AIEAVAISPWK	2	100.0%	1																									
				NDHQEDFWK	2	97.3%	1																									
				NDHQEDFWK	3	85.9%	1																									
				QHMDITGEENPLNK	3	98.3%	1																									
				RPLHSAQAVDVASASNFR	3	99.6%	1																									
				TYQLVYFLDK	2	92.5%	1																									
				VDIIPGFEFDR	2	99.9%	1																									
				VGEGPGVCWLAPEQTAGK	2	100.0%	1																									
				VKIEPGVDPDDTYNETPYEK	3	99.8%	1																									
				WGQIVLK	2	92.0%	1																									
				YSALIEVPDGFTAVMSASTWEK	2	100.0%	1																									
IPI00647418	NUDC	NPD011	100.0%	12.8	2	2	4	1	2,646,090	2,738,185	2,518,225	3,109,650	148,198	66,420	215,854	214,499	12.5	5.4	19.2	15.4	1.0	0.6	-1.1	0.6	1.2	0.1	-1.1	0.4	1.1	0.2	1.2	0.09
				GQPAIIDGELYNEVK	2	100.0%	2																									
				VEESSWLIEDGK	2	99.9%	2																									
IPI00647650	EIF3H	cDNA FLJ35809 fis, clone TESTI2006016, highly similar to Eukaryotic translation ini	99.6%	7.9	2	2	3	2	3,342,508	3,178,985	3,325,803	3,540,573	545,810	221,817	229,286	306,379	36.5	15.6	15.4	19.4	-1.1	0.8	-1.0	1	1.1	0.8	1.0	0.7	1.1	0.4	1.1	0.6
IPI00977658	EIF3H	Eukaryotic translation initiation factor 3 subunit H	99.6%	8.2	2	2	3	2	3,342,508	3,178,985	3,325,803	3,540,573	545,810	221,817	229,286	306,379	36.5	15.6	15.4	19.4	-1.1	0.8	-1.0	1	1.1	0.8	1.0	0.7	1.1	0.4	1.1	0.6
				ANITFEYMFEEVPIVIK	2	99.6%	2																									
				LFMAQALQEYNN	2	99.5%	1																									
IPI00647662	CNDP2	8 kDa protein	100.0%	30.4	1	1	1	1	634,942	462,424	605,474	636,150	31,554	74,920	33,604	51,960	11.1	36.2	12.4	18.3	-1.4	0.07	-1.0	0.5	1.0	1	1.3	0.1	1.4	0.09	1.1	0.6
				GSTDDKGPVAGWINALEAYQK	3	100.0%	1																									
IPI00647678	NARS	cDNA FLJ52703, highly similar to Asparaginyl-tRNA synthetase, cytoplasmic	100.0%	23.4	5	5	5	1	33,071,280	32,674,885	33,005,145	39,135,380	3,487,408	2,012,513	2,775,414	1,432,390	23.6	13.8	18.8	8.2	-1.0	0.9	-1.0	1	1.2	0.1	1.0	0.9	1.2	0.03	1.2	0.09
				IFDSEEILAGYK	2	100.0%	1																									
				LMTDTINEPILLCR	2	99.9%	1																									
				MNYSDAIVWLK	2	100.0%	1																									
				SPAGSIVHELNPNFQPPK	3	98.0%	1																									
				YGTCPHGGYGLGLER	3	100.0%	1																									

IPI00647775	MMS19	MMS19 nucleotide excision repair homolog	99.3%	4.0	1	1	1	2	225,810	242,424	283,824	369,708	64,456	46,740	54,783	25,338	63.8	43.1	43.2	15.3	1.1	0.8	1.3	0.5	1.6	0.09	1.2	0.6	1.5	0.04	1.3	0.2
IPI00973493	MMS19	isoform 2 of MMS19 nucleotide excision repair protein homolog	99.3%	3.8	1	1	1	2	225,810	242,424	283,824	369,708	64,456	46,740	54,783	25,338	63.8	43.1	43.2	15.3	1.1	0.8	1.3	0.5	1.6	0.09	1.2	0.6	1.5	0.04	1.3	0.2
				FAEFLLPLLIEK	2	99.3%	1																									
IPI00647859	RNPEP	Uncharacterized protein	100.0%	15.7	3	3	3	1	4,885,352	4,990,290	4,771,109	5,705,403	556,226	310,739	491,022	140,134	25.5	13.9	23.0	5.5	1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.7	1.1	0.07	1.2	0.1
				AFFPCFDTPAVK	2	81.3%	1																									
				VKIEPGVDPDDTYNETPYEK	3	99.8%	1																									
				YSALIEVPDGFTAVMSASTWEK	2	100.0%	1																									
IPI00651653	DDX17	isoform 3 of Probable ATP-dependent RNA helicase DDX17	100.0%	19.5	11	11	14	3	24,427,691	23,242,353	25,139,277	26,553,327	1,680,683	716,241	1,825,465	1,099,254	15.4	6.9	16.2	9.3	-1.1	0.5	1.0	0.8	1.1	0.3	1.1	0.4	1.1	0.04	1.1	0.5
IPI00651677	DDX17	isoform 2 of Probable ATP-dependent RNA helicase DDX17	100.0%	19.5	11	11	14	3	24,427,691	23,242,353	25,139,277	26,553,327	1,680,683	716,241	1,825,465	1,099,254	15.4	6.9	16.2	9.3	-1.1	0.5	1.0	0.8	1.1	0.3	1.1	0.4	1.1	0.04	1.1	0.5
IPI00952778	DDX17	Uncharacterized protein	100.0%	19.5	11	11	14	3	24,427,691	23,242,353	25,139,277	26,553,327	1,680,683	716,241	1,825,465	1,099,254	15.4	6.9	16.2	9.3	-1.1	0.5	1.0	0.8	1.1	0.3	1.1	0.4	1.1	0.04	1.1	0.5
				APILIATDVASR	2	100.0%	2																									
				CTYLVLDEADR	2	99.1%	1																									
				DMVGIAQTGSGK	2	99.7%	1																									
				FVINYDYPNSSEDYVHR	3	99.9%	1																									
				GDGPICLVLAPTR	2	99.3%	1																									
				LIQLMEEIMAEK	2	100.0%	2																									
				LIQLMEEIMAEKENK	3	99.7%	1																									
				NFYVEHPEVAR	2	99.9%	1																									
				SSQSSSQQFSGIGR	2	100.0%	2																									
				STCIYGGAPK	2	99.5%	1																									
				VLEEANQAINPK	2	99.9%	1																									
IPI00654754	RPS27A	RPS27A protein	100.0%	42.1	4	4	7	2	1,674,259	1,715,312	1,589,752	1,884,854	112,577	77,260	66,492	77,702	15.0	10.1	9.4	9.2	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.02
IPI01010447	UBC	10 kDa protein	100.0%	45.5	4	4	7	2	1,674,259	1,715,312	1,589,752	1,884,854	112,577	77,260	66,492	77,702	15.0	10.1	9.4	9.2	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.02
				IQDKEGIPPDQQR	2	99.9%	2																									
				TITLEVEPSDTIENVK	2	100.0%	2																									
				TITLEVEPSDTIENVKAK	3	86.9%	1																									
				TLSDYNIQK	2	100.0%	2																									
IPI00654777	EIF3F	cDNA FLJ36192 fis, clone TESTI2027450, highly similar to Eukaryotic translation ini	100.0%	18.3	5	5	5	3	9,061,677	10,909,061	9,592,479	10,884,938	1,070,594	1,442,002	1,186,662	1,053,917	26.4	29.6	27.7	21.7	1.2	0.3	1.1	0.7	1.2	0.3	-1.1	0.5	-1.0	1	1.1	0.4
IPI00941255	EIF3F	Eukaryotic translation initiation factor 3 subunit F	100.0%	19.1	5	5	5	3	9,061,677	10,909,061	9,592,479	10,884,938	1,070,594	1,442,002	1,186,662	1,053,917	26.4	29.6	27.7	21.7	1.2	0.3	1.1	0.7	1.2	0.3	-1.1	0.5	-1.0	1	1.1	0.4
IPI01013988	EIF3F	cDNA FLJ52696, highly similar to Eukaryotic translation initiation factor 3 subunit 5	100.0%	22.2	5	5	5	3	9,061,677	10,909,061	9,592,479	10,884,938	1,070,594	1,442,002	1,186,662	1,053,917	26.4	29.6	27.7	21.7	1.2	0.3	1.1	0.7	1.2	0.3	-1.1	0.5	-1.0	1	1.1	0.4
				AYVSTLMGVPGR	2	100.0%	1																									
				EAPNPIHLTVDTSLQNGR	3	100.0%	1																									
				FLMSLVNQVPK	2	100.0%	1																									
				LHPVILASIVDSYER	2	98.9%	1																									
				TMGVMFTPLTVK	2	99.6%	1																									
IPI00656107	TREH	isoform 2 of Trehalase	99.5%	4.0	1	1	1	2	1,546,155	1,615,695	1,818,990	1,791,210	154,203	72,055	88,738	88,387	22.3	10.0	10.9	11.0	1.0	0.7	1.2	0.2	1.2	0.2	1.1	0.1	1.1	0.2	-1.0	0.8
IPI00921204	TREH	Uncharacterized protein	99.5%	4.0	1	1	1	2	1,546,155	1,615,695	1,818,990	1,791,210	154,203	72,055	88,738	88,387	22.3	10.0	10.9	11.0	1.0	0.7	1.2	0.2	1.2	0.2	1.1	0.1	1.1	0.2	-1.0	0.8
				FVEFYYCYGHVPNGGRVYYLQR	3	99.5%	1																									
IPI00922301	-	Glutathione S-transferase	100.0%	18.2	3	3	3	4	6,319,728	6,964,588	6,543,651	7,253,923	1,411,753	864,989	883,689	509,923	50.0	27.8	30.2	15.7	1.1	0.7	1.0	0.9	1.1	0.6	-1.1	0.7	1.0	0.8	1.1	0.5
IPI00657682	GSTA1	Glutathione S-transferase A1	100.0%	18.5	3	3	3	4	6,319,728	6,964,588	6,543,651	7,253,923	1,411,753	864,989	883,689	509,923	50.0	27.8	30.2	15.7	1.1	0.7	1.0	0.9	1.1	0.6	-1.1	0.7	1.0	0.8	1.1	0.5
IPI00745233	GSTA2	Glutathione S-transferase A2	100.0%	18.5	3	3	3	4	6,319,728	6,964,588	6,543,651	7,253,923	1,411,753	864,989	883,689	509,923	50.0	27.8	30.2	15.7	1.1	0.7	1.0	0.9	1.1	0.6	-1.1	0.7	1.0	0.8	1.1	0.5
IPI01013892	GSTA2	Glutathione S-transferase	100.0%	18.5	3	3	3	4	6,319,728	6,964,588	6,543,651	7,253,923	1,411,753	864,989	883,689	509,923	50.0	27.8	30.2	15.7	1.1	0.7	1.0	0.9	1.1	0.6	-1.1	0.7	1.0	0.8	1.1	0.5
				AILNYIASK	2	100.0%	1																									
				NDGYLMFQQVPMVEIDGMK	3	88.3%	1																									
				WLLAAAGVEFEEK	2	100.0%	1																									
IPI00657713	P4HA2	Uncharacterized protein	99.8%	7.4	1	1	1	2	2,205,320	2,028,608	2,663,898	2,370,738	169,985	75,363	181,063	79,823	17.2	8.3	15.2	7.5	-1.1	0.4	1.2	0.1	1.1	0.4	1.3	0.01	1.2	0.01	-1.1	0.2
IPI00894468	P4HA2	Uncharacterized protein	99.8%	6.4	1	1	1	2	2,205,320	2,028,608	2,663,898	2,370,738	169,985	75,363	181,063	79,823	17.2	8.3	15.2	7.5	-1.1	0.4	1.2	0.1	1.1	0.4	1.3	0.01	1.2	0.01	-1.1	0.2
				YQAMLSVDDCFGMGR	2	97.7%	1																									
IPI00657751	PYGM	glycogen phosphorylase, muscle form isoform 2	100.0%	4.9	2	2	3	1	1,871,125	1,857,785	1,697,080	2,011,706	151,202	113,762	144,829	104,860	18.1	13.7	19.1	11.7	-1.0	0.9	-1.1	0.4	1.1	0.5	-1.1	0.4	1.1	0.3	1.2	0.1
				VIPAADLSEQISTAGTEASGTGNMK	2	100.0%	1																									
				VLYPNDNFFEGK	2	100.0%	2																									
IPI00657915	EHD1	cDNA FLJ55166, highly similar to EH-domain-containing protein 1	100.0%	5.1	2	2	2	3	2,340,034	2,799,010	2,394,144	2,711,976	208,754	66,846	145,749	113,794	20.0	5.3	13.6	9.4	1.2	0.09	1.0	0.8	1.2	0.2	-1.2	0.04	-1.0	0.5	1.1	0.1
IPI00852957	EHD1	Uncharacterized protein	100.0%	14.9	2	2	2	3	2,340,034	2,799,010	2,394,144	2,711,976	208,754	66,846	145,749	113,794	20.0	5.3	13.6	9.4	1.2	0.09	1.0	0.8	1.2	0.2	-1.2	0.04	-1.0	0.5	1.1	0.1
IPI00853038	EHD1	Uncharacterized protein	100.0%	15.2	2	2	2	3	2,340,034	2,799,010	2,394,144	2,711,976	208,754	66,846	145,749	113,794	20.0	5.3	13.6	9.4	1.2	0.09	1.0	0.8	1.2	0.2	-1.2	0.04	-1.0	0.5	1.1	0.1
				HLIEQDFPGMR	2	100.0%	1																									
				LNAFGNAFLNR	2	99.9%	1																									
IPI00658000	IGF2BP3	isoform 1 of Insulin-like growth factor 2 mRNA-binding protein 3	100.0%	20.2	8	8	11	1	36,411,302	37,825,468	33,038,622	39,940,078	2,632,152	1,702,407	3,095,872	1,331,128	16.2	10.1	21.0	7.5	1.0	0.7	-1.1	0.4	1.1	0.3	-1.1	0.2	1.1	0.4	1.2	0.07
				DQTPDENDQVVVK	2	100.0%	1																									
				IPVSGPFLVK	2	89.1%	1																									
				ITISPLQELTLYNPER	2	100.0%	1																									
				LLVPTQFVGAIIGK	2	94.8%	2																									
				LNGFQLENFTLK	2	99.7%	1																									
				LYIGNLSENAAPSDLESIFK	2	100.0%	2																									
				MVIITGPPEAQFK	2	100.0%	2																									
				VAYIPDEMAAQQNPLQQPR	3	100.0%	1																									
IPI00658011	DHRS11	isoform 2 of Dehydrogenase/reductase SDR family member 11	100.0%	11.1	2	2	3	1	2,676,393	2,532,831	2,605,708	2,894,002	128,485	118,880	135,218	131,721	10.7	10.5	11.6	10.2	-1.1	0.4	-1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.08	1.1	0.2
				AAATYEQMK	2	93.0%	1																									
				YAVTALTEGLR	2	99.9%	2																									
IPI00658014	DNPEP	Uncharacterized protein	100.0%	8.5	1	1	1	3	132,300	128,706	131,648	152,971	33,684	20,478	20,648	17,757	56.9	35.6	35.1	26.0	-1.0	0.9	-1.0	1	1.2	0.6	1.0	0.9	1.2	0.4	1.2	0.5
IPI00953251	DNPEP	cDNA FLJ58475, highly similar to Aspartyl aminopeptidase	100.0%	10.1	1	1	1	3	132,300	128,706	131,648	152,971	33,684	20,478	20,648	17,757	56.9	35.6	35.1	26.0	-1.0	0.9	-1.0	1	1.2	0.6	1.0	0.9	1.2	0.4	1.2	0.5
IPI01013435	DNPEP	Uncharacterized protein	100.0%	20.3	1	1	1	3	132,300	128,706	131,648	152,971	33,684	20,478	20,648	17,757	56.9	35.6	35.1	26.0	-1.0	0.9	-1.0	1	1.2	0.6	1.0	0.9	1.2	0.4	1.2	0.5
				NINENFGPNTEMHLVPILATAIQEELEK	3	99.3%	1																									
IPI00658086	ZYX	Uncharacterized protein	99.9%	6.4	1	1	1	4	2,045,512	2,036,284	1,915,666	2,241,170	266,918	110,855	160,068	88,412	29.2	12.2	18.7	8.8	-1.0	1	-1.1	0.7	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.1
IPI00871311	ZYX	cDNA FLJ53160, highly similar to Zyxin	99.9%	2.3	1	1	1	4	2,045,512	2,036,284	1,915,666	2,241,170	266,918	110,855	160,068	88,412	29.2	12.2	18.7	8.8	-1.0	1	-1.1	0.7	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.1
IPI00926316	ZYX	cDNA, FLJ79126, highly similar to Zyxin	99.9%	2.7	1	1	1	4	2,045,512	2,036,284	1,915,666	2,241,170	266,918	110,855	160,068	88,412	29.2	12.2	18.7	8.8	-1.0	1	-1.1	0.7	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.1
IPI00941977	ZYX	ZYX protein (Fragment)	99.9%	1.9	1	1	1	4	2,045,512	2,036,284	1,915,666	2,241,170	266,918	110,855	160,068	88,412	29.2	12.2	18.7	8.8	-1.0	1	-1.1	0.7	1.1	0.5	-1.1	0.6	1.1	0.2	1.2	0.1
				SPGAPGPLTLK	2	96.9%	1																									
IPI00658109	CKMT1B;CKMT1A	isoform 1 of Creatine kinase U-type, mitochondrial	100.0%	11.3	2	2	2	2	2,605,261	2,899,230	2,617,936	2,977,180	360,957	173,291	379,130	337,784	31.0	13.4	32.4	25.4	1.1	0.5	1.0	1	1.1	0.5	-1.1	0.5	1.0	0.8	1.1	0.5
IPI00877726	CKMT1B;CKMT1A	isoform 2 of Creatine kinase U-type, mitochondrial	100.0%	10.5	2	2	2	2	2,605,261	2,899,230	2,617,936	2,977,180	360,957	173,291	379,130	337,784	31.0	13.4	32.4	25.4	1.1	0.5	1.0	1	1.1	0.5	-1.1	0.5	1.0	0.8	1.1	0.5
				GTGGVDTAATGGVFDISNLDR	2	99.6%	1																									
				TVGMVAGDEETYEVFADLFDPVIQER	2	100.0%	1																									
IPI00719549	RBM14;RBM14-RBM4	RBM14-RBM4 protein isoform 1	100.0%	17.7	3	3	3	1	1,452,643	1,623,679	1,470,450	1,724,483	113,110	127,195	79,658	126,003	17.4	17.5	12.1	16.3	1.1	0.3	1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.6	1.2	0.1
				ATAPVPTVGEGYGYGHESELSQASAAAR	3	99.9%	1																									
				IFVGNVSAACTSQELR	2	100.0%	1																									
				VADLTEQYNEQYGAVR	2	99.6%	1																									
IPI00719553	PPP6R3	isoform 2 of Serine/threonine-protein phosphatase 6 regulatory subunit 3	100.0%	4.7	2	2	2	1	1,289,129	1,270,379	1,387,767	1,554,372	57,867	37,733	106,200	156,065	10.0	6.6	17.1	22.5	-1.0	0.8	1.1	0.4	1.2	0.2	1.1	0.3	1.2	0.1	1.1	0.4
				ETGFSQDSSLQQMQQMTSNFIDQFGFNDEK	3	98.1%	1																									
				QDVLNWLNEEK	2	99.9%	1																									
IPI00719600	CYFIP2	isoform 2 of Cytoplasmic FMR1-interacting protein 2	100.0%	1.8	2	2	3	4	1,064,840	964,203	1,072,027	1,105,544	33,688	52,023	89,545	35,794	7.1	12.1	18.7	7.2	-1.1	0.1	1.0	0.9	1.0	0.4	1.1	0.3	1.1	0.06	1.0	0.7
IPI00789699	CYFIP2	isoform 1 of Cytoplasmic FMR1-interacting protein 2	100.0%	1.8	2	2	3	4	1,064,840	964,203	1,072,027	1,105,544	33,688	52,023	89,545	35,794	7.1	12.1	18.7	7.2	-1.1	0.1	1.0	0.9	1.0	0.4	1.1	0.3	1.1	0.06	1.0	0.7
IPI00984777	CYFIP2	Uncharacterized protein	100.0%	1.9	2	2	3	4	1,064,840	964,203	1,072,027	1,105,544	33,688	52,023	89,545	35,794	7.1	12.1	18.7	7.2	-1.1	0.1	1.0	0.9	1.0	0.4	1.1	0.3	1.1	0.06	1.0	0.7
IPI01010578	CYFIP2	137 kDa protein	100.0%	2.0	2	2	3	4	1,064,840	964,203	1,072,027	1,105,544	33,688	52,023	89,545	35,794	7.1	12.1	18.7	7.2	-1.1	0.1	1.0	0.9	1.0	0.4	1.1	0.3	1.1	0.06	1.0	0.7
				FINMFAVLDELK	2	99.9%	2																									
				LGTPQQIAIAR	2	86.7%	1																									
IPI00719622	RPS28	40S ribosomal protein S28	100.0%	36.2	3	3	3	1	14,516,780	15,388,160	14,141,860	16,436,315	1,406,276	796,380	1,563,277	678,011	21.7	11.6	24.7	9.2	1.1	0.6	-1.0	0.9	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.2
				EGDVLTLLESER	2	100.0%	1																									
				GPVREGDVLTLLESER	3	99.3%	1																									
				VEFMDDTSR	2	99.9%	1																									
IPI00719669	MYL12B	Similar to Myosin regulatory light chain MRCL2	100.0%	45.4	7	8	13	1	12,919,011	13,021,199	12,913,326	14,806,187	1,071,789	400,745	680,753	313,575	18.6	6.9	11.8	4.7	1.0	0.9	-1.0	1	1.1	0.2	-1.0	0.9	1.1	0.008	1.1	0.04
				DGFIDKEDLHDMLASLGK	3	100.0%	2																									
				EAFNMIDQNR	2	100.0%	2																									
				ELLTTMGDR	2	100.0%	2																									
				ELLTTMGDRFTDEEVDELYR	3	99.9%	1																									
				FTDEEVDELYR	2	100.0%	2																									
				GNFNYIEFTR	2	100.0%	2																									
				NAFACFDEEATGTIQEDYLR	2	100.0%	1																									
				NAFACFDEEATGTIQEDYLR	3	100.0%	1																									
IPI00719690	SAMD9L	isoform 1 of Sterile alpha motif domain-containing protein 9-like	99.0%	2.2	2	2	2	1	7,086,720	7,312,670	6,752,770	7,791,330	487,836	329,468	268,731	218,464	15.4	10.1	8.9	6.3	1.0	0.7	-1.0	0.6	1.1	0.2	-1.1	0.2	1.1	0.3	1.2	0.02
				NFRCAVLKNK	2	86.6%	1																									
				YIEHYTLQPETGALNLIDPIHEFK	3	92.2%	1																									
IPI00736161	-	17 kDa protein	100.0%	13.4	2	2	2	1	2,832,931	3,133,964	2,917,921	3,387,933	121,338	147,984	137,055	235,142	9.6	10.6	10.5	15.5	1.1	0.2	1.0	0.7	1.2	0.07	-1.1	0.3	1.1	0.4	1.2	0.1
				LMELHGEGSSSGK	2	99.6%	1																									
				MMEIMTR	2	88.7%	1																									
IPI00981564	LOC100510292	putative alpha-1-antitrypsin-related protein-like	97.2%	2.4	1	1	1	2	2,054,880	1,987,440	2,212,535	2,108,010	219,509	114,903	179,482	49,350	23.9	12.9	18.1	5.2	-1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.3	1.1	0.4	-1.0	0.6
IPI00736763	SERPINA2	Putative alpha-1-antitrypsin-related protein	97.2%	2.4	1	1	1	2	2,054,880	1,987,440	2,212,535	2,108,010	219,509	114,903	179,482	49,350	23.9	12.9	18.1	5.2	-1.0	0.8	1.1	0.6	1.0	0.8	1.1	0.3	1.1	0.4	-1.0	0.6
				LVDTFLEDTK	2	97.2%	1																									
IPI00737545	PEAK1	Pseudopodium-enriched atypical kinase 1	97.6%	1.8	1	1	1	1	1,352,883	1,463,460	1,625,454	1,756,290	218,777	207,546	193,996	167,891	36.2	31.7	26.7	21.4	1.1	0.7	1.2	0.4	1.3	0.2	1.1	0.6	1.2	0.3	1.1	0.6
				LENLLLVHYQPGGTAQGFGPAEPSPTSSYPTR	3	96.5%	1																									
IPI00737736	-	similar to hCG1991922	100.0%	8.1	1	2	3	5	517,063	531,589	522,249	581,487	41,242	35,341	47,313	9,958	17.8	14.9	20.3	3.8	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00788220	-	similar to hCG1991922	100.0%	8.0	1	2	3	5	517,063	531,589	522,249	581,487	41,242	35,341	47,313	9,958	17.8	14.9	20.3	3.8	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00982055	HMGB1P40	high mobility group protein B1-like, partial	100.0%	11.8	1	2	3	5	517,063	531,589	522,249	581,487	41,242	35,341	47,313	9,958	17.8	14.9	20.3	3.8	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00982327	HMGB1P40	high mobility group protein B1-like, partial	100.0%	11.5	1	2	3	5	517,063	531,589	522,249	581,487	41,242	35,341	47,313	9,958	17.8	14.9	20.3	3.8	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.3
IPI00977902	LOC100508832	hypothetical protein LOC100508832	100.0%	5.4	1	2	3	5	517,063	531,589	522,249	581,487	41,242	35,341	47,313	9,958	17.8	14.9	20.3	3.8	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.3
				LGEMWNNTAADDKQPYEK	2	99.9%	1																									
				LGEMWNNTAADDKQPYEK	3	100.0%	2																									
IPI00737988	NKX1-1	LOW QUALITY PROTEIN: hypothetical protein LOC54729	91.2%	2.0	1	1	1	1	12,884,830	11,833,660	12,602,880	14,323,100	1,000,868	184,153	887,500	764,554	17.4	3.5	15.8	11.9	-1.1	0.4	-1.0	0.8	1.1	0.3	1.1	0.4	1.2	0.03	1.1	0.2
				ALAGAGGVGAAGSEPPNAGDPFK	3	91.2%	1																									
IPI00739387	FLJ45872	cDNA FLJ45872 fis, clone OCBBF3005843	93.1%	7.1	1	1	1	1	8,621,090	13,074,990	9,032,100	16,176,900	3,318,231	2,163,117	1,134,540	839,772	86.1	37.0	28.1	11.6	1.5	0.3	1.0	0.9	1.9	0.08	-1.4	0.1	1.2	0.2	1.8	0.001
				VLLLLFTSLCLK	3	93.1%	1																									
IPI00739539	POTEF	POTE ankyrin domain family member F	100.0%	5.2	7	9	11	1	164,156,799	160,009,650	154,462,430	179,585,560	########	6,134,599	########	5,924,304	14.6	8.6	15.0	7.4	-1.0	0.7	-1.1	0.5	1.1	0.2	-1.0	0.7	1.1	0.05	1.2	0.07
				AGFAGDDAPR	1	98.5%	1																									
				AVFPSIVGR	2	97.4%	1																									
				GILTLK	1	86.6%	1																									
				QEYDESGPSIVHR	2	100.0%	2																									
				QEYDESGPSIVHR	3	100.0%	1																									
				QEYDESGPSIVHRK	2	100.0%	2																									
				RGILTLK	2	89.1%	1																									
				SYELPDGQVITIGNER	1	98.1%	1																									
				SYELPDGQVITIGNER	3	100.0%	1																									
IPI00740026	LOC644578	hypothetical protein LOC644578	91.4%	6.7	1	1	1	1	5,416,360	6,797,220	5,880,390	7,521,460	809,297	1,026,142	754,568	339,079	33.4	33.8	28.7	10.1	1.3	0.3	1.1	0.7	1.4	0.04	-1.2	0.5	1.1	0.5	1.3	0.08
				SMPQVAVPDTMEEAAAGPKEK	3	88.6%	1																									
IPI00740286	LOC642781	Conserved hypothetical protein	99.5%	3.0	1	1	1	1	14,714,730	15,382,810	12,531,410	17,014,100	2,287,160	1,190,747	1,061,300	1,120,513	34.8	17.3	18.9	14.7	1.0	0.8	-1.2	0.4	1.2	0.4	-1.2	0.1	1.1	0.3	1.4	0.02
				VSEGLSFR	2	99.5%	1																									
IPI00740308	SLC45A1	Proton-associated sugar transporter A	91.3%	1.9	1	1	1	2	1,803,080	2,045,555	1,964,185	2,174,740	173,092	122,129	200,712	95,845	21.5	13.4	22.9	9.9	1.1	0.3	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.4	1.1	0.4
IPI00971085	SLC45A1	85 kDa protein	91.3%	1.8	1	1	1	2	1,803,080	2,045,555	1,964,185	2,174,740	173,092	122,129	200,712	95,845	21.5	13.4	22.9	9.9	1.1	0.3	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.4	1.1	0.4
				DIGIALADVTGNHK	2	84.8%	1																									
IPI00741635	ANKRD34C	ankyrin repeat domain-containing protein 34C	98.0%	1.3	1	1	1	1	29,141,200	35,715,700	27,966,600	37,448,300	3,008,897	3,666,816	2,889,501	1,824,792	23.1	23.0	23.1	10.9	1.2	0.2	-1.0	0.8	1.3	0.05	-1.3	0.1	1.0	0.7	1.3	0.02

				HLLDACK	2	98.0%	1																									
IPI00742127	-	Similar to Heterogeneous nuclear ribonucleoprotein A1 isoform a	100.0%	6.7	1	2	4	1	543,264	514,074	605,695	576,491	32,522	21,369	52,361	22,842	13.4	9.3	19.3	8.9	-1.1	0.5	1.1	0.3	1.1	0.4	1.2	0.1	1.1	0.08	-1.1	0.6
				GFGFVTYATVEEVDAAMNAR	2	100.0%	2																									
				GFGFVTYATVEEVDAAMNAR	3	100.0%	2																									
IPI00742191	-	Similar to ribosomal protein S14	100.0%	2.9	1	2	2	1	2,060,780	2,296,550	2,191,010	2,763,673	261,279	245,186	253,279	100,300	28.4	23.9	25.9	8.1	1.1	0.5	1.1	0.7	1.3	0.05	-1.0	0.8	1.2	0.1	1.3	0.07
				ELGITALHIK	2	99.0%	1																									
				ELGITALHIK	3	99.8%	1																									
IPI00742682	TPR	Nucleoprotein TPR	100.0%	8.7	15	16	17	1	72,913,502	74,962,234	72,726,336	85,353,968	6,389,491	2,146,841	3,634,591	3,119,883	19.6	6.4	11.2	8.2	1.0	0.8	-1.0	1	1.2	0.1	-1.0	0.6	1.1	0.03	1.2	0.03
				EGVQGPLNVSLSEEGK	2	96.6%	1																									
				ELENANDLLSATK	2	99.9%	1																									
				FEVAQVESLR	2	98.7%	1																									
				FLADQQSEIDGLK	2	100.0%	1																									
				GQNLLLTNLQTIQGILER	2	100.0%	2																									
				GQNLLLTNLQTIQGILER	3	100.0%	1																									
				LDELQASDVSVK	2	99.9%	1																									
				NIAIQSQFTR	2	100.0%	1																									
				NIEELQQQNQR	2	100.0%	1																									
				QEQIINTMTQDLR	2	99.9%	1																									
				RPPHPLPPRLTIHAPPQELGPPVQR	3	93.9%	1																									
				RPSTSQTVSTPAPVPVIESTEAIEAK	3	99.5%	1																									
				SLESQVENLQK	2	96.3%	1																									
				SQEQILEILR	2	99.9%	1																									
				TQYEELK	2	93.1%	1																									
				VLLMELEEAR	2	100.0%	1																									
IPI00742948	VIL1	Villin 1, isoform CRA_a	100.0%	2.6	1	1	1	1	3,244,465	3,526,965	3,037,570	3,631,500	358,083	170,807	215,189	250,799	24.7	10.8	15.8	15.4	1.1	0.5	-1.1	0.6	1.1	0.4	-1.2	0.1	1.0	0.7	1.2	0.1
				EVQGNESEAFR	2	100.0%	1																									
IPI00743469	TPD52L2	cDNA FLJ53635, highly similar to Homo sapiens tumor protein D52-like 2 (TPD52L2	100.0%	36.2	2	2	2	1	375,873	398,356	401,599	452,387	26,371	15,220	40,592	23,696	15.7	8.5	22.6	11.7	1.1	0.5	1.1	0.6	1.2	0.06	1.0	0.9	1.1	0.09	1.1	0.3
				TPAVEGLTEAEEEELRAELTKVEEEIVTLR	3	100.0%	1																									
				VVGDRENGSDNLPSSAGSGDKPLSDPAPF	3	100.0%	1																									
IPI00743654	NEB	Similar to Nebulin	99.4%	0.4	2	2	2	1	1,692,216	1,401,046	1,428,834	1,767,578	209,978	39,061	86,314	192,963	27.8	6.2	13.5	24.4	-1.2	0.2	-1.2	0.3	1.0	0.8	1.0	0.8	1.3	0.1	1.2	0.1
				GKYTFSPDTPHISHSKDMGK	3	96.7%	1																									
				QVSDILYK	2	81.8%	1																									
IPI00743873	MAP4	Uncharacterized protein	100.0%	3.8	2	2	2	1	981,731	1,055,471	1,030,049	1,283,982	38,478	38,528	83,851	46,161	8.8	8.2	18.2	8.0	1.1	0.2	1.0	0.6	1.3	0.001	-1.0	0.8	1.2	0.005	1.2	0.03
				TAGPIASAQK	2	99.8%	1																									
				TTTLSGTAPAAGVVPSR	2	100.0%	1																									
IPI00743914	IGF2BP2	isoform 3 of Insulin-like growth factor 2 mRNA-binding protein 2	100.0%	14.0	5	5	5	2	5,423,804	6,410,025	5,475,951	6,820,302	556,247	201,618	379,950	210,021	22.9	7.0	15.5	6.9	1.2	0.2	1.0	0.9	1.3	0.06	-1.2	0.06	1.1	0.2	1.2	0.01
IPI00922068	IGF2BP2	isoform 5 of Insulin-like growth factor 2 mRNA-binding protein 2	100.0%	15.2	5	5	5	2	5,423,804	6,410,025	5,475,951	6,820,302	556,247	201,618	379,950	210,021	22.9	7.0	15.5	6.9	1.2	0.2	1.0	0.9	1.3	0.06	-1.2	0.06	1.1	0.2	1.2	0.01
				DQTPDENEEVIVR	2	99.9%	1																									
				IAPAEGPDVSER	2	99.9%	1																									
				ISYIPDEEVSSPSPPQR	3	91.1%	1																									
				ITISSLQDLSIYNPER	2	99.0%	1																									
				TVNELQNLTSAEVIVPR	3	99.5%	1																									
IPI00743931	GORASP2	cDNA FLJ59712, highly similar to Golgi reassembly-stacking protein 2	100.0%	8.2	2	2	3	3	976,379	1,040,701	1,048,560	1,053,145	72,025	103,995	89,973	78,091	16.5	22.3	19.2	16.6	1.1	0.6	1.1	0.5	1.1	0.5	1.0	1	1.0	0.9	1.0	1
IPI00916299	GORASP2	cDNA FLJ54595, highly similar to Golgi reassembly-stacking protein 2	100.0%	9.4	2	2	3	3	976,379	1,040,701	1,048,560	1,053,145	72,025	103,995	89,973	78,091	16.5	22.3	19.2	16.6	1.1	0.6	1.1	0.5	1.1	0.5	1.0	1	1.0	0.9	1.0	1
IPI00941614	GORASP2	isoform 1 of Golgi reassembly-stacking protein 2	100.0%	8.4	2	2	3	3	976,379	1,040,701	1,048,560	1,053,145	72,025	103,995	89,973	78,091	16.5	22.3	19.2	16.6	1.1	0.6	1.1	0.5	1.1	0.5	1.0	1	1.0	0.9	1.0	1
				AGLEPFFDFIVSINGSR	2	100.0%	1																									
				ETSVTPSNLWGGQGLLGVSIR	2	100.0%	2																									
IPI00744135	RRBP1	isoform 2 of Ribosome-binding protein 1	100.0%	40.8	30	30	35	1	35,612,258	37,724,545	37,010,807	42,105,825	3,011,297	1,700,363	2,669,514	1,370,315	18.9	10.1	16.1	7.3	1.1	0.6	1.0	0.7	1.2	0.09	-1.0	0.8	1.1	0.08	1.1	0.1
				AAILETAPK	2	89.4%	1																									
				AGIIQDTWHK	3	96.7%	1																									
				AQEQQQQMAELHSK	3	100.0%	2																									
				DALNQATSQVESK	2	100.0%	1																									
				EHTSHLEAELEK	2	99.9%	1																									
				EQEITAVQAR	2	100.0%	1																									
				HLEEIVEK	2	100.0%	2																									
				HPPAPAEPSSDLASK	2	100.0%	1																									
				KLTSDLGR	2	81.1%	1																									
				LKELESQVSGLEK	2	99.9%	1																									
				LKGELESSDQVR	3	99.9%	1																									
				LLATEQEDAAVAK	2	100.0%	2																									
				LQQENSILR	2	98.0%	1																									
				LQSSEAEVR	2	89.3%	1																									
				LREAEETQSTLQAECDQYR	3	98.3%	1																									
				LTAEFEEAQTSACR	2	99.9%	1																									
				NTDVAQSPEAPKQEAPAK	3	91.3%	1																									
				QLLLESQSQLDAAK	2	100.0%	2																									
				QSDELALVR	2	88.6%	1																									
				QVLQLQASHR	2	88.0%	1																									
				SHVEDGDIAGAPASSPEAPPAEQDPVQLK	3	100.0%	1																									
				SIEALLEAGQAR	2	99.9%	1																									
				SILAETEGMLR	2	100.0%	2																									
				SVEEEEQVWR	2	100.0%	1																									
				TAGPLESSETEEASQLKER	3	98.7%	1																									
				TLQEQLENGPNTQLAR	2	100.0%	1																									
				TLVSTVGSMVFNEGEAQR	2	100.0%	1																									
				TQLEWTEAILEDEQTQR	3	100.0%	1																									
				VEPAVSSVVNSIQVLTSK	2	99.9%	1																									
				VGAAEEELQK	2	98.3%	1																									
IPI00744692	TALDO1	Transaldolase	100.0%	42.1	14	17	22	1	116,070,117	121,052,136	112,699,884	134,820,129	########	4,805,460	7,781,915	3,879,518	19.8	8.9	15.4	6.4	1.0	0.7	-1.0	0.8	1.2	0.1	-1.1	0.4	1.1	0.06	1.2	0.03
				ALAGCDFLTISPK	2	100.0%	2																									
				FAADAVK	2	99.7%	1																									
				ILDWHVANTDKK	2	100.0%	1																									
				ILDWHVANTDKK	3	93.7%	1																									
				LFVLFGAEILK	2	100.0%	1																									
				LGGSQEDQIK	2	100.0%	2																									
				LIELYK	2	95.0%	1																									
				LIELYKEAGISKDR	3	99.5%	1																									
				LLGELLQDNAK	2	100.0%	2																									
				LSFDKDAMVAR	2	99.3%	1																									
				LSFDKDAMVAR	3	99.9%	1																									
				LSSTWEGIQAGK	2	100.0%	2																									
				MESALDQLK	2	81.6%	1																									
				SYEPLEDPGVK	2	100.0%	1																									
				TIVMGASFR	2	99.5%	1																									
				WLHNEDQMAVEK	2	100.0%	2																									
				WLHNEDQMAVEK	3	100.0%	1																									
IPI00744711	PNPT1	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	96.6%	4.6	2	2	2	1	5,037,862	4,898,035	5,191,676	5,153,700	585,479	257,639	484,019	254,098	26.0	11.8	20.9	11.0	-1.0	0.8	1.0	0.8	1.0	0.9	1.1	0.6	1.1	0.5	-1.0	0.9
				FPEADPYEIIESFNVVAK	2	96.6%	1																									
				LLTDILGIEDYNGDMDFK	2	90.3%	1																									
IPI00744780	BCAS1	isoform 2 of Breast carcinoma-amplified sequence 1	100.0%	7.2	2	2	3	1	1,402,280	1,240,132	1,366,985	1,601,160	206,242	123,559	104,983	140,488	32.9	22.3	17.2	19.6	-1.1	0.5	-1.0	0.9	1.1	0.4	1.1	0.5	1.3	0.09	1.2	0.2
				MLDAQVQTDPVSIGPVGK	2	100.0%	2																									
				SKEVESALQTVDLNEGDAAPEPTEAK	3	100.0%	1																									
IPI00744835	PSAP	isoform Sap-mu-9 of Proactivator polypeptide	100.0%	16.3	7	8	12	3	14,379,988	14,747,372	14,276,348	16,538,068	889,527	586,950	844,732	459,764	13.8	8.9	13.2	6.2	1.0	0.7	-1.0	0.9	1.2	0.06	-1.0	0.7	1.1	0.04	1.2	0.05
IPI00873020	PSAP	Uncharacterized protein	100.0%	16.3	7	8	12	3	14,379,988	14,747,372	14,276,348	16,538,068	889,527	586,950	844,732	459,764	13.8	8.9	13.2	6.2	1.0	0.7	-1.0	0.9	1.2	0.06	-1.0	0.7	1.1	0.04	1.2	0.05
IPI01013537	PSAP	50 kDa protein	100.0%	19.1	7	8	12	3	14,379,988	14,747,372	14,276,348	16,538,068	889,527	586,950	844,732	459,764	13.8	8.9	13.2	6.2	1.0	0.7	-1.0	0.9	1.2	0.06	-1.0	0.7	1.1	0.04	1.2	0.05
				EIVDSYLPVILDIIK	2	100.0%	2																									
				EIVDSYLPVILDIIK	3	100.0%	1																									
				GCSFLPDPYQK	2	99.9%	2																									
				GEMSRPGEVCSALNLCESLQK	3	99.4%	1																									
				LGPGMADICK	2	100.0%	2																									
				LVGYLDR	2	99.5%	1																									
				QEILAALEK	2	99.4%	1																									
				SDVYCEVCEFLVK	2	100.0%	2																									
IPI00744919	ARFIP1	cDNA FLJ39190 fis, clone OCBBF2004647, highly similar to ARFAPTIN 1	100.0%	10.6	2	2	3	1	1,884,113	1,905,065	1,795,548	2,094,368	208,908	169,080	129,051	61,328	24.8	19.9	16.1	6.6	1.0	0.9	-1.0	0.7	1.1	0.4	-1.1	0.6	1.1	0.3	1.2	0.07
				LKTPGVDAPSWLEEQ	2	99.2%	1																									
				TDLEELNLGPR	2	99.9%	2																									
IPI00745267	TPM1	isoform 2 of Tropomyosin alpha-1 chain	100.0%	17.1	4	4	7	1	1,905,808	1,870,925	1,951,829	2,248,339	113,275	61,033	82,729	61,044	13.3	7.3	9.5	6.1	-1.0	0.8	1.0	0.8	1.2	0.03	1.0	0.5	1.2	0.002	1.2	0.02
				AQKDEEKMEIQEIQLK	3	92.3%	1																									
				ETAEADVASLNR	2	100.0%	2																									
				IQLVEEELDR	2	100.0%	2																									
				RIQLVEEELDR	2	100.0%	2																									
IPI00745433	EIF2C2	isoform 1 of Protein argonaute-2	99.9%	2.9	2	2	2	2	4,605,535	4,633,030	4,537,210	5,210,930	334,206	230,307	371,170	261,251	16.2	11.1	18.3	11.2	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.2
IPI00929290	EIF2C2	isoform 2 of Protein argonaute-2	99.9%	3.0	2	2	2	2	4,605,535	4,633,030	4,537,210	5,210,930	334,206	230,307	371,170	261,251	16.2	11.1	18.3	11.2	1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.1	1.1	0.2
				QEIIQDLAAMVR	2	95.6%	1																									
				YAQGADSVEPMFR	2	98.4%	1																									
IPI00745789	RPSAP19	Similar to 40S ribosomal protein SA-like protein	100.0%	13.8	2	2	3	1	2,106,877	2,291,515	2,367,220	2,573,903	230,072	46,061	211,439	126,373	24.4	4.5	20.0	11.0	1.1	0.5	1.1	0.4	1.2	0.1	1.0	0.7	1.1	0.09	1.1	0.4
				AIVAIENPADVSVISSR	2	100.0%	2																									
				FLAAGTHLGGTNLDFQMEQYIYK	3	100.0%	1																									
IPI00745800	GPX4	phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform B precurs	95.5%	3.1	1	1	1	1	1,629,950	1,676,668	1,474,173	1,565,883	200,405	99,121	118,584	97,423	27.5	13.2	18.0	13.9	1.0	0.8	-1.1	0.5	-1.0	0.8	-1.1	0.2	-1.1	0.4	1.1	0.6
				YAECGLR	2	82.9%	1																									
IPI00746059	HUWE1	HECT, UBA and WWE domain containing 1	98.8%	0.8	2	2	2	1	1,260,954	1,196,504	1,315,096	1,505,182	120,449	130,433	124,181	94,114	21.4	24.4	21.1	14.0	-1.1	0.7	1.0	0.8	1.2	0.1	1.1	0.5	1.3	0.09	1.1	0.3
				LLSLISIALPENK	2	96.0%	1																									
				QVVNQVWEAADVLIK	2	98.8%	1																									
IPI00746092	GLUD1	Glutamate dehydrogenase 1 variant (Fragment)	100.0%	10.0	2	2	2	1	2,104,833	2,246,907	2,202,727	2,454,450	184,185	137,964	130,135	90,527	19.6	13.7	13.2	8.3	1.1	0.6	1.0	0.7	1.2	0.1	-1.0	0.8	1.1	0.2	1.1	0.2
				GFIGPGIDVPAPDMSTGER	2	100.0%	1																									
				YSTDVSVDEVK	2	100.0%	1																									
IPI00746165	WDR1	isoform 1 of WD repeat-containing protein 1	100.0%	22.3	9	9	10	1	34,108,869	34,329,853	31,033,031	38,812,583	2,775,606	1,581,639	1,786,676	2,262,231	18.2	10.3	12.9	13.0	1.0	0.9	-1.1	0.4	1.1	0.2	-1.1	0.2	1.1	0.1	1.3	0.03
				CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR	3	100.0%	1																									
				DYSGQGVVK	2	99.8%	2																									
				GPVTDVAYSHDGAFLAVCDASK	3	100.0%	1																									
				IAVVGEGR	2	99.8%	1																									
				MTVDESGQLISCSMDDTVR	2	100.0%	1																									
				SIQCLTVHK	2	86.7%	1																									
				VFASLPQVER	2	89.8%	1																									
				YAPSGFYIASGDVSGK	2	100.0%	1																									
				YEYQPFAGK	2	99.7%	1																									
IPI00746326	PPM1G	Protein phosphatase 1G variant (Fragment)	100.0%	7.8	2	2	2	1	2,893,177	3,006,133	2,830,763	3,592,157	261,043	217,910	285,978	209,046	20.2	16.2	22.6	13.0	1.0	0.7	-1.0	0.9	1.2	0.07	-1.1	0.6	1.2	0.09	1.3	0.06

				NLPPEEQMISALPDIK	2	100.0%	1																									
				QLIVANAGDSR	2	99.7%	1																									
IPI00746554	RBM39	48 kDa protein	100.0%	7.6	2	2	2	1	1,102,202	1,056,550	1,132,140	1,126,093	83,111	56,627	84,275	38,384	16.9	12.0	16.6	7.6	-1.0	0.7	1.0	0.8	1.0	0.8	1.1	0.5	1.1	0.3	-1.0	0.9
				TDASSASSFLDSDELER	2	100.0%	1																									
				VLGVPIIVQASQAEK	2	98.5%	1																									
IPI00746581	C22orf36	isoform 2 of Leucine-rich repeat-containing protein C22orf36	91.8%	5.9	1	1	1	1	9,055,110	8,940,520	8,272,300	8,767,050	296,091	481,615	302,204	437,869	7.3	12.1	8.2	11.2	-1.0	0.8	-1.1	0.1	-1.0	0.6	-1.1	0.3	-1.0	0.8	1.1	0.4
				GYGLWACIR	2	91.8%	1																									
IPI00746756	ARHGAP44	Rho GTPase-activating protein 44	95.8%	3.1	1	1	1	2	1,384,595	1,364,040	1,440,775	1,427,585	128,418	144,256	142,672	132,852	20.7	23.7	22.1	20.8	-1.0	0.9	1.0	0.8	1.0	0.8	1.1	0.7	1.0	0.8	-1.0	0.9
IPI00791844	ARHGAP44	cDNA FLJ58097, moderately similar to Homo sapiens Rho GTPase activating protei	95.8%	3.1	1	1	1	2	1,384,595	1,364,040	1,440,775	1,427,585	128,418	144,256	142,672	132,852	20.7	23.7	22.1	20.8	-1.0	0.9	1.0	0.8	1.0	0.8	1.1	0.7	1.0	0.8	-1.0	0.9
				LPLTTLAQCLMEGSAILGDDTLLGK	3	95.8%	1																									
IPI00746777	ADH5;ADH5P4	Alcohol dehydrogenase class-3	100.0%	6.7	2	2	2	1	16,090,700	21,411,850	17,251,910	26,450,340	2,873,229	1,824,683	1,783,619	1,997,174	39.9	19.1	23.1	16.9	1.3	0.2	1.1	0.7	1.6	0.02	-1.2	0.1	1.2	0.1	1.5	0.009
				AFELMHSGK	2	99.9%	1																									
				VDEFVTHNLSFDEINK	3	99.5%	1																									
IPI00746782	MPST	3-mercaptopyruvate sulfurtransferase variant (Fragment)	100.0%	9.2	2	2	4	2	2,343,685	2,551,308	2,598,108	2,616,980	440,984	274,000	221,539	158,766	42.1	24.0	19.1	13.6	1.1	0.7	1.1	0.6	1.1	0.6	1.0	0.9	1.0	0.8	1.0	0.9
IPI00877618	MPST	Uncharacterized protein	100.0%	13.0	2	2	4	2	2,343,685	2,551,308	2,598,108	2,616,980	440,984	274,000	221,539	158,766	42.1	24.0	19.1	13.6	1.1	0.7	1.1	0.6	1.1	0.6	1.0	0.9	1.0	0.8	1.0	0.9
				AGQPLQLLDASWYLPK	2	100.0%	2																									
				ALVSAQWVAEALR	2	99.9%	2																									
IPI00746806	CTTN	cDNA FLJ54828, highly similar to Src substrate cortactin	100.0%	11.8	2	2	3	1	1,014,865	1,043,265	1,006,989	1,140,596	54,278	50,077	60,331	17,687	12.0	10.7	13.4	3.5	1.0	0.7	-1.0	0.9	1.1	0.08	-1.0	0.7	1.1	0.1	1.1	0.09
				GPVSGTEPEPVYSMEAADYR	2	100.0%	2																									
				NASTFEDVTQVSSAYQK	2	100.0%	1																									
IPI00746936	OSBP2	Oxysterol-binding protein 2	99.8%	4.6	2	2	2	4	1,489,072	1,662,140	1,494,626	1,760,616	172,147	121,577	190,847	98,644	25.9	16.4	28.6	12.5	1.1	0.4	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00877910	OSBP2	Oxysterol-binding protein	99.8%	5.6	2	2	2	4	1,489,072	1,662,140	1,494,626	1,760,616	172,147	121,577	190,847	98,644	25.9	16.4	28.6	12.5	1.1	0.4	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.5	1.2	0.3
IPI00878043	OSBP2	Oxysterol-binding protein	99.8%	4.6	2	2	2	4	1,489,072	1,662,140	1,494,626	1,760,616	172,147	121,577	190,847	98,644	25.9	16.4	28.6	12.5	1.1	0.4	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.5	1.2	0.3
IPI01013906	OSBP2	Oxysterol-binding protein	99.8%	5.7	2	2	2	4	1,489,072	1,662,140	1,494,626	1,760,616	172,147	121,577	190,847	98,644	25.9	16.4	28.6	12.5	1.1	0.4	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.5	1.2	0.3
				AKAVRVMNTHSDDSGDDDEATTPADK	3	95.2%	1																									
				IPMPVNFNEPLSMLQR	2	99.7%	1																									
IPI00747849	ATP1B1	isoform 1 of Sodium/potassium-transporting ATPase subunit beta-1	100.0%	8.9	2	2	3	3	2,479,873	2,533,727	2,465,710	2,724,077	85,622	151,939	259,918	110,074	7.7	13.4	23.6	9.0	1.0	0.8	-1.0	1	1.1	0.1	-1.0	0.8	1.1	0.3	1.1	0.4
IPI00871221	ATP1B1	isoform 2 of Sodium/potassium-transporting ATPase subunit beta-1	100.0%	9.0	2	2	3	3	2,479,873	2,533,727	2,465,710	2,724,077	85,622	151,939	259,918	110,074	7.7	13.4	23.6	9.0	1.0	0.8	-1.0	1	1.1	0.1	-1.0	0.8	1.1	0.3	1.1	0.4
IPI01009449	ATP1B1	cDNA FLJ51474, highly similar to Sodium/potassium-transporting ATPase subunit b	100.0%	9.2	2	2	3	3	2,479,873	2,533,727	2,465,710	2,724,077	85,622	151,939	259,918	110,074	7.7	13.4	23.6	9.0	1.0	0.8	-1.0	1	1.1	0.1	-1.0	0.8	1.1	0.3	1.1	0.4
				VAPPGLTQIPQIQK	2	99.5%	1																									
				YNPNVLPVQCTGK	2	99.9%	2																									
IPI00747859	ABHD14B	Uncharacterized protein	100.0%	22.1	3	4	4	1	5,078,517	5,434,404	5,186,328	5,809,006	508,034	265,914	462,357	176,722	22.4	10.9	19.9	6.8	1.1	0.6	1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.3	1.1	0.3
				EGTIQVQGQALFFR	2	98.0%	1																									
				FSVLLLHGIR	2	99.1%	1																									
				FSVLLLHGIR	3	93.5%	1																									
				TPALIVYGDQDPMGQTSFEHLK	3	100.0%	1																									
IPI00748037	NAPB	cDNA FLJ54102, highly similar to Beta-soluble NSF attachment protein	100.0%	4.3	1	1	1	4	372,012	367,716	389,216	396,782	35,425	26,152	61,622	42,705	21.3	15.9	35.4	24.1	-1.0	0.9	1.0	0.8	1.1	0.7	1.1	0.8	1.1	0.6	1.0	0.9
IPI00748905	NAPB	NAPB protein	100.0%	5.4	1	1	1	4	372,012	367,716	389,216	396,782	35,425	26,152	61,622	42,705	21.3	15.9	35.4	24.1	-1.0	0.9	1.0	0.8	1.1	0.7	1.1	0.8	1.1	0.6	1.0	0.9
IPI00908301	NAPB	cDNA FLJ52551, highly similar to Beta-soluble NSF attachment protein	100.0%	4.3	1	1	1	4	372,012	367,716	389,216	396,782	35,425	26,152	61,622	42,705	21.3	15.9	35.4	24.1	-1.0	0.9	1.0	0.8	1.1	0.7	1.1	0.8	1.1	0.6	1.0	0.9
IPI00942239	NAPB	Uncharacterized protein	100.0%	3.6	1	1	1	4	372,012	367,716	389,216	396,782	35,425	26,152	61,622	42,705	21.3	15.9	35.4	24.1	-1.0	0.9	1.0	0.8	1.1	0.7	1.1	0.8	1.1	0.6	1.0	0.9
				LDQWLTTMLLR	2	100.0%	1																									
IPI00748256	PSME1	proteasome activator complex subunit 1 isoform 2	100.0%	27.6	5	5	6	1	14,710,345	15,098,600	14,281,005	17,396,400	1,386,068	511,082	1,187,989	318,461	21.1	7.6	18.6	4.1	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.5	1.2	0.005	1.2	0.06
				IEDGNNFGVAVQEK	2	100.0%	2																									
				KISELDAFLKEPALNEANLSNLK	3	100.0%	1																									
				LEGFHTQISK	2	96.9%	1																									
				TENLLGSYFPK	2	100.0%	1																									
				VFELMTSLHTK	2	99.7%	1																									
IPI00748303	ZFR	Uncharacterized protein	91.7%	1.7	1	1	1	2	379,416	319,268	426,216	475,689	50,722	23,358	66,898	37,247	29.9	16.4	35.1	17.5	-1.2	0.3	1.1	0.6	1.3	0.2	1.3	0.2	1.5	0.007	1.1	0.5
IPI00784224	ZFR	Similar to Zinc finger RNA-binding protein	91.7%	1.7	1	1	1	2	379,416	319,268	426,216	475,689	50,722	23,358	66,898	37,247	29.9	16.4	35.1	17.5	-1.2	0.3	1.1	0.6	1.3	0.2	1.3	0.2	1.5	0.007	1.1	0.5
				VPTWSDFPSWAMELLVEK	2	91.8%	1																									
IPI00908824	-	Serine hydroxymethyltransferase	100.0%	13.2	4	4	6	2	2,405,641	2,433,473	2,621,624	2,714,040	214,704	136,383	187,019	53,781	20.0	12.5	16.0	4.4	1.0	0.9	1.1	0.5	1.1	0.2	1.1	0.4	1.1	0.1	1.0	0.7
IPI00748411	SHMT2	Serine hydroxymethyltransferase	100.0%	9.8	4	4	6	2	2,405,641	2,433,473	2,621,624	2,714,040	214,704	136,383	187,019	53,781	20.0	12.5	16.0	4.4	1.0	0.9	1.1	0.5	1.1	0.2	1.1	0.4	1.1	0.1	1.0	0.7
				AMADALLER	2	90.9%	1																									
				ISATSIFFESMPYK	2	100.0%	2																									
				VLELVSITANK	2	100.0%	2																									
				VVDFIDEGVNIGLEVK	2	100.0%	1																									
IPI00748490	AARSD1	alanyl-tRNA editing protein Aarsd1 isoform 1	97.8%	2.6	1	1	1	6	460,927	513,285	471,962	536,152	76,080	25,872	51,272	32,347	36.9	11.3	24.3	13.5	1.1	0.5	1.0	0.9	1.2	0.4	-1.1	0.5	1.0	0.6	1.1	0.3
IPI00914584	AARSD1	isoform 2 of Alanyl-tRNA editing protein Aarsd1	97.8%	2.9	1	1	1	6	460,927	513,285	471,962	536,152	76,080	25,872	51,272	32,347	36.9	11.3	24.3	13.5	1.1	0.5	1.0	0.9	1.2	0.4	-1.1	0.5	1.0	0.6	1.1	0.3
IPI00916173	AARSD1	Protein	97.8%	6.0	1	1	1	6	460,927	513,285	471,962	536,152	76,080	25,872	51,272	32,347	36.9	11.3	24.3	13.5	1.1	0.5	1.0	0.9	1.2	0.4	-1.1	0.5	1.0	0.6	1.1	0.3
IPI00916940	AARSD1	Uncharacterized protein	97.8%	3.0	1	1	1	6	460,927	513,285	471,962	536,152	76,080	25,872	51,272	32,347	36.9	11.3	24.3	13.5	1.1	0.5	1.0	0.9	1.2	0.4	-1.1	0.5	1.0	0.6	1.1	0.3
IPI00917260	AARSD1	Protein	97.8%	5.5	1	1	1	6	460,927	513,285	471,962	536,152	76,080	25,872	51,272	32,347	36.9	11.3	24.3	13.5	1.1	0.5	1.0	0.9	1.2	0.4	-1.1	0.5	1.0	0.6	1.1	0.3
IPI00917638	AARSD1	Uncharacterized protein	97.8%	8.6	1	1	1	6	460,927	513,285	471,962	536,152	76,080	25,872	51,272	32,347	36.9	11.3	24.3	13.5	1.1	0.5	1.0	0.9	1.2	0.4	-1.1	0.5	1.0	0.6	1.1	0.3
				ELSLDDPEVEQVSGR	2	97.8%	1																									
IPI00748640	MPI	cDNA FLJ56688, highly similar to Mannose-6-phosphate isomerase	100.0%	8.0	2	2	2	1	3,101,677	3,004,949	3,221,377	3,547,709	369,069	255,040	274,305	218,867	26.6	19.0	19.0	13.8	-1.0	0.8	1.0	0.8	1.1	0.3	1.1	0.6	1.2	0.1	1.1	0.4
				TLSQWIAENQDSLGSK	2	100.0%	1																									
				VVVEQLNLLVK	2	99.8%	1																									
IPI00748807	NUP160	isoform 1 of Nuclear pore complex protein Nup160	100.0%	2.9	2	2	2	2	3,893,615	4,179,190	5,042,825	5,433,005	626,132	205,785	600,044	471,832	36.0	11.0	26.6	19.4	1.1	0.7	1.3	0.2	1.4	0.09	1.2	0.2	1.3	0.04	1.1	0.6
IPI00978986	NUP160	140 kDa protein	100.0%	3.4	2	2	2	2	3,893,615	4,179,190	5,042,825	5,433,005	626,132	205,785	600,044	471,832	36.0	11.0	26.6	19.4	1.1	0.7	1.3	0.2	1.4	0.09	1.2	0.2	1.3	0.04	1.1	0.6
				LLSHGVPLPNWLINSYK	3	100.0%	1																									
				SQLQDLVEFPYVNLHNEVVGIIESR	3	100.0%	1																									
IPI00748826	MGLL	Uncharacterized protein	99.9%	7.6	1	1	1	3	317,543	332,453	375,105	363,030	23,151	13,608	38,014	11,207	16.3	9.2	22.7	6.9	1.0	0.6	1.2	0.2	1.1	0.1	1.1	0.3	1.1	0.1	-1.0	0.8
IPI00796800	MGLL	17 kDa protein	99.9%	13.6	1	1	1	3	317,543	332,453	375,105	363,030	23,151	13,608	38,014	11,207	16.3	9.2	22.7	6.9	1.0	0.6	1.2	0.2	1.1	0.1	1.1	0.3	1.1	0.1	-1.0	0.8
IPI00945201	MGLL	Protein	99.9%	10.1	1	1	1	3	317,543	332,453	375,105	363,030	23,151	13,608	38,014	11,207	16.3	9.2	22.7	6.9	1.0	0.6	1.2	0.2	1.1	0.1	1.1	0.3	1.1	0.1	-1.0	0.8
				VLNLVLPNLSLGPIDSSVLSR	2	100.0%	1																									
IPI00759596	HNRNPC	isoform 4 of Heterogeneous nuclear ribonucleoproteins C1/C2	100.0%	34.4	8	11	15	1	19,283,077	19,159,660	18,532,441	21,919,183	1,800,712	782,794	1,213,632	906,024	20.9	9.1	14.6	9.2	-1.0	1	-1.0	0.7	1.1	0.2	-1.0	0.7	1.1	0.05	1.2	0.06
				GFAFVQYVNER	2	100.0%	2																									
				KSDVEAIFSK	2	100.0%	1																									
				KSDVEAIFSK	3	96.8%	1																									
				MIAGQVLDINLAAEPK	2	100.0%	1																									
				MIAGQVLDINLAAEPK	3	99.1%	1																									
				SAAEMYGSSFDLDYDFQR	2	100.0%	2																									
				SAAEMYGSSFDLDYDFQR	3	100.0%	1																									
				SDVEAIFSK	2	100.0%	1																									
				VDSLLENLEK	2	100.0%	2																									
				VFIGNLNTLVVK	2	100.0%	2																									
				VPPPPPIAR	2	88.7%	1																									
IPI00759613	TTN	isoform 5 of Titin	99.8%	0.4	8	8	8	1	5,164,657	5,204,363	5,879,285	6,069,119	436,244	256,096	512,944	180,016	18.9	11.0	19.5	6.6	1.0	0.9	1.1	0.3	1.2	0.09	1.1	0.3	1.2	0.02	1.0	0.7
				AEDLSATVTDVVEGQEYSFR	3	97.1%	1																									
				ITQFLKAEASKEIAK	2	84.0%	1																									
				MPDDDGGDR	1	92.2%	1																									
				STVTIVDSKR	2	89.8%	1																									
				VLDTPGPPVNVTVK	2	90.2%	1																									
				VNTEDHQGEYVCEALNDSGK	3	87.7%	1																									
				VTGLSEGCEYFFR	3	94.3%	1																									
				YLISTEEVSYFNVQSR	3	85.6%	1																									
IPI00759646	ACP1	low molecular weight phosphotyrosine protein phosphatase isoform d	100.0%	33.9	3	3	3	1	14,479,589	16,901,078	15,025,583	19,061,432	1,938,823	1,615,989	1,135,562	1,130,773	29.9	21.4	16.9	13.3	1.2	0.4	1.0	0.8	1.3	0.08	-1.1	0.4	1.1	0.3	1.3	0.04
				LVTDQNISENWR	2	100.0%	1																									
				QVPSLDLK	2	99.1%	1																									
				VDSAATSGYEIGNPPDYR	2	100.0%	1																									
IPI00759705	PPP1R7	isoform 3 of Protein phosphatase 1 regulatory subunit 7	100.0%	16.1	3	3	3	2	2,019,074	2,284,096	2,120,576	2,551,293	161,886	111,710	176,255	74,303	17.9	10.9	18.6	6.5	1.1	0.2	1.1	0.7	1.3	0.02	-1.1	0.5	1.1	0.08	1.2	0.05
IPI00893943	PPP1R7	Uncharacterized protein	100.0%	16.4	3	3	3	2	2,019,074	2,284,096	2,120,576	2,551,293	161,886	111,710	176,255	74,303	17.9	10.9	18.6	6.5	1.1	0.2	1.1	0.7	1.3	0.02	-1.1	0.5	1.1	0.08	1.2	0.05
				GAGQQQSQEMMEVDR	2	100.0%	1																									
				IEGLQNLVNLR	2	99.8%	1																									
				LQNLDALTNLTVLSMQSNR	2	81.1%	1																									
IPI00759759	EPS8L2	isoform 2 of Epidermal growth factor receptor kinase substrate 8-like protein 2	100.0%	9.5	2	2	2	1	1,057,567	1,004,405	1,115,668	1,139,081	137,013	52,261	85,160	30,760	29.0	11.6	17.1	6.0	-1.1	0.7	1.1	0.7	1.1	0.6	1.1	0.3	1.1	0.06	1.0	0.8
				QQSGSELEELMNK	2	99.4%	1																									
				SQPVSQPLTYESGPDEVR	2	99.6%	1																									
IPI00759816	PPP1R7	isoform 4 of Protein phosphatase 1 regulatory subunit 7	100.0%	15.6	2	2	2	2	473,028	541,243	607,184	544,669	27,389	60,702	86,175	43,716	13.0	25.1	31.7	18.0	1.1	0.3	1.3	0.2	1.2	0.2	1.1	0.5	1.0	1	-1.1	0.5
IPI00893774	PPP1R7	Uncharacterized protein	100.0%	16.7	2	2	2	2	473,028	541,243	607,184	544,669	27,389	60,702	86,175	43,716	13.0	25.1	31.7	18.0	1.1	0.3	1.3	0.2	1.2	0.2	1.1	0.5	1.0	1	-1.1	0.5
				AIENIDTLTNLESLFLGK	2	100.0%	1																									
				LQNLDALTNLTVLSMQSNR	2	81.1%	1																									
IPI00760620	HNRNPA1P10	Similar to Heterogeneous nuclear ribonucleoprotein A1 isoform a	100.0%	35.2	9	9	12	1	11,625,760	11,698,704	11,881,363	12,722,067	869,825	397,081	597,777	271,784	16.7	7.6	11.3	4.8	1.0	0.9	1.0	0.8	1.1	0.3	1.0	0.8	1.1	0.07	1.1	0.2
				EDSQRPGAHLTVK	2	90.2%	1																									
				GFAFVTFDDHDSVDK	3	100.0%	1																									
				GFGFVTYATVEEVDAAMNAR	3	100.0%	2																									
				GGGFGGNDNFGR	2	98.0%	1																									
				KLFIGGLSFETTDESLR	2	100.0%	1																									
				LFIGGLSFETTDESLR	2	100.0%	3																									
				SESPKEPEQLRK	3	99.9%	1																									
				SSGPYGGGGQYFAK	2	100.0%	1																									
				WGTLTDCVVMR	2	99.9%	1																									
IPI00760735	LRRFIP2	isoform 3 of Leucine-rich repeat flightless-interacting protein 2	95.1%	14.0	1	1	1	1	677,200	672,940	645,462	770,766	89,933	59,751	54,375	28,506	29.7	19.9	18.8	8.3	-1.0	1	-1.0	0.8	1.1	0.4	-1.0	0.7	1.1	0.2	1.2	0.08
				AEQDITTLEQSISR	2	95.1%	1																									
IPI00760940	LOC723972;ANP32A	Hepatopoietin PCn127	100.0%	11.8	3	4	5	1	6,329,753	6,204,388	6,606,682	7,314,812	522,388	216,582	490,728	251,470	18.5	7.8	16.6	7.7	-1.0	0.8	1.0	0.7	1.2	0.1	1.1	0.5	1.2	0.01	1.1	0.2
				ELVLDNSR	2	95.1%	1																									
				SLDLFNCEVTNLNDYR	2	100.0%	2																									
				SLDLFNCEVTNLNDYR	3	100.0%	1																									
				SLDLFNCEVTNLNDYRENVFK	3	100.0%	1																									
IPI00782992	SRRM2	isoform 1 of Serine/arginine repetitive matrix protein 2	99.2%	1.1	2	2	2	2	3,302,335	3,211,095	3,032,795	3,703,590	280,032	220,361	142,437	120,564	19.0	15.3	10.5	7.3	-1.0	0.8	-1.1	0.4	1.1	0.2	-1.1	0.5	1.2	0.09	1.2	0.007
IPI01015893	SRRM2	KIAA0324	99.2%	1.4	2	2	2	2	3,302,335	3,211,095	3,032,795	3,703,590	280,032	220,361	142,437	120,564	19.0	15.3	10.5	7.3	-1.0	0.8	-1.1	0.4	1.1	0.2	-1.1	0.5	1.2	0.09	1.2	0.007
				IPAASAAAMNLASAR	2	99.2%	1																									
				TPQAPASANLVGPR	2	99.2%	1																									
IPI00783097	GARS	Glycyl-tRNA synthetase	100.0%	21.1	11	11	14	1	57,111,364	56,885,615	56,517,548	66,068,674	3,286,264	2,042,717	3,872,597	2,094,717	12.9	8.0	15.3	7.1	-1.0	1	-1.0	0.9	1.2	0.05	-1.0	0.9	1.2	0.01	1.2	0.06
				APQVDVDKAVAELK	3	99.9%	1																									
				CSVLPLSQNQEFMPFVK	2	100.0%	1																									
				LGDAVEQGVINNTVLGYFIGR	3	100.0%	1																									
				LLEFNQGK	2	99.2%	1																									
				LPFAAAQIGNSFR	2	100.0%	1																									
				NNIIQTWR	2	95.0%	2																									
				SPITGNDLSPPVSFNLMFK	2	100.0%	2																									
				TFFSFPAVVAPFK	2	100.0%	1																									
				TLYVEEVVPNVIEPSFGLGR	2	99.8%	1																									
				TVNVVQFEPSK	2	100.0%	2																									
				YPLFEGQETGKK	3	97.7%	1																									
IPI00783271	LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial	100.0%	10.9	11	11	11	1	27,359,795	28,838,149	28,853,265	31,840,656	2,174,496	1,305,803	1,892,258	908,381	17.8	10.1	14.7	6.4	1.1	0.6	1.1	0.6	1.2	0.09	1.0	1	1.1	0.1	1.1	0.2
				AGDMENAENILTVMR	2	100.0%	1																									
				GDVENIEVVQK	2	96.5%	1																									

				IQEENVIPR	2	99.7%	1																									
				LANQFAIYKPVTDFFLQLVDAGK	3	97.1%	1																									
				LIASYCNVGDIEGASK	2	96.7%	1																									
				LLMSEDYFTQAMEVK	2	100.0%	1																									
				MEEANIQPNR	2	96.6%	1																									
				MLNGLEDSIGLSK	2	99.8%	1																									
				SMNINLWSEITELLYK	2	100.0%	1																									
				SNTLPISLQSIR	2	87.0%	1																									
				VIEEQLEPAVEK	2	98.9%	1																									
IPI00783313	PYGL	Glycogen phosphorylase, liver form	100.0%	21.0	12	12	15	3	34,419,920	36,751,666	32,113,238	44,557,532	5,755,731	2,760,031	4,942,369	2,385,910	37.4	16.8	34.4	12.0	1.1	0.7	-1.1	0.8	1.3	0.1	-1.1	0.4	1.2	0.06	1.4	0.05
IPI00943894	PYGL	glycogen phosphorylase, liver form isoform 2	100.0%	21.9	12	12	15	3	34,419,920	36,751,666	32,113,238	44,557,532	5,755,731	2,760,031	4,942,369	2,385,910	37.4	16.8	34.4	12.0	1.1	0.7	-1.1	0.8	1.3	0.1	-1.1	0.4	1.2	0.06	1.4	0.05
IPI00977162	PYGL	Uncharacterized protein	100.0%	21.7	12	12	15	3	34,419,920	36,751,666	32,113,238	44,557,532	5,755,731	2,760,031	4,942,369	2,385,910	37.4	16.8	34.4	12.0	1.1	0.7	-1.1	0.8	1.3	0.1	-1.1	0.4	1.2	0.06	1.4	0.05
				DFNVGDYIQAVLDR	3	100.0%	1																									
				DGWQVEEADDWLR	2	100.0%	1																									
				EYYEALPELK	2	99.3%	1																									
				FSQFLETEYK	2	99.9%	1																									
				GAGTVFDAFPDQVAIQLNDTHPALAIPELMR	3	100.0%	1																									
				HLEIIYEINQK	2	99.9%	1																									
				LAACFLDSMATLGLAAYGYGIR	2	100.0%	2																									
				LVIDQIDNGFFSPK	2	100.0%	1																									
				VFADYEAYVK	2	99.8%	1																									
				VIPATDLSEQISTAGTEASGTGNMK	3	99.9%	1																									
				VLYPNDNFFEGK	2	100.0%	2																									
				VSLAEK	1	91.7%	2																									
IPI00783378	UBE2O	Ubiquitin-conjugating enzyme E2 O	94.3%	1.2	1	1	1	1	1,708,830	1,739,020	1,788,600	1,824,660	168,688	242,389	134,569	106,767	22.1	31.2	16.8	13.1	1.0	0.9	1.0	0.7	1.1	0.6	1.0	0.9	1.0	0.8	1.0	0.8
				SGYPDIGFPLFPLSK	2	94.3%	1																									
IPI00783625	SERPINB5	isoform 1 of Serpin B5	100.0%	9.1	2	2	2	1	4,898,823	4,768,650	5,361,937	5,739,560	342,093	312,210	691,094	402,889	15.6	14.6	28.8	15.7	-1.0	0.8	1.1	0.6	1.2	0.2	1.1	0.5	1.2	0.09	1.1	0.6
				DLTDGHFENILADNSVNDQTK	3	99.8%	1																									
				SLNLSTEFISSTK	2	100.0%	1																									
IPI00783835	LTN1	E3 ubiquitin-protein ligase listerin	98.3%	0.8	1	1	1	4	659,633	653,455	871,273	774,600	38,007	60,788	94,570	45,927	12.9	20.8	24.3	13.3	-1.0	0.9	1.3	0.07	1.2	0.09	1.3	0.09	1.2	0.2	-1.1	0.4
IPI00793009	LTN1	Uncharacterized protein	98.3%	1.7	1	1	1	4	659,633	653,455	871,273	774,600	38,007	60,788	94,570	45,927	12.9	20.8	24.3	13.3	-1.0	0.9	1.3	0.07	1.2	0.09	1.3	0.09	1.2	0.2	-1.1	0.4
IPI00942336	LTN1	54 kDa protein	98.3%	2.9	1	1	1	4	659,633	653,455	871,273	774,600	38,007	60,788	94,570	45,927	12.9	20.8	24.3	13.3	-1.0	0.9	1.3	0.07	1.2	0.09	1.3	0.09	1.2	0.2	-1.1	0.4
IPI01012824	LTN1	isoform 1 of E3 ubiquitin-protein ligase listerin	98.3%	0.8	1	1	1	4	659,633	653,455	871,273	774,600	38,007	60,788	94,570	45,927	12.9	20.8	24.3	13.3	-1.0	0.9	1.3	0.07	1.2	0.09	1.3	0.09	1.2	0.2	-1.1	0.4
				NFLTSLVAGLSTER	2	98.3%	1																									
IPI00783872	CAPRIN1	isoform 1 of Caprin-1	100.0%	11.6	5	5	8	3	6,525,880	6,909,559	7,077,438	7,417,853	288,098	451,705	504,682	333,355	9.9	14.6	16.0	10.1	1.1	0.5	1.1	0.4	1.1	0.08	1.0	0.8	1.1	0.4	1.0	0.6
IPI00873926	CAPRIN1	isoform 2 of Caprin-1	100.0%	11.8	5	5	8	3	6,525,880	6,909,559	7,077,438	7,417,853	288,098	451,705	504,682	333,355	9.9	14.6	16.0	10.1	1.1	0.5	1.1	0.4	1.1	0.08	1.0	0.8	1.1	0.4	1.0	0.6
IPI00982178	CAPRIN1	70 kDa protein	100.0%	13.1	5	5	8	3	6,525,880	6,909,559	7,077,438	7,417,853	288,098	451,705	504,682	333,355	9.9	14.6	16.0	10.1	1.1	0.5	1.1	0.4	1.1	0.08	1.0	0.8	1.1	0.4	1.0	0.6
				LNEQYEHASIHLWDLLEGK	3	100.0%	1																									
				LNQDQLDAVSK	2	100.0%	2																									
				QGLNGVPILSEEELSLLDEFYK	2	100.0%	2																									
				TVLELQYVLDKLGDDEVR	2	96.9%	1																									
				YQEVTNNLEFAK	2	100.0%	2																									
IPI00783982	COPG	Coatomer subunit gamma	100.0%	21.6	13	14	15	1	52,703,740	54,986,688	54,529,137	60,274,875	4,160,661	2,276,910	3,666,924	2,018,820	17.7	9.3	15.0	7.5	1.0	0.6	1.0	0.8	1.1	0.1	-1.0	0.9	1.1	0.1	1.1	0.2
				ALNAGYILNGLTVSIPGLER	2	100.0%	1																									
				ALQQYTLEPSEKPFDLK	3	100.0%	1																									
				ELAPAVSVLQLFCSSPK	2	99.5%	1																									
				EMSCIAEDVIIVTSSLTK	2	100.0%	1																									
				FGAQNEEMLPSILVLLK	2	99.6%	1																									
				ILHLLGQEGPK	2	97.1%	1																									
				ILHLLGQEGPK	3	98.7%	1																									
				QEIFQEQLAAVPEFR	2	99.8%	1																									
				QISSFMSEISDEFK	2	100.0%	1																									
				SIATLAITTLLK	2	100.0%	2																									
				SLEELPVDIILASVG	2	99.7%	1																									
				SVPLATAPMAEQR	2	93.2%	1																									
				TLEEAVGNIVK	2	99.4%	1																									
				VVLEHEEVR	2	99.7%	1																									
IPI00784090	CCT8	T-complex protein 1 subunit theta	100.0%	43.4	20	20	25	1	47,433,217	47,320,505	45,476,833	52,574,551	4,018,415	1,898,224	2,951,407	1,428,603	18.9	9.0	14.5	6.1	-1.0	1	-1.0	0.7	1.1	0.3	-1.0	0.6	1.1	0.06	1.2	0.06
				APGFAQMLK	2	100.0%	1																									
				AVDDGVNTFK	2	100.0%	1																									
				DMLEAGILDTYLGK	2	100.0%	2																									
				EDGAISTIVLR	2	82.4%	1																									
				ELEVQHPAAK	2	99.4%	1																									
				FAEAFEAIPR	2	100.0%	1																									
				GEENLMDAQVK	2	100.0%	2																									
				GSTDNLMDDIER	2	100.0%	2																									
				HFSGLEEAVYR	2	99.3%	1																									
				IAVYSCPFDGMITETK	2	97.7%	1																									
				IGLSVSEVIEGYEIACR	2	100.0%	1																									
				LATNAAVTVLR	2	100.0%	2																									
				LFVTNDAATILR	2	100.0%	1																									
				LIAQACVSIFPDSGHFNVDNIR	3	95.8%	1																									
				LVPGGGATEIELAK	2	88.3%	1																									
				MVINHLEK	2	85.5%	1																									
				NVGLDIEAEVPAVK	2	100.0%	2																									
				TAEELMNFSK	2	100.0%	1																									
				TVGATALPR	2	98.5%	1																									
				YNIMLVR	2	99.0%	1																									
IPI00784154	HSPD1	60 kDa heat shock protein, mitochondrial	100.0%	62.7	29	35	49	1	280,481,131	294,819,541	284,107,300	324,417,315	########	6,889,546	########	########	18.9	5.2	17.6	8.1	1.1	0.6	1.0	0.9	1.2	0.1	-1.0	0.7	1.1	0.06	1.1	0.1
				AAVEEGIVLGGGCALLR	2	100.0%	1																									
				ALMLQGVDLLADAVAVTMGPK	2	100.0%	1																									
				APGFGDNR	2	99.9%	2																									
				APGFGDNRK	2	100.0%	1																									
				CEFQDAYVLLSEK	2	100.0%	2																									
				CIPALDSLTPANEDQK	2	100.0%	2																									
				DDAMLLK	2	99.4%	1																									
				DMAIATGGAVFGEEGLTLNLEDVQPHDLGK	3	100.0%	1																									
				GIIDPTK	1	98.4%	1																									
				GVMLAVDAVIAELK	2	100.0%	1																									
				GYISPYFINTSK	2	100.0%	1																									
				IGIEIIK	2	86.2%	1																									
				IGIEIIKR	2	97.8%	1																									
				IMQSSSEVGYDAMAGDFVNMVEK	2	100.0%	2																									
				ISSIQSIVPALEIANAHR	2	100.0%	1																									
				ISSIQSIVPALEIANAHR	3	100.0%	1																									
				KPLVIIAEDVDGEALSTLVLNR	3	100.0%	2																									
				LSDGVAVLK	1	99.1%	1																									
				LSDGVAVLK	2	99.6%	1																									
				LVQDVANNTNEEAGDGTTTATVLAR	2	100.0%	2																									
				LVQDVANNTNEEAGDGTTTATVLAR	3	100.0%	1																									
				NAGVEGSLIVEK	2	100.0%	2																									
				PVTTPEEIAQVATISANGDK	2	81.5%	1																									
				PVTTPEEIAQVATISANGDKEIGNIISDAMK	3	99.5%	1																									
				TLKIPAMTIAK	3	100.0%	1																									
				TLNDELEIIEGMK	2	100.0%	2																									
				TLNDELEIIEGMKFDR	2	100.0%	1																									
				TLNDELEIIEGMKFDR	3	99.7%	2																									
				TVIIEQSWGSPK	2	100.0%	2																									
				VGEVIVTK	1	99.1%	1																									
				VGEVIVTK	2	100.0%	1																									
				VGEVIVTKDDAMLLK	2	100.0%	2																									
				VGEVIVTKDDAMLLK	3	100.0%	2																									
				VGLQVVAVK	2	100.0%	2																									
				VTDALNATR	2	100.0%	2																									
IPI00784156	AP2B1	isoform 1 of AP-2 complex subunit beta	100.0%	16.7	10	10	11	3	6,589,779	7,292,125	7,155,538	7,677,080	665,279	281,575	554,306	85,765	22.6	8.6	17.3	2.5	1.1	0.4	1.1	0.5	1.2	0.2	-1.0	0.8	1.1	0.3	1.1	0.4
IPI00784366	AP2B1	isoform 2 of AP-2 complex subunit beta	100.0%	16.4	10	10	11	3	6,589,779	7,292,125	7,155,538	7,677,080	665,279	281,575	554,306	85,765	22.6	8.6	17.3	2.5	1.1	0.4	1.1	0.5	1.2	0.2	-1.0	0.8	1.1	0.3	1.1	0.4
IPI00790702	AP2B1	Beta adaptin subunit	100.0%	17.7	10	10	11	3	6,589,779	7,292,125	7,155,538	7,677,080	665,279	281,575	554,306	85,765	22.6	8.6	17.3	2.5	1.1	0.4	1.1	0.5	1.2	0.2	-1.0	0.8	1.1	0.3	1.1	0.4
				AAMIWIVGEYAER	2	100.0%	2																									
				APEVSQYIYQVYDSILK	2	92.8%	1																									
				CVSTLLDLIQTK	2	100.0%	1																									
				LAPPLVTLLSGEPEVQYVALR	2	99.9%	1																									
				LASQANIAQVLAELKEYATEVDVDFVR	3	100.0%	1																									
				LHDINAQMVEDQGFLDSLR	3	100.0%	1																									
				LTNGIWILAELR	2	100.0%	1																									
				MEPLNNLQVAVK	2	99.8%	1																									
				SQPDMAIMAVNSFVK	2	99.7%	1																									
				YNDPIYVK	2	99.7%	1																									
IPI00784201	CEP290	isoform 1 of Centrosomal protein of 290 kDa	91.8%	0.6	1	1	1	2	1,219,850	1,206,910	1,429,295	1,265,550	56,093	61,081	74,442	86,841	10.3	11.3	11.7	15.3	-1.0	0.9	1.2	0.05	1.0	0.7	1.2	0.05	1.0	0.6	-1.1	0.2
IPI00794668	CEP290	isoform 2 of Centrosomal protein of 290 kDa	91.8%	0.9	1	1	1	2	1,219,850	1,206,910	1,429,295	1,265,550	56,093	61,081	74,442	86,841	10.3	11.3	11.7	15.3	-1.0	0.9	1.2	0.05	1.0	0.7	1.2	0.05	1.0	0.6	-1.1	0.2
				LTSGLQGKPLTDNK	2	86.7%	1																									
IPI00784299	WDR81	isoform 2 of WD repeat-containing protein 81	94.6%	2.8	1	1	1	7	705,741	876,546	698,704	772,761	90,209	81,455	29,696	34,586	28.6	20.8	9.5	10.0	1.2	0.2	-1.0	0.9	1.1	0.5	-1.3	0.09	-1.1	0.3	1.1	0.1
IPI00917671	WDR81	WD repeat-containing protein 81 isoform 1	94.6%	1.0	1	1	1	7	705,741	876,546	698,704	772,761	90,209	81,455	29,696	34,586	28.6	20.8	9.5	10.0	1.2	0.2	-1.0	0.9	1.1	0.5	-1.3	0.09	-1.1	0.3	1.1	0.1
IPI00924963	WDR81	cDNA FLJ51331, highly similar to WD repeat protein 81	94.6%	3.3	1	1	1	7	705,741	876,546	698,704	772,761	90,209	81,455	29,696	34,586	28.6	20.8	9.5	10.0	1.2	0.2	-1.0	0.9	1.1	0.5	-1.3	0.09	-1.1	0.3	1.1	0.1
IPI00926441	WDR81	Uncharacterized protein	94.6%	3.3	1	1	1	7	705,741	876,546	698,704	772,761	90,209	81,455	29,696	34,586	28.6	20.8	9.5	10.0	1.2	0.2	-1.0	0.9	1.1	0.5	-1.3	0.09	-1.1	0.3	1.1	0.1
IPI00927804	WDR81	WD repeat-containing protein 81 isoform 3	94.6%	2.6	1	1	1	7	705,741	876,546	698,704	772,761	90,209	81,455	29,696	34,586	28.6	20.8	9.5	10.0	1.2	0.2	-1.0	0.9	1.1	0.5	-1.3	0.09	-1.1	0.3	1.1	0.1
IPI00943756	WDR81	isoform 1 of WD repeat-containing protein 81	94.6%	2.1	1	1	1	7	705,741	876,546	698,704	772,761	90,209	81,455	29,696	34,586	28.6	20.8	9.5	10.0	1.2	0.2	-1.0	0.9	1.1	0.5	-1.3	0.09	-1.1	0.3	1.1	0.1
IPI01009619	WDR81	WD repeat-containing protein 81 isoform 4	94.6%	2.7	1	1	1	7	705,741	876,546	698,704	772,761	90,209	81,455	29,696	34,586	28.6	20.8	9.5	10.0	1.2	0.2	-1.0	0.9	1.1	0.5	-1.3	0.09	-1.1	0.3	1.1	0.1
				LSSENFRGTLTSLALLPTK	3	94.6%	1																									
IPI00784490	SDK1	isoform 1 of Protein sidekick-1	96.1%	0.7	1	1	1	4	260,736	237,325	275,989	287,301	46,988	24,172	28,996	9,604	40.3	22.8	23.5	7.5	-1.1	0.7	1.1	0.8	1.1	0.6	1.2	0.3	1.2	0.09	1.0	0.7
IPI00902868	SDK1	Uncharacterized protein	96.1%	0.7	1	1	1	4	260,736	237,325	275,989	287,301	46,988	24,172	28,996	9,604	40.3	22.8	23.5	7.5	-1.1	0.7	1.1	0.8	1.1	0.6	1.2	0.3	1.2	0.09	1.0	0.7
IPI00942650	SDK1	isoform 3 of Protein sidekick-1	96.1%	0.7	1	1	1	4	260,736	237,325	275,989	287,301	46,988	24,172	28,996	9,604	40.3	22.8	23.5	7.5	-1.1	0.7	1.1	0.8	1.1	0.6	1.2	0.3	1.2	0.09	1.0	0.7
IPI01014396	SDK1	Uncharacterized protein	96.1%	3.5	1	1	1	4	260,736	237,325	275,989	287,301	46,988	24,172	28,996	9,604	40.3	22.8	23.5	7.5	-1.1	0.7	1.1	0.8	1.1	0.6	1.2	0.3	1.2	0.09	1.0	0.7
				YLVSISAFNAAGDGPK	2	96.1%	1																									
IPI00784614	9-Sep	septin-9 isoform a	100.0%	21.7	9	10	14	1	9,288,365	10,231,549	10,410,976	11,305,296	1,082,600	367,291	836,692	348,769	26.1	8.0	18.0	6.9	1.1	0.4	1.1	0.4	1.2	0.1	1.0	0.8	1.1	0.07	1.1	0.4
				ADTLTLEER	2	100.0%	1																									
				APVDFGYVGIDSILEQMR	2	100.0%	2																									
				APVDFGYVGIDSILEQMR	3	100.0%	1																									

				DITSSIHFEAYR	2	100.0%	2																									
				LGDSSGPALKR	2	90.7%	1																									
				LTVIDTPGFGDHINNENCWQPIMK	3	100.0%	1																									
				RVELSGPK	2	93.2%	1																									
				SQEATEAAPSCVGDMADTPR	2	100.0%	1																									
				VPEVPTAPATDAAPK	2	100.0%	2																									
				YLQEEVNINR	2	100.0%	2																									
IPI00784782	FLJ13224	Conserved hypothetical protein	93.8%	12.0	1	1	1	1	5,418,570	5,981,540	5,433,860	5,779,910	626,731	415,081	245,785	291,552	25.9	15.5	10.1	11.3	1.1	0.5	1.0	1	1.1	0.6	-1.1	0.3	-1.0	0.7	1.1	0.4
				EALAVSPTPTLQVNAPGAK	3	93.8%	1																									
IPI00784808	9-Sep	septin-9 isoform b	100.0%	20.0	8	9	13	2	7,110,857	7,685,529	7,619,686	8,534,766	720,402	325,526	583,164	277,395	22.7	9.5	17.1	7.3	1.1	0.5	1.1	0.6	1.2	0.1	-1.0	0.9	1.1	0.08	1.1	0.2
IPI00784936	9-Sep	septin-9 isoform c	100.0%	20.4	8	9	13	2	7,110,857	7,685,529	7,619,686	8,534,766	720,402	325,526	583,164	277,395	22.7	9.5	17.1	7.3	1.1	0.5	1.1	0.6	1.2	0.1	-1.0	0.9	1.1	0.08	1.1	0.2
				ADTLTLEER	2	100.0%	1																									
				APVDFGYVGIDSILEQMR	2	100.0%	2																									
				APVDFGYVGIDSILEQMR	3	100.0%	1																									
				DITSSIHFEAYR	2	100.0%	2																									
				LTVIDTPGFGDHINNENCWQPIMK	3	100.0%	1																									
				RVELSGPK	2	93.2%	1																									
				SQEATEAAPSCVGDMADTPR	2	100.0%	1																									
				VPEVPTAPATDAAPK	2	100.0%	2																									
				YLQEEVNINR	2	100.0%	2																									
IPI00784835	9-Sep	septin-9 isoform f	100.0%	11.9	3	3	6	3	1,062,209	1,035,864	1,056,077	1,228,566	83,912	35,262	116,066	60,710	17.7	7.6	24.6	11.1	-1.0	0.8	-1.0	1	1.2	0.1	1.0	0.9	1.2	0.03	1.2	0.2
IPI00883870	9-Sep	septin-9 isoform d	100.0%	8.4	3	3	6	3	1,062,209	1,035,864	1,056,077	1,228,566	83,912	35,262	116,066	60,710	17.7	7.6	24.6	11.1	-1.0	0.8	-1.0	1	1.2	0.1	1.0	0.9	1.2	0.03	1.2	0.2
IPI01010880	9-Sep	41 kDa protein	100.0%	11.1	3	3	6	3	1,062,209	1,035,864	1,056,077	1,228,566	83,912	35,262	116,066	60,710	17.7	7.6	24.6	11.1	-1.0	0.8	-1.0	1	1.2	0.1	1.0	0.9	1.2	0.03	1.2	0.2
				APVDFGYVGIDSILEQMR	2	100.0%	2																									
				DITSSIHFEAYR	2	100.0%	2																									
				YLQEEVNINR	2	100.0%	2																									
IPI00784869	DNAH10	isoform 1 of Dynein heavy chain 10, axonemal	98.9%	1.3	2	2	2	1	3,836,179	3,346,369	4,758,490	3,737,740	550,217	339,819	462,126	413,757	32.1	22.7	21.7	24.8	-1.1	0.5	1.2	0.2	-1.0	0.9	1.4	0.04	1.1	0.5	-1.3	0.1
				DMWAHLLELQPQTGESSSGISRDDYIGQVAK	3	95.4%	1																									
				LLVFMDDMNMPRVDEYGTQQPIALLK	3	93.1%	1																									
IPI00785096	BZW1	isoform 1 of Basic leucine zipper and W2 domain-containing protein 1	99.7%	12.4	4	4	4	3	6,732,535	6,735,297	6,473,238	8,033,184	629,395	329,024	427,302	383,264	20.9	10.9	14.8	10.7	1.0	1	-1.0	0.7	1.2	0.1	-1.0	0.6	1.2	0.03	1.2	0.03
IPI00916112	BZW1	cDNA FLJ55501, highly similar to Rattus norvegicus basic leucine zipper and W2 do	99.7%	12.3	4	4	4	3	6,732,535	6,735,297	6,473,238	8,033,184	629,395	329,024	427,302	383,264	20.9	10.9	14.8	10.7	1.0	1	-1.0	0.7	1.2	0.1	-1.0	0.6	1.2	0.03	1.2	0.03
IPI00916503	BZW1	cDNA FLJ55789, highly similar to Rattus norvegicus basic leucine zipper and W2 do	99.7%	11.5	4	4	4	3	6,732,535	6,735,297	6,473,238	8,033,184	629,395	329,024	427,302	383,264	20.9	10.9	14.8	10.7	1.0	1	-1.0	0.7	1.2	0.1	-1.0	0.6	1.2	0.03	1.2	0.03
				AEVLSEEPILK	2	89.0%	1																									
				EGVSAAFAVK	2	92.4%	1																									
				LMELFPANK	2	99.5%	1																									
				QYSPLLAAFTTQGQSELTLLLK	2	99.2%	1																									
IPI00787316	-	Putative uncharacterized protein	100.0%	20.8	2	2	3	1	7,612,035	7,878,180	7,588,185	8,454,205	759,957	364,670	632,733	292,446	22.3	10.4	18.7	7.7	1.0	0.8	-1.0	1	1.1	0.3	-1.0	0.7	1.1	0.3	1.1	0.2
				HTGPGILSMANAGPNTNDSQIFICTAK	3	100.0%	1																									
				VSFELFADK	2	100.0%	2																									
IPI00787323	LOC728638	Similar to Keratin, type II cytoskeletal 8	100.0%	36.6	27	43	71	2	293,683,612	294,535,201	285,228,362	328,388,007	########	########	########	9,246,460	14.8	8.4	14.7	6.3	1.0	1	-1.0	0.8	1.1	0.1	-1.0	0.7	1.1	0.05	1.2	0.07
IPI00985064	LOC728638	Conserved hypothetical protein	100.0%	39.7	27	43	71	2	293,683,612	294,535,201	285,228,362	328,388,007	########	########	########	9,246,460	14.8	8.4	14.7	6.3	1.0	1	-1.0	0.8	1.1	0.1	-1.0	0.7	1.1	0.05	1.2	0.07
				AEAESMYQIK	2	100.0%	2																									
				AEAESMYQIKYEELQSLAGK	3	100.0%	1																									
				ASLEAAIADAEQR	2	100.0%	2																									
				ASLEAAIADAEQRGELAIK	2	100.0%	2																									
				ASLEAAIADAEQRGELAIK	3	99.9%	1																									
				ASLEAAIADAEQRGELAIKDANAK	2	94.9%	1																									
				ASLEAAIADAEQRGELAIKDANAK	3	100.0%	1																									
				DVDEAYMNK	2	100.0%	2																									
				DVDEAYMNKVELESR	2	100.0%	2																									
				DVDEAYMNKVELESR	3	100.0%	2																									
				DVDEAYMNKVELESRLEGLTDEINFLR	3	100.0%	2																									
				EYQELMNVK	1	99.2%	1																									
				EYQELMNVK	2	99.9%	1																									
				GELAIK	1	96.9%	2																									
				GELAIKDANAK	2	99.8%	1																									
				GELAIKDANAK	3	99.0%	1																									
				KDVDEAYMNKVELESR	3	84.6%	1																									
				LEGLTDEINFLR	2	100.0%	2																									
				LQAEIEGLK	1	100.0%	1																									
				LQAEIEGLK	2	99.8%	2																									
				LQAEIEGLKGQR	2	99.9%	2																									
				LSELEAALQR	1	88.7%	1																									
				LSELEAALQR	2	100.0%	3																									
				LSELEAALQR	3	97.2%	1																									
				QLETLGQEK	1	99.2%	1																									
				QLETLGQEK	2	99.9%	2																									
				QLREYQELMNVK	2	99.1%	2																									
				QLREYQELMNVK	3	84.3%	1																									
				RQLETLGQEK	2	100.0%	3																									
				SLDMDSIIAEVK	1	100.0%	2																									
				SLDMDSIIAEVK	2	100.0%	3																									
				SNMDNMFESYINNLR	2	100.0%	2																									
				SNMDNMFESYINNLR	3	100.0%	1																									
				SNMDNMFESYINNLRR	3	99.9%	2																									
				TEMENEFVLIK	2	100.0%	2																									
				TEMENEFVLIKK	2	100.0%	2																									
				TEMENEFVLIKK	3	100.0%	2																									
				VELESRLEGLTDEINFLR	2	99.7%	1																									
				VELESRLEGLTDEINFLR	3	100.0%	1																									
				WSLLQQQK	1	96.6%	1																									
				WSLLQQQK	2	99.9%	2																									
				YEELQSLAGK	1	100.0%	2																									
				YEELQSLAGK	2	99.9%	2																									
IPI00788011	LOC100506332	s-phase kinase-associated protein 1-like isoform 1	100.0%	8.6	1	1	1	2	6,296,350	6,166,475	5,960,225	6,926,963	517,176	298,258	425,087	309,520	18.4	10.8	16.0	10.0	-1.0	0.8	-1.1	0.6	1.1	0.3	-1.0	0.7	1.1	0.1	1.2	0.1
IPI00979350	LOC100506332	s-phase kinase-associated protein 1-like isoform 2	100.0%	8.3	1	1	1	2	6,296,350	6,166,475	5,960,225	6,926,963	517,176	298,258	425,087	309,520	18.4	10.8	16.0	10.0	-1.0	0.8	-1.1	0.6	1.1	0.3	-1.0	0.7	1.1	0.1	1.2	0.1
				RTDDIPVWDQEFLK	2	100.0%	1																									
IPI00788157	XRN2	isoform 2 of 5'-3' exoribonuclease 2	100.0%	7.3	4	4	4	1	6,058,803	6,169,830	5,890,067	6,942,477	483,302	185,114	324,673	208,840	17.8	6.7	12.3	6.7	1.0	0.8	-1.0	0.8	1.1	0.1	-1.0	0.5	1.1	0.02	1.2	0.03
				DQPAFTPSGILTPHALGSR	3	93.8%	1																									
				NLTVILSDASAPGEGEHK	3	98.8%	1																									
				NSLGGDVLFVGK	2	99.9%	1																									
				YAWQGVALLPFVDER	2	99.9%	1																									
IPI00788602	TATDN1	9 kDa protein	100.0%	29.5	2	2	3	2	1,176,497	1,145,247	1,075,540	1,260,480	123,123	28,929	64,353	41,962	23.4	5.7	13.4	7.4	-1.0	0.8	-1.1	0.5	1.1	0.5	-1.1	0.4	1.1	0.05	1.2	0.04
IPI01012335	TATDN1	Uncharacterized protein	100.0%	37.1	2	2	3	2	1,176,497	1,145,247	1,075,540	1,260,480	123,123	28,929	64,353	41,962	23.4	5.7	13.4	7.4	-1.0	0.8	-1.1	0.5	1.1	0.5	-1.1	0.4	1.1	0.05	1.2	0.04
				FMITGGNLQDSK	2	98.5%	1																									
				HQDDLQDVIGR	2	100.0%	2																									
IPI00788630	KLC4	isoform 2 of Kinesin light chain 4	100.0%	16.0	2	2	2	5	1,339,282	1,285,897	1,258,891	1,528,762	126,054	78,883	94,805	90,954	21.1	13.7	16.8	13.3	-1.0	0.7	-1.1	0.6	1.1	0.3	-1.0	0.8	1.2	0.08	1.2	0.07
IPI00909371	KLC4	cDNA FLJ58264, highly similar to Kinesin light chain 4	100.0%	3.9	2	2	2	5	1,339,282	1,285,897	1,258,891	1,528,762	126,054	78,883	94,805	90,954	21.1	13.7	16.8	13.3	-1.0	0.7	-1.1	0.6	1.1	0.3	-1.0	0.8	1.2	0.08	1.2	0.07
IPI00945157	KLC4	Uncharacterized protein	100.0%	25.6	2	2	2	5	1,339,282	1,285,897	1,258,891	1,528,762	126,054	78,883	94,805	90,954	21.1	13.7	16.8	13.3	-1.0	0.7	-1.1	0.6	1.1	0.3	-1.0	0.8	1.2	0.08	1.2	0.07
IPI00947002	KLC4	Uncharacterized protein	100.0%	22.8	2	2	2	5	1,339,282	1,285,897	1,258,891	1,528,762	126,054	78,883	94,805	90,954	21.1	13.7	16.8	13.3	-1.0	0.7	-1.1	0.6	1.1	0.3	-1.0	0.8	1.2	0.08	1.2	0.07
IPI00947288	KLC4	Uncharacterized protein	100.0%	25.0	2	2	2	5	1,339,282	1,285,897	1,258,891	1,528,762	126,054	78,883	94,805	90,954	21.1	13.7	16.8	13.3	-1.0	0.7	-1.1	0.6	1.1	0.3	-1.0	0.8	1.2	0.08	1.2	0.07
				LSQEEILGSTR	2	100.0%	1																									
				LVSQGLEALR	2	99.7%	1																									
IPI00788666	LOXHD1	lipoxygenase homology domain-containing protein 1 isoform 1	97.5%	0.7	1	1	1	2	2,163,910	2,250,080	2,265,495	2,321,085	158,085	97,671	83,918	96,973	16.3	9.7	8.3	9.3	1.0	0.7	1.0	0.6	1.1	0.4	1.0	0.9	1.0	0.6	1.0	0.7
IPI01009573	LOXHD1	isoform 1 of Lipoxygenase homology domain-containing protein 1	97.5%	0.8	1	1	1	2	2,163,910	2,250,080	2,265,495	2,321,085	158,085	97,671	83,918	96,973	16.3	9.7	8.3	9.3	1.0	0.7	1.0	0.6	1.1	0.4	1.0	0.9	1.0	0.6	1.0	0.7
				KAGTNSPIFIQIYGQK	2	89.9%	1																									
IPI00788719	ACY1	aminoacylase-1 isoform d	100.0%	15.6	4	4	5	2	5,375,699	5,126,385	5,067,241	6,048,716	516,215	450,603	336,767	539,684	21.5	19.7	14.9	20.0	-1.0	0.7	-1.1	0.6	1.1	0.4	-1.0	0.9	1.2	0.2	1.2	0.2
IPI00945211	ACY1	Uncharacterized protein	100.0%	11.4	4	4	5	2	5,375,699	5,126,385	5,067,241	6,048,716	516,215	450,603	336,767	539,684	21.5	19.7	14.9	20.0	-1.0	0.7	-1.1	0.6	1.1	0.4	-1.0	0.9	1.2	0.2	1.2	0.2
				AVGVPALGFSPMNR	2	99.9%	2																									
				DMNLTLEPEIMPAATDNR	2	100.0%	1																									
				EGSVTSVNLTK	2	98.8%	1																									
				LLPALASVPALPSDS	2	93.1%	1																									
IPI00788781	FABP5	Uncharacterized protein	99.9%	10.9	1	1	1	1	1,908,680	2,366,527	2,023,537	2,332,767	160,523	207,773	207,570	136,685	18.8	19.6	22.9	13.1	1.2	0.1	1.1	0.7	1.2	0.08	-1.2	0.3	-1.0	0.9	1.2	0.2
				TTQFSCTLGEK	2	99.6%	1																									
IPI00788782	ATP1A3	Uncharacterized protein	100.0%	5.4	4	4	6	1	10,156,978	10,927,663	10,178,418	11,356,865	933,433	448,862	902,386	324,225	20.6	9.2	19.8	6.4	1.1	0.5	1.0	1	1.1	0.3	-1.1	0.5	1.0	0.5	1.1	0.3
				ADIGVAMGIAGSDVSK	2	100.0%	2																									
				GAAGSQAAGPR	1	95.4%	1																									
				LNIPVSQVNPR	2	99.9%	2																									
				MTVAHMWFDNQIHEADTTEDQSGTSFDK	3	99.6%	1																									
IPI00788840	NAP1L4	Uncharacterized protein	100.0%	21.4	3	3	3	5	1,519,363	1,567,214	1,476,658	1,850,731	155,006	118,841	102,092	52,511	22.8	17.0	15.5	6.3	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.6	1.2	0.06	1.3	0.01
IPI00979151	NAP1L4	Uncharacterized protein	100.0%	28.6	3	3	3	5	1,519,363	1,567,214	1,476,658	1,850,731	155,006	118,841	102,092	52,511	22.8	17.0	15.5	6.3	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.6	1.2	0.06	1.3	0.01
IPI00979847	NAP1L4	Uncharacterized protein	100.0%	29.7	3	3	3	5	1,519,363	1,567,214	1,476,658	1,850,731	155,006	118,841	102,092	52,511	22.8	17.0	15.5	6.3	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.6	1.2	0.06	1.3	0.01
IPI00984634	NAP1L4	Uncharacterized protein	100.0%	35.5	3	3	3	5	1,519,363	1,567,214	1,476,658	1,850,731	155,006	118,841	102,092	52,511	22.8	17.0	15.5	6.3	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.6	1.2	0.06	1.3	0.01
IPI01010987	NAP1L4	Uncharacterized protein	100.0%	27.1	3	3	3	5	1,519,363	1,567,214	1,476,658	1,850,731	155,006	118,841	102,092	52,511	22.8	17.0	15.5	6.3	1.0	0.8	-1.0	0.8	1.2	0.1	-1.1	0.6	1.2	0.06	1.3	0.01
				FYEEVHDLER	2	100.0%	1																									
				LDNVPHTPSSYIETLPK	3	100.0%	1																									
				YAALYQPLFDK	2	99.7%	1																									
IPI00788848	FABP1	Uncharacterized protein	100.0%	34.7	3	4	6	1	13,276,130	13,928,655	12,975,690	14,953,555	701,994	410,368	743,000	542,409	11.8	6.6	12.8	8.1	1.0	0.4	-1.0	0.8	1.1	0.1	-1.1	0.3	1.1	0.2	1.2	0.06
				FTITAGSK	2	95.9%	1																									
				VIQNEFTVGEECELETMTGEK	2	100.0%	2																									
				YQLQSQENFEAFMK	2	100.0%	2																									
				YQLQSQENFEAFMK	3	98.9%	1																									
IPI00788896	PSMB3	13 kDa protein	100.0%	28.6	2	3	3	2	3,330,393	3,847,490	4,041,917	4,070,420	269,676	242,764	266,983	159,493	18.1	14.1	14.8	8.8	1.2	0.2	1.2	0.1	1.2	0.05	1.1	0.6	1.1	0.5	1.0	0.9
IPI00789577	PSMB3	12 kDa protein	100.0%	29.9	2	3	3	2	3,330,393	3,847,490	4,041,917	4,070,420	269,676	242,764	266,983	159,493	18.1	14.1	14.8	8.8	1.2	0.2	1.2	0.1	1.2	0.05	1.1	0.6	1.1	0.5	1.0	0.9
				FGIQAQMVTTDFQK	2	100.0%	1																									
				LYIGLAGLATDVQTVAQR	2	100.0%	1																									
				LYIGLAGLATDVQTVAQR	3	100.0%	1																									
IPI00788938	LDHB	L-lactate dehydrogenase	100.0%	37.9	7	8	14	1	41,071,716	39,562,867	39,687,216	46,668,095	3,507,233	2,006,998	3,751,794	2,152,199	19.1	11.3	21.1	10.3	-1.0	0.7	-1.0	0.8	1.1	0.2	1.0	1	1.2	0.04	1.2	0.1
				ITVVGVGQVGMACAISILGK	3	100.0%	1																									
				IVADKDYSVTANSK	2	100.0%	2																									
				IVADKDYSVTANSK	3	100.0%	2																									
				IVVVTAGVR	2	100.0%	1																									
				LIAPVAEEEATVPNNK	2	100.0%	2																									
				SLADELALVDVLEDK	2	100.0%	2																									
				SLADELALVDVLEDKLK	3	99.9%	1																									
				VIGSGCNLDSAR	2	100.0%	3																									
IPI00788942	RUVBL1	isoform 2 of RuvB-like 1	100.0%	19.2	6	6	7	1	###########	###########	###########	###########	########	9,571,037	########	########	3.7	2.0	5.1	5.1	1.1	0.004	1.0	0.2	1.1	0.03	-1.0	0.2	1.0	0.9	1.0	0.3

				EACGVIVELIK	3	90.8%	1																									
				GLGLDESGLAK	2	100.0%	1																									
				LDPSIFESLQK	2	100.0%	1																									
				QAASGLVGQENAR	2	100.0%	2																									
				TISHVIIGLK	3	100.0%	1																									
				VPFCPMVGSEVYSTEIKK	3	99.6%	1																									
IPI00789008	FLOT2	Flotillin-2	99.0%	2.3	1	1	1	2	3,151,570	3,711,835	3,043,960	4,037,545	271,227	149,313	245,360	198,022	19.2	9.0	18.0	11.0	1.2	0.1	-1.0	0.8	1.3	0.03	-1.2	0.05	1.1	0.2	1.3	0.01
IPI00795979	FLOT2	Uncharacterized protein	99.0%	2.1	1	1	1	2	3,151,570	3,711,835	3,043,960	4,037,545	271,227	149,313	245,360	198,022	19.2	9.0	18.0	11.0	1.2	0.1	-1.0	0.8	1.3	0.03	-1.2	0.05	1.1	0.2	1.3	0.01
				SAFSEEVNIK	2	99.0%	1																									
IPI00789041	PNN	isoform 1 of Pinin	100.0%	8.1	4	4	4	1	7,566,783	8,187,129	8,588,173	9,315,094	550,593	508,403	684,710	582,880	16.3	13.9	17.8	14.0	1.1	0.4	1.1	0.3	1.2	0.06	1.0	0.7	1.1	0.2	1.1	0.4
				DLIQDQNMDEK	2	99.4%	1																									
				IFGLLMGTLQK	2	100.0%	1																									
				QQDSQPEEVMDVLEMVENVK	3	93.7%	1																									
				VELAQLQEEWNEHNAK	3	83.0%	1																									
IPI00789078	SOD1	Superoxide dismutase	100.0%	8.9	1	1	1	1	1,544,590	1,509,570	1,301,400	1,547,215	113,596	114,455	47,033	157,341	16.5	17.0	8.1	22.7	-1.0	0.8	-1.2	0.08	1.0	1	-1.2	0.1	1.0	0.9	1.2	0.2
				HVGDLGNVTADK	2	99.8%	1																									
IPI00789119	PSMB6	20 kDa protein	100.0%	16.3	3	3	5	1	8,095,998	8,696,100	8,144,243	9,213,833	416,048	433,147	510,755	331,550	11.5	11.1	14.0	8.1	1.1	0.3	1.0	0.9	1.1	0.07	-1.1	0.4	1.1	0.4	1.1	0.1
				LAAIAESGVER	2	99.9%	2																									
				QVLLGDQIPK	2	98.7%	1																									
				TTTGSYIANR	2	99.9%	2																									
IPI00789127	-	30 kDa protein	100.0%	6.7	1	1	1	1	369,118	382,340	312,668	408,144	36,866	34,869	31,369	15,492	22.3	20.4	22.4	8.5	1.0	0.8	-1.2	0.3	1.1	0.4	-1.2	0.2	1.1	0.5	1.3	0.03
				NQGGYGGSSSSSSYGSGR	2	100.0%	1																									
IPI00789135	-	Protein	100.0%	14.7	2	3	3	1	2,809,873	2,795,210	2,819,695	3,196,964	248,805	159,562	376,069	130,997	19.8	12.8	29.8	9.2	-1.0	1	1.0	1	1.1	0.2	1.0	1	1.1	0.09	1.1	0.4
				FSPLTTNLINLLAENGR	2	100.0%	1																									
				FSPLTTNLINLLAENGR	3	99.9%	1																									
				VAASVLNPYVK	2	97.7%	1																									
IPI00789155	CALU	calumenin isoform c precurosr	100.0%	28.5	7	8	8	2	15,848,960	17,561,760	16,794,845	18,747,804	2,177,379	1,633,967	1,868,945	575,793	30.7	20.8	24.9	6.9	1.1	0.5	1.1	0.8	1.2	0.3	-1.0	0.8	1.1	0.5	1.1	0.4
IPI00941900	CALU	isoform 1 of Calumenin	100.0%	29.2	7	8	8	2	15,848,960	17,561,760	16,794,845	18,747,804	2,177,379	1,633,967	1,868,945	575,793	30.7	20.8	24.9	6.9	1.1	0.5	1.1	0.8	1.2	0.3	-1.0	0.8	1.1	0.5	1.1	0.4
				EEIVDKYDLFVGSQATDFGEALVR	3	100.0%	1																									
				HLVYESDQNKDGK	3	100.0%	1																									
				IDGDKDGFVTVDELKDWIK	3	100.0%	1																									
				LTKEEIVDKYDLFVGSQATDFGEALVR	3	99.8%	1																									
				MADKDGDLIATK	2	99.1%	1																									
				TFDQLTPEESKER	2	99.2%	1																									
				TFDQLTPEESKER	3	99.6%	1																									
				WIYEDVER	2	99.9%	1																									
IPI00789159	SNORD4A;RPL23A	Uncharacterized protein	99.9%	10.3	2	2	3	2	5,223,355	5,119,258	5,179,832	5,543,106	581,412	315,215	213,865	301,399	24.9	13.8	9.2	12.2	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.4
IPI00793523	SNORD4A;RPL23A	Uncharacterized protein	99.9%	12.7	2	2	3	2	5,223,355	5,119,258	5,179,832	5,543,106	581,412	315,215	213,865	301,399	24.9	13.8	9.2	12.2	-1.0	0.9	-1.0	0.9	1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.4
				LAPDYDALDVANK	2	99.8%	2																									
				WAPAPPK	2	88.6%	1																									
IPI00789253	FAM49B	33 kDa protein	100.0%	11.2	2	2	3	1	1,230,274	1,412,864	1,321,881	1,519,520	126,117	70,400	109,503	47,971	22.9	11.1	18.5	7.1	1.1	0.2	1.1	0.6	1.2	0.08	-1.1	0.5	1.1	0.2	1.1	0.1
				DAEGILEDLQSYR	2	100.0%	2																									
				INNVPAEGENEVNNELANR	3	93.4%	1																									
IPI00789285	TXNDC17	11 kDa protein	100.0%	33.7	2	2	2	1	3,656,779	3,841,050	3,867,398	4,041,352	155,251	157,255	266,021	129,993	9.5	9.2	15.4	7.2	1.1	0.4	1.1	0.5	1.1	0.09	1.0	0.9	1.1	0.4	1.0	0.6
				LVESECLQANLVEMLFSED	2	100.0%	1																									
				YEEVSVSGFEEFHR	3	99.9%	1																									
IPI00789296	SRP14	8 kDa protein	96.1%	14.3	1	1	1	1	31,569,700	24,049,300	32,100,400	23,331,100	1,502,068	2,255,936	2,710,257	1,203,106	10.6	21.0	18.9	11.5	-1.3	0.02	1.0	0.9	-1.4	0.003	1.3	0.05	-1.0	0.8	-1.4	0.02
				RLPLPFPTLY	2	96.1%	1																									
IPI00789370	SHMT2	serine hydroxymethyltransferase, mitochondrial isoform 3	100.0%	23.8	8	8	11	1	6,198,429	6,012,846	6,772,022	7,193,704	579,299	236,821	488,241	399,168	20.9	8.8	16.1	12.4	-1.0	0.8	1.1	0.5	1.2	0.2	1.1	0.2	1.2	0.03	1.1	0.5
				AALEALGSCLNNK	2	100.0%	2																									
				AMADALLER	2	90.9%	1																									
				GLELIASENFCSR	2	96.9%	1																									
				IMGLDLPDGGHLTHGYMSDVKR	3	95.8%	1																									
				ISATSIFFESMPYK	2	100.0%	2																									
				VLELVSITANK	2	100.0%	2																									
				VVDFIDEGVNIGLEVK	2	100.0%	1																									
				YYGGAEVVDEIELLCQR	2	100.0%	1																									
IPI00789398	LY75	isoform 3 of Lymphocyte antigen 75	98.8%	2.0	2	2	2	2	1,798,046	1,353,103	1,529,248	1,564,632	330,079	120,907	72,382	31,061	41.1	20.0	10.6	4.4	-1.3	0.3	-1.2	0.5	-1.1	0.5	1.1	0.2	1.2	0.2	1.0	0.7
IPI00789911	LY75	isoform 2 of Lymphocyte antigen 75	98.8%	2.0	2	2	2	2	1,798,046	1,353,103	1,529,248	1,564,632	330,079	120,907	72,382	31,061	41.1	20.0	10.6	4.4	-1.3	0.3	-1.2	0.5	-1.1	0.5	1.1	0.2	1.2	0.2	1.0	0.7
				FLAGLSTDGFWDIQTFK	2	98.8%	1																									
				WTDQDDDEDLVDTCAFLHIK	3	90.9%	1																									
IPI00789437	NAP1L4	Uncharacterized protein	100.0%	14.0	3	4	5	1	1,597,616	1,632,851	1,534,527	1,959,733	155,431	85,709	108,363	84,922	21.8	11.7	15.8	9.7	1.0	0.8	-1.0	0.7	1.2	0.08	-1.1	0.5	1.2	0.03	1.3	0.01
				FYEEVHDLER	2	100.0%	1																									
				NVDMLSELVQEYDEPILK	2	100.0%	2																									
				NVDMLSELVQEYDEPILK	3	99.6%	1																									
				YAALYQPLFDK	2	99.7%	1																									
IPI00789452	WDR61	23 kDa protein	100.0%	19.3	2	2	2	1	1,115,121	1,227,320	1,385,908	1,835,047	173,639	123,483	235,876	109,966	34.8	22.5	38.1	13.4	1.1	0.6	1.2	0.4	1.6	0.008	1.1	0.6	1.5	0.006	1.3	0.1
				SLTFSPDSQLLVTASDDGYIK	2	100.0%	1																									
				YLASGAIDGIINIFDIATGK	2	99.6%	1																									
IPI00789454	TCEB1	9 kDa protein	100.0%	28.6	2	2	3	2	513,480	479,238	519,498	559,927	48,630	18,726	35,997	9,085	21.2	8.7	15.5	3.6	-1.1	0.5	1.0	0.9	1.1	0.4	1.1	0.4	1.2	0.005	1.1	0.3
IPI00973924	TCEB1	Uncharacterized protein	100.0%	24.2	2	2	3	2	513,480	479,238	519,498	559,927	48,630	18,726	35,997	9,085	21.2	8.7	15.5	3.6	-1.1	0.5	1.0	0.9	1.1	0.4	1.1	0.4	1.2	0.005	1.1	0.3
				EHALTSGTIK	1	100.0%	1																									
				TYGGCEGPDAMYVK	2	100.0%	2																									
IPI00789589	ACAA1	12 kDa protein	100.0%	18.6	1	1	1	2	45,254	58,969	44,100	67,503	7,689	5,357	8,330	10,830	38.0	20.3	42.2	35.9	1.3	0.2	-1.0	0.9	1.5	0.1	-1.3	0.2	1.1	0.5	1.5	0.1
IPI00924606	ACAA1	13 kDa protein	100.0%	17.4	1	1	1	2	45,254	58,969	44,100	67,503	7,689	5,357	8,330	10,830	38.0	20.3	42.2	35.9	1.3	0.2	-1.0	0.9	1.5	0.1	-1.3	0.2	1.1	0.5	1.5	0.1
				GGFKDTTPDELLSAVMTAVLK	3	100.0%	1																									
IPI00789605	MYL6	isoform Smooth muscle of Myosin light polypeptide 6	100.0%	55.6	8	10	16	2	30,772,053	32,167,535	31,069,373	36,330,443	2,494,202	1,284,466	2,108,502	1,100,216	18.1	8.9	15.2	6.8	1.0	0.6	1.0	0.9	1.2	0.08	-1.0	0.7	1.1	0.04	1.2	0.06
IPI00796366	MYL6	cDNA FLJ56329, highly similar to Myosin light polypeptide 6	100.0%	35.3	8	10	16	2	30,772,053	32,167,535	31,069,373	36,330,443	2,494,202	1,284,466	2,108,502	1,100,216	18.1	8.9	15.2	6.8	1.0	0.6	1.0	0.9	1.2	0.08	-1.0	0.7	1.1	0.04	1.2	0.06
				ALGQNPTNAEVLK	2	100.0%	2																									
				DQGTYEDYVEGLR	2	100.0%	2																									
				EAFQLFDR	2	88.6%	1																									
				EGNGTVMGAEIR	2	95.8%	1																									
				HVLVTLGEK	2	100.0%	2																									
				ILYSQCGDVMR	2	100.0%	2																									
				NKDQGTYEDYVEGLR	2	100.0%	2																									
				NKDQGTYEDYVEGLR	3	100.0%	1																									
				VLDFEHFLPMLQTVAK	2	100.0%	1																									
				VLDFEHFLPMLQTVAK	3	100.0%	2																									
IPI00789638	PSMA4	Proteasome subunit beta type	100.0%	25.7	5	5	6	2	5,920,023	6,245,635	5,834,846	7,145,666	507,789	240,283	432,188	300,248	19.2	8.6	16.6	9.4	1.1	0.6	-1.0	0.9	1.2	0.07	-1.1	0.4	1.1	0.05	1.2	0.04
IPI00795606	PSMA4	26 kDa protein	100.0%	26.5	5	5	6	2	5,920,023	6,245,635	5,834,846	7,145,666	507,789	240,283	432,188	300,248	19.2	8.6	16.6	9.4	1.1	0.6	-1.0	0.9	1.2	0.07	-1.1	0.4	1.1	0.05	1.2	0.04
				ATCIGNNSAAAVSMLK	2	100.0%	1																									
				HYGFQLYQSDPSGNYGGWK	3	96.3%	1																									
				LLDEVFFSEK	2	100.0%	2																									
				SALALAIK	2	99.7%	1																									
				VEIATLTR	2	88.9%	1																									
IPI00789691	FLOT1	Flotillin 1	98.5%	9.4	1	1	1	8	572,310	538,125	551,064	561,680	41,713	19,628	26,852	24,434	16.3	8.2	10.9	9.7	-1.1	0.5	-1.0	0.7	-1.0	0.8	1.0	0.7	1.0	0.5	1.0	0.8
IPI00792079	FLOT1	Flotillin 1	98.5%	9.7	1	1	1	8	572,310	538,125	551,064	561,680	41,713	19,628	26,852	24,434	16.3	8.2	10.9	9.7	-1.1	0.5	-1.0	0.7	-1.0	0.8	1.0	0.7	1.0	0.5	1.0	0.8
IPI00892989	FLOT1	Flotillin 1	98.5%	15.7	1	1	1	8	572,310	538,125	551,064	561,680	41,713	19,628	26,852	24,434	16.3	8.2	10.9	9.7	-1.1	0.5	-1.0	0.7	-1.0	0.8	1.0	0.7	1.0	0.5	1.0	0.8
IPI00893081	FLOT1	Flotillin 1	98.5%	13.0	1	1	1	8	572,310	538,125	551,064	561,680	41,713	19,628	26,852	24,434	16.3	8.2	10.9	9.7	-1.1	0.5	-1.0	0.7	-1.0	0.8	1.0	0.7	1.0	0.5	1.0	0.8
IPI00893481	FLOT1	Flotillin 1	98.5%	10.9	1	1	1	8	572,310	538,125	551,064	561,680	41,713	19,628	26,852	24,434	16.3	8.2	10.9	9.7	-1.1	0.5	-1.0	0.7	-1.0	0.8	1.0	0.7	1.0	0.5	1.0	0.8
IPI00894145	FLOT1	Flotillin 1	98.5%	8.6	1	1	1	8	572,310	538,125	551,064	561,680	41,713	19,628	26,852	24,434	16.3	8.2	10.9	9.7	-1.1	0.5	-1.0	0.7	-1.0	0.8	1.0	0.7	1.0	0.5	1.0	0.8
IPI00894525	FLOT1	Flotillin 1	98.5%	12.2	1	1	1	8	572,310	538,125	551,064	561,680	41,713	19,628	26,852	24,434	16.3	8.2	10.9	9.7	-1.1	0.5	-1.0	0.7	-1.0	0.8	1.0	0.7	1.0	0.5	1.0	0.8
IPI00941052	FLOT1	Flotillin 1	98.5%	7.7	1	1	1	8	572,310	538,125	551,064	561,680	41,713	19,628	26,852	24,434	16.3	8.2	10.9	9.7	-1.1	0.5	-1.0	0.7	-1.0	0.8	1.0	0.7	1.0	0.5	1.0	0.8
				TEAEIAHIALETLEGHQR	3	98.5%	1																									
IPI00789792	DCTN2	cDNA FLJ77785	100.0%	25.5	6	6	9	1	6,658,344	6,867,000	6,545,332	7,272,518	390,308	272,662	431,779	188,004	13.1	8.9	14.8	5.8	1.0	0.7	-1.0	0.9	1.1	0.2	-1.0	0.5	1.1	0.3	1.1	0.2
				DNTTLLTQVQTTMR	2	99.9%	1																									
				LLGPDAAINLTDPDGALAK	2	100.0%	2																									
				LLLQLEATK	2	99.7%	2																									
				LTELETAVR	2	98.9%	1																									
				VSALDLAVLDQVEAR	2	100.0%	2																									
				WSPIASTLPELVQR	2	100.0%	1																									
IPI00789806	LAP3	isoform 2 of Cytosol aminopeptidase	100.0%	19.1	6	6	6	1	9,622,039	9,932,689	9,294,125	11,171,004	594,695	426,583	584,039	416,738	13.8	9.6	14.1	8.3	1.0	0.7	-1.0	0.7	1.2	0.07	-1.1	0.4	1.1	0.07	1.2	0.03
				GITFDSGGISIK	2	99.9%	1																									
				GSPNANEPPLVFVGK	2	96.1%	1																									
				LNLPINIIGLAPLCENMPSGK	2	82.1%	1																									
				LYGSGDQEAWQK	2	99.5%	1																									
				QLMETPANEMTPTR	2	100.0%	1																									
				TFYGLHQDFPSVVLVGLGK	3	100.0%	1																									
IPI00790016	NAP1L4	Uncharacterized protein	100.0%	9.9	1	1	1	1	1,491,462	1,353,877	1,762,185	1,538,254	139,881	95,834	99,802	106,533	21.0	15.8	12.7	15.5	-1.1	0.4	1.2	0.2	1.0	0.8	1.3	0.02	1.1	0.2	-1.1	0.2
				LTDQVMQNPR	2	100.0%	1																									
IPI00790124	GRB2	18 kDa protein	100.0%	12.8	2	3	3	1	4,863,107	4,956,880	4,540,840	5,539,593	533,916	262,762	202,047	370,411	24.6	11.9	10.0	15.0	1.0	0.9	-1.1	0.6	1.1	0.3	-1.1	0.2	1.1	0.2	1.2	0.05
				HDGAFLIR	2	99.9%	1																									
				VLNEECDQNWYK	2	100.0%	1																									
				VLNEECDQNWYK	3	80.4%	1																									
IPI00790166	MGLL	cDNA FLJ54260, highly similar to Monoglyceride lipase	99.9%	6.7	2	2	2	1	996,735	1,064,240	1,295,098	1,270,415	98,936	64,594	95,712	85,977	22.2	13.6	16.5	15.1	1.1	0.6	1.3	0.06	1.3	0.07	1.2	0.08	1.2	0.09	-1.0	0.9
				VCFGIQLLNAVSR	2	99.9%	1																									
				YEELAR	1	94.8%	1																									
IPI00790203	LTA4H	LTA4H protein	100.0%	8.7	1	1	1	1	763,290	787,510	927,780	817,125	71,775	66,191	39,886	105,344	21.0	18.8	9.6	28.8	1.0	0.8	1.2	0.08	1.1	0.7	1.2	0.1	1.0	0.8	-1.1	0.4
				EDDLNSFNATDLK	2	100.0%	1																									
IPI00790291	RPL7P32;RPL7	Uncharacterized protein	100.0%	9.1	1	1	1	2	593,086	627,810	588,534	688,474	60,481	26,820	64,929	52,515	22.8	9.6	24.7	17.1	1.1	0.6	-1.0	1	1.2	0.3	-1.1	0.6	1.1	0.3	1.2	0.3
IPI00793342	RPL7P32;RPL7	Uncharacterized protein	100.0%	10.2	1	1	1	2	593,086	627,810	588,534	688,474	60,481	26,820	64,929	52,515	22.8	9.6	24.7	17.1	1.1	0.6	-1.0	1	1.2	0.3	-1.1	0.6	1.1	0.3	1.2	0.3
				QIFNGTFVK	2	90.0%	1																									
IPI00790304	VDAC1	Uncharacterized protein	100.0%	22.3	3	3	3	1	5,951,068	6,368,880	5,747,043	7,246,170	893,088	338,511	520,159	388,197	33.6	11.9	20.2	12.0	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.3	0.05
				VTQSNFAVGYK	2	99.8%	1																									
				WNTDNTLGTEITVEDQLAR	3	99.6%	1																									
				WTEYGLTFTEK	2	99.9%	1																									
IPI00790342	RPL6	60S ribosomal protein L6	100.0%	12.5	3	4	6	2	4,868,204	5,569,204	4,865,278	6,188,032	313,403	467,645	443,437	244,688	14.4	18.8	20.4	8.8	1.1	0.2	-1.0	1	1.3	0.01	-1.1	0.3	1.1	0.3	1.3	0.03
IPI00867533	RPL6	60S ribosomal protein L6	100.0%	12.5	3	4	6	2	4,868,204	5,569,204	4,865,278	6,188,032	313,403	467,645	443,437	244,688	14.4	18.8	20.4	8.8	1.1	0.2	-1.0	1	1.3	0.01	-1.1	0.3	1.1	0.3	1.3	0.03
				ASITPGTILIILTGR	2	100.0%	2																									
				ASITPGTILIILTGR	3	100.0%	1																									
				HLTDAYFK	2	100.0%	2																									
				VLATVTKPVGGDK	2	99.9%	1																									
IPI00790462	PTGES3	cDNA FLJ50819, highly similar to Prostaglandin E synthase 3	100.0%	30.8	3	3	4	1	3,389,991	3,604,548	3,514,594	4,078,449	375,483	102,318	253,146	109,129	24.8	6.4	16.1	6.0	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.8	1.1	0.01	1.2	0.08
				HLNEIDLFHCIDPNDSK	3	100.0%	1																									
				KGESGQSWPR	2	100.0%	2																									
				LTFSCLGGSDNFK	2	100.0%	1																									
IPI00790570	RAB2A	Protein	100.0%	26.9	2	2	2	1	1,410,935	1,365,623	1,304,412	1,454,090	109,449	74,373	49,896	49,447	17.4	12.2	8.6	7.6	-1.0	0.7	-1.1	0.4	1.0	0.7	-1.0	0.5	1.1	0.4	1.1	0.07

				DTFNHLTTWLEDAR	2	99.9%	1																									
				TASNVEEAFINTAK	2	99.7%	1																									
IPI00791300	-	cDNA FLJ61645, highly similar to Homo sapiens nitrilase family, member 2 (NIT2), r	100.0%	8.1	1	1	2	3	1,421,338	1,301,358	1,293,753	1,366,298	173,479	40,377	101,889	45,627	27.3	6.9	17.6	7.5	-1.1	0.5	-1.1	0.5	-1.0	0.8	-1.0	0.9	1.0	0.3	1.1	0.5
IPI00790618	NIT2	10 kDa protein	100.0%	13.0	1	1	2	3	1,421,338	1,301,358	1,293,753	1,366,298	173,479	40,377	101,889	45,627	27.3	6.9	17.6	7.5	-1.1	0.5	-1.1	0.5	-1.0	0.8	-1.0	0.9	1.0	0.3	1.1	0.5
IPI00945908	NIT2	Protein	100.0%	4.5	1	1	2	3	1,421,338	1,301,358	1,293,753	1,366,298	173,479	40,377	101,889	45,627	27.3	6.9	17.6	7.5	-1.1	0.5	-1.1	0.5	-1.0	0.8	-1.0	0.9	1.0	0.3	1.1	0.5
				LALIQLQISSIK	2	100.0%	2																									
IPI00790636	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	28.9	10	11	12	1	11,112,497	11,223,177	11,128,493	12,805,958	1,079,559	461,847	730,668	254,381	21.7	9.2	14.7	4.4	1.0	0.9	1.0	1	1.2	0.2	-1.0	0.9	1.1	0.02	1.2	0.08
				CIALAQLLVEQNFPAIAIHR	3	100.0%	2																									
				DFLLKPELLR	2	99.3%	1																									
				DFLLKPELLR	3	90.9%	1																									
				FMQDPMEIFVDDETK	2	99.8%	1																									
				GSYVSIHSSGFR	2	99.7%	1																									
				HFILDECDK	2	99.7%	1																									
				ILVATNLFGR	2	98.9%	1																									
				MLEQLDMR	2	100.0%	1																									
				NCPHIVVGTPGR	2	99.8%	1																									
				RDVQEIFR	2	98.1%	1																									
				VNIAFNYDMPEDSDTYLHR	3	100.0%	1																									
IPI00790695	RPL30	6 kDa protein	100.0%	31.4	1	1	1	2	996,865	1,172,550	1,122,820	1,294,950	71,553	112,032	97,573	133,486	16.1	21.4	19.4	23.1	1.2	0.2	1.1	0.3	1.3	0.08	-1.0	0.7	1.1	0.5	1.2	0.3
IPI00794121	RPL30	11 kDa protein	100.0%	16.7	1	1	1	2	996,865	1,172,550	1,122,820	1,294,950	71,553	112,032	97,573	133,486	16.1	21.4	19.4	23.1	1.2	0.2	1.1	0.3	1.3	0.08	-1.0	0.7	1.1	0.5	1.2	0.3
				VCTLAIIDPGDSDIIR	2	99.7%	1																									
IPI00790804	TFG	Uncharacterized protein	100.0%	24.8	2	2	2	1	1,806,962	1,779,920	1,782,171	1,928,842	149,423	84,982	117,860	43,597	18.5	10.7	14.8	5.1	-1.0	0.9	-1.0	0.9	1.1	0.5	1.0	1	1.1	0.2	1.1	0.3
				LLDSLEPPGEPGPSTNIPENDTVDGREEK	3	100.0%	1																									
				LLSNDEVTIK	2	100.0%	1																									
IPI00790831	LMNB1	Uncharacterized protein	100.0%	32.3	9	11	18	1	36,499,647	37,337,708	38,188,492	42,039,994	1,907,118	1,224,088	2,104,085	1,394,622	11.7	7.3	12.3	7.4	1.0	0.7	1.0	0.6	1.2	0.05	1.0	0.7	1.1	0.04	1.1	0.2
				CQSLTEDLEFR	2	99.7%	1																									
				DAALATALGDKK	2	100.0%	2																									
				DAALATALGDKK	3	99.7%	1																									
				DQMQQQLNDYEQLLDVK	2	100.0%	2																									
				IESLSSQLSNLQK	2	100.0%	2																									
				IQELEDLLAK	2	99.9%	1																									
				LSSEMNTSTVNSAR	2	100.0%	2																									
				LYKEELEQTYHAK	3	99.0%	1																									
				SLEGDLEDLKDQIAQLEASLAAAK	2	100.0%	2																									
				SLEGDLEDLKDQIAQLEASLAAAK	3	100.0%	2																									
				SMYEEEINETR	2	100.0%	2																									
IPI00790844	DHRS11	Uncharacterized protein	100.0%	14.3	1	1	1	1	2,891,355	2,772,180	2,794,690	3,538,900	339,956	144,378	220,150	135,374	26.3	11.7	17.6	8.6	-1.0	0.8	-1.0	0.8	1.2	0.1	1.0	0.9	1.3	0.005	1.3	0.02
				LALVTGASGGIGAAVAR	2	99.8%	1																									
IPI00791026	MYO1C	56 kDa protein	100.0%	7.4	3	3	4	1	1,396,287	1,302,668	1,374,780	1,480,814	107,056	75,903	60,892	94,766	17.1	13.0	9.9	14.3	-1.1	0.5	-1.0	0.9	1.1	0.6	1.1	0.5	1.1	0.2	1.1	0.4
				KRPETVATQFK	2	99.5%	1																									
				MSLLQLVEILQSK	2	100.0%	2																									
				TLFATEDALEVR	2	95.4%	1																									
IPI00791083	PSMA4	20 kDa protein	100.0%	10.9	2	2	3	1	4,302,269	4,425,563	4,213,131	5,173,686	503,092	149,322	295,062	170,323	26.2	7.5	15.7	7.4	1.0	0.8	-1.0	0.9	1.2	0.2	-1.1	0.5	1.2	0.01	1.2	0.02
				LLDEVFFSEK	2	100.0%	2																									
				TTIFSPEGR	2	98.2%	1																									
IPI00791180	ARHGDIA	9 kDa protein	100.0%	36.7	3	3	4	1	3,303,508	3,180,343	3,042,541	3,362,866	318,501	210,153	190,132	139,152	21.6	14.8	14.0	9.3	-1.0	0.8	-1.1	0.5	1.0	0.9	-1.0	0.6	1.1	0.5	1.1	0.2
				AEEYEFLTPVEEAPK	2	100.0%	2																									
				IDKTDYMVGSYGPR	2	100.0%	1																									
				TDYMVGSYGPR	2	100.0%	1																									
IPI00796346	-	12 kDa protein	100.0%	10.7	1	1	1	2	1,660,903	2,052,780	1,609,105	1,963,215	164,778	195,465	150,098	258,593	22.2	21.3	20.9	29.5	1.2	0.2	-1.0	0.8	1.2	0.4	-1.3	0.1	-1.0	0.8	1.2	0.3
IPI00791185	TCEB1	Uncharacterized protein	100.0%	12.5	1	1	1	2	1,660,903	2,052,780	1,609,105	1,963,215	164,778	195,465	150,098	258,593	22.2	21.3	20.9	29.5	1.2	0.2	-1.0	0.8	1.2	0.4	-1.3	0.1	-1.0	0.8	1.2	0.3
				LISSDGHEFIVK	2	100.0%	1																									
IPI00791226	SEC13	Uncharacterized protein	96.8%	12.8	1	1	1	4	545,834	478,563	584,463	566,117	32,675	38,992	60,685	19,977	13.4	18.2	23.2	7.9	-1.1	0.2	1.1	0.6	1.0	0.6	1.2	0.2	1.2	0.08	-1.0	0.8
IPI00852657	SEC13	Uncharacterized protein	96.8%	10.9	1	1	1	4	545,834	478,563	584,463	566,117	32,675	38,992	60,685	19,977	13.4	18.2	23.2	7.9	-1.1	0.2	1.1	0.6	1.0	0.6	1.2	0.2	1.2	0.08	-1.0	0.8
IPI00852874	SEC13	Uncharacterized protein	96.8%	20.0	1	1	1	4	545,834	478,563	584,463	566,117	32,675	38,992	60,685	19,977	13.4	18.2	23.2	7.9	-1.1	0.2	1.1	0.6	1.0	0.6	1.2	0.2	1.2	0.08	-1.0	0.8
IPI00853116	SEC13	cDNA FLJ59881, highly similar to SEC13-related protein	96.8%	5.7	1	1	1	4	545,834	478,563	584,463	566,117	32,675	38,992	60,685	19,977	13.4	18.2	23.2	7.9	-1.1	0.2	1.1	0.6	1.0	0.6	1.2	0.2	1.2	0.08	-1.0	0.8
				NGGQILIADLR	2	96.8%	1																									
IPI00791265	SNORD54;RPS20	Uncharacterized protein	100.0%	24.6	2	2	2	4	2,492,335	2,454,990	2,228,850	2,991,567	226,249	123,980	117,702	223,305	20.3	11.3	11.8	16.7	-1.0	0.9	-1.1	0.3	1.2	0.2	-1.1	0.2	1.2	0.07	1.3	0.02
IPI00791752	SNORD54;RPS20	7 kDa protein	100.0%	25.4	2	2	2	4	2,492,335	2,454,990	2,228,850	2,991,567	226,249	123,980	117,702	223,305	20.3	11.3	11.8	16.7	-1.0	0.9	-1.1	0.3	1.2	0.2	-1.1	0.2	1.2	0.07	1.3	0.02
IPI00795078	SNORD54;RPS20	5 kDa protein	100.0%	34.9	2	2	2	4	2,492,335	2,454,990	2,228,850	2,991,567	226,249	123,980	117,702	223,305	20.3	11.3	11.8	16.7	-1.0	0.9	-1.1	0.3	1.2	0.2	-1.1	0.2	1.2	0.07	1.3	0.02
IPI00796373	SNORD54;RPS20	Uncharacterized protein	100.0%	32.6	2	2	2	4	2,492,335	2,454,990	2,228,850	2,991,567	226,249	123,980	117,702	223,305	20.3	11.3	11.8	16.7	-1.0	0.9	-1.1	0.3	1.2	0.2	-1.1	0.2	1.2	0.07	1.3	0.02
				DTGKTPVEPEVAIHR	3	100.0%	1																									
				TPVEPEVAIHR	3	100.0%	1																									
IPI00791367	PPIB	20 kDa protein	100.0%	42.7	8	9	15	1	36,615,695	36,502,710	35,633,610	39,215,640	3,198,409	1,967,799	2,340,504	1,373,533	19.5	12.1	14.7	7.8	-1.0	1	-1.0	0.8	1.1	0.5	-1.0	0.8	1.1	0.3	1.1	0.2
				DFMIQGGDFTR	2	100.0%	2																									
				DKPLKDVIIADCGK	3	99.9%	1																									
				DTNGSQFFITTVK	2	100.0%	2																									
				FPDENFK	2	97.8%	1																									
				IEVEKPFAIAKE	2	99.2%	2																									
				TAWLDGK	2	99.4%	2																									
				VIKDFMIQGGDFTR	2	100.0%	2																									
				VIKDFMIQGGDFTR	3	100.0%	1																									
				VLEGMEVVR	2	100.0%	2																									
IPI00791490	PDXK	29 kDa protein	100.0%	22.8	4	5	5	1	6,772,627	6,518,036	7,042,338	7,153,632	397,457	396,372	421,394	264,685	13.1	13.6	13.4	8.3	-1.0	0.7	1.0	0.7	1.1	0.4	1.1	0.4	1.1	0.2	1.0	0.8
				GQVLNSDELQELYEGLR	2	100.0%	1																									
				GQVLNSDELQELYEGLR	3	99.9%	1																									
				RNPAGSVVMER	2	82.5%	1																									
				VVPLADIITPNQFEAELLSGR	2	99.8%	1																									
				YDYVLTGYTR	2	100.0%	1																									
IPI00791537	CAND2	isoform 1 of Cullin-associated NEDD8-dissociated protein 2	91.6%	1.5	1	1	1	1	4,471,830	4,622,990	5,152,620	5,148,720	299,789	210,506	337,363	321,267	15.0	10.2	14.6	14.0	1.0	0.7	1.2	0.2	1.2	0.2	1.1	0.2	1.1	0.2	-1.0	1
				EYQVETIVDTLCTNMRSDK	3	91.6%	1																									
IPI00791573	SUGT1	isoform 2 of Suppressor of G2 allele of SKP1 homolog	100.0%	11.1	2	2	3	2	2,486,128	2,064,355	2,061,619	2,715,233	639,634	186,290	311,221	216,581	57.5	20.2	33.8	17.8	-1.2	0.6	-1.2	0.6	1.1	0.7	-1.0	1	1.3	0.05	1.3	0.1
IPI00828150	SUGT1	isoform 1 of Suppressor of G2 allele of SKP1 homolog	100.0%	10.1	2	2	3	2	2,486,128	2,064,355	2,061,619	2,715,233	639,634	186,290	311,221	216,581	57.5	20.2	33.8	17.8	-1.2	0.6	-1.2	0.6	1.1	0.7	-1.0	1	1.3	0.05	1.3	0.1
				FFQSFSDALIDEDPQAALEELTK	2	100.0%	2																									
				SLELNPNNSTAMLR	2	98.1%	1																									
IPI00791583	FLOT1	Flotillin 1	98.5%	12.3	2	2	2	4	1,352,970	1,396,933	1,308,277	1,355,875	76,428	65,868	106,144	52,032	12.6	10.5	18.1	8.6	1.0	0.7	-1.0	0.7	1.0	1	-1.1	0.5	-1.0	0.6	1.0	0.7
IPI00827631	FLOT1	Flotillin 1	98.5%	13.0	2	2	2	4	1,352,970	1,396,933	1,308,277	1,355,875	76,428	65,868	106,144	52,032	12.6	10.5	18.1	8.6	1.0	0.7	-1.0	0.7	1.0	1	-1.1	0.5	-1.0	0.6	1.0	0.7
IPI00892615	FLOT1	Flotillin 1	98.5%	17.0	2	2	2	4	1,352,970	1,396,933	1,308,277	1,355,875	76,428	65,868	106,144	52,032	12.6	10.5	18.1	8.6	1.0	0.7	-1.0	0.7	1.0	1	-1.1	0.5	-1.0	0.6	1.0	0.7
IPI00893347	FLOT1	Flotillin 1	98.5%	13.4	2	2	2	4	1,352,970	1,396,933	1,308,277	1,355,875	76,428	65,868	106,144	52,032	12.6	10.5	18.1	8.6	1.0	0.7	-1.0	0.7	1.0	1	-1.1	0.5	-1.0	0.6	1.0	0.7
				AQADLAYQLQVAK	2	96.2%	1																									
				TEAEIAHIALETLEGHQR	3	98.5%	1																									
IPI00791634	PHB	Uncharacterized protein	100.0%	16.9	3	3	5	3	2,800,771	2,894,346	2,972,918	3,244,354	213,188	123,297	197,334	94,557	17.0	9.5	14.8	6.5	1.0	0.7	1.1	0.6	1.2	0.09	1.0	0.7	1.1	0.05	1.1	0.2
IPI01011045	PHB	Uncharacterized protein	100.0%	16.7	3	3	5	3	2,800,771	2,894,346	2,972,918	3,244,354	213,188	123,297	197,334	94,557	17.0	9.5	14.8	6.5	1.0	0.7	1.1	0.6	1.2	0.09	1.0	0.7	1.1	0.05	1.1	0.2
IPI01011461	PHB	Uncharacterized protein	100.0%	15.9	3	3	5	3	2,800,771	2,894,346	2,972,918	3,244,354	213,188	123,297	197,334	94,557	17.0	9.5	14.8	6.5	1.0	0.7	1.1	0.6	1.2	0.09	1.0	0.7	1.1	0.05	1.1	0.2
				FDAGELITQR	2	100.0%	2																									
				IFTSIGEDYDER	2	100.0%	2																									
				ILFRPVASQLPR	2	98.5%	1																									
IPI00791788	TSTA3	cDNA FLJ39433 fis, clone PROST2004142, highly similar to GDP-L-fucose syntheta	100.0%	11.8	1	1	1	5	339,070	337,353	397,993	445,573	37,798	7,747	34,158	32,840	24.9	5.1	19.2	16.5	-1.0	1	1.2	0.3	1.3	0.07	1.2	0.2	1.3	0.03	1.1	0.3
IPI00909958	TSTA3	cDNA FLJ57685, highly similar to GDP-L-fucose synthetase	100.0%	10.7	1	1	1	5	339,070	337,353	397,993	445,573	37,798	7,747	34,158	32,840	24.9	5.1	19.2	16.5	-1.0	1	1.2	0.3	1.3	0.07	1.2	0.2	1.3	0.03	1.1	0.3
IPI00981359	TSTA3	Uncharacterized protein	100.0%	7.1	1	1	1	5	339,070	337,353	397,993	445,573	37,798	7,747	34,158	32,840	24.9	5.1	19.2	16.5	-1.0	1	1.2	0.3	1.3	0.07	1.2	0.2	1.3	0.03	1.1	0.3
IPI01012947	TSTA3	Uncharacterized protein	100.0%	9.6	1	1	1	5	339,070	337,353	397,993	445,573	37,798	7,747	34,158	32,840	24.9	5.1	19.2	16.5	-1.0	1	1.2	0.3	1.3	0.07	1.2	0.2	1.3	0.03	1.1	0.3
IPI00984362	TSTA3	Uncharacterized protein	100.0%	16.5	1	1	1	5	339,070	337,353	397,993	445,573	37,798	7,747	34,158	32,840	24.9	5.1	19.2	16.5	-1.0	1	1.2	0.3	1.3	0.07	1.2	0.2	1.3	0.03	1.1	0.3
				VVADGAGLPGEDWVFVSSK	2	100.0%	1																									
IPI00791920	RPL23	13 kDa protein	100.0%	31.2	3	3	4	3	6,922,568	7,047,212	6,845,294	8,201,638	554,641	266,629	601,317	422,348	17.9	8.5	19.6	11.5	1.0	0.8	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.05	1.2	0.1
IPI00794091	RPL23	Uncharacterized protein	100.0%	33.3	3	3	4	3	6,922,568	7,047,212	6,845,294	8,201,638	554,641	266,629	601,317	422,348	17.9	8.5	19.6	11.5	1.0	0.8	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.05	1.2	0.1
IPI00795751	RPL23	Uncharacterized protein	100.0%	41.8	3	3	4	3	6,922,568	7,047,212	6,845,294	8,201,638	554,641	266,629	601,317	422,348	17.9	8.5	19.6	11.5	1.0	0.8	-1.0	0.9	1.2	0.1	-1.0	0.8	1.2	0.05	1.2	0.1
				ISLGLPVGAVINCADNTGAK	2	100.0%	1																									
				LNRLPAAGVGDMVMATVK	3	99.9%	1																									
				LPAAGVGDMVMATVK	2	100.0%	2																									
IPI00791938	LLGL1	LLGL1 protein	97.3%	1.1	1	1	1	2	2,399,175	2,430,255	2,326,975	2,538,045	173,164	136,313	137,058	126,408	16.1	12.5	13.2	11.1	1.0	0.9	-1.0	0.8	1.1	0.5	-1.0	0.6	1.0	0.6	1.1	0.3
IPI00854741	LLGL1	Lethal(2) giant larvae protein homolog 1	97.3%	1.1	1	1	1	2	2,399,175	2,430,255	2,326,975	2,538,045	173,164	136,313	137,058	126,408	16.1	12.5	13.2	11.1	1.0	0.9	-1.0	0.8	1.1	0.5	-1.0	0.6	1.0	0.6	1.1	0.3
				APVVAIAVLDGR	2	97.3%	1																									
IPI00791971	ME1;NME1-NME2;NM	9 kDa protein	100.0%	36.5	2	2	3	1	10,736,303	11,036,621	9,822,928	11,604,476	629,913	626,219	657,979	507,341	13.1	12.7	15.0	9.8	1.0	0.7	-1.1	0.3	1.1	0.3	-1.1	0.2	1.1	0.5	1.2	0.06
				NIIHGSDSVESAEK	3	100.0%	1																									
				VMLGETNPADSKPGTIR	2	100.0%	2																									
IPI00792035	GLOD4	isoform 3 of Glyoxalase domain-containing protein 4	100.0%	34.2	5	5	7	1	7,261,218	7,843,441	7,677,172	8,844,711	716,704	256,738	722,232	266,198	22.1	7.3	21.0	6.7	1.1	0.5	1.1	0.7	1.2	0.09	-1.0	0.8	1.1	0.03	1.2	0.2
				ALLGYADNQCK	2	100.0%	2																									
				LGNDFMGITLASSQAVSNAR	3	100.0%	1																									
				SLNYWCNLLGMK	2	100.0%	1																									
				TMVGFGPEDDHFVAELTYNYGVGDYK	3	100.0%	1																									
				VTLAVSDLQK	2	99.9%	2																									
IPI00792043	DDX39B;SNORD84	cDNA FLJ53073, highly similar to Spliceosome RNA helicase Bat1	100.0%	35.1	10	10	11	2	12,266,208	12,222,686	12,142,870	14,133,158	1,248,184	539,601	779,334	517,560	22.8	9.9	14.4	8.2	-1.0	1	-1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.03	1.2	0.07
IPI00893580	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	37.5	10	10	11	2	12,266,208	12,222,686	12,142,870	14,133,158	1,248,184	539,601	779,334	517,560	22.8	9.9	14.4	8.2	-1.0	1	-1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.03	1.2	0.07
				CIALAQLLVEQNFPAIAIHR	3	100.0%	2																									
				FMQDPMEIFVDDETK	2	99.8%	1																									
				GLAITFVSDENDAK	2	100.0%	1																									
				HFILDECDK	2	99.7%	1																									
				ILNDVQDR	2	99.9%	1																									
				ILVATNLFGR	2	98.9%	1																									
				MLEQLDMR	2	100.0%	1																									
				NCPHIVVGTPGR	2	99.8%	1																									
				RDVQEIFR	2	98.1%	1																									
				VNIAFNYDMPEDSDTYLHR	3	100.0%	1																									
IPI00792054	SCRN2	30 kDa protein	100.0%	18.1	3	3	3	1	3,918,947	3,968,380	3,803,691	4,627,317	466,831	160,840	382,534	189,493	26.6	9.1	22.5	9.2	1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.7	1.2	0.03	1.2	0.09
				EPVGEGEALLGMDLLR	2	99.7%	1																									
				LQCTYIEVEQVSK	2	94.7%	1																									
				NISNQLSIGTDISAQHPELR	3	100.0%	1																									
IPI00792088	ACTL6A	Protein	100.0%	31.7	3	3	3	1	5,031,124	5,374,739	4,840,993	5,206,993	436,244	257,691	149,058	294,168	19.4	10.7	6.9	12.6	1.1	0.5	-1.0	0.7	1.0	0.7	-1.1	0.1	-1.0	0.7	1.1	0.3
				NGMVEDWDSFQAILDHTYK	3	98.6%	1																									
				QGGPTYYIDTNALR	2	99.9%	1																									
				SEASLHPVLMSEAPWNTR	3	100.0%	1																									
IPI00792135	ATP5H	ATP5H protein (Fragment)	100.0%	8.8	1	1	1	2	1,073,270	1,133,125	1,018,763	1,389,625	134,194	99,035	84,990	117,923	28.0	19.5	18.7	19.0	1.1	0.7	-1.1	0.7	1.3	0.1	-1.1	0.4	1.2	0.1	1.4	0.03
IPI01012080	ATP5H	11 kDa protein	100.0%	8.8	1	1	1	2	1,073,270	1,133,125	1,018,763	1,389,625	134,194	99,035	84,990	117,923	28.0	19.5	18.7	19.0	1.1	0.7	-1.1	0.7	1.3	0.1	-1.1	0.4	1.2	0.1	1.4	0.03
				SWNETLTSR	2	99.1%	1																									
IPI00792159	RPL4	11 kDa protein	100.0%	10.7	1	1	2	1	1,102,297	1,202,627	967,187	1,318,153	79,968	68,619	34,318	57,929	16.2	12.8	7.9	9.8	1.1	0.4	-1.1	0.2	1.2	0.06	-1.2	0.02	1.1	0.2	1.4	0.0008
				AAAAAAALQAK	2	99.9%	2																									
IPI00792207	ALDH2	aldehyde dehydrogenase, mitochondrial isoform 2 precursor	100.0%	21.3	7	7	10	1	17,617,160	17,977,350	16,280,400	20,258,545	1,595,218	924,454	1,192,606	664,104	20.3	11.5	16.4	7.3	1.0	0.8	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.08	1.2	0.02

				ANNSTYGLAAAVFTK	2	99.4%	1																									
				ELGEYGLQAYTEVK	2	100.0%	2																									
				GYFIQPTVFGDVQDGMTIAK	2	100.0%	1																									
				LGPALATGNVVVMK	2	99.9%	2																									
				LLCGGGIAADR	2	95.4%	1																									
				TFVQEDIYDEFVER	2	100.0%	2																									
				VIQVAAGSSNLK	2	96.6%	1																									
IPI00792218	PSMA4	proteasome subunit alpha type-4 isoform 2	100.0%	12.6	2	2	2	1	1,321,049	1,409,441	1,251,675	1,642,870	102,533	54,388	103,797	180,264	17.4	8.6	18.5	24.5	1.1	0.5	-1.1	0.6	1.2	0.2	-1.1	0.2	1.2	0.3	1.3	0.1
				ATCIGNNSAAAVSMLK	2	100.0%	1																									
				SALALAIK	2	99.7%	1																									
IPI00792258	DHRS11	17 kDa protein	100.0%	7.3	1	1	2	1	2,172,970	2,106,770	2,182,617	2,381,710	201,204	104,696	93,087	143,223	20.7	11.1	9.5	13.5	-1.0	0.8	1.0	1	1.1	0.4	1.0	0.6	1.1	0.2	1.1	0.3
				YAVTALTEGLR	2	99.9%	2																									
IPI00792330	ARF4	Uncharacterized protein	100.0%	30.7	3	4	5	1	11,531,216	12,141,212	13,474,937	13,546,386	792,469	563,228	936,112	435,026	15.4	10.4	15.5	7.2	1.1	0.5	1.2	0.2	1.2	0.06	1.1	0.3	1.1	0.08	1.0	0.9
				IQEVADELQK	2	99.9%	1																									
				LGEIVTTIPTIGFNVETVEYK	2	100.0%	2																									
				LGEIVTTIPTIGFNVETVEYK	3	100.0%	1																									
				MLLVDELR	2	94.7%	1																									
IPI00792538	APEX1	Protein	100.0%	19.3	2	2	3	1	7,526,257	7,748,043	7,653,550	8,746,720	494,474	324,377	533,705	216,635	14.7	9.4	15.6	5.5	1.0	0.7	1.0	0.9	1.2	0.05	-1.0	0.9	1.1	0.03	1.1	0.09
				GLDWVKEEAPDILCLQETK	3	99.4%	1																									
				ICSWNVDGLR	2	99.9%	2																									
IPI00792542	ACY1	Uncharacterized protein	100.0%	14.5	3	3	3	2	7,369,338	7,861,913	8,061,233	8,229,942	854,181	630,554	669,191	369,141	25.9	17.9	18.6	10.0	1.1	0.7	1.1	0.5	1.1	0.4	1.0	0.8	1.0	0.6	1.0	0.8
IPI00946958	ACY1	23 kDa protein	100.0%	16.4	3	3	3	2	7,369,338	7,861,913	8,061,233	8,229,942	854,181	630,554	669,191	369,141	25.9	17.9	18.6	10.0	1.1	0.7	1.1	0.5	1.1	0.4	1.0	0.8	1.0	0.6	1.0	0.8
				GPEEEHPSVTLFR	3	99.3%	1																									
				PDYGAAVAFFEETAR	2	90.9%	1																									
				TVQPKPDYGAAVAFFEETAR	3	100.0%	1																									
IPI00792607	SNRPA1	cDNA FLJ75425, highly similar to Homo sapiens small nuclear ribonucleoprotein pol	99.5%	16.0	2	2	2	2	1,112,583	1,226,775	1,244,526	1,377,609	252,640	280,465	120,801	220,184	50.8	51.1	21.7	35.7	1.1	0.8	1.1	0.7	1.2	0.5	1.0	1	1.1	0.7	1.1	0.6
IPI00797067	SNRPA1	U2 snRNP-specific A' protein	99.5%	18.2	2	2	2	2	1,112,583	1,226,775	1,244,526	1,377,609	252,640	280,465	120,801	220,184	50.8	51.1	21.7	35.7	1.1	0.8	1.1	0.7	1.2	0.5	1.0	1	1.1	0.7	1.1	0.6
				GYKIPVIENLGATLDQFDAIDFSDNEIR	3	98.9%	1																									
				IPVIENLGATLDQFDAIDFSDNEIR	2	99.5%	1																									
IPI00792647	LSS	Uncharacterized protein	100.0%	5.0	1	1	1	1	1,670,950	1,681,590	1,593,478	1,761,595	98,107	75,896	76,281	52,648	13.1	10.1	10.7	6.7	1.0	0.9	-1.0	0.6	1.1	0.4	-1.1	0.4	1.0	0.4	1.1	0.1
				ILGVGPDDPDLVR	2	99.9%	1																									
IPI00792667	PNPO	cDNA FLJ59599, highly similar to Pyridoxine-5'-phosphate oxidase	100.0%	11.0	2	2	2	1	4,865,368	4,674,318	4,623,717	5,429,265	329,071	223,730	263,326	188,676	15.1	10.7	12.7	7.8	-1.0	0.6	-1.1	0.6	1.1	0.2	-1.0	0.9	1.2	0.03	1.2	0.04
				EAFEETHLTSLDPVK	2	99.9%	1																									
				GEEDWLYER	2	99.9%	1																									
IPI00792673	ETFA	24 kDa protein	100.0%	33.6	5	5	6	1	5,108,682	5,650,422	5,648,423	6,434,453	480,627	202,141	451,448	181,173	21.0	8.0	17.9	6.3	1.1	0.3	1.1	0.4	1.3	0.05	-1.0	1	1.1	0.02	1.1	0.1
				AAVDAGFVPNDMQVGQTGK	2	100.0%	2																									
				DPEAPIFQVADYGIVADLFK	2	100.0%	1																									
				GTSFDAAATSGGSASSEK	2	100.0%	1																									
				LEVAPISDIIAIK	2	99.9%	1																									
				TIVAINKDPEAPIFQVADYGIVADLFK	3	100.0%	1																									
IPI00793930	TUBA1B	TUBA1B protein	100.0%	22.1	4	4	6	3	13,307,575	13,562,479	13,263,959	15,195,204	1,095,441	460,508	867,679	592,060	18.4	7.6	14.6	8.7	1.0	0.8	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.06	1.1	0.1
IPI00930688	TUBA1B	Tubulin alpha-1B chain	100.0%	16.4	4	4	6	3	13,307,575	13,562,479	13,263,959	15,195,204	1,095,441	460,508	867,679	592,060	18.4	7.6	14.6	8.7	1.0	0.8	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.06	1.1	0.1
IPI00792677	TUBA4A;TUBA1B	cDNA FLJ60097, highly similar to Tubulin alpha-ubiquitous chain	100.0%	17.8	4	4	6	3	13,307,575	13,562,479	13,263,959	15,195,204	1,095,441	460,508	867,679	592,060	18.4	7.6	14.6	8.7	1.0	0.8	-1.0	1	1.1	0.2	-1.0	0.8	1.1	0.06	1.1	0.1
				AVCMLSNTTAIAEAWAR	3	100.0%	1																									
				AVFVDLEPTVIDEVR	2	100.0%	3																									
				EDMAALEKDYEEVGVDSVEGEGEEEGEEY	2	100.0%	1																									
				SIQFVDWCPTGFK	2	100.0%	1																									
IPI00792679	FAM194A	isoform 2 of Protein FAM194A	98.1%	3.1	1	1	1	1	905,615	885,451	1,015,035	1,058,903	109,108	93,252	141,631	99,589	26.9	23.6	31.2	21.0	-1.0	0.9	1.1	0.6	1.2	0.3	1.1	0.5	1.2	0.2	1.0	0.8
				ESEQELEAPETFSEEYLWK	2	98.1%	1																									
IPI00792746	GRB2	19 kDa protein	100.0%	16.0	2	2	2	1	10,280,587	8,766,843	11,080,677	11,829,393	672,037	367,577	1,159,318	1,310,737	14.6	9.4	23.4	24.8	-1.2	0.08	1.1	0.6	1.2	0.3	1.3	0.1	1.3	0.08	1.1	0.7
				FGNDVQHFK	3	99.8%	1																									
				RGDFIHVMDNSDPNWWK	3	100.0%	1																									
IPI00792753	QARS	cDNA FLJ55601, highly similar to Glutaminyl-tRNA synthetase	100.0%	13.8	2	2	2	3	239,241	251,588	246,391	278,546	25,451	12,335	23,320	5,212	23.8	11.0	21.2	4.2	1.1	0.7	1.0	0.8	1.2	0.2	-1.0	0.8	1.1	0.08	1.1	0.2
IPI00924591	QARS	Uncharacterized protein	100.0%	21.4	2	2	2	3	239,241	251,588	246,391	278,546	25,451	12,335	23,320	5,212	23.8	11.0	21.2	4.2	1.1	0.7	1.0	0.8	1.2	0.2	-1.0	0.8	1.1	0.08	1.1	0.2
IPI00925012	QARS	Uncharacterized protein	100.0%	12.8	2	2	2	3	239,241	251,588	246,391	278,546	25,451	12,335	23,320	5,212	23.8	11.0	21.2	4.2	1.1	0.7	1.0	0.8	1.2	0.2	-1.0	0.8	1.1	0.08	1.1	0.2
				EAATQAQQTLGSTIDK	2	100.0%	1																									
				ECGVGVIVTPEQIEEAVEAAINR	3	100.0%	1																									
IPI00792875	SERPINB5	Uncharacterized protein	100.0%	21.7	2	2	2	1	4,904,083	4,760,080	5,240,640	5,493,363	407,491	339,164	443,992	361,034	18.6	15.9	18.9	14.7	-1.0	0.8	1.1	0.6	1.1	0.3	1.1	0.4	1.2	0.2	1.0	0.7
				DVPFGFQTVTSDVNK	2	99.6%	1																									
				SLNLSTEFISSTK	2	100.0%	1																									
IPI00792984	ARPP19	14 kDa protein	100.0%	26.7	2	2	2	1	2,837,059	2,674,309	2,680,759	3,190,831	311,744	141,993	301,121	277,528	24.6	11.9	25.1	19.5	-1.1	0.6	-1.1	0.7	1.1	0.4	1.0	1	1.2	0.1	1.2	0.2
				SEHNMLPWSLQPSIPNSLEEMEDK	3	90.4%	1																									
				YFDSGDYNMAK	2	100.0%	1																									
IPI00793137	-	Uncharacterized protein	100.0%	20.3	5	5	8	1	7,802,764	8,185,762	8,029,590	9,107,624	442,523	335,429	437,554	441,678	12.7	9.2	12.2	10.8	1.0	0.5	1.0	0.7	1.2	0.07	-1.0	0.8	1.1	0.1	1.1	0.1
				AIVAIENPADVSVISSR	2	100.0%	2																									
				FAAATGATPIAGR	2	100.0%	2																									
				KSDGIYIINLK	3	99.3%	1																									
				LLVVTDPR	2	99.9%	1																									
				YVDIAIPCNNK	2	100.0%	2																									
IPI00793141	MAPK3	Uncharacterized protein	99.5%	7.4	1	1	1	1	365,802	354,723	355,033	419,358	36,172	18,482	26,668	21,420	22.1	11.7	16.8	11.4	-1.0	0.8	-1.0	0.8	1.1	0.2	1.0	1	1.2	0.05	1.2	0.1
				YTQLQYIGEGAYGMVSSAYDHVR	3	99.3%	1																									
IPI00793199	ANXA4	annexin A4	100.0%	70.1	22	26	34	1	111,620,670	114,584,802	112,479,677	131,171,863	8,296,948	3,649,747	8,366,658	4,020,149	16.6	7.1	16.6	6.9	1.0	0.8	1.0	0.9	1.2	0.07	-1.0	0.8	1.1	0.02	1.2	0.08
				AASGFNAMEDAQTLR	2	100.0%	2																									
				AASGFNAMEDAQTLRK	2	100.0%	1																									
				AASGFNAMEDAQTLRK	3	100.0%	1																									
				AEIDMLDIR	2	100.0%	1																									
				DEGNYLDDALVR	2	100.0%	2																									
				DIEQSIK	1	95.0%	1																									
				FLTVLCSR	2	99.3%	1																									
				GAGTDEGCLIEILASR	2	100.0%	2																									
				GLGTDDNTLIR	2	100.0%	2																									
				GLGTDEDAIISVLAYR	2	100.0%	2																									
				GLGTDEDAIISVLAYR	3	90.7%	1																									
				ISQTYQQQYGR	2	100.0%	2																									
				NHLLHVFDEYK	3	98.4%	1																									
				NHLLHVFDEYKR	3	100.0%	1																									
				QDAQDLYEAGEK	2	100.0%	2																									
				QDAQDLYEAGEKK	3	97.7%	1																									
				SAYFAEK	2	90.3%	1																									
				SELSGNFEQVIVGMMTPTVLYDVQELRR	3	100.0%	1																									
				SETSGSFEDALLAIVK	2	100.0%	2																									
				SLEDDIRSDTSFMFQR	2	85.4%	1																									
				SLEDDIRSDTSFMFQR	3	100.0%	1																									
				VLLVLCGGDD	1	100.0%	1																									
				VLVSLSAGGR	2	100.0%	1																									
				VLVSLSAGGRDEGNYLDDALVR	2	99.9%	1																									
				VLVSLSAGGRDEGNYLDDALVR	3	100.0%	1																									
				WGTDEVK	2	82.3%	1																									
IPI00793205	SRSF9	cDNA FLJ56571, highly similar to Splicing factor, arginine/serine-rich 9	100.0%	8.8	1	1	1	1	3,147,135	3,526,950	3,295,905	3,792,010	389,709	169,384	201,473	392,577	27.7	10.7	13.7	23.2	1.1	0.4	1.0	0.7	1.2	0.3	-1.1	0.4	1.1	0.6	1.2	0.3
				IYVGNLPTDVR	2	99.7%	1																									
IPI00793211	-	41 kDa protein	100.0%	3.3	1	1	2	1	1,149,270	1,276,403	1,035,483	1,298,103	111,640	108,436	76,231	43,458	21.7	19.0	16.5	7.5	1.1	0.4	-1.1	0.4	1.1	0.3	-1.2	0.1	1.0	0.9	1.3	0.02
				LDYDEDASAMLK	2	100.0%	2																									
IPI00793232	PNPO	cDNA FLJ59109, highly similar to Pyridoxine-5'-phosphate oxidase	100.0%	18.7	2	2	2	1	5,124,955	4,913,528	4,840,677	5,648,445	293,639	256,347	290,038	249,911	12.8	11.7	13.4	9.9	-1.0	0.6	-1.1	0.5	1.1	0.2	-1.0	0.9	1.1	0.07	1.2	0.07
				GEEDWLYER	2	99.9%	1																									
				SSQIGAVVSHQSSVIPDREYLR	3	98.5%	1																									
IPI00793299	BAG6	large proline-rich protein BAG6 isoform c	99.3%	2.9	2	2	2	2	2,291,057	2,380,602	1,697,370	1,852,232	196,847	158,002	234,210	255,063	19.2	14.8	30.9	30.8	1.0	0.7	-1.3	0.09	-1.2	0.2	-1.4	0.04	-1.3	0.1	1.1	0.7
IPI00829720	BAG6	large proline-rich protein BAG6 isoform d	99.3%	2.4	2	2	2	2	2,291,057	2,380,602	1,697,370	1,852,232	196,847	158,002	234,210	255,063	19.2	14.8	30.9	30.8	1.0	0.7	-1.3	0.09	-1.2	0.2	-1.4	0.04	-1.3	0.1	1.1	0.7
				AGSSESIAAFIQR	2	94.7%	1																									
				LLGNTFVALSDLR	2	98.6%	1																									
IPI00793319	GSTP1	Uncharacterized protein	100.0%	62.6	9	10	20	1	50,389,930	51,545,310	46,207,320	56,305,615	5,214,434	2,204,316	3,449,760	2,073,451	23.1	9.6	16.7	8.2	1.0	0.8	-1.1	0.5	1.1	0.3	-1.1	0.2	1.1	0.2	1.2	0.04
				AFLASPEYVNLPINGNGK	2	100.0%	3																									
				AFLASPEYVNLPINGNGKQ	2	100.0%	3																									
				ASCLYGQLPK	2	100.0%	2																									
				DQQEAALVDMVNDGVEDLR	2	100.0%	2																									
				DQQEAALVDMVNDGVEDLR	3	100.0%	1																									
				EEVVTVETWQEGSLK	2	100.0%	1																									
				FQDGDLTLYQSNTILR	2	100.0%	3																									
				MLLADQGQSWK	2	100.0%	2																									
				MPPYTVVYFPVR	2	100.0%	2																									
				TLGLYGK	1	97.4%	1																									
IPI00793341	RPL4	11 kDa protein	100.0%	35.9	2	2	2	2	1,222,708	1,438,626	1,474,654	1,655,441	107,050	99,255	173,821	103,135	19.6	15.4	26.4	13.9	1.2	0.2	1.2	0.3	1.4	0.02	1.0	0.9	1.2	0.2	1.1	0.4
IPI00908376	RPL4	cDNA FLJ51018, highly similar to 60S ribosomal protein L4	100.0%	25.2	2	2	2	2	1,222,708	1,438,626	1,474,654	1,655,441	107,050	99,255	173,821	103,135	19.6	15.4	26.4	13.9	1.2	0.2	1.2	0.3	1.4	0.02	1.0	0.9	1.2	0.2	1.1	0.4
				APIRPDIVNFVHTNLR	3	100.0%	1																									
				QPYAVSELAGHQTSAESWGTGR	3	99.9%	1																									
IPI00793433	PDXK	Uncharacterized protein	94.2%	32.2	1	1	1	1	3,292,680	3,079,500	3,796,220	3,554,150	344,232	245,341	432,432	335,580	23.4	17.8	25.5	21.1	-1.1	0.6	1.2	0.4	1.1	0.6	1.2	0.2	1.2	0.3	-1.1	0.7
				AATFPLQVLGFEIDAVNSVQFSNHTETR	3	94.2%	1																									
IPI00793443	IPO5	isoform 1 of Importin-5	100.0%	14.0	10	12	13	4	12,659,945	13,311,812	13,196,029	15,031,138	1,216,571	619,015	991,552	284,943	21.5	10.4	16.8	4.2	1.1	0.6	1.0	0.7	1.2	0.1	-1.0	0.9	1.1	0.04	1.1	0.1
IPI00937471	IPO5	isoform 2 of Importin-5	100.0%	14.8	10	12	13	4	12,659,945	13,311,812	13,196,029	15,031,138	1,216,571	619,015	991,552	284,943	21.5	10.4	16.8	4.2	1.1	0.6	1.0	0.7	1.2	0.1	-1.0	0.9	1.1	0.04	1.1	0.1
IPI00939304	IPO5	isoform 3 of Importin-5	100.0%	13.7	10	12	13	4	12,659,945	13,311,812	13,196,029	15,031,138	1,216,571	619,015	991,552	284,943	21.5	10.4	16.8	4.2	1.1	0.6	1.0	0.7	1.2	0.1	-1.0	0.9	1.1	0.04	1.1	0.1
IPI01012384	IPO5	Protein	100.0%	13.9	10	12	13	4	12,659,945	13,311,812	13,196,029	15,031,138	1,216,571	619,015	991,552	284,943	21.5	10.4	16.8	4.2	1.1	0.6	1.0	0.7	1.2	0.1	-1.0	0.9	1.1	0.04	1.1	0.1
				AIGTEPDSDVLSEIMHSFAK	3	99.2%	1																									
				EFQQYLPVVMGPLMK	2	99.9%	1																									
				EHIMQMLQNPDWK	2	99.2%	1																									
				FLFDSVSSQNVGLR	2	99.5%	1																									
				FMQDASDVMQLLLK	2	100.0%	2																									
				LCGDTSLNNMQR	2	99.8%	1																									
				LVLEQVVTSIASVADTAEEK	2	99.9%	1																									
				LVLEQVVTSIASVADTAEEK	3	99.9%	1																									
				SLVEIADTVPK	2	100.0%	1																									
				VIAALLQTMEDQGNQR	2	99.9%	1																									
				VIAALLQTMEDQGNQR	3	99.9%	1																									
				VQAHAAAALINFTEDCPK	3	91.7%	1																									
IPI00793589	RPN1	cDNA FLJ51740, highly similar to Dolichyl-diphosphooligosaccharide--proteinglycos	100.0%	4.0	2	2	2	1	5,202,047	5,318,877	4,915,632	5,752,567	504,252	336,701	278,548	356,719	21.7	14.2	12.7	13.9	1.0	0.9	-1.1	0.6	1.1	0.4	-1.1	0.4	1.1	0.4	1.2	0.1
				ALTSEIALLQSR	2	100.0%	1																									
				SEDLLDYGPFR	2	97.6%	1																									
IPI00793767	ARHGDIA	22 kDa protein	100.0%	23.5	4	4	5	1	3,362,590	3,269,652	3,319,191	3,666,385	260,006	152,759	185,774	109,141	17.3	10.5	12.5	6.7	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.8	1.1	0.07	1.1	0.1
				AEEYEFLTPVEEAPK	2	100.0%	2																									

				EIVSGMK	1	98.7%	1																									
				SIQEIQELDKDDESLRK	3	100.0%	1																									
				YIQHTYR	2	99.4%	1																									
IPI00793812	LTA4H	cDNA FLJ51009, highly similar to Leukotriene A-4 hydrolase	100.0%	20.5	7	7	8	1	8,233,703	8,590,053	8,778,103	9,441,778	740,712	424,550	545,344	248,142	20.1	11.1	13.9	5.9	1.0	0.7	1.1	0.6	1.1	0.2	1.0	0.8	1.1	0.1	1.1	0.3
				AILPCQDTPSVK	2	99.9%	1																									
				EDDLNSFNATDLK	2	100.0%	1																									
				GSPMEISLPIALSK	2	99.9%	1																									
				HFNALGGWGELQNSVK	2	98.8%	1																									
				LVVDLTDIDPDVAYSSVPYEK	2	100.0%	1																									
				SAYEFSETESMLK	2	100.0%	2																									
				SSALQWLTPEQTSGK	2	99.9%	1																									
IPI00793841	BCAS1	53 kDa protein	100.0%	6.3	2	2	4	1	1,540,888	1,505,993	1,573,542	1,757,812	115,920	137,452	86,843	95,193	16.8	20.4	12.3	12.1	-1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.7	1.2	0.2	1.1	0.2
				MLDAQVQTDPVSIGPVGK	2	100.0%	2																									
				TGDQAADSSLGSVK	2	100.0%	2																									
IPI00793890	ERLIN2	15 kDa protein	100.0%	14.8	1	1	1	1	670,320	668,998	500,633	517,715	62,543	69,054	14,079	28,421	20.9	23.1	6.3	12.3	-1.0	1	-1.3	0.05	-1.3	0.06	-1.3	0.07	-1.3	0.08	1.0	0.6
				LALQQDLTSMAPGLVIQAVR	3	99.9%	1																									
IPI00794061	SNORD54;RPS20	7 kDa protein	100.0%	18.8	1	1	2	2	628,408	656,313	691,483	669,045	110,892	44,607	51,613	33,169	39.5	15.2	16.7	11.1	1.0	0.8	1.1	0.6	1.1	0.7	1.1	0.6	1.0	0.8	-1.0	0.7
IPI00795919	SNORD54;RPS20	Pseudogene candidate	100.0%	31.6	1	1	2	2	628,408	656,313	691,483	669,045	110,892	44,607	51,613	33,169	39.5	15.2	16.7	11.1	1.0	0.8	1.1	0.6	1.1	0.7	1.1	0.6	1.0	0.8	-1.0	0.7
				LIDLHSPSEIVK	2	100.0%	2																									
IPI00794087	RPL4	7 kDa protein	100.0%	24.6	1	1	1	2	612,318	733,563	699,222	825,223	59,859	60,211	60,029	66,872	21.9	18.4	19.2	18.1	1.2	0.2	1.1	0.3	1.3	0.05	-1.0	0.7	1.1	0.3	1.2	0.2
IPI00794736	RPL4	12 kDa protein	100.0%	14.8	1	1	1	2	612,318	733,563	699,222	825,223	59,859	60,211	60,029	66,872	21.9	18.4	19.2	18.1	1.2	0.2	1.1	0.3	1.3	0.05	-1.0	0.7	1.1	0.3	1.2	0.2
				APIRPDIVNFVHTNLR	3	100.0%	1																									
IPI00794332	BCAS1	Protein	100.0%	7.3	1	1	2	3	457,955	344,617	492,935	613,595	62,089	53,763	53,809	62,789	30.3	34.9	24.4	22.9	-1.3	0.2	1.1	0.7	1.3	0.1	1.4	0.09	1.8	0.01	1.2	0.2
IPI00807587	BCAS1	BCAS1 protein	100.0%	4.7	1	1	2	3	457,955	344,617	492,935	613,595	62,089	53,763	53,809	62,789	30.3	34.9	24.4	22.9	-1.3	0.2	1.1	0.7	1.3	0.1	1.4	0.09	1.8	0.01	1.2	0.2
IPI00908415	BCAS1	cDNA, FLJ78937, highly similar to Rattus norvegicus breast carcinoma amplified se	100.0%	7.2	1	1	2	3	457,955	344,617	492,935	613,595	62,089	53,763	53,809	62,789	30.3	34.9	24.4	22.9	-1.3	0.2	1.1	0.7	1.3	0.1	1.4	0.09	1.8	0.01	1.2	0.2
				MLDAQVQTDPVSIGPVGK	2	100.0%	2																									
IPI00794383	PSMD6	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 6, isoform CRA_d	100.0%	7.4	2	2	2	1	2,155,069	2,403,160	2,141,160	2,447,044	206,947	81,889	210,506	40,597	21.5	7.6	22.0	3.7	1.1	0.3	-1.0	1	1.1	0.2	-1.1	0.3	1.0	0.6	1.1	0.2
				IGLFYMDNDLITR	2	99.7%	1																									
				SLDWQIDVDLLNK	2	99.9%	1																									
IPI00794397	CHMP4A	charged multivesicular body protein 4a	97.7%	5.3	1	1	1	4	1,331,773	1,677,118	1,558,440	2,042,395	196,418	225,144	210,236	148,997	33.0	30.0	30.2	16.3	1.3	0.3	1.2	0.5	1.5	0.02	-1.1	0.7	1.2	0.2	1.3	0.1
IPI00975824	CHMP4A	Uncharacterized protein	97.7%	6.6	1	1	1	4	1,331,773	1,677,118	1,558,440	2,042,395	196,418	225,144	210,236	148,997	33.0	30.0	30.2	16.3	1.3	0.3	1.2	0.5	1.5	0.02	-1.1	0.7	1.2	0.2	1.3	0.1
IPI00978991	CHMP4A	Uncharacterized protein	97.7%	8.4	1	1	1	4	1,331,773	1,677,118	1,558,440	2,042,395	196,418	225,144	210,236	148,997	33.0	30.0	30.2	16.3	1.3	0.3	1.2	0.5	1.5	0.02	-1.1	0.7	1.2	0.2	1.3	0.1
IPI00983078	TM9SF1	cDNA FLJ61658, highly similar to Transmembrane 9 superfamily protein member 1	97.7%	1.7	1	1	1	4	1,331,773	1,677,118	1,558,440	2,042,395	196,418	225,144	210,236	148,997	33.0	30.0	30.2	16.3	1.3	0.3	1.2	0.5	1.5	0.02	-1.1	0.7	1.2	0.2	1.3	0.1
				EAIENATTNAEVLR	2	97.7%	1																									
IPI00794417	HSPH1	Heat shock 105kDa/110kDa protein 1	100.0%	13.1	1	1	1	1	413,620	393,340	438,345	409,647	22,728	24,764	43,860	25,251	12.3	14.1	22.4	13.8	-1.1	0.6	1.1	0.6	-1.0	0.9	1.1	0.4	1.0	0.7	-1.1	0.6
				SVNEVMEWMNNVMNAQAK	2	100.0%	1																									
IPI00794544	TRIM16L	cDNA FLJ57635, moderately similar to Tripartite motif-containing protein 16	91.6%	10.7	1	1	1	2	6,237,705	5,895,245	6,158,700	6,356,695	565,324	482,377	606,991	350,956	20.3	18.3	22.0	12.4	-1.1	0.7	-1.0	0.9	1.0	0.9	1.0	0.7	1.1	0.5	1.0	0.8
IPI00795649	TRIM16L	19 kDa protein	91.6%	6.4	1	1	1	2	6,237,705	5,895,245	6,158,700	6,356,695	565,324	482,377	606,991	350,956	20.3	18.3	22.0	12.4	-1.1	0.7	-1.0	0.9	1.0	0.9	1.0	0.7	1.1	0.5	1.0	0.8
				TSPAGSCTGGR	2	91.6%	1																									
IPI00794549	SHMT2	Serine hydroxymethyltransferase	100.0%	8.8	3	3	4	1	1,982,719	2,026,975	2,185,408	2,275,273	151,363	105,340	143,086	41,789	17.1	11.6	14.6	4.1	1.0	0.8	1.1	0.4	1.1	0.1	1.1	0.4	1.1	0.06	1.0	0.6
				AMADALLER	2	90.9%	1																									
				VLELVSITANK	2	100.0%	2																									
				VVDFIDEGVNIGLEVK	2	100.0%	1																									
IPI00794561	RAB2A	cDNA FLJ51998, highly similar to Ras-related protein Rab-2A	100.0%	30.3	4	4	4	2	3,689,555	3,422,066	3,533,812	3,599,100	195,830	177,128	151,155	89,809	11.9	11.6	9.6	5.6	-1.1	0.3	-1.0	0.5	-1.0	0.7	1.0	0.6	1.1	0.4	1.0	0.7
IPI01014788	RAB2A	RAB2	100.0%	34.3	4	4	4	2	3,689,555	3,422,066	3,533,812	3,599,100	195,830	177,128	151,155	89,809	11.9	11.6	9.6	5.6	-1.1	0.3	-1.0	0.5	-1.0	0.7	1.0	0.6	1.1	0.4	1.0	0.7
				DTFNHLTTWLEDAR	2	99.9%	1																									
				IQEGVFDINNEANGIK	2	99.2%	1																									
				LQIWDTAGQESFR	2	100.0%	1																									
				TASNVEEAFINTAK	2	99.7%	1																									
IPI00794572	SHMT2	Serine hydroxymethyltransferase	100.0%	23.1	7	7	10	1	4,439,057	4,581,117	4,796,634	5,103,912	378,670	206,954	351,679	142,970	19.1	10.1	16.4	6.3	1.0	0.8	1.1	0.5	1.1	0.2	1.0	0.6	1.1	0.07	1.1	0.4
				AALEALGSCLNNK	2	100.0%	2																									
				AMADALLER	2	90.9%	1																									
				CGQLVRMAIRAQHSNAAQTQTGEANR	3	93.4%	1																									
				GLELIASENFCSR	2	96.9%	1																									
				ISATSIFFESMPYK	2	100.0%	2																									
				VLELVSITANK	2	100.0%	2																									
				VVDFIDEGVNIGLEVK	2	100.0%	1																									
IPI00794573	GSR	20 kDa protein	100.0%	25.1	2	2	2	1	1,832,165	1,835,943	1,928,809	2,099,860	61,526	65,512	85,159	88,695	7.5	8.0	9.9	9.4	1.0	1	1.1	0.4	1.1	0.04	1.1	0.4	1.1	0.04	1.1	0.2
				LGGTCVNVGCVPK	2	100.0%	1																									
				QEPQPQGPPPAAGAVASYDYLVIGGGSGGLASAR	3	98.8%	1																									
IPI00794618	PTDSS1	PTDSS1 protein	95.2%	4.3	1	1	1	1	4,546,240	4,656,270	4,079,820	5,425,060	582,042	236,555	492,685	302,626	28.6	11.4	27.0	12.5	1.0	0.9	-1.1	0.6	1.2	0.2	-1.1	0.3	1.2	0.08	1.3	0.05
				MEYAVNCHVITWER	2	95.8%	1																									
IPI00794673	CCT8	cDNA FLJ59382, highly similar to T-complex protein 1 subunit theta	100.0%	27.8	11	11	16	1	20,942,503	20,633,530	20,322,860	22,652,119	1,272,034	766,784	1,128,114	406,450	13.6	8.3	12.4	4.0	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	0.8	1.1	0.05	1.1	0.1
				AVDDGVNTFK	2	100.0%	1																									
				DMLEAGILDTYLGK	2	100.0%	2																									
				FAEAFEAIPR	2	100.0%	1																									
				GEENLMDAQVK	2	100.0%	2																									
				GSTDNLMDDIER	2	100.0%	2																									
				IAVYSCPFDGMITETK	2	97.7%	1																									
				IGLSVSEVIEGYEIACR	2	100.0%	1																									
				LATNAAVTVLR	2	100.0%	2																									
				NVGLDIEAEVPAVK	2	100.0%	2																									
				TAEELMNFSK	2	100.0%	1																									
				YNIMLVR	2	99.0%	1																									
IPI00794745	RPL30	Uncharacterized protein	100.0%	21.4	1	1	2	1	4,857,333	4,786,000	5,340,133	5,341,833	476,064	355,726	334,225	275,289	21.9	16.6	14.0	11.5	-1.0	0.9	1.1	0.4	1.1	0.4	1.1	0.3	1.1	0.3	1.0	1
				LVILANNCPALR	2	100.0%	2																									
IPI00794755	SLC9A3R1	26 kDa protein	100.0%	25.1	3	3	4	1	4,209,130	3,909,338	3,592,400	4,407,135	399,486	169,574	344,846	211,822	21.2	9.7	21.5	10.8	-1.1	0.5	-1.2	0.3	1.0	0.7	-1.1	0.4	1.1	0.1	1.2	0.08
				AQEAPGQAEPPAAAEVQGAGNENEPR	3	100.0%	1																									
				LLVVDPETDEQLQK	2	100.0%	2																									
				LVEVNGENVEKETHQQVVSR	3	100.0%	1																									
IPI00794777	PRDX2	Uncharacterized protein	100.0%	40.4	5	6	11	1	14,307,727	15,327,343	15,669,127	17,078,250	1,030,698	230,117	750,316	512,508	16.1	3.4	10.7	6.7	1.1	0.4	1.1	0.3	1.2	0.04	1.0	0.7	1.1	0.01	1.1	0.2
				ATAVVDGAFK	2	100.0%	2																									
				ATAVVDGAFKEVK	2	99.6%	1																									
				EGGLGPLNIPLLADVTR	2	100.0%	2																									
				KEGGLGPLNIPLLADVTR	2	100.0%	2																									
				KEGGLGPLNIPLLADVTR	3	100.0%	2																									
				LGCEVLGVSVDSQFTHLAWINTPR	3	100.0%	2																									
IPI00794787	POF1B	isoform 3 of Protein POF1B	100.0%	6.9	2	2	2	1	4,639,830	5,058,300	5,132,243	5,764,377	124,358	304,846	294,122	230,443	6.0	13.5	12.8	8.9	1.1	0.2	1.1	0.2	1.2	0.003	1.0	0.9	1.1	0.1	1.1	0.1
				LTTYPQTTIR	2	94.6%	1																									
				YFGELLADLSR	2	99.5%	1																									
IPI00794839	PSMC5	25 kDa protein	100.0%	30.0	4	4	5	1	5,726,775	5,594,858	5,960,855	6,180,583	460,968	270,225	348,852	243,562	18.0	10.8	13.1	8.8	-1.0	0.8	1.0	0.7	1.1	0.4	1.1	0.4	1.1	0.1	1.0	0.6
				FVVDVDKNIDINDVTPNCR	3	99.9%	1																									
				IEELQLIVNDK	2	100.0%	2																									
				LLREELQLLQEQGSYVGEVVR	3	100.0%	1																									
				VPDSTYEMIGGLDK	2	100.0%	1																									
IPI00794843	SPTLC3	isoform 1 of Serine palmitoyltransferase 3	92.7%	4.0	1	1	1	1	2,383,240	3,125,420	3,049,360	3,164,230	331,201	450,879	275,562	201,196	31.1	32.3	20.2	14.2	1.3	0.2	1.3	0.2	1.3	0.08	-1.0	0.9	1.0	0.9	1.0	0.7
				GVTEFFGLDPHEVDVLMGTFTK	3	92.7%	1																									
IPI00794900	MTHFD1	cDNA FLJ56016, highly similar to C-1-tetrahydrofolate synthase, cytoplasmic	100.0%	17.1	14	14	16	1	55,140,515	59,057,235	55,777,681	68,478,600	5,278,113	2,754,195	4,192,605	2,649,267	21.4	10.4	16.8	8.7	1.1	0.5	1.0	0.9	1.2	0.05	-1.1	0.5	1.2	0.04	1.2	0.03
				AYIQENLELVEK	2	100.0%	1																									
				EIGLLSEEVELYGETK	2	99.9%	1																									
				GALALAQAVQR	2	100.0%	1																									
				IYGADDIELLPEAQHK	2	97.1%	1																									
				KVVGDVAYDEAK	2	89.3%	1																									
				LAILQVGNR	2	94.1%	1																									
				LDIDPETITWQR	2	100.0%	2																									
				QGFGNLPICMAK	2	100.0%	1																									
				QPSQGPTFGIK	2	87.3%	1																									
				TDPTTLTDEEINR	2	100.0%	2																									
				TDTESELDLISR	2	100.0%	1																									
				TPVPSDIDISR	2	99.0%	1																									
				WMIQYNNLNLK	2	94.1%	1																									
				YVVVTGITPTPLGEGK	2	100.0%	1																									
IPI00794911	COPG	Coatomer subunit gamma	100.0%	25.3	11	12	13	1	50,215,014	52,344,125	50,841,637	56,929,395	3,829,937	2,256,893	3,276,212	2,011,199	17.1	9.6	14.4	7.9	1.0	0.6	1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.1	0.2
				ALNAGYILNGLTVSIPGLER	2	100.0%	1																									
				ALQQYTLEPSEKPFDLK	3	100.0%	1																									
				FGAQNEEMLPSILVLLK	2	99.6%	1																									
				ILHLLGQEGPK	2	97.1%	1																									
				ILHLLGQEGPK	3	98.7%	1																									
				QEIFQEQLAAVPEFR	2	99.8%	1																									
				QISSFMSEISDEFK	2	100.0%	1																									
				SIATLAITTLLK	2	100.0%	2																									
				SLEELPVDIILASVG	2	99.7%	1																									
				SVPLATAPMAEQR	2	93.2%	1																									
				TLEEAVGNIVK	2	99.4%	1																									
				VVLEHEEVR	2	99.7%	1																									
IPI00795109	RAN;RANP1	cDNA, FLJ79092, highly similar to GTP-binding nuclear protein Ran	100.0%	28.9	3	3	5	1	2,941,870	3,260,410	3,158,820	3,719,316	280,469	122,892	177,773	146,933	21.3	8.4	12.6	8.8	1.1	0.3	1.1	0.5	1.3	0.04	-1.0	0.7	1.1	0.04	1.2	0.04
				NLQYYDISAK	2	100.0%	2																									
				SNYNFEKPFLWLAR	3	100.0%	1																									
				VCENIPIVLCGNK	2	100.0%	2																									
IPI00795163	CDV3	Uncharacterized protein	100.0%	21.3	1	1	1	1	613,974	635,473	602,916	731,319	66,697	32,028	34,750	29,874	24.3	11.3	12.9	9.1	1.0	0.8	-1.0	0.9	1.2	0.1	-1.1	0.5	1.2	0.06	1.2	0.02
				KTPQGPPEIYSDTQFPSLQSTAK	3	100.0%	1																									
IPI00795241	ENOPH1	isoform 2 of Enolase-phosphatase E1	100.0%	36.5	2	2	2	1	1,159,793	1,246,913	1,497,390	1,328,037	45,078	150,280	92,193	44,961	8.7	27.0	13.8	7.6	1.1	0.6	1.3	0.01	1.1	0.03	1.2	0.2	1.1	0.6	-1.1	0.1
				IADSIGCSTNNILFLTDVTR	2	99.6%	1																									
				LLFGHSTEGDILELVDGHFDTK	3	100.0%	1																									
IPI00795257	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	100.0%	55.0	17	25	42	1	261,926,804	282,264,691	261,629,588	319,209,180	########	########	########	########	21.4	8.6	19.5	9.6	1.1	0.5	-1.0	1	1.2	0.08	-1.1	0.4	1.1	0.07	1.2	0.06
				AENGKLVINGNPITIFQER	3	99.9%	1																									
				AENGKLVINGNPITIFQERDPSK	3	99.9%	1																									
				GALQNIIPASTGAAK	1	100.0%	1																									
				GALQNIIPASTGAAK	2	100.0%	2																									
				IISNASCTTNCLAPLAK	2	100.0%	2																									
				IISNASCTTNCLAPLAK	3	100.0%	1																									
				IKWGDAGAEYVVESTGVFTTMEK	3	99.9%	1																									
				LISWYDNEFGYSNR	2	100.0%	3																									
				LISWYDNEFGYSNR	3	100.0%	1																									
				LTGMAFR	2	100.0%	2																									
				LVINGNPITIFQER	2	100.0%	2																									
				LVINGNPITIFQER	3	100.0%	1																									

				LVINGNPITIFQERDPSK	2	100.0%	2																									
				LVINGNPITIFQERDPSK	3	100.0%	2																									
				RVIISAPSADAPMFVMGVNHEK	3	100.0%	1																									
				VIISAPSADAPMFVMGVNHEK	2	100.0%	2																									
				VIISAPSADAPMFVMGVNHEK	3	100.0%	2																									
				VIPELNGK	1	98.0%	1																									
				VPTANVSVVDLTCR	2	100.0%	4																									
				VVDLMAHMASK	3	99.2%	1																									
				VVDLMAHMASKE	2	100.0%	2																									
				VVDLMAHMASKE	3	99.8%	2																									
				WGDAGAEYVVESTGVFTTMEK	2	100.0%	2																									
				WGDAGAEYVVESTGVFTTMEK	3	100.0%	2																									
				YDNSLK	1	99.3%	1																									
IPI00795310	-	10 kDa protein	100.0%	38.4	2	2	2	1	1,002,426	1,057,358	709,084	1,043,892	130,024	78,898	68,319	66,211	29.0	16.7	21.5	14.2	1.1	0.7	-1.4	0.08	1.0	0.8	-1.5	0.01	-1.0	0.9	1.5	0.008
				DFNHINVELSLLGK	2	99.9%	1																									
				TILSNQTVDIPENVDITLK	2	100.0%	1																									
IPI00795334	CBR1	Uncharacterized protein	100.0%	19.8	3	3	5	3	3,873,312	3,911,959	3,967,107	4,256,718	101,183	210,968	292,469	145,612	5.8	12.1	16.5	7.7	1.0	0.9	1.0	0.8	1.1	0.06	1.0	0.9	1.1	0.2	1.1	0.4
IPI00909888	CBR1	cDNA FLJ60474, highly similar to Carbonyl reductase	100.0%	25.4	3	3	5	3	3,873,312	3,911,959	3,967,107	4,256,718	101,183	210,968	292,469	145,612	5.8	12.1	16.5	7.7	1.0	0.9	1.0	0.8	1.1	0.06	1.0	0.9	1.1	0.2	1.1	0.4
IPI00974490	CBR1	Uncharacterized protein	100.0%	24.7	3	3	5	3	3,873,312	3,911,959	3,967,107	4,256,718	101,183	210,968	292,469	145,612	5.8	12.1	16.5	7.7	1.0	0.9	1.0	0.8	1.1	0.06	1.0	0.9	1.1	0.2	1.1	0.4
				EYGGLDVLVNNAGIAFK	2	100.0%	2																									
				GQAAVQQLQAEGLSPR	2	100.0%	2																									
				LFSGDVVLTAR	2	99.8%	1																									
IPI00795545	EPS8L1	isoform 4 of Epidermal growth factor receptor kinase substrate 8-like protein 1	100.0%	6.6	2	2	2	1	403,825	440,982	424,740	500,799	33,336	32,897	34,046	35,092	18.5	16.7	17.9	15.7	1.1	0.5	1.1	0.7	1.2	0.08	-1.0	0.7	1.1	0.2	1.2	0.2
				APEPQLSPGSDASEVR	2	99.5%	1																									
				DLEPESEPQLESETAGK	2	100.0%	1																									
IPI00795816	SHMT2	serine hydroxymethyltransferase, mitochondrial isoform 2 precursor	100.0%	21.5	7	7	10	1	4,324,137	4,455,405	4,835,248	5,182,306	440,189	223,892	455,890	167,984	22.8	11.2	21.1	7.3	1.0	0.8	1.1	0.4	1.2	0.1	1.1	0.5	1.2	0.03	1.1	0.5
				AALEALGSCLNNK	2	100.0%	2																									
				AMADALLER	2	90.9%	1																									
				CGQLVRMAIRAQHSNAAQTQTGEANR	3	93.4%	1																									
				ISATSIFFESMPYK	2	100.0%	2																									
				VLELVSITANK	2	100.0%	2																									
				VVDFIDEGVNIGLEVK	2	100.0%	1																									
				YYGGAEVVDEIELLCQR	2	100.0%	1																									
IPI00795857	RPP14	Hydroxyacyl-thioester dehydratase type 2, mitochondrial	93.1%	5.4	1	1	1	1	16,063,650	14,612,930	13,398,600	15,312,200	982,901	1,175,191	1,686,711	1,407,939	13.7	18.0	28.2	20.6	-1.1	0.4	-1.2	0.2	-1.0	0.7	-1.1	0.6	1.0	0.7	1.1	0.4
				KTVMEGWVK	3	93.1%	1																									
IPI00795892	PFN2	Uncharacterized protein	100.0%	45.1	3	3	4	2	2,743,112	2,676,976	2,736,352	2,998,677	158,544	108,597	150,663	64,395	12.9	9.1	12.3	4.8	-1.0	0.7	-1.0	1	1.1	0.2	1.0	0.8	1.1	0.03	1.1	0.1
IPI00945855	PFN2	Uncharacterized protein	100.0%	45.1	3	3	4	2	2,743,112	2,676,976	2,736,352	2,998,677	158,544	108,597	150,663	64,395	12.9	9.1	12.3	4.8	-1.0	0.7	-1.0	1	1.1	0.2	1.0	0.8	1.1	0.03	1.1	0.1
				DSLYVDGDCTMDIR	2	97.4%	1																									
				EGFFTNGLTLGAK	2	95.2%	1																									
				SQGGEPTYNVAVGR	2	100.0%	2																									
IPI00795920	EEF1D	Uncharacterized protein	100.0%	11.3	2	2	4	1	765,074	698,088	684,621	796,442	66,553	46,235	60,252	60,545	19.5	14.8	19.7	17.0	-1.1	0.4	-1.1	0.4	1.0	0.7	-1.0	0.9	1.1	0.2	1.2	0.2
				FYEQMNGPVAGASR	2	100.0%	2																									
				SIQLDGLVWGASK	2	100.0%	2																									
IPI00796075	C1QBP	20 kDa protein	100.0%	27.0	3	3	4	1	4,730,613	5,142,352	4,680,013	5,330,582	465,670	199,211	431,369	212,200	22.0	8.7	20.6	8.9	1.1	0.4	-1.0	0.9	1.1	0.3	-1.1	0.4	1.0	0.5	1.1	0.2
				EVSFQSTGESEWK	2	99.5%	1																									
				MSGGWELELNGTEAK	2	100.0%	2																									
				VEEQEPELTSTPNFVVEVIK	3	85.5%	1																									
IPI00796114	C6orf103	cDNA FLJ11889 fis, clone HEMBA1007251, weakly similar to Homo sapiens F-box p	96.1%	1.5	1	1	1	2	2,331,570	2,549,815	2,565,225	2,705,450	219,991	206,142	187,233	51,648	21.1	18.1	16.3	4.3	1.1	0.5	1.1	0.4	1.2	0.2	1.0	1	1.1	0.5	1.1	0.5
IPI00964550	C6orf103	isoform 1 of Calpain-7-like protein	96.1%	0.7	1	1	1	2	2,331,570	2,549,815	2,565,225	2,705,450	219,991	206,142	187,233	51,648	21.1	18.1	16.3	4.3	1.1	0.5	1.1	0.4	1.2	0.2	1.0	1	1.1	0.5	1.1	0.5
				VQITKPPPNFK	2	93.1%	1																									
IPI00796161	EIF3E	20 kDa protein	100.0%	29.7	4	4	4	2	5,035,319	4,914,975	5,104,556	5,750,388	293,699	247,596	276,959	154,826	13.0	11.3	12.1	6.0	-1.0	0.8	1.0	0.9	1.1	0.06	1.0	0.6	1.2	0.02	1.1	0.08
IPI01015563	EIF3E	Protein	100.0%	29.8	4	4	4	2	5,035,319	4,914,975	5,104,556	5,750,388	293,699	247,596	276,959	154,826	13.0	11.3	12.1	6.0	-1.0	0.8	1.0	0.9	1.1	0.06	1.0	0.6	1.2	0.02	1.1	0.08
				HLVFPLLEFLSVK	2	99.7%	1																									
				LDLLSDTNMVDFAMDVYK	2	100.0%	1																									
				MFEDPETTR	2	93.2%	1																									
				QLQAETEPIVK	2	100.0%	1																									
IPI00796198	PSMB6	12 kDa protein	100.0%	18.4	2	2	3	1	6,603,983	6,867,840	6,321,403	7,291,613	290,994	303,258	421,793	311,715	9.9	9.9	14.9	9.6	1.0	0.5	-1.0	0.6	1.1	0.1	-1.1	0.3	1.1	0.4	1.2	0.1
				LAAIAESGVER	2	99.9%	2																									
				QVLLGDQIPK	2	98.7%	1																									
IPI00796237	DUSP3	DUSP3 protein	100.0%	18.8	2	2	3	2	1,782,450	1,723,328	1,746,603	2,068,668	116,268	73,516	125,360	85,921	14.6	9.5	16.1	9.3	-1.0	0.7	-1.0	0.8	1.2	0.08	1.0	0.9	1.2	0.02	1.2	0.07
IPI00980124	DUSP3	Conserved hypothetical protein	100.0%	19.9	2	2	3	2	1,782,450	1,723,328	1,746,603	2,068,668	116,268	73,516	125,360	85,921	14.6	9.5	16.1	9.3	-1.0	0.7	-1.0	0.8	1.2	0.08	1.0	0.9	1.2	0.02	1.2	0.07
				AADFIDQALAQK	2	99.9%	2																									
				ANDTQEFNLSAYFER	2	99.6%	1																									
IPI00796241	PROSC	14 kDa protein	100.0%	10.6	1	1	2	1	947,898	1,002,670	973,872	901,873	88,547	82,055	92,793	76,302	20.9	18.3	21.3	18.9	1.1	0.7	1.0	0.8	-1.1	0.7	-1.0	0.8	-1.1	0.4	-1.1	0.6
				TFGENYVQELLEK	2	100.0%	2																									
IPI00796284	EEF1D	cDNA FLJ57946, highly similar to Elongation factor 1-delta	100.0%	13.5	3	3	5	2	1,987,749	1,902,882	1,887,627	2,122,124	161,285	86,707	111,605	128,992	18.1	10.2	13.2	13.6	-1.0	0.7	-1.1	0.6	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.2
IPI01013278	EEF1D	elongation factor 1-delta isoform 5	100.0%	14.1	3	3	5	2	1,987,749	1,902,882	1,887,627	2,122,124	161,285	86,707	111,605	128,992	18.1	10.2	13.2	13.6	-1.0	0.7	-1.1	0.6	1.1	0.5	-1.0	0.9	1.1	0.2	1.1	0.2
				FYEQMNGPVAGASR	2	100.0%	2																									
				QENGASVILR	2	99.9%	1																									
				SIQLDGLVWGASK	2	100.0%	2																									
IPI00796450	LYST	isoform 1 of Lysosomal-trafficking regulator	97.6%	0.6	1	1	1	1	5,222,590	5,383,510	5,049,560	5,654,750	315,641	671,030	249,526	363,408	13.5	27.9	11.1	14.4	1.0	0.8	-1.0	0.7	1.1	0.4	-1.1	0.7	1.1	0.7	1.1	0.2
				VGSQEAFYLYACGPNHTSVMPCK	3	86.6%	1																									
IPI00796527	TPD52	Uncharacterized protein	100.0%	26.1	2	2	2	3	766,742	764,169	798,556	886,889	81,550	27,674	98,724	53,378	23.8	8.1	27.6	13.5	-1.0	1	1.0	0.8	1.2	0.3	1.0	0.8	1.2	0.08	1.1	0.5
IPI00976904	TPD52	Prostate leucine zipper isoform 5	100.0%	19.2	2	2	2	3	766,742	764,169	798,556	886,889	81,550	27,674	98,724	53,378	23.8	8.1	27.6	13.5	-1.0	1	1.0	0.8	1.2	0.3	1.0	0.8	1.2	0.08	1.1	0.5
IPI00982396	TPD52	Protein	100.0%	19.6	2	2	2	3	766,742	764,169	798,556	886,889	81,550	27,674	98,724	53,378	23.8	8.1	27.6	13.5	-1.0	1	1.0	0.8	1.2	0.3	1.0	0.8	1.2	0.08	1.1	0.5
				ELAKVEEEIQTLSQVLAAK	3	100.0%	1																									
				LGINSLQELK	2	100.0%	1																									
IPI00796630	C1QBP	16 kDa protein	100.0%	19.3	2	2	3	1	2,048,093	2,137,097	2,103,123	2,362,557	100,428	106,896	157,997	95,888	11.0	11.2	16.8	9.1	1.0	0.6	1.0	0.8	1.2	0.05	-1.0	0.9	1.1	0.2	1.1	0.2
				EVSFQSTGESEWK	2	99.5%	1																									
				MSGGWELELNGTEAK	2	100.0%	2																									
IPI00796705	LIMA1	cDNA FLJ55990, highly similar to LIM domain and actin-binding protein 1	100.0%	18.1	8	9	11	1	13,649,230	14,379,569	15,312,303	15,966,262	538,819	639,588	1,225,925	465,085	8.8	10.0	17.9	6.5	1.1	0.4	1.1	0.2	1.2	0.01	1.1	0.5	1.1	0.08	1.0	0.6
				IAWPPPTELGSSGSALEEGIK	2	99.9%	1																									
				ISANENSLAVR	2	100.0%	2																									
				NENEEILERPAQLANAR	3	100.0%	1																									
				QSSSTNYTNELK	2	99.9%	1																									
				SEVQQPVHPKPLSPDSR	3	87.4%	1																									
				SLNWSSFVDNTFAEEFTTQNQK	2	83.9%	1																									
				SLNWSSFVDNTFAEEFTTQNQK	3	100.0%	1																									
				SPPEALVQGR	2	99.9%	1																									
				SQDVELWEGEVVK	2	100.0%	2																									
IPI00796739	CRABP1	Uncharacterized protein	100.0%	31.6	2	2	2	1	7,493,488	7,450,697	7,328,142	8,679,200	601,344	376,087	371,336	627,630	17.9	11.3	11.3	16.2	-1.0	1	-1.0	0.8	1.2	0.2	-1.0	0.8	1.2	0.1	1.2	0.1
				IHCTQTLLEGDGPK	2	99.9%	1																									
				SLATWENENK	2	98.9%	1																									
IPI00796919	GLB1	Beta-galactosidase	96.5%	4.8	2	2	2	3	1,133,663	1,221,374	1,065,143	1,274,775	92,304	103,764	55,570	47,981	18.2	19.0	11.7	8.4	1.1	0.5	-1.1	0.5	1.1	0.2	-1.1	0.2	1.0	0.7	1.2	0.02
IPI00927191	GLB1	isoform 3 of Beta-galactosidase	96.5%	5.4	2	2	2	3	1,133,663	1,221,374	1,065,143	1,274,775	92,304	103,764	55,570	47,981	18.2	19.0	11.7	8.4	1.1	0.5	-1.1	0.5	1.1	0.2	-1.1	0.2	1.0	0.7	1.2	0.02
IPI01012577	GLB1	isoform 1 of Beta-galactosidase	96.5%	5.2	2	2	2	3	1,133,663	1,221,374	1,065,143	1,274,775	92,304	103,764	55,570	47,981	18.2	19.0	11.7	8.4	1.1	0.5	-1.1	0.5	1.1	0.2	-1.1	0.2	1.0	0.7	1.2	0.02
				AYVAVDGIPQGVLER	2	96.5%	1																									
				SSDPDYLAAVDKWLGVLLPK	3	91.5%	1																									
IPI00796925	-	15 kDa protein	93.8%	9.5	1	1	1	1	1,837,547	2,058,262	1,675,270	1,910,820	171,566	324,602	155,448	151,719	20.9	35.3	20.8	17.8	1.1	0.6	-1.1	0.5	1.0	0.8	-1.2	0.3	-1.1	0.7	1.1	0.3
				TPWTCVSVASVR	2	91.6%	1																									
IPI00797038	PCK2	isoform 1 of Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	100.0%	3.4	2	2	2	1	9,721,465	9,009,150	9,076,290	9,370,460	299,331	327,125	439,871	523,272	6.9	8.1	10.8	12.5	-1.1	0.1	-1.1	0.3	-1.0	0.6	1.0	0.9	1.0	0.6	1.0	0.7
				DFWEQEVR	2	82.7%	1																									
				GQLGNWMSPADFQR	2	98.2%	1																									
IPI00797126	NACA	nascent polypeptide-associated complex subunit alpha isoform a	100.0%	4.5	6	6	10	1	16,102,323	17,588,821	15,967,145	20,254,441	1,788,369	1,119,001	1,636,911	1,200,862	24.8	14.2	22.9	13.3	1.1	0.5	-1.0	1	1.3	0.09	-1.1	0.4	1.2	0.1	1.3	0.07
				DIELVMSQANVSR	2	99.6%	2																									
				GAPTPPAVTPPSPK	2	84.3%	1																									
				GPAIPSPKGDPTSPAVIPLSPKK	2	81.8%	1																									
				IEDLSQQAQLAAAEK	2	99.2%	2																									
				NNSNDIVNAIMELTM	2	100.0%	2																									
				SPASDTYIVFGEAK	2	100.0%	2																									
IPI00797148	HNRNPA1	isoform 2 of Heterogeneous nuclear ribonucleoprotein A1	100.0%	40.8	9	10	13	1	8,019,867	8,366,932	8,003,143	8,799,858	475,942	289,555	408,528	169,501	13.3	7.7	11.4	4.3	1.0	0.6	-1.0	1	1.1	0.2	-1.0	0.5	1.1	0.2	1.1	0.1
				EDSQRPGAHLTVK	2	90.2%	1																									
				GFGFVTYATVEEVDAAMNAR	3	100.0%	2																									
				KLFIGGLSFETTDESLR	2	100.0%	1																									
				KLFIGGLSFETTDESLR	3	99.5%	1																									
				LFIGGLSFETTDESLR	2	100.0%	3																									
				NQGGYGGSSSSSSYGSGR	2	100.0%	1																									
				SESPKEPEQLRK	3	99.9%	1																									
				SHFEQWGTLTDCVVMR	2	100.0%	1																									
				SSGPYGGGGQYFAK	2	100.0%	1																									
				WGTLTDCVVMR	2	99.9%	1																									
IPI00797323	TXNDC17	9 kDa protein	100.0%	17.5	1	1	1	1	878,660	966,205	803,810	1,042,590	61,045	65,911	69,368	34,955	15.5	15.3	19.3	7.5	1.1	0.4	-1.1	0.4	1.2	0.05	-1.2	0.1	1.1	0.3	1.3	0.02
				SWCPDCVQAEPVVR	2	98.7%	1																									
IPI00797373	DOCK8	isoform 1 of Dedicator of cytokinesis protein 8	94.9%	0.5	1	1	1	4	10,399,300	10,070,650	9,666,850	11,379,250	1,231,316	1,036,441	643,089	806,582	26.5	23.0	14.9	15.9	-1.0	0.8	-1.1	0.6	1.1	0.5	-1.0	0.7	1.1	0.3	1.2	0.1
IPI00856108	DOCK8	isoform 2 of Dedicator of cytokinesis protein 8	94.9%	0.5	1	1	1	4	10,399,300	10,070,650	9,666,850	11,379,250	1,231,316	1,036,441	643,089	806,582	26.5	23.0	14.9	15.9	-1.0	0.8	-1.1	0.6	1.1	0.5	-1.0	0.7	1.1	0.3	1.2	0.1
IPI00945728	DOCK8	8 kDa protein	94.9%	15.2	1	1	1	4	10,399,300	10,070,650	9,666,850	11,379,250	1,231,316	1,036,441	643,089	806,582	26.5	23.0	14.9	15.9	-1.0	0.8	-1.1	0.6	1.1	0.5	-1.0	0.7	1.1	0.3	1.2	0.1
IPI00977252	DOCK8	Uncharacterized protein	94.9%	20.0	1	1	1	4	10,399,300	10,070,650	9,666,850	11,379,250	1,231,316	1,036,441	643,089	806,582	26.5	23.0	14.9	15.9	-1.0	0.8	-1.1	0.6	1.1	0.5	-1.0	0.7	1.1	0.3	1.2	0.1
				MATLPSAERR	2	94.9%	1																									
IPI00797535	LYPLA1	10 kDa protein	100.0%	12.6	1	1	1	2	1,038,783	1,006,908	1,121,843	1,221,202	66,699	77,238	136,249	155,298	14.4	17.2	27.2	28.4	-1.0	0.8	1.1	0.6	1.2	0.3	1.1	0.5	1.2	0.3	1.1	0.6
IPI00909991	LYPLA1	cDNA FLJ52008, highly similar to Acyl-protein thioesterase 1	100.0%	5.6	1	1	1	2	1,038,783	1,006,908	1,121,843	1,221,202	66,699	77,238	136,249	155,298	14.4	17.2	27.2	28.4	-1.0	0.8	1.1	0.6	1.2	0.3	1.1	0.5	1.2	0.3	1.1	0.6
				TLVNPANVTFK	2	99.4%	1																									
IPI00797536	RPRD1B	Regulation of nuclear pre-mRNA domain containing 1B	100.0%	8.1	1	1	2	1	2,364,860	2,429,260	2,552,835	3,054,830	335,124	517,924	202,591	212,289	31.7	47.7	17.8	15.5	1.0	0.9	1.1	0.6	1.3	0.1	1.1	0.8	1.3	0.3	1.2	0.1
				ALQDLENAASGDATVR	2	100.0%	2																									
IPI00797560	ARHGDIA	cDNA FLJ50748, highly similar to Rho GDP-dissociation inhibitor 1	100.0%	13.5	2	2	2	2	1,399,210	1,399,466	1,499,764	1,624,376	135,915	68,162	94,320	69,062	21.7	10.9	14.1	9.5	1.0	1	1.1	0.6	1.2	0.2	1.1	0.4	1.2	0.05	1.1	0.3
IPI00797924	ARHGDIA	rho GDP-dissociation inhibitor 1 isoform b	100.0%	15.0	2	2	2	2	1,399,210	1,399,466	1,499,764	1,624,376	135,915	68,162	94,320	69,062	21.7	10.9	14.1	9.5	1.0	1	1.1	0.6	1.2	0.2	1.1	0.4	1.2	0.05	1.1	0.3
				SIQEIQELDKDDESLRK	3	100.0%	1																									
				YIQHTYR	2	99.4%	1																									
IPI00797679	ITPA	Inosine triphosphatase (Nucleoside triphosphate pyrophosphatase), isoform CRA_b	100.0%	9.2	1	1	1	1	294,171	290,419	296,963	406,595	31,672	22,147	40,254	45,789	24.1	17.1	30.3	25.2	-1.0	0.9	1.0	1	1.4	0.08	1.0	0.9	1.4	0.05	1.4	0.1
				ALLELQEYFGSLAA	2	99.9%	1																									
IPI00797743	FDFT1	21 kDa protein	100.0%	16.4	2	2	2	2	1,250,948	1,398,790	1,250,036	1,349,201	51,628	80,427	46,855	31,255	9.2	12.9	8.4	5.2	1.1	0.2	-1.0	1	1.1	0.1	-1.1	0.1	-1.0	0.6	1.1	0.1
IPI01015743	FDFT1	Uncharacterized protein	100.0%	19.3	2	2	2	2	1,250,948	1,398,790	1,250,036	1,349,201	51,628	80,427	46,855	31,255	9.2	12.9	8.4	5.2	1.1	0.2	-1.0	1	1.1	0.1	-1.1	0.1	-1.0	0.6	1.1	0.1
				ALDTLEDDMTISVEK	2	98.1%	1																									
				SFAAVIQALDGEMR	2	100.0%	1																									
IPI00797763	CGN	Cingulin	100.0%	8.8	1	1	1	2	449,290	399,728	392,665	434,215	42,811	35,375	29,340	40,408	21.3	19.8	16.7	20.8	-1.1	0.4	-1.1	0.3	-1.0	0.8	-1.0	0.9	1.1	0.5	1.1	0.4
IPI00852984	CGN	Cingulin	100.0%	5.2	1	1	1	2	449,290	399,728	392,665	434,215	42,811	35,375	29,340	40,408	21.3	19.8	16.7	20.8	-1.1	0.4	-1.1	0.3	-1.0	0.8	-1.0	0.9	1.1	0.5	1.1	0.4
				FITEPVSGAEMGTLR	2	100.0%	1																									
IPI00797822	PHB2	cDNA FLJ56579, highly similar to Prohibitin-2	100.0%	31.8	6	7	8	1	8,028,761	8,873,629	8,192,785	9,830,398	647,867	222,756	563,634	263,720	18.0	5.6	15.4	6.0	1.1	0.3	1.0	0.9	1.2	0.03	-1.1	0.3	1.1	0.02	1.2	0.03

				FNASQLITQR	2	99.9%	2																									
				IGGVQQDTILAEGLHFR	3	100.0%	1																									
				IPWFQYPIIYDIR	2	99.9%	1																									
				IYLTADNLVLNLQDESFTR	2	100.0%	1																									
				IYLTADNLVLNLQDESFTR	3	100.0%	1																									
				LGLDYEER	2	99.9%	1																									
				VLSRPNAQELPSMYQR	3	95.0%	1																									
IPI00797907	WDR61	cDNA FLJ61675, highly similar to WD repeat protein 61	100.0%	13.5	1	1	1	1	1,023,200	1,001,925	888,920	930,025	158,802	26,574	82,076	37,356	34.7	5.9	20.7	9.0	-1.0	0.9	-1.2	0.5	-1.1	0.6	-1.1	0.2	-1.1	0.2	1.0	0.7
				ENSETVVTGSLDDLVK	2	100.0%	1																									
IPI00797968	-	11 kDa protein	100.0%	50.0	3	3	3	1	8,643,010	9,833,740	10,102,915	10,185,095	756,623	759,127	1,369,768	719,307	19.6	17.3	30.3	15.8	1.1	0.3	1.2	0.4	1.2	0.2	1.0	0.9	1.0	0.7	1.0	1
				DNYVPEVSALDQEIIEVDPDTK	2	100.0%	1																									
				LLDFGSLSNLQVTQPTVGMNFK	3	100.0%	1																									
				RDNYVPEVSALDQEIIEVDPDTKEMLK	3	97.9%	1																									
IPI00798071	NAP1L4	Uncharacterized protein	100.0%	24.1	6	7	8	2	4,303,547	4,214,841	4,591,018	4,985,561	209,192	220,778	194,137	169,427	10.9	11.7	9.5	7.6	-1.0	0.8	1.1	0.3	1.2	0.04	1.1	0.2	1.2	0.02	1.1	0.2
IPI00941463	NAP1L4	Nucleosome assembly protein 1-like 4	100.0%	24.8	6	7	8	2	4,303,547	4,214,841	4,591,018	4,985,561	209,192	220,778	194,137	169,427	10.9	11.7	9.5	7.6	-1.0	0.8	1.1	0.3	1.2	0.04	1.1	0.2	1.2	0.02	1.1	0.2
				ASGDGESLDEDSEFTLASDFEIGHFFR	3	100.0%	1																									
				FYEEVHDLER	2	100.0%	1																									
				LDNVPHTPSSYIETLPK	3	100.0%	1																									
				LTDQVMQNPR	2	100.0%	1																									
				NVDMLSELVQEYDEPILK	2	100.0%	2																									
				NVDMLSELVQEYDEPILK	3	99.6%	1																									
				YAALYQPLFDK	2	99.7%	1																									
IPI00798089	RAB2A	Uncharacterized protein	100.0%	13.8	2	2	2	1	3,524,330	3,633,133	3,787,444	4,186,295	263,428	292,932	367,085	346,358	16.7	18.0	21.7	18.5	1.0	0.8	1.1	0.6	1.2	0.2	1.0	0.8	1.2	0.3	1.1	0.5
				DTFNHLTTWLEDAR	2	99.9%	1																									
				YIIIGDTGVGK	2	99.8%	1																									
IPI00798190	MSI2	11 kDa protein	100.0%	31.3	2	2	2	1	2,686,398	2,806,994	2,508,038	2,822,388	218,183	84,792	158,487	179,122	18.2	6.8	14.1	14.2	1.0	0.6	-1.1	0.5	1.1	0.6	-1.1	0.1	1.0	0.9	1.1	0.2
				GFGFVTFADPASVDK	2	99.1%	1																									
				MFIGGLSWQTSPDSLR	2	100.0%	1																									
IPI00798211	TBCB	Uncharacterized protein	100.0%	9.4	2	2	3	1	5,343,530	5,835,520	5,178,125	5,810,920	202,780	414,250	253,027	351,599	8.5	15.9	10.9	13.5	1.1	0.3	-1.0	0.6	1.1	0.3	-1.1	0.2	-1.0	1	1.1	0.2
				LGEYEDVSR	2	99.2%	1																									
				YTISQEAYDQR	2	100.0%	2																									
IPI00798278	CDV3	isoform 2 of Protein CDV3 homolog	100.0%	25.8	2	2	2	4	1,002,244	1,055,269	969,190	1,155,366	108,863	37,135	63,013	44,005	24.3	7.9	14.5	8.5	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00964446	CDV3	protein CDV3 homolog isoform c	100.0%	50.0	2	2	2	4	1,002,244	1,055,269	969,190	1,155,366	108,863	37,135	63,013	44,005	24.3	7.9	14.5	8.5	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00966255	CDV3	Uncharacterized protein	100.0%	50.9	2	2	2	4	1,002,244	1,055,269	969,190	1,155,366	108,863	37,135	63,013	44,005	24.3	7.9	14.5	8.5	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00966539	CDV3	Protein	100.0%	29.3	2	2	2	4	1,002,244	1,055,269	969,190	1,155,366	108,863	37,135	63,013	44,005	24.3	7.9	14.5	8.5	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
				KTPQGPPEIYSDTQFPSLQSTAK	3	100.0%	1																									
				TAPVQAPPAPVIVTETPEPAMTSGVYRPPGAR	3	98.7%	1																									
IPI00798302	EIF4B	cDNA FLJ59405, highly similar to Eukaryotic translation initiation factor 4B	100.0%	6.3	2	2	2	1	4,631,674	4,622,503	3,820,293	5,035,975	149,835	457,739	167,757	304,193	7.2	22.1	9.8	13.5	-1.0	1	-1.2	0.007	1.1	0.3	-1.2	0.2	1.1	0.5	1.3	0.008
				RGDDSFGDKYR	3	99.1%	1																									
				SPPYTAFLGNLPYDVTEESIKEFFR	3	100.0%	1																									
IPI00798401	-	cDNA FLJ50992, highly similar to Coronin-1C	99.9%	13.3	3	3	3	3	3,712,081	3,455,710	3,371,688	4,354,004	359,506	122,571	133,017	135,978	21.7	7.9	8.8	7.0	-1.1	0.5	-1.1	0.4	1.2	0.2	-1.0	0.7	1.3	0.001	1.3	0.0009
IPI00867509	CORO1C	Coronin-1C_i3 protein	99.9%	11.0	3	3	3	3	3,712,081	3,455,710	3,371,688	4,354,004	359,506	122,571	133,017	135,978	21.7	7.9	8.8	7.0	-1.1	0.5	-1.1	0.4	1.2	0.2	-1.0	0.7	1.3	0.001	1.3	0.0009
IPI00943173	CORO1C	Coronin-1C	99.9%	12.2	3	3	3	3	3,712,081	3,455,710	3,371,688	4,354,004	359,506	122,571	133,017	135,978	21.7	7.9	8.8	7.0	-1.1	0.5	-1.1	0.4	1.2	0.2	-1.0	0.7	1.3	0.001	1.3	0.0009
				AIFLADGNVFTTGFSR	2	93.7%	1																									
				KSDLFQDDLYPDTAGPEAALEAEEWFEGK	3	99.9%	1																									
				VTWDSSFCAVNPR	2	95.6%	1																									
IPI00807498	CCDC6	CCDC6 protein (Fragment)	98.2%	9.9	2	2	2	2	4,382,170	4,554,800	4,615,535	4,674,950	396,930	89,607	278,136	146,999	20.3	4.4	13.5	7.0	1.0	0.7	1.1	0.6	1.1	0.5	1.0	0.8	1.0	0.5	1.0	0.9
IPI00956015	CCDC6	Coiled-coil domain-containing protein 6	98.2%	5.6	2	2	2	2	4,382,170	4,554,800	4,615,535	4,674,950	396,930	89,607	278,136	146,999	20.3	4.4	13.5	7.0	1.0	0.7	1.1	0.6	1.1	0.5	1.0	0.8	1.0	0.5	1.0	0.9
				AEQEEEFISNTLFK	2	96.9%	1																									
				EKIDLENTLEQEQEALVNR	3	98.2%	1																									
IPI00807557	PA2G4	PA2G4 protein (Fragment)	100.0%	33.5	12	12	15	1	41,714,695	44,395,245	40,835,630	46,974,185	4,284,164	980,429	2,071,267	1,452,194	23.0	4.9	11.3	6.9	1.1	0.6	-1.0	0.9	1.1	0.3	-1.1	0.2	1.1	0.2	1.2	0.04
				AAHLCAEAALR	3	81.1%	1																									
				AFFSEVER	2	99.6%	1																									
				ALLQSSASR	2	100.0%	2																									
				EGEFVAQFK	2	98.4%	1																									
				FTVLLMPNGPMR	2	96.9%	1																									
				GDAMIMEETGK	2	100.0%	2																									
				HELLQPFNVLYEK	2	100.0%	1																									
				ITSGPFEPDLYK	2	100.0%	1																									
				LVKPGNQNTQVTEAWNK	3	100.0%	2																									
				MGVVECAK	2	98.2%	1																									
				SDQDYILK	2	98.1%	1																									
				SLVEASSSGVSVLSLCEK	2	99.3%	1																									
IPI00815732	PAICS	multifunctional protein ADE2 isoform 1	100.0%	11.1	4	4	4	1	9,156,718	8,722,488	8,843,091	9,608,648	573,505	398,970	843,971	386,568	14.0	10.2	21.3	9.0	-1.0	0.6	-1.0	0.8	1.0	0.5	1.0	0.9	1.1	0.1	1.1	0.4
				ACGNFGIPCELR	2	98.4%	1																									
				ASILNTWISLK	2	100.0%	1																									
				EIVLADVIDNDSWR	2	99.7%	1																									
				EVTPEGLQMVK	2	98.5%	1																									
IPI00815784	PPP2CA	Serine/threonine-protein phosphatase	100.0%	22.0	5	5	5	1	9,454,760	9,830,902	9,536,294	10,401,132	657,101	262,754	619,274	313,892	15.5	6.0	14.5	6.8	1.0	0.6	1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.1	0.2
				CGNQAAIMELDDTLK	2	99.9%	1																									
				ELDQWIEQLNECK	2	100.0%	1																									
				QITQVYGFYDECLR	2	100.0%	1																									
				SPDTNYLFMGDYVDR	2	100.0%	1																									
				YSFLQFDPAPR	2	100.0%	1																									
IPI00815843	RPL14	RPL14 protein (Fragment)	100.0%	18.6	2	2	2	2	8,526,757	8,662,990	8,802,257	9,091,900	401,840	249,819	392,968	378,146	10.5	6.5	10.0	9.3	1.0	0.8	1.0	0.6	1.1	0.3	1.0	0.8	1.0	0.4	1.0	0.6
IPI00925323	RPL14	60S ribosomal protein L14	100.0%	10.8	2	2	2	2	8,526,757	8,662,990	8,802,257	9,091,900	401,840	249,819	392,968	378,146	10.5	6.5	10.0	9.3	1.0	0.8	1.0	0.6	1.1	0.3	1.0	0.8	1.0	0.4	1.0	0.6
				ALVDGPCTQVR	2	99.8%	1																									
				LVAIVDVIDQNR	2	99.9%	1																									
IPI00816063	RPL12	isoform 2 of 60S ribosomal protein L12	100.0%	34.9	3	3	6	1	5,231,210	5,455,115	5,274,080	6,099,725	320,422	245,469	339,558	386,351	13.7	10.1	14.4	14.2	1.0	0.6	1.0	0.9	1.2	0.1	-1.0	0.7	1.1	0.2	1.2	0.1
				CTGGEVGATSALAPK	2	100.0%	2																									
				EILGTAQSVGCNVDGR	2	100.0%	2																									
				HSGNITFDEIVNIAR	2	100.0%	2																									
IPI00816128	MUC5AC;MUC5B	Gastric mucin (Fragment)	100.0%	15.0	12	12	20	1	31,777,490	32,478,292	31,353,078	36,862,370	3,033,306	1,096,247	2,569,183	1,343,892	21.3	7.6	18.3	8.2	1.0	0.8	-1.0	0.9	1.2	0.2	-1.0	0.7	1.1	0.04	1.2	0.09
				CGLTDSETCLK	2	100.0%	1																									
				DGVCTKPMTTCPK	2	100.0%	2																									
				FHPGDVIYHTTDGTGGCISAR	3	100.0%	2																									
				GQTCGLCGNFNSIQADDFR	2	100.0%	2																									
				QCSILHGPTFAACHAHVEPAR	3	100.0%	1																									
				SLSEGDITCSVGFIPVDGCICPK	2	100.0%	2																									
				SVVGDVLEFGNSWK	2	100.0%	2																									
				TQAACPNIR	2	99.9%	2																									
				TSIFINLSPEFK	2	100.0%	2																									
				VCGLCGNFDDIAVNDFATR	2	100.0%	2																									
				WSCQEVPCPGTCSVLGGAHFSTFDGK	3	99.9%	1																									
				YAQHWCSQLTDADGPFGR	3	100.0%	1																									
IPI00816513	MSH2	Uncharacterized protein	99.6%	8.3	1	1	1	4	78,945	70,325	65,425	70,946	8,436	4,637	4,051	1,237	23.9	14.7	13.9	3.9	-1.1	0.4	-1.2	0.2	-1.1	0.4	-1.1	0.4	1.0	0.9	1.1	0.3
IPI00940255	MSH2	Uncharacterized protein	99.6%	2.9	1	1	1	4	78,945	70,325	65,425	70,946	8,436	4,637	4,051	1,237	23.9	14.7	13.9	3.9	-1.1	0.4	-1.2	0.2	-1.1	0.4	-1.1	0.4	1.0	0.9	1.1	0.3
IPI00940797	MSH2	Uncharacterized protein	99.6%	2.6	1	1	1	4	78,945	70,325	65,425	70,946	8,436	4,637	4,051	1,237	23.9	14.7	13.9	3.9	-1.1	0.4	-1.2	0.2	-1.1	0.4	-1.1	0.4	1.0	0.9	1.1	0.3
IPI00942418	MSH2	46 kDa protein	99.6%	3.4	1	1	1	4	78,945	70,325	65,425	70,946	8,436	4,637	4,051	1,237	23.9	14.7	13.9	3.9	-1.1	0.4	-1.2	0.2	-1.1	0.4	-1.1	0.4	1.0	0.9	1.1	0.3
				LNLVEAFVEDAELR	2	99.6%	1																									
IPI00816829	TWF1	isoform 4 of Twinfilin-1	99.9%	5.2	1	1	1	1	840,167	879,450	915,370	863,343	85,746	35,525	14,920	25,069	22.8	9.0	3.6	6.5	1.0	0.7	1.1	0.4	1.0	0.8	1.0	0.4	-1.0	0.7	-1.1	0.1
				INEVQTDVGVDTK	2	100.0%	1																									
IPI00827967	C9orf86	isoform 2 of Putative GTP-binding protein Parf	100.0%	9.0	4	4	6	2	3,124,062	3,404,615	3,544,560	3,581,181	133,588	125,076	171,235	128,205	9.6	8.2	10.8	8.0	1.1	0.2	1.1	0.09	1.1	0.04	1.0	0.5	1.1	0.4	1.0	0.9
IPI00827972	C9orf86	isoform 1 of Putative GTP-binding protein Parf	100.0%	9.1	4	4	6	2	3,124,062	3,404,615	3,544,560	3,581,181	133,588	125,076	171,235	128,205	9.6	8.2	10.8	8.0	1.1	0.2	1.1	0.09	1.1	0.04	1.0	0.5	1.1	0.4	1.0	0.9
				FFNIPFLQLQR	2	100.0%	2																									
				NIPAGLQSMNQALQR	2	100.0%	2																									
				PFVEEYIPTQEIQVTSIHWSYK	3	99.8%	1																									
				TAADELEAFLGGGAPGGR	2	90.5%	1																									
IPI00828110	SF3B3	isoform 3 of Splicing factor 3B subunit 3	100.0%	17.8	5	5	6	1	13,622,695	13,399,655	12,714,065	14,246,250	934,578	371,711	591,269	504,355	15.3	6.2	10.4	7.9	-1.0	0.8	-1.1	0.4	1.0	0.6	-1.1	0.4	1.1	0.2	1.1	0.08
				AGNGQWASVIR	2	99.9%	1																									
				HIANYISGIQTIGHR	3	100.0%	1																									
				NENQLIIFADDTYPR	2	100.0%	1																									
				TPVEEVPAAIAPFQGR	2	99.8%	2																									
				VIVSDVQESFIWVR	2	100.0%	1																									
IPI00829824	PRKCSH	PRKCSH protein (Fragment)	100.0%	18.2	3	3	6	1	9,095,123	9,911,317	9,003,243	9,798,827	1,326,838	901,218	451,422	406,048	32.6	20.3	11.2	9.3	1.1	0.6	-1.0	1	1.1	0.6	-1.1	0.4	-1.0	0.9	1.1	0.2
				AQQEQELAADAFK	2	100.0%	2																									
				LWEEQLAAAK	2	100.0%	2																									
				SLEDQVEMLR	2	100.0%	2																									
IPI00830052	HSPA1L	64 kDa protein	100.0%	2.9	1	1	1	1	1,227,510	1,141,303	1,117,058	1,355,243	74,474	119,167	117,191	115,420	13.6	23.4	23.5	19.0	-1.1	0.6	-1.1	0.4	1.1	0.4	-1.0	0.9	1.2	0.2	1.2	0.2
				MDKAKIHDIVLVGGSTR	3	97.4%	1																									
IPI00843759	YTHDF1	isoform 1 of YTH domain family protein 1	97.7%	2.7	1	1	1	2	1,855,655	1,982,995	1,935,855	2,050,170	85,247	101,833	179,854	144,976	10.3	11.5	20.8	15.8	1.1	0.4	1.0	0.7	1.1	0.3	-1.0	0.8	1.0	0.7	1.1	0.6
IPI01012814	YTHDF1	55 kDa protein	97.7%	3.0	1	1	1	2	1,855,655	1,982,995	1,935,855	2,050,170	85,247	101,833	179,854	144,976	10.3	11.5	20.8	15.8	1.1	0.4	1.0	0.7	1.1	0.3	-1.0	0.8	1.0	0.7	1.1	0.6
				SGPVMGGGLPPPPIK	2	97.7%	1																									
IPI00843765	SPTAN1	isoform 3 of Spectrin alpha chain, brain	100.0%	55.1	113	130	161	2	189,544,623	194,974,937	188,203,485	218,811,898	########	6,097,452	########	5,432,489	18.4	7.0	14.7	5.6	1.0	0.8	-1.0	0.9	1.2	0.1	-1.0	0.6	1.1	0.02	1.2	0.05
IPI01009172	SPTAN1	282 kDa protein	100.0%	55.1	113	130	161	2	189,544,623	194,974,937	188,203,485	218,811,898	########	6,097,452	########	5,432,489	18.4	7.0	14.7	5.6	1.0	0.8	-1.0	0.9	1.2	0.1	-1.0	0.6	1.1	0.02	1.2	0.05
				ADVVESWIGEK	2	99.9%	1																									
				AGTFQAFEQFGQQLLAHGHYASPEIK	3	99.4%	1																									
				AINVQEEK	1	100.0%	1																									
				AKLDENSAFLQFNWK	3	99.5%	1																									
				ALINADELASDVAGAEALLDR	2	100.0%	2																									
				ALINADELASDVAGAEALLDR	3	100.0%	1																									
				ALSSEGKPYVTKEELYQNLTR	3	100.0%	1																									
				AQLADSFHLQQFFR	2	100.0%	1																									
				ASAFNSWFENAEEDLTDPVR	2	100.0%	2																									
				ASAFNSWFENAEEDLTDPVR	3	100.0%	1																									
				CTELNQAWSSLGK	2	99.9%	1																									
				DADETKEWIEEK	3	96.6%	1																									
				DAEELEKWIQEK	2	98.9%	1																									
				DCEQAENWMAAR	2	99.8%	1																									
				DLAALEDKVK	2	97.8%	1																									
				DLAALGDK	2	83.8%	1																									
				DLAALGDKVNSLGETAER	3	100.0%	1																									
				DLASVQALLR	2	100.0%	1																									
				DLIGVQNLLK	2	94.8%	1																									
				DLMSWINGIR	2	100.0%	2																									
				DLNSQADSLMTSSAFDTSQVK	2	100.0%	1																									
				DLNSQADSLMTSSAFDTSQVK	3	93.0%	1																									

				DLSSVQTLLTK	2	100.0%	2																									
				DLTGVQNLR	2	99.9%	1																									
				DLTNVQNLQK	2	100.0%	1																									
				DLTSWVTEMK	2	100.0%	1																									
				DMDDEESWIK	2	100.0%	2																									
				DSDELKSWVNEK	2	86.8%	1																									
				DTEQVDNWMSK	2	100.0%	1																									
				DVDEIEAWISEK	2	100.0%	2																									
				DVDETISWIK	2	100.0%	1																									
				DVEDEETWIR	2	100.0%	2																									
				DVTGAEALLER	2	99.9%	1																									
				EAALTSEEVGADLEQVEVLQK	3	100.0%	1																									
				EANELQQWINEK	2	100.0%	2																									
				EELITNWEQIR	2	99.8%	1																									
				EELYQNLTR	2	96.4%	1																									
				EKEPIVGSTDYGKDEDSAEALLK	3	99.9%	1																									
				ELPTAFDYVEFTR	2	100.0%	2																									
				ENLLEEQGSIALR	2	100.0%	2																									
				EQLMASDDFGRDLASVQALLR	3	100.0%	1																									
				FEEFQTDMAAHEER	2	86.2%	1																									
				FLADFR	2	99.3%	2																									
				FLADFRDLTSWVTEMK	3	88.0%	1																									
				FLSDFR	2	92.1%	2																									
				GKDLIGVQNLLK	2	99.2%	1																									
				GKDLIGVQNLLK	3	99.7%	1																									
				GLVSSDELAK	2	98.5%	1																									
				GLVSSDELAKDVTGAEALLER	2	100.0%	1																									
				GLVSSDELAKDVTGAEALLER	3	100.0%	1																									
				GNAMVEEGHFAAEDVK	2	100.0%	1																									
				GRELPTAFDYVEFTR	3	99.9%	1																									
				GVIDMGNSLIER	2	100.0%	2																									
				HALLEADVAAHQDR	3	100.0%	1																									
				HQAFEAELHANADR	3	99.9%	1																									
				HQALQAEIAGHEPR	3	100.0%	2																									
				HQLLEADISAHEDR	3	90.2%	1																									
				IAALQAFADQLIAAGHYAK	2	100.0%	2																									
				IAALQAFADQLIAAGHYAK	3	100.0%	2																									
				IDGITIQAR	2	99.2%	1																									
				ITALDEFATK	2	100.0%	1																									
				KASAFNSWFENAEEDLTDPVR	3	100.0%	1																									
				KFDDFQK	2	99.2%	1																									
				KGDILTLLNSTNK	2	100.0%	1																									
				KGDILTLLNSTNKDWWK	3	100.0%	1																									
				KIEDLGAAMEEALILDNK	2	100.0%	1																									
				KIEDLGAAMEEALILDNK	3	99.7%	1																									
				KVEDLFLTFAK	2	100.0%	2																									
				LAALADQWQFLVQK	2	100.0%	2																									
				LAQFVEHWK	2	100.0%	2																									
				LAQFVEHWK	3	98.7%	1																									
				LDENSAFLQFNWK	2	100.0%	2																									
				LDETGNLMISEGHFASETIR	3	99.9%	1																									
				LEESLEYQQFVANVEEEEAWINEK	2	100.0%	1																									
				LEESLEYQQFVANVEEEEAWINEK	3	100.0%	1																									
				LFGAAEVQR	2	100.0%	1																									
				LGDSHDLQR	2	100.0%	1																									
				LGESQTLQQFSR	2	100.0%	2																									
				LIQEQHPEEELIK	2	100.0%	1																									
				LIQNNHYAMEDVATR	3	100.0%	1																									
				LIQSHPESAEDLQEK	3	99.9%	1																									
				LKDLNSQADSLMTSSAFDTSQVK	3	100.0%	1																									
				LLEATELK	2	97.6%	1																									
				LLVGSEDYGR	2	100.0%	1																									
				LQQSHPLSATQIQVK	3	100.0%	1																									
				LQTASDESYKDPTNIQSK	3	100.0%	2																									
				LSDDNTIGKEEIQQR	2	100.0%	1																									
				LSDDNTIGKEEIQQR	3	100.0%	1																									
				LTVLSEER	2	99.9%	1																									
				MMLDQCLELQLFHR	3	98.1%	1																									
				MNEVISLWK	2	100.0%	1																									
				MQHNLEQQIQAR	2	100.0%	1																									
				MTLVASEDYGDTLAAIQGLLK	2	100.0%	2																									
				MTLVASEDYGDTLAAIQGLLK	3	100.0%	1																									
				MTLVASEDYGDTLAAIQGLLKK	3	99.2%	1																									
				NQALNTDNYGHDLASVQALQR	3	100.0%	2																									
				NTTGVTEEALK	2	99.4%	1																									
				NTTGVTEEALKEFSMMFK	2	100.0%	1																									
				NTTGVTEEALKEFSMMFK	3	100.0%	1																									
				NVEDIELWLYEVEGHLASDDYGK	3	100.0%	1																									
				QDEVNAAWQR	2	100.0%	1																									
				QEAFLLNEDLGDSLDSVEALLK	2	100.0%	2																									
				QEAFLLNEDLGDSLDSVEALLK	3	100.0%	1																									
				QEAFLLNEDLGDSLDSVEALLKK	3	100.0%	1																									
				QEFAQHANAFHQWIQETR	3	100.0%	1																									
				QETFDAGLQAFQQEGIANITALK	3	100.0%	1																									
				QETFDAGLQAFQQEGIANITALKDQLLAAK	3	100.0%	2																									
				QGFVPAAYVK	2	99.6%	1																									
				QQYEQCMDLQLFYR	2	97.2%	1																									
				REELITNWEQIR	2	100.0%	1																									
				REELITNWEQIR	3	98.9%	1																									
				RQDLEDSLQAQQYFADANEAESWMR	3	100.0%	1																									
				SADESGQALLAAGHYASDEVR	3	100.0%	1																									
				SADESGQALLAAGHYASDEVREK	3	99.9%	1																									
				SLQQLAEER	2	99.8%	1																									
				SQLLGSAHEVQR	2	100.0%	2																									
				SQLLGSAHEVQR	3	97.0%	1																									
				SSEEIESAFR	2	100.0%	1																									
				SSLSSAQADFNQLAELDR	2	100.0%	2																									
				SSLSSAQADFNQLAELDR	3	100.0%	1																									
				TATDEAYKDPSNLQGK	2	100.0%	1																									
				TATDEAYKDPSNLQGK	3	100.0%	1																									
				VASNPYTWFTMEALEETWR	2	100.0%	1																									
				VLETAEDIQER	2	100.0%	2																									
				VNDVCTNGQDLIKK	2	97.6%	1																									
				VNEVNQFAAK	2	100.0%	1																									
				VNSLGETAER	2	99.6%	1																									
				WSQLLANSAAR	2	100.0%	2																									
				YEALKEPMVAR	2	99.8%	1																									
				YTEHSTVGLAQQWDQLDQLGMR	3	100.0%	2																									
IPI00843904	AKR1C2	Aldo-keto reductase family 1, member C2 variant (Fragment)	100.0%	13.6	2	2	2	1	1,854,984	1,782,463	1,805,366	2,093,547	268,290	91,797	155,992	101,486	32.3	11.5	19.3	10.8	-1.0	0.8	-1.0	0.9	1.1	0.4	1.0	0.9	1.2	0.05	1.2	0.2
				ILFDTVDLCATWEAMEK	2	99.4%	1																									
				LNDGHFMPVLGFGTYAPAEVPK	3	100.0%	1																									
IPI00843910	FUCA1	Tissue alpha-L-fucosidase	99.8%	4.1	1	1	1	1	1,795,960	1,869,070	1,497,081	2,020,170	270,997	161,619	158,448	178,627	33.7	19.3	23.7	19.8	1.0	0.8	-1.2	0.4	1.1	0.5	-1.2	0.1	1.1	0.5	1.3	0.06
				DNYPPGFSYADFGPQFTAR	2	99.2%	1																									
IPI00843975	EZR	Ezrin	100.0%	39.6	21	25	35	1	80,330,811	81,724,607	84,321,615	92,538,001	5,432,045	2,670,910	4,658,853	1,813,525	15.1	7.3	12.4	4.4	1.0	0.8	1.0	0.6	1.2	0.09	1.0	0.6	1.1	0.01	1.1	0.2
				AKEAQDDLVK	2	99.9%	1																									
				APDFVFYAPR	2	100.0%	2																									
				DNAMLEYLK	2	98.7%	1																									
				EVWYFGLHYVDNK	2	100.0%	1																									
				FVIKPIDKK	2	87.7%	1																									
				FVIKPIDKK	3	97.1%	1																									
				FYPEDVAEELIQDITQK	2	100.0%	2																									
				FYPEDVAEELIQDITQK	3	100.0%	2																									
				GTDLWLGVDALGLNIYEK	2	99.8%	1																									
				GTDLWLGVDALGLNIYEKDDK	3	93.0%	1																									
				IALLEEAR	2	86.6%	1																									
				IAQDLEMYGINYFEIK	2	100.0%	2																									
				IGFPWSEIR	2	100.0%	2																									
				ILQLCMGNHELYMR	3	99.9%	1																									
				IQVWHAEHR	2	100.0%	1																									
				KENPLQFK	2	98.6%	1																									
				LFFLQVK	2	92.1%	1																									
				NISFNDKK	2	99.8%	2																									
				QLLTLSSELSQAR	2	100.0%	2																									
				RKEDEVEEWQHR	3	100.0%	1																									
				RKPDTIEVQQMK	2	100.0%	2																									
				RKPDTIEVQQMK	3	100.0%	1																									
				SGYLSSER	2	100.0%	2																									
				VTTMDAELEFAIQPNTTGK	2	100.0%	2																									
				VTTMDAELEFAIQPNTTGK	3	99.8%	1																									
IPI00844172	MYO6	Myosin	100.0%	8.4	9	9	9	2	11,540,397	12,006,665	12,086,527	13,463,200	1,079,434	458,918	567,663	585,440	20.9	8.6	10.5	9.7	1.0	0.7	1.0	0.7	1.2	0.2	1.0	0.9	1.1	0.09	1.1	0.1
IPI00941711	MYO6	Uncharacterized protein	100.0%	8.2	9	9	9	2	11,540,397	12,006,665	12,086,527	13,463,200	1,079,434	458,918	567,663	585,440	20.9	8.6	10.5	9.7	1.0	0.7	1.0	0.7	1.2	0.2	1.0	0.9	1.1	0.09	1.1	0.1
				FNEVVSVLK	2	95.8%	1																									
				IQAEVEAQLAR	2	100.0%	1																									
				IVEANPLLEAFGNAK	2	98.0%	1																									
				LHLSSPDNFR	2	98.7%	1																									
				NLEISIDTLMAK	2	96.7%	1																									
				SSEELLSALQK	2	99.9%	1																									

				STMMTQEQIQK	2	97.9%	1																									
				SVTDYAQQNPAAQIPAR	3	99.9%	1																									
				TQLNLLLDK	2	91.2%	1																									
IPI00844215	SPTAN1	isoform 1 of Spectrin alpha chain, brain	100.0%	56.6	117	136	167	1	206,383,713	212,414,786	205,094,280	239,678,881	########	6,787,503	########	6,524,386	19.4	7.2	15.2	6.1	1.0	0.8	-1.0	1	1.2	0.1	-1.0	0.6	1.1	0.02	1.2	0.05
				ADVVESWIGEK	2	99.9%	1																									
				AGTFQAFEQFGQQLLAHGHYASPEIK	3	99.4%	1																									
				AINVQEEK	1	100.0%	1																									
				AKLDENSAFLQFNWK	3	99.5%	1																									
				ALINADELASDVAGAEALLDR	2	100.0%	2																									
				ALINADELASDVAGAEALLDR	3	100.0%	1																									
				ALSSEGKPYVTKEELYQNLTR	3	100.0%	1																									
				AQLADSFHLQQFFR	2	100.0%	1																									
				ASAFNSWFENAEEDLTDPVR	2	100.0%	2																									
				ASAFNSWFENAEEDLTDPVR	3	100.0%	1																									
				CTELNQAWSSLGK	2	99.9%	1																									
				DADETKEWIEEK	3	96.6%	1																									
				DAEELEKWIQEK	2	98.9%	1																									
				DCEQAENWMAAR	2	99.8%	1																									
				DLAALEDKVK	2	97.8%	1																									
				DLAALGDK	2	83.8%	1																									
				DLAALGDKVNSLGETAER	3	100.0%	1																									
				DLASVQALLR	2	100.0%	1																									
				DLIGVQNLLK	2	94.8%	1																									
				DLMSWINGIR	2	100.0%	2																									
				DLNSQADSLMTSSAFDTSQVK	2	100.0%	1																									
				DLNSQADSLMTSSAFDTSQVK	3	93.0%	1																									
				DLSSVQTLLTK	2	100.0%	2																									
				DLTGVQNLR	2	99.9%	1																									
				DLTNVQNLQK	2	100.0%	1																									
				DLTSWVTEMK	2	100.0%	1																									
				DMDDEESWIK	2	100.0%	2																									
				DSDELKSWVNEK	2	86.8%	1																									
				DTEQVDNWMSK	2	100.0%	1																									
				DVDEIEAWISEK	2	100.0%	2																									
				DVDETISWIK	2	100.0%	1																									
				DVEDEETWIR	2	100.0%	2																									
				DVTGAEALLER	2	99.9%	1																									
				EAALTSEEVGADLEQVEVLQK	3	100.0%	1																									
				EANELQQWINEK	2	100.0%	2																									
				EELITNWEQIR	2	99.8%	1																									
				EELYQNLTR	2	96.4%	1																									
				EKEPIVGSTDYGKDEDSAEALLK	3	99.9%	1																									
				ELPTAFDYVEFTR	2	100.0%	2																									
				ENLLEEQGSIALR	2	100.0%	2																									
				EQLMASDDFGRDLASVQALLR	3	100.0%	1																									
				FEEFQTDMAAHEER	2	86.2%	1																									
				FLADFR	2	99.3%	2																									
				FLADFRDLTSWVTEMK	3	88.0%	1																									
				FLSDFR	2	92.1%	2																									
				GKDLIGVQNLLK	2	99.2%	1																									
				GKDLIGVQNLLK	3	99.7%	1																									
				GLVSSDELAK	2	98.5%	1																									
				GLVSSDELAKDVTGAEALLER	2	100.0%	1																									
				GLVSSDELAKDVTGAEALLER	3	100.0%	1																									
				GNAMVEEGHFAAEDVK	2	100.0%	1																									
				GRELPTAFDYVEFTR	3	99.9%	1																									
				GVIDMGNSLIER	2	100.0%	2																									
				HALLEADVAAHQDR	3	100.0%	1																									
				HQAFEAELHANADR	3	99.9%	1																									
				HQAFEAELSANQSR	2	100.0%	1																									
				HQAFEAEVQANSGAIVK	3	90.0%	1																									
				HQALQAEIAGHEPR	3	100.0%	2																									
				HQLLEADISAHEDR	3	90.2%	1																									
				IAALQAFADQLIAAGHYAK	2	100.0%	2																									
				IAALQAFADQLIAAGHYAK	3	100.0%	2																									
				IDGITIQAR	2	99.2%	1																									
				ITALDEFATK	2	100.0%	1																									
				KASAFNSWFENAEEDLTDPVR	2	97.1%	1																									
				KASAFNSWFENAEEDLTDPVR	3	100.0%	1																									
				KFDDFQK	2	99.2%	1																									
				KGDILTLLNSTNK	2	100.0%	1																									
				KGDILTLLNSTNKDWWK	3	100.0%	1																									
				KIEDLGAAMEEALILDNK	2	100.0%	1																									
				KIEDLGAAMEEALILDNK	3	99.7%	1																									
				KVEDLFLTFAK	2	100.0%	2																									
				LAALADQWQFLVQK	2	100.0%	2																									
				LAQFVEHWK	2	100.0%	2																									
				LAQFVEHWK	3	98.7%	1																									
				LDENSAFLQFNWK	2	100.0%	2																									
				LDETGNLMISEGHFASETIR	3	99.9%	1																									
				LEESLEYQQFVANVEEEEAWINEK	2	100.0%	1																									
				LEESLEYQQFVANVEEEEAWINEK	3	100.0%	1																									
				LFGAAEVQR	2	100.0%	1																									
				LGDSHDLQR	2	100.0%	1																									
				LGESQTLQQFSR	2	100.0%	2																									
				LIQEQHPEEELIK	2	100.0%	1																									
				LIQNNHYAMEDVATR	3	100.0%	1																									
				LIQSHPESAEDLQEK	3	99.9%	1																									
				LKDLNSQADSLMTSSAFDTSQVK	3	100.0%	1																									
				LLEATELK	2	97.6%	1																									
				LLVGSEDYGR	2	100.0%	1																									
				LQQSHPLSATQIQVK	3	100.0%	1																									
				LQTASDESYKDPTNIQSK	3	100.0%	2																									
				LSDDNTIGKEEIQQR	2	100.0%	1																									
				LSDDNTIGKEEIQQR	3	100.0%	1																									
				LTVLSEER	2	99.9%	1																									
				MKQVEELYHSLLELGEK	3	97.5%	1																									
				MMLDQCLELQLFHR	3	98.1%	1																									
				MNEVISLWK	2	100.0%	1																									
				MQHNLEQQIQAR	2	100.0%	1																									
				MTLVASEDYGDTLAAIQGLLK	2	100.0%	2																									
				MTLVASEDYGDTLAAIQGLLK	3	100.0%	1																									
				MTLVASEDYGDTLAAIQGLLKK	3	99.2%	1																									
				NQALNTDNYGHDLASVQALQR	3	100.0%	2																									
				NTTGVTEEALK	2	99.4%	1																									
				NTTGVTEEALKEFSMMFK	2	100.0%	1																									
				NTTGVTEEALKEFSMMFK	3	100.0%	1																									
				NVEDIELWLYEVEGHLASDDYGK	3	100.0%	1																									
				QDEVNAAWQR	2	100.0%	1																									
				QEAFLLNEDLGDSLDSVEALLK	2	100.0%	2																									
				QEAFLLNEDLGDSLDSVEALLK	3	100.0%	1																									
				QEAFLLNEDLGDSLDSVEALLKK	3	100.0%	1																									
				QEFAQHANAFHQWIQETR	3	100.0%	1																									
				QETFDAGLQAFQQEGIANITALK	3	100.0%	1																									
				QETFDAGLQAFQQEGIANITALKDQLLAAK	3	100.0%	2																									
				QGFVPAAYVK	2	99.6%	1																									
				QQYEQCMDLQLFYR	2	97.2%	1																									
				QVEELYHSLLELGEK	2	99.9%	1																									
				QVEELYHSLLELGEK	3	93.0%	1																									
				REELITNWEQIR	2	100.0%	1																									
				REELITNWEQIR	3	98.9%	1																									
				RQDLEDSLQAQQYFADANEAESWMR	3	100.0%	1																									
				SADESGQALLAAGHYASDEVR	3	100.0%	1																									
				SADESGQALLAAGHYASDEVREK	3	99.9%	1																									
				SLQQLAEER	2	99.8%	1																									
				SQLLGSAHEVQR	2	100.0%	2																									
				SQLLGSAHEVQR	3	97.0%	1																									
				SSEEIESAFR	2	100.0%	1																									
				SSLSSAQADFNQLAELDR	2	100.0%	2																									
				SSLSSAQADFNQLAELDR	3	100.0%	1																									
				TATDEAYKDPSNLQGK	2	100.0%	1																									
				TATDEAYKDPSNLQGK	3	100.0%	1																									
				VASNPYTWFTMEALEETWR	2	100.0%	1																									
				VLETAEDIQER	2	100.0%	2																									
				VNDVCTNGQDLIKK	2	97.6%	1																									
				VNEVNQFAAK	2	100.0%	1																									
				VNSLGETAER	2	99.6%	1																									
				WSQLLANSAAR	2	100.0%	2																									
				YEALKEPMVAR	2	99.8%	1																									
				YTEHSTVGLAQQWDQLDQLGMR	3	100.0%	2																									
IPI00844296	MUC17	Mucin-17	93.3%	6.7	1	1	1	1	5,342,390	5,212,050	4,238,820	6,014,060	144,032	282,755	253,750	266,040	6.0	12.1	13.4	9.9	-1.0	0.7	-1.3	0.005	1.1	0.06	-1.2	0.03	1.2	0.07	1.4	0.001
				NIIAVALLMLGK	2	93.3%	1																									
IPI00844363	TOMM34	cDNA FLJ26027 fis, clone PNC04328, highly similar to Homo sapiens translocase of	96.0%	8.2	1	1	1	1	1,330,645	1,326,045	1,577,200	1,322,525	97,404	112,015	131,205	18,718	16.4	18.9	18.6	3.2	-1.0	1	1.2	0.2	-1.0	0.9	1.2	0.2	-1.0	1	-1.2	0.1
				SSFADISNLLQIEPR	2	96.0%	1																									
IPI00844375	PSMB2	Proteasome beta 2 subunit variant (Fragment)	100.0%	6.0	1	1	1	1	1,285,717	1,189,317	1,062,703	1,343,387	170,112	18,108	150,139	125,343	29.6	3.4	31.6	20.9	-1.1	0.6	-1.2	0.4	1.0	0.8	-1.1	0.4	1.1	0.3	1.3	0.2
				NGYELSPTAAANFTR	2	100.0%	1																									
IPI00844412	-	Similar to Nuclear protein Hcc-1	100.0%	10.3	2	2	2	1	2,594,497	2,841,060	2,829,847	3,174,350	338,422	160,914	213,182	178,788	29.2	12.7	16.9	12.6	1.1	0.5	1.1	0.6	1.2	0.2	-1.0	1	1.1	0.2	1.1	0.3

				FGISSVPTK	2	99.0%	1																									
				FGLNVSSISR	2	99.8%	1																									
IPI00844508	CGN	cingulin	100.0%	9.7	9	9	10	1	79,935,345	80,402,393	75,248,320	91,047,270	6,359,330	3,373,055	4,918,811	2,821,010	17.8	9.4	14.6	6.9	1.0	0.9	-1.1	0.6	1.1	0.1	-1.1	0.4	1.1	0.04	1.2	0.02
				AVAGQGELTR	2	99.9%	2																									
				FDSQLGGQAR	2	87.0%	1																									
				FITEPVSGAEMGTLR	2	100.0%	1																									
				GPVDHGVQIR	3	88.9%	1																									
				ILGLEQQLK	2	90.0%	1																									
				LETELDEEKNTVELLTDR	3	92.6%	1																									
				LQGLEQEAENK	2	99.5%	1																									
				QALQQLQAQLEDYKEK	3	92.4%	1																									
				SHSQASLAGPGPVDPSNR	3	90.7%	1																									
IPI00844513	-	Similar to Chain , Heat-Shock Cognate 70kd Protein (44kd Atpase N-Terminal) (E.C	100.0%	21.7	5	5	9	1	24,717,440	25,121,075	23,060,945	27,496,560	1,817,922	1,119,183	1,562,397	1,209,281	16.5	10.0	15.2	9.8	1.0	0.9	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.05
				DAGTIAGLNVLR	2	100.0%	2																									
				FDDAVVQSDMK	2	100.0%	2																									
				HQVAMNPTNTVFDAK	2	94.8%	1																									
				MKEIAEAYLGK	2	100.0%	2																									
				RFDDAVVQSDMK	2	100.0%	2																									
IPI00844578	DHX9	ATP-dependent RNA helicase A	100.0%	23.0	24	26	29	1	242,381,541	244,953,505	231,890,312	271,031,444	########	########	########	########	17.1	11.3	12.6	9.7	1.0	0.9	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.2	1.2	0.06
				AAECNIVVTQPR	2	99.4%	1																									
				DINTDFLLVVLR	2	100.0%	1																									
				DVVQAYPEVR	2	95.4%	1																									
				GISHVIVDEIHER	3	100.0%	1																									
				GMTLVTPLQLLLFASK	2	100.0%	2																									
				HLEMNPHFGSHR	3	99.9%	1																									
				KVFDPVPVGVTK	2	99.9%	1																									
				LAAQSCALSLVR	2	100.0%	1																									
				LAQFEPSQR	2	87.1%	1																									
				LETHMTPEMFR	3	94.6%	1																									
				LQISHEAAACITGLR	2	99.4%	1																									
				MGGEEAEIR	2	95.3%	1																									
				NELMYQLEQDHDLQAILQER	3	99.4%	1																									
				PSAAGINLMIGSTR	2	99.8%	1																									
				QISRPSAAGINLMIGSTR	3	99.8%	1																									
				QPAIISQLDPVNER	2	100.0%	1																									
				RISAVSVAER	2	99.9%	1																									
				RLNMATLR	2	99.5%	1																									
				SSVNCPFSSQDMK	2	100.0%	2																									
				TPLHEIALSIK	2	98.9%	1																									
				TPLHEIALSIK	3	99.9%	1																									
				TTQVPQFILDDFIQNDR	2	100.0%	1																									
				TTQVPQFILDDFIQNDR	3	100.0%	1																									
				VQSDGQIVLVDDWIK	2	98.9%	1																									
				YPSPFFVFGEK	2	100.0%	2																									
				YQILPLHSQIPR	3	88.4%	1																									
IPI00844588	TSNAX	Translin-associated factor X, isoform CRA_a	99.8%	10.8	1	1	1	1	1,163,430	1,150,185	1,067,645	1,275,153	103,864	50,766	76,131	68,342	20.0	9.9	15.9	12.0	-1.0	0.9	-1.1	0.5	1.1	0.4	-1.1	0.4	1.1	0.2	1.2	0.08
				SLISMDEINK	2	99.7%	1																									
IPI00845324	GREB1L	isoform 3 of GREB1-like protein	91.6%	1.1	1	1	1	2	1,267,095	1,161,210	1,285,980	1,405,815	169,187	35,540	121,715	218,000	29.9	6.8	21.2	34.7	-1.1	0.6	1.0	0.9	1.1	0.6	1.1	0.4	1.2	0.3	1.1	0.6
IPI00885180	GREB1L	isoform 1 of GREB1-like protein	91.6%	1.0	1	1	1	2	1,267,095	1,161,210	1,285,980	1,405,815	169,187	35,540	121,715	218,000	29.9	6.8	21.2	34.7	-1.1	0.6	1.0	0.9	1.1	0.6	1.1	0.4	1.2	0.3	1.1	0.6
				EVIRGPTVALDLSGKEQER	2	87.9%	1																									
IPI00845339	HSPA1A;HSPA1B	cDNA FLJ54370, highly similar to Heat shock 70 kDa protein 1	100.0%	47.1	25	27	33	1	83,551,125	87,286,386	84,126,962	97,865,537	7,075,511	2,995,818	6,202,967	3,392,398	18.9	7.7	16.5	7.8	1.0	0.6	1.0	1	1.2	0.1	-1.0	0.7	1.1	0.05	1.2	0.09
				AFYPEEISSMVLTK	2	100.0%	2																									
				ARFEELCSDLFR	2	96.6%	1																									
				ATAGDTHLGGEDFDNR	2	100.0%	2																									
				ATAGDTHLGGEDFDNR	3	99.9%	1																									
				CQEVISWLDANTLAEKDEFEHK	3	99.9%	1																									
				DAGVIAGLNVLR	2	100.0%	1																									
				DNNLLGR	2	96.6%	1																									
				ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK	3	99.9%	1																									
				FEELCSDLFR	2	100.0%	1																									
				FELSGIPPAPR	2	98.9%	1																									
				FGDPVVQSDMK	2	99.9%	1																									
				GGSGSGPTIEEVD	1	88.5%	1																									
				HWPFQVINDGDKPK	3	100.0%	2																									
				ITITNDKGR	2	99.5%	1																									
				KFGDPVVQSDMK	2	100.0%	2																									
				LLQDFFNGR	2	95.2%	1																									
				LVNHFVEEFK	2	100.0%	2																									
				LVNHFVEEFK	3	99.9%	1																									
				LVNHFVEEFKR	3	100.0%	1																									
				MKEIAEAYLGYPVTNAVITVPAYFNDSQR	3	100.0%	1																									
				NALESYAFNMK	2	100.0%	1																									
				NAVITVPAYFNDSQR	2	99.9%	1																									
				NQVALNPQNTVFDAK	2	100.0%	2																									
				SAVEDEGLK	2	95.9%	1																									
				SINPDEAVAYGAAVQAAILMGDK	2	100.0%	1																									
				TTPSYVAFTDTER	2	100.0%	1																									
				YKAEDEVQR	2	99.9%	1																									
IPI00845444	MAT2B	isoform 5 of Methionine adenosyltransferase 2 subunit beta	100.0%	14.5	1	1	1	3	658,213	683,093	724,467	750,533	83,552	30,755	79,058	34,717	28.4	10.1	24.4	10.3	1.0	0.8	1.1	0.6	1.1	0.3	1.1	0.6	1.1	0.2	1.0	0.8
IPI00974257	MAT2B	Uncharacterized protein	100.0%	10.3	1	1	1	3	658,213	683,093	724,467	750,533	83,552	30,755	79,058	34,717	28.4	10.1	24.4	10.3	1.0	0.8	1.1	0.6	1.1	0.3	1.1	0.6	1.1	0.2	1.0	0.8
IPI00981635	MAT2B	Uncharacterized protein	100.0%	14.6	1	1	1	3	658,213	683,093	724,467	750,533	83,552	30,755	79,058	34,717	28.4	10.1	24.4	10.3	1.0	0.8	1.1	0.6	1.1	0.3	1.1	0.6	1.1	0.2	1.0	0.8
				VLVTGATGLLGR	2	99.9%	1																									
IPI00845461	ATL3	Uncharacterized protein	92.7%	3.7	1	1	1	2	6,257,850	6,813,300	6,515,425	6,872,175	529,651	248,935	674,806	246,574	18.9	8.2	23.2	8.0	1.1	0.4	1.0	0.8	1.1	0.3	-1.0	0.7	1.0	0.9	1.1	0.6
IPI01012574	ATL3	59 kDa protein	92.7%	4.0	1	1	1	2	6,257,850	6,813,300	6,515,425	6,872,175	529,651	248,935	674,806	246,574	18.9	8.2	23.2	8.0	1.1	0.4	1.0	0.8	1.1	0.3	-1.0	0.7	1.0	0.9	1.1	0.6
				ESGHSNWLGDPEEPLTGFSWR	3	92.7%	1																									
IPI00845521	KIAA1217	isoform 3 of Sickle tail protein homolog	100.0%	2.4	2	2	2	1	406,079	421,842	415,553	481,029	28,073	33,800	13,989	26,320	15.5	17.9	7.5	12.2	1.0	0.7	1.0	0.8	1.2	0.09	-1.0	0.9	1.1	0.2	1.2	0.06
				GDAPVDKVELSEDSPNSEQDLEK	3	99.5%	1																									
				SMVVPGNATIPR	2	100.0%	1																									
IPI00847255	EML6	isoform 2 of Echinoderm microtubule-associated protein-like 6	97.9%	1.1	1	1	1	2	1,571,365	1,392,455	1,474,295	1,822,805	187,292	137,369	72,024	196,681	26.7	22.1	10.9	24.1	-1.1	0.5	-1.1	0.6	1.2	0.4	1.1	0.6	1.3	0.1	1.2	0.2
IPI00895879	EML6	isoform 1 of Echinoderm microtubule-associated protein-like 6	97.9%	1.0	1	1	1	2	1,571,365	1,392,455	1,474,295	1,822,805	187,292	137,369	72,024	196,681	26.7	22.1	10.9	24.1	-1.1	0.5	-1.1	0.6	1.2	0.4	1.1	0.6	1.3	0.1	1.2	0.2
				YLAVASHDNFVDIYNVLTSK	3	97.9%	1																									
IPI00847300	-	Similar to Voltage-dependent anion-selective channel protein 1	100.0%	18.3	3	3	4	1	4,706,027	5,011,963	4,537,477	5,137,333	474,226	194,782	298,098	126,902	22.5	8.7	14.7	5.5	1.1	0.6	-1.0	0.8	1.1	0.4	-1.1	0.2	1.0	0.6	1.1	0.1
				TDEFQLHTNVNDGTEFGGSIYQK	3	100.0%	2																									
				WTEYGLTFTEK	2	99.9%	1																									
				YQIDPDACFSAK	2	98.9%	1																									
IPI00847335	-	FLJ45422 protein	99.5%	8.4	1	1	1	1	6,608,220	6,555,700	6,565,960	7,455,040	769,162	290,140	510,098	720,718	26.0	9.9	17.4	21.6	-1.0	1	-1.0	1	1.1	0.4	1.0	1	1.1	0.3	1.1	0.3
				FIAVGYVDDTEFVR	2	99.5%	1																									
IPI00847504	PLCL2	isoform 1 of Inactive phospholipase C-like protein 2	99.8%	5.3	2	2	2	1	2,207,461	1,989,720	2,447,833	2,320,979	269,315	359,902	429,882	245,119	27.3	40.5	39.3	23.6	-1.1	0.6	1.1	0.6	1.1	0.8	1.2	0.4	1.2	0.5	-1.1	0.8
				GWAAVGGALPTSPGPSLGAKGALKAGVGEDGVGGGF	3	95.2%	1																									
				LSSNCSGVEGDVTDEDEGAEMSQR	3	96.7%	1																									
IPI00847543	TRANK1	TPR and ankyrin repeat-containing protein 1	97.3%	0.6	1	1	1	1	457,753	429,220	319,994	464,201	75,326	25,734	25,475	36,021	36.8	13.4	17.8	17.4	-1.1	0.7	-1.4	0.1	1.0	0.9	-1.3	0.02	1.1	0.5	1.5	0.01
				DLAVLLCNKSNAFFSLGK	3	97.3%	1																									
IPI00847558	-	Similar to Non-POU domain-containing octamer-binding protein	100.0%	9.1	3	3	4	1	2,451,733	2,299,390	2,084,619	2,632,651	198,908	146,807	74,265	71,277	18.1	14.3	8.0	6.1	-1.1	0.6	-1.2	0.1	1.1	0.4	-1.1	0.2	1.1	0.08	1.3	0.0007
				FAQPGSFEYEYAMR	2	100.0%	2																									
				RMEELHNQEVQK	3	100.0%	1																									
				TLAEIAK	1	98.8%	1																									
IPI00847646	TNKS1BP1	isoform 2 of 182 kDa tankyrase-1-binding protein	100.0%	9.0	5	5	5	1	7,809,910	8,605,923	8,202,658	9,972,053	739,244	411,135	800,005	403,149	21.2	10.7	21.8	9.0	1.1	0.4	1.1	0.7	1.3	0.03	-1.0	0.7	1.2	0.05	1.2	0.08
				ESAVGQMGWSGGLSLR	2	100.0%	1																									
				GWVGEFSLSVGPQR	2	93.9%	1																									
				SKDLAEVGEGGGHSQAR	3	100.0%	1																									
				SQEADVQDWEFR	2	99.9%	1																									
				SYQFGIIGNDR	2	97.8%	1																									
IPI00847766	RPSAP58	Similar to Potential laminin-binding protein	100.0%	32.9	7	8	12	1	10,658,005	11,279,683	11,156,379	12,449,970	734,934	327,546	701,200	535,855	15.4	6.5	14.1	9.6	1.1	0.5	1.0	0.6	1.2	0.08	-1.0	0.9	1.1	0.1	1.1	0.2
				AIVAIENPADVSVISSR	2	100.0%	2																									
				FAAATGATPIAGR	2	100.0%	2																									
				FLAAGTHLGGTNLDFQMEQYIYK	3	100.0%	1																									
				GAHSVGLMWWMLAR	2	99.9%	1																									
				KSDGIYIINLK	2	99.9%	2																									
				KSDGIYIINLK	3	99.3%	1																									
				LLVVTDPR	2	99.9%	1																									
				YVDIAIPCNNK	2	100.0%	2																									
IPI00847789	HCFC1	isoform 3 of Host cell factor 1	99.6%	3.7	1	1	1	1	428,025	414,037	478,435	469,027	40,775	55,073	33,945	42,017	21.3	29.7	15.9	20.0	-1.0	0.8	1.1	0.4	1.1	0.5	1.2	0.3	1.1	0.5	-1.0	0.9
				MYVFGGWVPLVMDDVK	2	99.6%	1																									
IPI00848097	CLEC18C	Putative uncharacterized protein	97.1%	5.6	1	1	1	1	2,447,720	3,036,570	2,483,200	3,416,530	475,641	480,987	542,303	457,350	43.5	35.4	48.8	29.9	1.2	0.4	1.0	1	1.4	0.2	-1.2	0.5	1.1	0.6	1.4	0.2
				KGAWCSLCTASVSCCFK	2	97.1%	1																									
IPI00848226	GNB2L1	Guanine nucleotide-binding protein subunit beta-2-like 1	100.0%	32.8	7	8	9	1	21,279,065	22,232,531	21,235,184	25,094,286	1,792,364	405,361	1,211,401	522,216	18.8	4.1	12.8	4.7	1.0	0.6	-1.0	1	1.2	0.1	-1.0	0.5	1.1	0.003	1.2	0.02
				DGQAMLWDLNEGK	2	100.0%	2																									
				DVLSVAFSSDNR	2	99.6%	1																									
				FSPNSSNPIIVSCGWDK	2	100.0%	1																									
				GHNGWVTQIATTPQFPDMILSASR	3	100.0%	1																									
				IIVDELKQEVISTSSK	2	100.0%	1																									
				IIVDELKQEVISTSSK	3	99.9%	1																									
				LTRDETNYGIPQR	3	87.6%	1																									
				VWQVTIGTR	2	100.0%	1																									
IPI00848320	ATP6V1B2	ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain containi	100.0%	16.5	4	4	4	1	1,845,008	2,013,284	2,324,829	2,266,666	188,542	87,484	257,413	145,193	22.9	9.7	24.8	14.3	1.1	0.4	1.3	0.2	1.2	0.1	1.2	0.3	1.1	0.2	-1.0	0.8
				AVVGEEALTSDDLLYLEFLQK	2	98.6%	1																									
				IYPEEMIQTGISAIDGMNSIAR	3	99.9%	1																									
				TPVSEDMLGR	2	98.5%	1																									
				TVFETLDIGWQLLR	2	99.8%	1																									
IPI00852591	SF1	splicing factor 1 isoform 5	100.0%	8.2	3	3	3	1	1,300,879	1,239,041	1,250,319	1,440,364	97,334	55,131	105,087	74,978	16.7	10.0	18.8	11.6	-1.0	0.6	-1.0	0.7	1.1	0.3	1.0	0.9	1.2	0.06	1.2	0.2
				AYIVQLQIEDLTR	2	99.9%	1																									
				TVIPGMPTVIPPGLTR	2	93.5%	1																									
				VMIPQDEYPEINFVGLLIGPR	3	100.0%	1																									
IPI00852597	CTSD	Uncharacterized protein	100.0%	32.1	6	7	11	1	15,804,705	16,364,109	15,920,360	18,005,707	1,286,363	812,834	832,510	550,759	18.2	11.1	11.7	6.8	1.0	0.7	1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.1	1.1	0.07
				AYWQVHLDQVEVASGLTLCK	3	98.7%	1																									
				DPDAQPGGELMLGGTDSK	2	100.0%	2																									
				EGCEAIVDTGTSLMVGPVDEVR	2	100.0%	1																									

				FDGILGMAYPR	2	100.0%	2																									
				ISVNNVLPVFDNLMQQK	2	100.0%	2																									
				ISVNNVLPVFDNLMQQK	3	100.0%	2																									
				QVFGEATK	2	95.4%	1																									
IPI00852685	DIAPH1	isoform 1 of Protein diaphanous homolog 1	100.0%	11.0	9	10	10	7	6,336,622	6,139,367	6,694,967	7,044,710	520,770	220,248	427,756	192,507	18.4	8.0	14.3	6.1	-1.0	0.7	1.1	0.6	1.1	0.3	1.1	0.3	1.1	0.01	1.1	0.5
IPI00884341	DIAPH1	isoform 2 of Protein diaphanous homolog 1	100.0%	11.2	9	10	10	7	6,336,622	6,139,367	6,694,967	7,044,710	520,770	220,248	427,756	192,507	18.4	8.0	14.3	6.1	-1.0	0.7	1.1	0.6	1.1	0.3	1.1	0.3	1.1	0.01	1.1	0.5
IPI00924442	DIAPH1	Uncharacterized protein	100.0%	11.5	9	10	10	7	6,336,622	6,139,367	6,694,967	7,044,710	520,770	220,248	427,756	192,507	18.4	8.0	14.3	6.1	-1.0	0.7	1.1	0.6	1.1	0.3	1.1	0.3	1.1	0.01	1.1	0.5
IPI00936125	DIAPH1	Diaphanous 1	100.0%	11.0	9	10	10	7	6,336,622	6,139,367	6,694,967	7,044,710	520,770	220,248	427,756	192,507	18.4	8.0	14.3	6.1	-1.0	0.7	1.1	0.6	1.1	0.3	1.1	0.3	1.1	0.01	1.1	0.5
IPI00936881	DIAPH1	Uncharacterized protein	100.0%	11.2	9	10	10	7	6,336,622	6,139,367	6,694,967	7,044,710	520,770	220,248	427,756	192,507	18.4	8.0	14.3	6.1	-1.0	0.7	1.1	0.6	1.1	0.3	1.1	0.3	1.1	0.01	1.1	0.5
IPI00978163	DIAPH1	Uncharacterized protein	100.0%	11.1	9	10	10	7	6,336,622	6,139,367	6,694,967	7,044,710	520,770	220,248	427,756	192,507	18.4	8.0	14.3	6.1	-1.0	0.7	1.1	0.6	1.1	0.3	1.1	0.3	1.1	0.01	1.1	0.5
IPI01009439	DIAPH1	protein diaphanous homolog 1 isoform 2	100.0%	11.1	9	10	10	7	6,336,622	6,139,367	6,694,967	7,044,710	520,770	220,248	427,756	192,507	18.4	8.0	14.3	6.1	-1.0	0.7	1.1	0.6	1.1	0.3	1.1	0.3	1.1	0.01	1.1	0.5
				AGCAVTSLLASELTK	2	91.8%	1																									
				EIENEDMR	2	90.3%	1																									
				EQLIDMNAEGDETGVMDSLLEALQSGAAFR	3	100.0%	1																									
				FENNELFAK	2	97.7%	1																									
				LGLHQVLQDLR	3	89.2%	1																									
				NSETFPTILEEAK	2	99.9%	1																									
				NVILEVNEAVLTESMIQNLIK	3	100.0%	1																									
				TAQNLSIFLGSFR	2	99.9%	1																									
				VGCLQLINALITPAEELDFR	2	100.0%	1																									
				VGCLQLINALITPAEELDFR	3	100.0%	1																									
IPI00852796	CAPZA2	20 kDa protein	100.0%	16.1	2	2	3	3	3,115,284	3,353,838	3,359,699	3,595,850	374,523	130,997	318,561	179,034	26.9	8.7	21.2	11.1	1.1	0.6	1.1	0.6	1.2	0.3	1.0	1	1.1	0.3	1.1	0.5
IPI00952611	CAPZA2	cDNA FLJ51827, highly similar to F-actin capping protein alpha-2 subunit	100.0%	16.3	2	2	3	3	3,115,284	3,353,838	3,359,699	3,595,850	374,523	130,997	318,561	179,034	26.9	8.7	21.2	11.1	1.1	0.6	1.1	0.6	1.2	0.3	1.0	1	1.1	0.3	1.1	0.5
IPI00985078	CAPZA2	Uncharacterized protein	100.0%	19.2	2	2	3	3	3,115,284	3,353,838	3,359,699	3,595,850	374,523	130,997	318,561	179,034	26.9	8.7	21.2	11.1	1.1	0.6	1.1	0.6	1.2	0.3	1.0	1	1.1	0.3	1.1	0.5
				FIIHAPPGEFNEVFNDVR	3	100.0%	1																									
				LLLNNDNLLR	2	100.0%	2																									
IPI00852838	SELENBP1	Selenium binding protein 1	100.0%	15.7	3	3	3	1	1,687,083	1,766,910	1,794,673	2,009,817	123,130	95,444	98,646	50,551	16.3	12.1	12.3	5.6	1.0	0.6	1.1	0.5	1.2	0.04	1.0	0.8	1.1	0.05	1.1	0.09
				GGFVLLDGETFEVK	2	99.9%	1																									
				HNVMISTEWAAPNVLR	2	99.8%	1																									
				NTGTEAPDYLATVDVDPK	2	100.0%	1																									
IPI00852891	PLXNB2	Plexin B2	99.9%	7.9	1	1	1	1	3,556,185	3,625,965	3,389,195	4,073,255	312,479	161,048	294,921	142,579	19.7	9.9	19.5	7.8	1.0	0.8	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.07	1.2	0.07
				AMTLQEAEAFVGAER	2	99.5%	1																									
IPI00852953	SELENBP1	Uncharacterized protein	100.0%	22.2	1	1	1	2	202,713	230,998	211,160	264,704	12,343	11,039	11,121	16,448	13.6	10.7	11.8	13.9	1.1	0.1	1.0	0.6	1.3	0.02	-1.1	0.2	1.1	0.1	1.3	0.03
IPI01008815	SELENBP1	Selenium binding protein 1 (Fragment)	100.0%	14.3	1	1	1	2	202,713	230,998	211,160	264,704	12,343	11,039	11,121	16,448	13.6	10.7	11.8	13.9	1.1	0.1	1.0	0.6	1.3	0.02	-1.1	0.2	1.1	0.1	1.3	0.03
				NTGTEAPDYLATVDVDPK	2	100.0%	1																									
IPI00853023	QPRT	Uncharacterized protein	100.0%	28.5	4	4	4	1	14,951,490	14,559,735	14,015,815	16,653,180	1,086,860	638,619	681,285	577,531	16.3	9.8	10.9	7.8	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.0	0.6	1.1	0.04	1.2	0.02
				CSGIASAAAAAVEAAR	2	100.0%	1																									
				GPAHCLLLGER	3	86.4%	1																									
				VALNTLAR	2	99.8%	1																									
				YGLLVGGAASHR	3	99.4%	1																									
IPI00853068	HBA1;HBA2	Hemoglobin alpha-2	100.0%	22.7	2	2	3	1	11,902,265	10,547,375	12,192,295	11,689,925	884,812	373,592	353,609	573,809	16.6	7.9	6.5	11.0	-1.1	0.2	1.0	0.8	-1.0	0.8	1.2	0.01	1.1	0.1	-1.0	0.5
				MFLSFPTTK	2	100.0%	2																									
				TYFPHFDLSHGSAQVK	3	100.0%	1																									
IPI00853149	TMEM131	Transmembrane protein 131	97.9%	0.4	1	1	1	1	12,437,740	12,240,050	11,485,060	13,257,920	983,007	798,050	888,891	787,901	17.7	14.6	17.3	13.3	-1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.5	1.1	0.4	1.2	0.2
				NSSSTSSR	2	84.0%	1																									
IPI00853173	KIAA1217	isoform 4 of Sickle tail protein homolog	100.0%	4.0	2	2	2	4	406,079	421,842	415,553	481,029	28,073	33,800	13,989	26,320	15.5	17.9	7.5	12.2	1.0	0.7	1.0	0.8	1.2	0.09	-1.0	0.9	1.1	0.2	1.2	0.06
IPI00855886	KIAA1217	isoform 7 of Sickle tail protein homolog	100.0%	3.9	2	2	2	4	406,079	421,842	415,553	481,029	28,073	33,800	13,989	26,320	15.5	17.9	7.5	12.2	1.0	0.7	1.0	0.8	1.2	0.09	-1.0	0.9	1.1	0.2	1.2	0.06
IPI00878042	KIAA1217	isoform 5 of Sickle tail protein homolog	100.0%	2.6	2	2	2	4	406,079	421,842	415,553	481,029	28,073	33,800	13,989	26,320	15.5	17.9	7.5	12.2	1.0	0.7	1.0	0.8	1.2	0.09	-1.0	0.9	1.1	0.2	1.2	0.06
IPI01010021	KIAA1217	isoform 6 of Sickle tail protein homolog	100.0%	3.8	2	2	2	4	406,079	421,842	415,553	481,029	28,073	33,800	13,989	26,320	15.5	17.9	7.5	12.2	1.0	0.7	1.0	0.8	1.2	0.09	-1.0	0.9	1.1	0.2	1.2	0.06
				GDAPVDKVELSEDSPNSEQDLEK	3	99.5%	1																									
				SMVVPGNATIPR	2	100.0%	1																									
IPI00853290	SEC31A	Uncharacterized protein	100.0%	1.5	1	1	2	1	273,450	287,976	302,485	332,663	17,856	18,321	27,604	28,871	14.6	14.2	20.4	19.4	1.1	0.6	1.1	0.4	1.2	0.1	1.1	0.7	1.2	0.2	1.1	0.5
				NPAVLSAASFDGR	2	99.9%	2																									
IPI00853306	RCN2	Uncharacterized protein	100.0%	19.0	3	3	3	1	20,250,731	23,905,102	22,427,056	27,325,365	3,208,166	2,041,492	2,358,739	1,864,544	35.4	19.1	23.5	15.3	1.2	0.4	1.1	0.6	1.3	0.09	-1.1	0.6	1.1	0.3	1.2	0.1
				LSEEEILENPDLFLTSEATDYGR	2	100.0%	1																									
				WDPTANEDPEWILVEK	2	99.4%	1																									
				WDPTANEDPEWILVEKDR	3	85.1%	1																									
IPI00853369	PLXNB2	Plexin-B2	99.9%	1.5	2	2	2	1	6,536,965	6,845,535	6,150,745	7,150,465	516,149	167,878	478,758	270,223	17.7	5.5	17.4	8.5	1.0	0.6	-1.1	0.6	1.1	0.3	-1.1	0.2	1.0	0.4	1.2	0.1
				AMTLQEAEAFVGAER	2	99.5%	1																									
				EASPNPEDGIVR	2	99.3%	1																									
IPI00853455	-	Protein	100.0%	24.3	6	8	13	1	19,694,805	20,107,686	19,278,872	22,123,612	1,658,953	1,027,090	1,086,538	689,991	18.8	11.4	12.6	7.0	1.0	0.8	-1.0	0.8	1.1	0.2	-1.0	0.6	1.1	0.1	1.1	0.06
				AIGAVPLIQGEYMIPCEK	2	100.0%	2																									
				AIGAVPLIQGEYMIPCEK	3	100.0%	1																									
				AYWQVHLDQVEVASGLTLCK	3	98.7%	1																									
				DPDAQPGGELMLGGTDSK	2	100.0%	2																									
				FDGILGMAYPR	2	100.0%	2																									
				ISVNNVLPVFDNLMQQK	2	100.0%	2																									
				ISVNNVLPVFDNLMQQK	3	100.0%	2																									
				QVFGEATK	2	95.4%	1																									
IPI00853525	APOA1	Uncharacterized protein	100.0%	21.6	4	4	4	1	8,849,370	9,716,225	9,470,560	10,595,040	947,716	155,277	481,268	216,658	24.0	3.6	11.4	4.6	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.6	1.1	0.01	1.1	0.07
				EQLGPVTQEFWDNLEK	2	93.2%	1																									
				LLDNWDSVTSTFSK	2	100.0%	1																									
				QGLLPVLESFK	2	97.6%	1																									
				VSFLSALEEYTK	2	100.0%	1																									
IPI00853609	PSMD4	Uncharacterized protein	100.0%	23.6	3	3	4	1	8,287,013	8,752,030	8,105,672	9,834,713	524,488	599,729	598,503	516,137	14.2	15.3	16.5	11.7	1.1	0.6	-1.0	0.8	1.2	0.07	-1.1	0.5	1.1	0.2	1.2	0.06
				AAAASAAEAGIATTGTEDSDDALLK	3	99.8%	1																									
				MTISQQEFGR	2	99.9%	2																									
				NAMGSLASQATK	2	97.4%	1																									
IPI00854567	KIAA1598	isoform 2 of Shootin-1	99.7%	2.2	1	1	1	1	836,578	952,710	865,775	1,018,850	109,575	75,716	86,065	112,830	29.3	17.8	22.2	24.8	1.1	0.4	1.0	0.8	1.2	0.3	-1.1	0.5	1.1	0.6	1.2	0.3
				LVEVIEEVNK	2	92.8%	1																									
IPI00854592	TPM3	Tropomyosin 3	100.0%	6.7	2	2	3	1	3,025,234	3,218,272	3,289,434	3,591,324	179,060	134,331	250,419	107,103	13.2	9.3	17.0	6.7	1.1	0.4	1.1	0.4	1.2	0.03	1.0	0.8	1.1	0.06	1.1	0.3
				IQVLQQQADDAEER	2	100.0%	2																									
				KIQVLQQQADDAEER	3	100.0%	1																									
IPI00854835	STAM	Uncharacterized protein	100.0%	9.1	1	1	1	2	1,126,793	1,113,900	1,194,165	1,188,265	88,168	68,149	69,483	45,244	17.5	13.7	13.0	8.5	-1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.4	1.1	0.4	-1.0	0.9
IPI01013719	STAM	cDNA FLJ57683, highly similar to Signal transducing adapter molecule 1	100.0%	4.0	1	1	1	2	1,126,793	1,113,900	1,194,165	1,188,265	88,168	68,149	69,483	45,244	17.5	13.7	13.0	8.5	-1.0	0.9	1.1	0.6	1.1	0.6	1.1	0.4	1.1	0.4	-1.0	0.9
				AGEIITVLDDSDPNWWK	2	99.8%	1																									
IPI00855788	NUSAP1	isoform 4 of Nucleolar and spindle-associated protein 1	98.9%	4.7	1	1	1	1	11,352,300	11,984,760	14,057,170	13,401,000	935,550	836,798	1,572,106	353,929	18.4	15.6	25.0	5.9	1.1	0.6	1.2	0.2	1.2	0.09	1.2	0.3	1.1	0.2	-1.0	0.7
				TVRVDPDSQNHEKQESQDLR	3	98.9%	1																									
IPI00856037	HNRNPR	heterogeneous nuclear ribonucleoprotein R isoform 3	100.0%	15.7	6	6	8	2	4,242,389	4,227,716	4,337,747	4,832,677	286,070	185,923	205,231	184,082	15.1	9.8	10.6	8.5	-1.0	1	1.0	0.8	1.1	0.1	1.0	0.7	1.1	0.05	1.1	0.1
IPI00910614	HNRNPR	heterogeneous nuclear ribonucleoprotein R isoform 4	100.0%	15.8	6	6	8	2	4,242,389	4,227,716	4,337,747	4,832,677	286,070	185,923	205,231	184,082	15.1	9.8	10.6	8.5	-1.0	1	1.0	0.8	1.1	0.1	1.0	0.7	1.1	0.05	1.1	0.1
				DLYEDELVPLFEK	2	100.0%	1																									
				LCDSYEIRPGK	2	99.3%	1																									
				LMMDPLSGQNR	2	100.0%	2																									
				NLATTVTEEILEK	2	100.0%	1																									
				TGYTLDVTTGQR	2	100.0%	2																									
				VWGNVVTVEWADPVEEPDPEVMAK	2	100.0%	1																									
IPI00856038	HNRNPR	cDNA FLJ53358, highly similar to Heterogeneous nuclear ribonucleoprotein R	100.0%	6.2	3	3	4	1	2,556,458	2,547,700	2,546,766	2,907,650	147,488	122,500	138,527	107,062	12.9	10.8	12.2	8.2	-1.0	1	-1.0	1	1.1	0.09	-1.0	1	1.1	0.06	1.1	0.07
				DLYEDELVPLFEK	2	100.0%	1																									
				LMMDPLSGQNR	2	100.0%	2																									
				NLATTVTEEILEK	2	100.0%	1																									
IPI00856045	AHNAK2	isoform 1 of Protein AHNAK2	100.0%	1.7	6	6	6	2	13,602,330	13,728,895	12,898,975	14,199,580	790,619	641,311	816,079	95,961	13.0	10.5	14.2	1.5	1.0	0.9	-1.1	0.6	1.0	0.5	-1.1	0.4	1.0	0.5	1.1	0.2
IPI00884904	AHNAK2	isoform 3 of Protein AHNAK2	100.0%	1.8	6	6	6	2	13,602,330	13,728,895	12,898,975	14,199,580	790,619	641,311	816,079	95,961	13.0	10.5	14.2	1.5	1.0	0.9	-1.1	0.6	1.0	0.5	-1.1	0.4	1.0	0.5	1.1	0.2
				KSGLLWFWLPNIGFSSSVDETGVDSKNDVQR	3	91.6%	1																									
				LPEGQVPEGAGLK	2	99.9%	1																									
				MSLSSMEVDVQAPR	2	99.5%	1																									
				SIEASVDVSAPK	2	99.9%	1																									
				VEADVSLPSMQGDLK	2	100.0%	1																									
				VEADVSLSSMQGDLK	2	99.9%	1																									
IPI00867659	CORO1B	Similar to Protein tyrosine phosphatase receptor type C-associated protein	100.0%	7.1	2	2	3	2	2,054,535	2,156,533	2,086,233	2,448,318	149,557	102,795	132,204	118,409	16.3	10.7	14.2	10.8	1.0	0.6	1.0	0.9	1.2	0.07	-1.0	0.7	1.1	0.1	1.2	0.08
IPI00908316	CORO1B	cDNA FLJ60046, highly similar to Coronin-1B	100.0%	6.9	2	2	3	2	2,054,535	2,156,533	2,086,233	2,448,318	149,557	102,795	132,204	118,409	16.3	10.7	14.2	10.8	1.0	0.6	1.0	0.9	1.2	0.07	-1.0	0.7	1.1	0.1	1.2	0.08
				NDQCYEDIR	2	93.7%	1																									
				VGIIAWHPTAR	3	100.0%	2																									
IPI00867679	PSMA6	cDNA FLJ51729, highly similar to Proteasome subunit alpha type 6	100.0%	25.1	4	4	4	1	11,549,510	12,389,195	10,692,800	14,367,020	1,259,921	908,176	923,559	944,223	24.4	16.4	19.3	14.7	1.1	0.6	-1.1	0.6	1.2	0.1	-1.2	0.2	1.2	0.2	1.3	0.02
				ILTEAEIDAHLVALAERD	3	97.0%	1																									
				ITENIGCVMTGMTADSR	2	100.0%	1																									
				LLDSSTVTHLFK	3	100.0%	1																									
				QTESTSFLEK	2	90.1%	1																									
IPI00868715	CENPE	isoform 2 of Centromere-associated protein E	97.1%	0.5	1	1	1	1	1,780,987	1,825,190	1,461,877	1,809,997	286,862	96,607	167,544	150,871	36.0	11.8	25.6	18.6	1.0	0.9	-1.2	0.4	1.0	0.9	-1.2	0.1	-1.0	0.9	1.2	0.2
				NELQQMLESVIAEK	2	97.1%	1																									
IPI00868717	PRRC1	isoform 4 of Protein PRRC1	100.0%	9.0	2	2	3	3	2,466,762	2,449,355	2,451,777	2,827,940	140,182	135,499	167,111	59,700	12.7	12.4	15.2	4.7	-1.0	0.9	-1.0	0.9	1.1	0.05	1.0	1	1.2	0.03	1.2	0.09
IPI00868764	PRRC1	isoform 5 of Protein PRRC1	100.0%	6.7	2	2	3	3	2,466,762	2,449,355	2,451,777	2,827,940	140,182	135,499	167,111	59,700	12.7	12.4	15.2	4.7	-1.0	0.9	-1.0	0.9	1.1	0.05	1.0	1	1.2	0.03	1.2	0.09
IPI00942375	PRRC1	Uncharacterized protein	100.0%	9.0	2	2	3	3	2,466,762	2,449,355	2,451,777	2,827,940	140,182	135,499	167,111	59,700	12.7	12.4	15.2	4.7	-1.0	0.9	-1.0	0.9	1.1	0.05	1.0	1	1.2	0.03	1.2	0.09
				GQDEASAGGIWGFIK	2	100.0%	2																									
				SGGELDIVVTSNK	2	99.9%	1																									
IPI00868816	RPL12P38	Pseudogene candidate	100.0%	13.7	1	1	2	1	3,126,760	3,155,185	3,186,085	3,703,930	272,369	180,190	273,916	217,166	19.5	12.8	19.2	13.1	1.0	0.9	1.0	0.9	1.2	0.1	1.0	0.9	1.2	0.09	1.2	0.2
				QAQIEVVPSASALIIK	2	100.0%	2																									
IPI00869000	C12orf51	probable E3 ubiquitin-protein ligase C12orf51	98.4%	0.4	1	1	1	2	1,745,000	1,888,365	1,910,790	1,880,805	65,759	175,599	179,367	90,222	8.4	20.8	21.0	10.7	1.1	0.5	1.1	0.4	1.1	0.3	1.0	0.9	-1.0	1	-1.0	0.9
IPI00942832	C12orf51	isoform 1 of Probable E3 ubiquitin-protein ligase C12orf51	98.4%	0.4	1	1	1	2	1,745,000	1,888,365	1,910,790	1,880,805	65,759	175,599	179,367	90,222	8.4	20.8	21.0	10.7	1.1	0.5	1.1	0.4	1.1	0.3	1.0	0.9	-1.0	1	-1.0	0.9
				DGGPDTAHVPPYPMK	2	97.5%	1																									
IPI00869333	LOC727896	Pseudogene candidate	100.0%	19.9	2	2	2	1	1,491,757	1,378,401	1,600,177	1,648,769	144,994	52,222	127,081	116,878	21.7	8.5	17.8	15.9	-1.1	0.5	1.1	0.6	1.1	0.4	1.2	0.1	1.2	0.07	1.0	0.8
				RPSPDEPMTNLELK	2	99.9%	1																									
				TTDFSDFLSIVGCTK	2	100.0%	1																									
IPI00871174	MYCBP	C-Myc-binding protein	99.6%	19.4	1	1	1	1	5,297,950	5,146,320	6,391,240	5,405,640	313,443	851,339	367,830	252,154	13.2	37.0	12.9	10.4	-1.0	0.9	1.2	0.05	1.0	0.8	1.2	0.2	1.1	0.8	-1.2	0.06
				VLVALYEEPEKPNSALDFLK	3	99.6%	1																									
IPI00871535	SPTAN1	isoform 2 of Spectrin alpha chain, brain	100.0%	50.0	101	120	150	2	183,331,175	188,067,373	182,274,308	212,363,448	########	5,551,813	########	5,889,169	19.0	6.6	14.7	6.2	1.0	0.8	-1.0	1	1.2	0.1	-1.0	0.7	1.1	0.02	1.2	0.05
IPI00879810	SPTAN1	Uncharacterized protein	100.0%	50.0	101	120	150	2	183,331,175	188,067,373	182,274,308	212,363,448	########	5,551,813	########	5,889,169	19.0	6.6	14.7	6.2	1.0	0.8	-1.0	1	1.2	0.1	-1.0	0.7	1.1	0.02	1.2	0.05
				ADVVESWIGEK	2	99.9%	1																									
				AGTFQAFEQFGQQLLAHGHYASPEIK	3	99.4%	1																									
				AINVQEEK	1	100.0%	1																									
				AKLDENSAFLQFNWK	3	99.5%	1																									
				ALINADELASDVAGAEALLDR	2	100.0%	2																									
				ALINADELASDVAGAEALLDR	3	100.0%	1																									
				ALSSEGKPYVTKEELYQNLTR	3	100.0%	1																									
				AQLADSFHLQQFFR	2	100.0%	1																									
				ASAFNSWFENAEEDLTDPVR	2	100.0%	2																									
				ASAFNSWFENAEEDLTDPVR	3	100.0%	1																									
				CTELNQAWSSLGK	2	99.9%	1																									

				DADETKEWIEEK	3	96.6%	1																									
				DCEQAENWMAAR	2	99.8%	1																									
				DLAALEDKVK	2	97.8%	1																									
				DLAALGDK	2	83.8%	1																									
				DLAALGDKVNSLGETAER	3	100.0%	1																									
				DLASVQALLR	2	100.0%	1																									
				DLIGVQNLLK	2	94.8%	1																									
				DLMSWINGIR	2	100.0%	2																									
				DLNSQADSLMTSSAFDTSQVK	2	100.0%	1																									
				DLNSQADSLMTSSAFDTSQVK	3	93.0%	1																									
				DLSSVQTLLTK	2	100.0%	2																									
				DLTGVQNLR	2	99.9%	1																									
				DLTNVQNLQK	2	100.0%	1																									
				DLTSWVTEMK	2	100.0%	1																									
				DMDDEESWIK	2	100.0%	2																									
				DVDEIEAWISEK	2	100.0%	2																									
				DVDETISWIK	2	100.0%	1																									
				DVEDEETWIR	2	100.0%	2																									
				DVTGAEALLER	2	99.9%	1																									
				EAALTSEEVGADLEQVEVLQK	3	100.0%	1																									
				EANELQQWINEK	2	100.0%	2																									
				EELITNWEQIR	2	99.8%	1																									
				EELYQNLTR	2	96.4%	1																									
				EKEPIVGSTDYGKDEDSAEALLK	3	99.9%	1																									
				ELPTAFDYVEFTR	2	100.0%	2																									
				ENLLEEQGSIALR	2	100.0%	2																									
				EQLMASDDFGRDLASVQALLR	3	100.0%	1																									
				FEEFQTDMAAHEER	2	86.2%	1																									
				FLADFR	2	99.3%	2																									
				FLSDFR	2	92.1%	2																									
				GKDLIGVQNLLK	2	99.2%	1																									
				GKDLIGVQNLLK	3	99.7%	1																									
				GLVSSDELAK	2	98.5%	1																									
				GLVSSDELAKDVTGAEALLER	2	100.0%	1																									
				GLVSSDELAKDVTGAEALLER	3	100.0%	1																									
				GVIDMGNSLIER	2	100.0%	2																									
				HALLEADVAAHQDR	3	100.0%	1																									
				HQAFEAELHANADR	3	99.9%	1																									
				HQAFEAELSANQSR	2	100.0%	1																									
				HQAFEAEVQANSGAIVK	3	90.0%	1																									
				HQALQAEIAGHEPR	3	100.0%	2																									
				IAALQAFADQLIAAGHYAK	2	100.0%	2																									
				IAALQAFADQLIAAGHYAK	3	100.0%	2																									
				ITALDEFATK	2	100.0%	1																									
				KASAFNSWFENAEEDLTDPVR	2	97.1%	1																									
				KASAFNSWFENAEEDLTDPVR	3	100.0%	1																									
				KFDDFQK	2	99.2%	1																									
				KGDILTLLNSTNK	2	100.0%	1																									
				KIEDLGAAMEEALILDNK	2	100.0%	1																									
				KIEDLGAAMEEALILDNK	3	99.7%	1																									
				KVEDLFLTFAK	2	100.0%	2																									
				LAALADQWQFLVQK	2	100.0%	2																									
				LAQFVEHWK	2	100.0%	2																									
				LAQFVEHWK	3	98.7%	1																									
				LDENSAFLQFNWK	2	100.0%	2																									
				LEESLEYQQFVANVEEEEAWINEK	2	100.0%	1																									
				LEESLEYQQFVANVEEEEAWINEK	3	100.0%	1																									
				LFGAAEVQR	2	100.0%	1																									
				LGDSHDLQR	2	100.0%	1																									
				LGESQTLQQFSR	2	100.0%	2																									
				LIQEQHPEEELIK	2	100.0%	1																									
				LIQNNHYAMEDVATR	3	100.0%	1																									
				LIQSHPESAEDLQEK	3	99.9%	1																									
				LKDLNSQADSLMTSSAFDTSQVK	3	100.0%	1																									
				LLEATELK	2	97.6%	1																									
				LLVGSEDYGR	2	100.0%	1																									
				LQQSHPLSATQIQVK	3	100.0%	1																									
				LSDDNTIGKEEIQQR	2	100.0%	1																									
				LSDDNTIGKEEIQQR	3	100.0%	1																									
				LTVLSEER	2	99.9%	1																									
				MKQVEELYHSLLELGEK	3	97.5%	1																									
				MNEVISLWK	2	100.0%	1																									
				MQHNLEQQIQAR	2	100.0%	1																									
				MTLVASEDYGDTLAAIQGLLK	2	100.0%	2																									
				MTLVASEDYGDTLAAIQGLLK	3	100.0%	1																									
				NQALNTDNYGHDLASVQALQR	3	100.0%	2																									
				NTTGVTEEALK	2	99.4%	1																									
				NTTGVTEEALKEFSMMFK	2	100.0%	1																									
				NTTGVTEEALKEFSMMFK	3	100.0%	1																									
				NVEDIELWLYEVEGHLASDDYGK	3	100.0%	1																									
				QDEVNAAWQR	2	100.0%	1																									
				QEAFLLNEDLGDSLDSVEALLK	2	100.0%	2																									
				QEAFLLNEDLGDSLDSVEALLK	3	100.0%	1																									
				QEAFLLNEDLGDSLDSVEALLKK	3	100.0%	1																									
				QEFAQHANAFHQWIQETR	3	100.0%	1																									
				QETFDAGLQAFQQEGIANITALK	3	100.0%	1																									
				QETFDAGLQAFQQEGIANITALKDQLLAAK	3	100.0%	2																									
				QGFVPAAYVK	2	99.6%	1																									
				QVEELYHSLLELGEK	2	99.9%	1																									
				QVEELYHSLLELGEK	3	93.0%	1																									
				REELITNWEQIR	2	100.0%	1																									
				REELITNWEQIR	3	98.9%	1																									
				RQDLEDSLQAQQYFADANEAESWMR	3	100.0%	1																									
				SADESGQALLAAGHYASDEVR	3	100.0%	1																									
				SADESGQALLAAGHYASDEVREK	3	99.9%	1																									
				SLQQLAEER	2	99.8%	1																									
				SQLLGSAHEVQR	2	100.0%	2																									
				SQLLGSAHEVQR	3	97.0%	1																									
				SSEEIESAFR	2	100.0%	1																									
				SSLSSAQADFNQLAELDR	2	100.0%	2																									
				SSLSSAQADFNQLAELDR	3	100.0%	1																									
				TATDEAYKDPSNLQGK	2	100.0%	1																									
				TATDEAYKDPSNLQGK	3	100.0%	1																									
				VASNPYTWFTMEALEETWR	2	100.0%	1																									
				VLETAEDIQER	2	100.0%	2																									
				VNEVNQFAAK	2	100.0%	1																									
				WSQLLANSAAR	2	100.0%	2																									
				YEALKEPMVAR	2	99.8%	1																									
				YTEHSTVGLAQQWDQLDQLGMR	3	100.0%	2																									
IPI00871646	RPLP0P6	60S acidic ribosomal protein P0-like	100.0%	25.2	6	6	11	1	14,404,212	13,812,430	14,211,307	16,262,365	1,097,667	114,210	973,570	235,291	17.0	1.9	15.3	3.2	-1.0	0.6	-1.0	0.9	1.1	0.2	1.0	0.7	1.2	1.00E-05	1.1	0.1
				AGAIAPCEVTVPAQNTGLGPEK	2	100.0%	2																									
				CFIVGADNVGSK	2	100.0%	2																									
				GHLENNPALEK	2	100.0%	2																									
				GTIEILSDVQLIK	2	100.0%	2																									
				IIQLLDDYPK	2	100.0%	1																									
				TSFFQALGITTK	2	100.0%	2																									
IPI00871666	ANK3	ankyrin-3 isoform 2	100.0%	7.8	5	5	5	4	2,434,831	2,407,977	2,505,526	2,797,218	217,852	115,252	189,179	152,392	20.0	10.7	16.9	12.2	-1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.7	1.2	0.08	1.1	0.3
IPI00921566	ANK3	Ankyrin-3	100.0%	1.8	5	5	5	4	2,434,831	2,407,977	2,505,526	2,797,218	217,852	115,252	189,179	152,392	20.0	10.7	16.9	12.2	-1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.7	1.2	0.08	1.1	0.3
IPI00967150	ANK3	ankyrin-3 isoform 3	100.0%	4.2	5	5	5	4	2,434,831	2,407,977	2,505,526	2,797,218	217,852	115,252	189,179	152,392	20.0	10.7	16.9	12.2	-1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.7	1.2	0.08	1.1	0.3
IPI00967510	ANK3	ankyrin-3 isoform 4	100.0%	4.2	5	5	5	4	2,434,831	2,407,977	2,505,526	2,797,218	217,852	115,252	189,179	152,392	20.0	10.7	16.9	12.2	-1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.7	1.2	0.08	1.1	0.3
				IDIVTLLEGPIFDYGNISGTR	2	99.9%	1																									
				INRIDIVTLLEGPIFDYGNISGTR	3	89.8%	1																									
				LIIEETKPCVPVSMK	2	97.4%	1																									
				LVEMGPAGAQFLGPVIVEIPHFGSMR	3	97.8%	1																									
				NATTDALTSVLTK	2	99.3%	1																									
IPI00871968	ANK3	Uncharacterized protein	100.0%	3.4	2	2	2	2	924,316	977,010	1,026,724	1,020,650	81,967	55,382	71,460	70,219	19.8	12.7	15.6	15.4	1.1	0.6	1.1	0.4	1.1	0.4	1.1	0.6	1.0	0.6	-1.0	1
IPI00909984	ANK3	Ankyrin G119	100.0%	3.5	2	2	2	2	924,316	977,010	1,026,724	1,020,650	81,967	55,382	71,460	70,219	19.8	12.7	15.6	15.4	1.1	0.6	1.1	0.4	1.1	0.4	1.1	0.6	1.0	0.6	-1.0	1
				ATFSPIVTVEPR	2	99.8%	1																									
				LVEMGPAGAQFLGPVIVEIPHFGSMR	3	97.8%	1																									
IPI00871988	SFXN3	cDNA FLJ58980, highly similar to Sideroflexin-3	98.9%	4.0	1	1	1	1	4,874,670	3,972,630	5,513,340	5,063,530	220,110	361,196	402,551	533,038	10.1	20.3	16.3	23.5	-1.2	0.07	1.1	0.2	1.0	0.8	1.4	0.02	1.3	0.1	-1.1	0.5
				NLLLSGAQLEASR	2	96.1%	1																									
IPI00872013	QSOX1	17 kDa protein	100.0%	12.3	1	1	1	1	580,105	599,303	546,148	592,070	57,401	46,883	61,220	45,355	22.1	17.5	25.1	17.1	1.0	0.8	-1.1	0.7	1.0	0.9	-1.1	0.5	-1.0	0.9	1.1	0.6
				SALYSPSDPLTLLQADTVR	2	100.0%	1																									
IPI00872250	PDZK1P1;PDZK1P2	isoform 1 of Putative PDZ domain-containing protein 1P	97.2%	3.5	1	1	1	2	1,002,830	689,265	1,161,155	667,728	106,080	88,684	192,272	78,526	23.7	28.8	37.0	26.3	-1.5	0.05	1.2	0.5	-1.5	0.03	1.7	0.06	-1.0	0.9	-1.7	0.04
IPI00900383	PDZK1P1;PDZK1P2	isoform 2 of Putative PDZ domain-containing protein 1P	97.2%	5.2	1	1	1	2	1,002,830	689,265	1,161,155	667,728	106,080	88,684	192,272	78,526	23.7	28.8	37.0	26.3	-1.5	0.05	1.2	0.5	-1.5	0.03	1.7	0.06	-1.0	0.9	-1.7	0.04
				DIDSGSPAEEAGLK	2	97.2%	1																									
IPI00872664	USP14	Ubiquitin carboxyl-terminal hydrolase	100.0%	26.3	9	9	10	1	14,465,307	16,552,530	14,956,253	18,696,290	1,819,408	1,119,780	1,753,404	522,073	28.1	15.1	26.2	6.2	1.1	0.4	1.0	0.9	1.3	0.08	-1.1	0.5	1.1	0.1	1.3	0.1
				AQLFALTGVQPAR	2	99.9%	1																									
				ASGEMASAQYITAALR	2	100.0%	1																									
				EKFEGVELNTDEPPMVFK	3	99.9%	1																									
				FEGVELNTDEPPMVFK	2	100.0%	1																									
				FPLMLDMYELCTPELQEK	2	99.7%	1																									
				LEAIEDDSVKETDSSSASAATPSK	3	100.0%	1																									
				LPAYLTIQMVR	2	100.0%	2																									
				RVEIMEEESEQ	2	100.0%	1																									
				SLIDQFFGVEFETTMK	2	100.0%	1																									
IPI00872684	EZR	cDNA FLJ54141, highly similar to Ezrin	100.0%	36.8	18	20	29	1	58,902,471	61,013,997	61,311,615	68,284,291	4,399,100	2,101,792	3,515,554	1,694,873	16.7	7.7	12.8	5.6	1.0	0.7	1.0	0.7	1.2	0.1	1.0	0.9	1.1	0.03	1.1	0.1

				AKEAQDDLVK	2	99.9%	1																									
				APDFVFYAPR	2	100.0%	2																									
				DNAMLEYLK	2	98.7%	1																									
				FVIKPIDKK	2	87.7%	1																									
				FVIKPIDKK	3	97.1%	1																									
				FYPEDVAEELIQDITQK	2	100.0%	2																									
				FYPEDVAEELIQDITQK	3	100.0%	2																									
				GTDLWLGVDALGLNIYEK	2	99.8%	1																									
				IALLEEAR	2	86.6%	1																									
				IAQDLEMYGINYFEIK	2	100.0%	2																									
				IGFPWSEIR	2	100.0%	2																									
				ILQLCMGNHELYMR	3	99.9%	1																									
				IQVWHAEHR	2	100.0%	1																									
				KENPLQFK	2	98.6%	1																									
				LFFLQVK	2	92.1%	1																									
				NISFNDKK	2	99.8%	2																									
				QLLTLSSELSQAR	2	100.0%	2																									
				RKEDEVEEWQHR	3	100.0%	1																									
				SGYLSSER	2	100.0%	2																									
				VTTMDAELEFAIQPNTTGK	2	100.0%	2																									
IPI00872777	SAFB2	Uncharacterized protein	100.0%	5.3	2	2	2	2	250,929	281,679	251,101	281,700	13,613	19,181	25,008	18,473	12.1	15.2	22.3	14.7	1.1	0.2	1.0	1	1.1	0.2	-1.1	0.4	1.0	1	1.1	0.4
IPI00942551	SAFB2	44 kDa protein	100.0%	6.7	2	2	2	2	250,929	281,679	251,101	281,700	13,613	19,181	25,008	18,473	12.1	15.2	22.3	14.7	1.1	0.2	1.0	1	1.1	0.2	-1.1	0.4	1.0	1	1.1	0.4
				SEPVKEESSELEQPFAQDTSSVGPDR	3	100.0%	1																									
				SEPVKEESSELEQPFAQDTSSVGPDRK	3	99.3%	1																									
IPI00872780	ANXA4	cDNA FLJ51794, highly similar to Annexin A4	100.0%	65.6	20	24	32	1	92,858,322	96,904,206	93,152,046	110,688,645	7,872,361	3,234,258	6,630,243	4,226,480	19.0	7.5	15.9	8.5	1.0	0.6	1.0	1	1.2	0.08	-1.0	0.6	1.1	0.03	1.2	0.06
				AASGFNAMEDAQTLR	2	100.0%	2																									
				AASGFNAMEDAQTLRK	2	100.0%	1																									
				AASGFNAMEDAQTLRK	3	100.0%	1																									
				AEIDMLDIR	2	100.0%	1																									
				DEGNYLDDALVR	2	100.0%	2																									
				DIEQSIK	1	95.0%	1																									
				FLTVLCSR	2	99.3%	1																									
				GAGTDEGCLIEILASR	2	100.0%	2																									
				GLGTDDNTLIR	2	100.0%	2																									
				GLGTDEDAIISVLAYR	2	100.0%	2																									
				GLGTDEDAIISVLAYR	3	90.7%	1																									
				ISQTYQQQYGR	2	100.0%	2																									
				NHLLHVFDEYK	3	98.4%	1																									
				QDAQDLYEAGEK	2	100.0%	2																									
				QDAQDLYEAGEKK	3	97.7%	1																									
				SAYFAEK	2	90.3%	1																									
				SETSGSFEDALLAIVK	2	100.0%	2																									
				SLEDDIRSDTSFMFQR	2	85.4%	1																									
				SLEDDIRSDTSFMFQR	3	100.0%	1																									
				VLLVLCGGDD	1	100.0%	1																									
				VLVSLSAGGR	2	100.0%	1																									
				VLVSLSAGGRDEGNYLDDALVR	2	99.9%	1																									
				VLVSLSAGGRDEGNYLDDALVR	3	100.0%	1																									
				WGTDEVK	2	82.3%	1																									
IPI00873286	EIF3CL;EIF3C	cDNA FLJ55750, highly similar to Eukaryotic translation initiation factor 3 subunit 8	100.0%	7.5	5	5	5	4	4,290,618	4,346,564	4,059,201	4,766,928	216,076	148,774	245,121	118,265	11.3	7.7	13.5	5.6	1.0	0.8	-1.1	0.5	1.1	0.09	-1.1	0.3	1.1	0.06	1.2	0.03
IPI00939953	EIF3CL;EIF3C	Uncharacterized protein	100.0%	7.5	5	5	5	4	4,290,618	4,346,564	4,059,201	4,766,928	216,076	148,774	245,121	118,265	11.3	7.7	13.5	5.6	1.0	0.8	-1.1	0.5	1.1	0.09	-1.1	0.3	1.1	0.06	1.2	0.03
IPI01010538	EIF3CL;EIF3C	cDNA FLJ30804 fis, clone FEBRA2001267, highly similar to Eukaryotic translation i	100.0%	7.0	5	5	5	4	4,290,618	4,346,564	4,059,201	4,766,928	216,076	148,774	245,121	118,265	11.3	7.7	13.5	5.6	1.0	0.8	-1.1	0.5	1.1	0.09	-1.1	0.3	1.1	0.06	1.2	0.03
IPI01014204	EIF3CL;EIF3C	91 kDa protein	100.0%	7.0	5	5	5	4	4,290,618	4,346,564	4,059,201	4,766,928	216,076	148,774	245,121	118,265	11.3	7.7	13.5	5.6	1.0	0.8	-1.1	0.5	1.1	0.09	-1.1	0.3	1.1	0.06	1.2	0.03
				KLNEILQAR	2	95.1%	1																									
				LGSLVENNER	2	99.9%	1																									
				QGTYGGYFR	2	89.1%	1																									
				TEPTAQQNLALQLAEK	2	100.0%	1																									
				TMVQLGICAFR	2	99.9%	1																									
IPI00873466	HPRT1	Uncharacterized protein	100.0%	16.5	3	3	4	1	3,903,280	4,318,352	4,262,173	4,949,635	386,721	192,083	289,567	219,145	22.2	10.0	15.2	9.9	1.1	0.4	1.1	0.5	1.3	0.05	-1.0	0.9	1.1	0.06	1.2	0.09
				DLNHVCVISETGK	2	87.4%	1																									
				FFADLLDYIK	2	100.0%	1																									
				VIGGDDLSTLTGK	2	100.0%	2																									
IPI00873472	SEC24A	isoform 1 of Protein transport protein Sec24A	99.6%	1.4	1	1	1	1	927,308	1,464,642	936,691	911,199	214,212	507,987	137,312	90,075	51.7	77.6	32.8	22.1	1.6	0.4	1.0	1	-1.0	0.9	-1.6	0.4	-1.6	0.3	-1.0	0.9
				DALVNAVIDSLSAYR	2	99.6%	1																									
IPI00873730	LOC100292653	nuclear envelope pore membrane protein POM 121-like	97.3%	5.0	1	1	1	1	1,297,608	1,573,970	1,518,829	1,946,490	212,728	28,984	175,011	66,957	36.7	4.1	25.8	7.7	1.2	0.3	1.2	0.4	1.5	0.04	-1.0	0.8	1.2	0.0009	1.3	0.07
				SGSEAWLVAALSLAFLICQMR	2	97.3%	1																									
IPI00876921	LYPLA2	Lysophospholipase II	100.0%	37.4	2	2	2	1	2,025,915	1,980,428	1,920,193	2,294,638	214,286	111,969	182,030	183,250	23.7	12.6	21.2	17.9	-1.0	0.9	-1.1	0.7	1.1	0.4	-1.0	0.8	1.2	0.2	1.2	0.2
				ETAAVIFLHGLGDTGHSWADALSTIR	3	89.0%	1																									
				IPVTLNMK	2	99.6%	1																									
IPI00876962	INF2	isoform 2 of Inverted formin-2	100.0%	10.6	7	7	7	2	14,277,949	14,449,023	15,803,606	16,768,137	1,121,080	558,110	1,141,838	401,183	17.6	8.6	16.2	5.4	1.0	0.9	1.1	0.4	1.2	0.09	1.1	0.3	1.2	0.01	1.1	0.5
IPI00895800	INF2	Uncharacterized protein	100.0%	10.5	7	7	7	2	14,277,949	14,449,023	15,803,606	16,768,137	1,121,080	558,110	1,141,838	401,183	17.6	8.6	16.2	5.4	1.0	0.9	1.1	0.4	1.2	0.09	1.1	0.3	1.2	0.01	1.1	0.5
				ALDELFEAIEQK	2	97.8%	1																									
				EHNSMWASLSSPDAEAVEPDFSSIER	3	99.8%	1																									
				GWDLVDAVTPGPQPTLEQLEEGGPRPLER	3	100.0%	1																									
				LASADHFYLLLLAIPCYQLR	3	93.2%	1																									
				NEFIGLQLLDVLAR	2	99.4%	1																									
				SSQLLWEALESLVNR	3	99.8%	1																									
				VSASVAEVQEQYTER	2	99.7%	1																									
IPI00877624	PACSIN2	Protein kinase C and casein kinase substrate in neurons 2	100.0%	13.2	2	2	3	2	4,319,613	3,867,235	4,033,243	4,274,933	315,676	257,369	307,403	235,859	16.3	14.9	17.0	12.3	-1.1	0.3	-1.1	0.5	-1.0	0.9	1.0	0.7	1.1	0.3	1.1	0.6
IPI00879955	PACSIN2	Protein kinase C and casein kinase substrate in neurons 2	100.0%	12.9	2	2	3	2	4,319,613	3,867,235	4,033,243	4,274,933	315,676	257,369	307,403	235,859	16.3	14.9	17.0	12.3	-1.1	0.3	-1.1	0.5	-1.0	0.9	1.0	0.7	1.1	0.3	1.1	0.6
				AYAQQLTEWAR	2	100.0%	2																									
				VSELHLEVK	3	97.4%	1																									
IPI00877635	RD43;RPL3;LOC653	Ribosomal protein L3, isoform CRA_b	100.0%	9.7	2	2	2	1	2,166,796	2,241,976	2,176,891	2,523,364	186,722	97,181	173,805	103,808	19.3	9.7	17.9	9.2	1.0	0.7	1.0	1	1.2	0.1	-1.0	0.8	1.1	0.08	1.2	0.1
				NNASTDYDLSDK	2	100.0%	1																									
				SINPLGGFVHYGEVTNDFVMLK	3	100.0%	1																									
IPI00877787	RD43;RPL3;LOC653	Uncharacterized protein	100.0%	14.0	2	2	2	1	1,913,378	1,773,584	1,861,551	2,012,233	92,853	90,705	72,535	84,769	10.9	11.4	8.7	9.4	-1.1	0.3	-1.0	0.7	1.1	0.5	1.0	0.5	1.1	0.09	1.1	0.2
				ERLEQQVPVNQVFGQDEMIDVIGVTK	3	100.0%	1																									
				NNASTDYDLSDK	2	100.0%	1																									
IPI00877836	SNAP29	Synaptosomal-associated protein	99.5%	8.1	1	1	1	1	2,731,395	2,977,190	2,871,845	3,139,645	316,182	158,539	141,995	178,156	25.9	11.9	11.1	12.7	1.1	0.5	1.1	0.7	1.1	0.3	-1.0	0.6	1.1	0.5	1.1	0.3
				GAGSAMSTDAYPK	2	99.5%	1																									
IPI00877922	-	13 kDa protein	100.0%	23.9	2	2	3	2	1,404,553	1,403,901	1,732,430	1,892,987	209,566	135,274	83,036	229,129	33.4	21.6	10.7	27.1	-1.0	1	1.2	0.2	1.3	0.2	1.2	0.07	1.3	0.1	1.1	0.5
IPI01008747	RPS4X	Uncharacterized protein	100.0%	22.1	2	2	3	2	1,404,553	1,403,901	1,732,430	1,892,987	209,566	135,274	83,036	229,129	33.4	21.6	10.7	27.1	-1.0	1	1.2	0.2	1.3	0.2	1.2	0.07	1.3	0.1	1.1	0.5
				ECLPLIIFLR	2	99.3%	1																									
				TDITYPAGFMDVISIDK	2	100.0%	2																									
IPI00877935	EIF3L	Uncharacterized protein	90.7%	7.7	1	1	1	1	829,452	845,806	1,081,740	816,002	63,142	89,175	117,175	55,472	17.0	23.6	24.2	15.2	1.0	0.9	1.3	0.09	-1.0	0.9	1.3	0.1	-1.0	0.8	-1.3	0.07
				VYEIQDIYENSWTK	2	90.7%	1																									
IPI00877999	RD43;RPL3;LOC653	35 kDa protein	100.0%	11.5	2	2	3	2	4,520,355	4,615,738	4,126,221	5,114,465	471,423	323,093	375,880	145,834	23.3	15.7	20.4	6.4	1.0	0.9	-1.1	0.5	1.1	0.3	-1.1	0.4	1.1	0.2	1.2	0.06
IPI00878524	RD43;RPL3;LOC653	Protein	100.0%	13.4	2	2	3	2	4,520,355	4,615,738	4,126,221	5,114,465	471,423	323,093	375,880	145,834	23.3	15.7	20.4	6.4	1.0	0.9	-1.1	0.5	1.1	0.3	-1.1	0.4	1.1	0.2	1.2	0.06
				ERLEQQVPVNQVFGQDEMIDVIGVTK	3	100.0%	1																									
				HGSLGFLPR	2	100.0%	2																									
IPI00878105	-	12 kDa protein	100.0%	18.1	1	1	1	1	667,169	742,026	345,846	624,266	101,330	74,330	31,183	72,281	34.0	22.4	20.2	25.9	1.1	0.6	-1.9	0.03	-1.1	0.7	-2.1	0.001	-1.2	0.3	1.8	0.008
				TILSNQTVDIPENVDITLK	2	100.0%	1																									
IPI00878126	UBE2K	ubiquitin-conjugating enzyme E2 K isoform 2	100.0%	17.2	2	2	2	1	2,240,664	2,389,497	2,253,553	2,237,053	124,665	44,033	120,137	158,920	12.4	4.1	11.9	15.9	1.1	0.3	1.0	0.9	-1.0	1	-1.1	0.3	-1.1	0.4	-1.0	0.9
				GEIAGPPDTPYEGGR	2	87.8%	1																									
				VDLVDENFTELR	2	99.9%	1																									
IPI00878218	ATP5O	Mitochondrial ATP synthase, O subunit variant (Fragment)	100.0%	17.8	3	4	4	1	4,880,148	5,044,245	4,912,515	5,446,729	619,377	265,318	535,925	177,811	28.4	11.8	24.4	7.3	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.8	1.1	0.2	1.1	0.4
				FSPLTTNLINLLAENGR	2	100.0%	1																									
				FSPLTTNLINLLAENGR	3	99.9%	1																									
				SFLSQGQVLK	2	85.3%	1																									
				VAASVLNPYVK	2	97.7%	1																									
IPI00878254	COMT	Uncharacterized protein	100.0%	28.3	5	6	7	1	8,132,328	8,838,142	9,303,083	9,638,521	710,622	341,510	553,957	212,486	19.5	8.6	13.3	4.9	1.1	0.4	1.1	0.2	1.2	0.1	1.1	0.5	1.1	0.08	1.0	0.6
				KYDVDTLDMVFLDHWK	3	98.3%	1																									
				LITIEINPDCAAITQR	3	100.0%	1																									
				VTLVVGASQDIIPQLK	2	99.8%	1																									
				YDVDTLDMVFLDHWK	2	100.0%	1																									
				YDVDTLDMVFLDHWK	3	100.0%	1																									
				YLPDTLLLEECGLLR	2	100.0%	2																									
IPI00878298	EIF3L	Uncharacterized protein	99.9%	10.2	1	1	1	1	373,834	424,641	431,589	416,281	45,760	16,412	17,138	11,849	27.4	8.6	8.9	6.4	1.1	0.3	1.2	0.3	1.1	0.4	1.0	0.8	-1.0	0.7	-1.0	0.5
				LAGFLDLTEQEFR	2	100.0%	1																									
IPI00980488	LOC100508181	ran-specific GTPase-activating protein-like	100.0%	12.6	2	2	3	4	2,091,637	2,128,630	2,022,104	2,169,828	87,404	53,221	98,311	51,659	9.3	5.6	10.9	5.3	1.0	0.7	-1.0	0.6	1.0	0.5	-1.1	0.4	1.0	0.6	1.1	0.2
IPI00878440	RANBP1	Uncharacterized protein	100.0%	13.3	2	2	3	4	2,091,637	2,128,630	2,022,104	2,169,828	87,404	53,221	98,311	51,659	9.3	5.6	10.9	5.3	1.0	0.7	-1.0	0.6	1.0	0.5	-1.1	0.4	1.0	0.6	1.1	0.2
IPI00878950	RANBP1	cDNA FLJ57507, highly similar to Ran-specific GTPase-activating protein	100.0%	10.8	2	2	3	4	2,091,637	2,128,630	2,022,104	2,169,828	87,404	53,221	98,311	51,659	9.3	5.6	10.9	5.3	1.0	0.7	-1.0	0.6	1.0	0.5	-1.1	0.4	1.0	0.6	1.1	0.2
IPI01014561	RANBP1	Uncharacterized protein	100.0%	13.5	2	2	3	4	2,091,637	2,128,630	2,022,104	2,169,828	87,404	53,221	98,311	51,659	9.3	5.6	10.9	5.3	1.0	0.7	-1.0	0.6	1.0	0.5	-1.1	0.4	1.0	0.6	1.1	0.2
				FASENDLPEWK	2	100.0%	2																									
				TLEEDEEELFK	2	100.0%	1																									
IPI00878669	CBX1	Uncharacterized protein	100.0%	22.8	3	3	4	2	6,755,743	6,950,870	5,817,308	7,459,320	630,110	334,535	367,445	379,958	20.9	10.8	14.1	11.4	1.0	0.8	-1.2	0.2	1.1	0.4	-1.2	0.05	1.1	0.3	1.3	0.01
IPI01014449	CBX1	Uncharacterized protein	100.0%	25.6	3	3	4	2	6,755,743	6,950,870	5,817,308	7,459,320	630,110	334,535	367,445	379,958	20.9	10.8	14.1	11.4	1.0	0.8	-1.2	0.2	1.1	0.4	-1.2	0.05	1.1	0.3	1.3	0.01
				IIGATDSSGELMFLMK	2	100.0%	2																									
				NSDEADLVPAK	2	100.0%	1																									
				VEEVLEEEEEEYVVEK	2	100.0%	1																									
IPI00878677	SF3A1	29 kDa protein	100.0%	8.9	1	1	1	1	1,039,863	1,112,608	1,052,875	1,211,310	98,931	60,623	108,897	77,818	21.3	12.2	23.1	14.4	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.3	1.2	0.3
				ASKPLPPAPAPDEYLVSPITGEK	3	100.0%	1																									
IPI00878697	SUN2	SUN domain-containing protein 2 isoform a	97.2%	4.3	1	1	1	1	2,606,700	2,438,369	3,096,010	3,245,140	370,400	252,780	434,443	155,198	31.8	23.2	31.4	10.7	-1.1	0.7	1.2	0.4	1.2	0.2	1.3	0.2	1.3	0.03	1.0	0.8
				VTETEPVSSFPAGYSDVDQQSSSSRLRSAVSR	3	97.2%	1																									
IPI00878765	COMT	Protein	100.0%	9.9	1	1	1	2	343,158	328,388	372,920	403,224	29,311	32,607	26,604	32,345	19.1	22.2	16.0	17.9	-1.0	0.7	1.1	0.5	1.2	0.2	1.1	0.3	1.2	0.1	1.1	0.5
IPI00878855	COMT	Uncharacterized protein	100.0%	6.4	1	1	1	2	343,158	328,388	372,920	403,224	29,311	32,607	26,604	32,345	19.1	22.2	16.0	17.9	-1.0	0.7	1.1	0.5	1.2	0.2	1.1	0.3	1.2	0.1	1.1	0.5
				YDVDTLDMVFLDHWK	3	100.0%	1																									
IPI00878795	RANBP1	Uncharacterized protein	100.0%	20.8	1	1	2	1	642,256	648,506	602,723	690,438	46,974	29,200	36,137	10,573	16.4	10.1	13.4	3.4	1.0	0.9	-1.1	0.5	1.1	0.4	-1.1	0.4	1.1	0.2	1.1	0.07
				FASENDLPEWK	2	100.0%	2																									
IPI00878827	RD43;RPL3;LOC653	20 kDa protein	100.0%	5.0	1	1	2	1	3,562,920	3,729,846	3,126,128	4,195,880	423,966	302,187	360,390	109,223	26.6	18.1	25.8	5.8	1.0	0.8	-1.1	0.5	1.2	0.2	-1.2	0.2	1.1	0.2	1.3	0.04
				HGSLGFLPR	2	100.0%	2																									
IPI00878833	TES	9 kDa protein	100.0%	43.0	2	2	2	1	1,385,439	1,498,417	1,294,772	1,558,093	226,784	118,099	140,008	57,530	36.6	17.6	24.2	8.3	1.1	0.7	-1.1	0.7	1.1	0.5	-1.2	0.3	1.0	0.7	1.2	0.1
				NVMILTNPVAAK	2	100.0%	1																									
				NVSINTVTYEWAPPVQNQALAR	2	89.6%	1																									
IPI00878953	APOE	MRNA for apolipoprotein E	100.0%	8.3	2	2	2	3	3,015,760	3,191,455	3,068,833	3,484,340	120,748	148,853	136,273	183,049	9.0	10.4	9.9	11.8	1.1	0.4	1.0	0.8	1.2	0.07	-1.0	0.6	1.1	0.2	1.1	0.1
IPI00879368	APOE	Uncharacterized protein	100.0%	11.1	2	2	2	3	3,015,760	3,191,455	3,068,833	3,484,340	120,748	148,853	136,273	183,049	9.0	10.4	9.9	11.8	1.1	0.4	1.0	0.8	1.2	0.07	-1.0	0.6	1.1	0.2	1.1	0.1
IPI00879456	APOE	Uncharacterized protein	100.0%	11.0	2	2	2	3	3,015,760	3,191,455	3,068,833	3,484,340	120,748	148,853	136,273	183,049	9.0	10.4	9.9	11.8	1.1	0.4	1.0	0.8	1.2	0.07	-1.0	0.6	1.1	0.2	1.1	0.1

				GEVQAMLGQSTEELR	2	100.0%	1																									
				LGPLVEQGR	2	89.4%	1																									
IPI00879051	-	15 kDa protein	100.0%	25.6	3	4	6	1	2,408,683	2,378,339	2,322,261	2,567,089	236,354	132,301	130,309	108,903	21.9	12.4	12.6	9.5	-1.0	0.9	-1.0	0.8	1.1	0.6	-1.0	0.8	1.1	0.3	1.1	0.2
				GEHPGLSIGDVAK	2	99.4%	1																									
				IKGEHPGLSIGDVAK	3	100.0%	2																									
				LGEMWNNTAADDKQPYEK	2	99.9%	1																									
				LGEMWNNTAADDKQPYEK	3	100.0%	2																									
IPI00879132	CBX1	Uncharacterized protein	100.0%	16.4	2	2	2	1	3,480,293	3,590,667	3,409,840	3,860,473	284,202	117,327	262,821	216,847	18.3	7.3	17.2	12.6	1.0	0.7	-1.0	0.9	1.1	0.3	-1.1	0.5	1.1	0.3	1.1	0.2
				KKVEEVLEEEEEEYVVEK	3	99.9%	1																									
				VEEVLEEEEEEYVVEK	2	100.0%	1																									
IPI00879160	RANBP1	14 kDa protein	100.0%	25.0	2	2	3	1	2,070,457	1,909,177	1,773,985	2,037,947	95,908	164,269	228,967	88,015	10.4	19.2	28.9	9.7	-1.1	0.4	-1.2	0.3	-1.0	0.8	-1.1	0.6	1.1	0.5	1.1	0.3
				AWVWNTHADFADECPKPELLAIR	3	100.0%	1																									
				FLNAENAQK	2	99.9%	2																									
IPI00879328	CTSD	30 kDa protein	100.0%	19.6	4	5	9	1	10,146,895	10,628,623	9,776,290	11,494,050	941,228	618,022	507,205	440,186	20.7	13.0	11.6	8.6	1.0	0.7	-1.0	0.7	1.1	0.2	-1.1	0.3	1.1	0.3	1.2	0.03
				DPDAQPGGELMLGGTDSK	2	100.0%	2																									
				FDGILGMAYPR	2	100.0%	2																									
				ISVNNVLPVFDNLMQQK	2	100.0%	2																									
				ISVNNVLPVFDNLMQQK	3	100.0%	2																									
				QVFGEATK	2	95.4%	1																									
IPI00219153	RPL22	60S ribosomal protein L22	100.0%	16.3	1	1	1	1	2,064,695	2,229,610	2,140,980	2,387,825	79,409	128,117	192,702	108,169	8.6	12.9	20.1	10.1	1.1	0.3	1.0	0.7	1.2	0.04	-1.0	0.7	1.1	0.4	1.1	0.3
				AGNLGGGVVTIER	2	100.0%	1																									
IPI00879501	HNRNPA1L2	Heterogeneous nuclear ribonucleoprotein A1-like 2	100.0%	9.1	2	2	4	1	1,557,922	1,583,267	1,633,252	1,820,219	76,101	90,981	120,387	58,398	10.9	12.9	16.5	7.2	1.0	0.8	1.0	0.6	1.2	0.03	1.0	0.7	1.1	0.06	1.1	0.2
				EDSQRPGAHLTVK	2	90.2%	1																									
				LFIGGLSFETTDESLR	2	100.0%	3																									
IPI00879638	DDX17	cDNA FLJ58652, highly similar to Probable ATP-dependent RNA helicase DDX17	100.0%	12.6	5	5	8	1	14,900,181	14,230,372	15,498,083	16,164,304	1,068,063	169,797	1,269,381	866,130	16.0	2.7	18.3	12.0	-1.0	0.6	1.0	0.7	1.1	0.4	1.1	0.4	1.1	0.09	1.0	0.7
				APILIATDVASR	2	100.0%	2																									
				CTYLVLDEADR	2	99.1%	1																									
				ELAQQVQQVADDYGK	2	100.0%	2																									
				LIQLMEEIMAEK	2	100.0%	2																									
				LIQLMEEIMAEKENK	3	99.7%	1																									
IPI00879666	RANBP1	Uncharacterized protein	100.0%	31.2	4	4	6	2	3,339,405	3,240,251	2,977,360	3,443,965	184,765	162,908	283,208	104,425	12.4	11.2	21.3	6.8	-1.0	0.7	-1.1	0.3	1.0	0.6	-1.1	0.4	1.1	0.3	1.2	0.2
IPI01015397	RANBP1	RAN binding protein 1, isoform CRA_b	100.0%	42.4	4	4	6	2	3,339,405	3,240,251	2,977,360	3,443,965	184,765	162,908	283,208	104,425	12.4	11.2	21.3	6.8	-1.0	0.7	-1.1	0.3	1.0	0.6	-1.1	0.4	1.1	0.3	1.2	0.2
				AWVWNTHADFADECPKPELLAIR	3	100.0%	1																									
				FASENDLPEWK	2	100.0%	2																									
				FLNAENAQK	2	99.9%	2																									
				ICANHYITPMMELKPNAGSDR	3	98.6%	1																									
IPI00879681	RANGAP1	cDNA FLJ51385, highly similar to Ran GTPase-activating protein 1	100.0%	5.1	2	2	3	1	3,015,010	2,962,165	2,940,495	3,317,395	227,672	155,635	347,971	185,481	16.9	11.8	26.5	12.5	-1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.4
				AFNSSSFNSNTFLTR	2	81.6%	1																									
				VINLNDNTFTEK	2	100.0%	2																									
IPI00879701	LOC100287852	protein FAM136A-like, partial	100.0%	10.7	1	1	2	1	703,447	789,080	657,657	753,520	28,080	69,422	39,733	34,088	8.9	19.7	13.5	10.1	1.1	0.3	-1.1	0.4	1.1	0.3	-1.2	0.1	-1.0	0.7	1.1	0.1
				CVDDHMHLIPTMTK	2	98.9%	2																									
IPI00879729	SCIN	isoform 3 of Adseverin	100.0%	7.5	3	3	3	1	11,561,450	12,253,250	11,386,870	13,349,330	981,265	518,708	1,012,141	488,638	19.0	9.5	19.9	8.2	1.1	0.6	-1.0	0.9	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.1
				LPQNSGYIWVGK	2	98.5%	1																									
				MYLETDPSGR	2	99.4%	1																									
				TAEEFLQQMNYSK	2	99.9%	1																									
IPI00879764	TTC38	6 kDa protein	99.8%	22.6	1	1	1	2	784,838	803,790	872,123	846,813	65,943	42,667	66,320	84,886	18.8	11.9	17.0	22.4	1.0	0.8	1.1	0.4	1.1	0.6	1.1	0.4	1.1	0.7	-1.0	0.8
IPI00910722	TTC38	cDNA FLJ58627	99.8%	2.9	1	1	1	2	784,838	803,790	872,123	846,813	65,943	42,667	66,320	84,886	18.8	11.9	17.0	22.4	1.0	0.8	1.1	0.4	1.1	0.6	1.1	0.4	1.1	0.7	-1.0	0.8
				LPLSTTSNEACK	2	99.5%	1																									
IPI00879792	CYB5R3	Cytochrome b5 reductase 3	100.0%	7.5	1	1	1	1	1,747,740	1,657,068	1,775,358	1,549,320	68,624	48,327	95,078	45,551	8.8	6.5	12.0	6.6	-1.1	0.3	1.0	0.8	-1.1	0.04	1.1	0.3	-1.1	0.1	-1.1	0.06
				GPSGLLVYQGK	2	100.0%	1																									
IPI00883655	DPYSL2	dihydropyrimidinase-related protein 2 isoform 1	100.0%	34.4	14	15	21	1	20,926,413	22,292,278	21,413,624	24,089,557	2,175,556	923,319	1,446,742	570,017	23.3	9.3	15.1	5.3	1.1	0.6	1.0	0.9	1.2	0.2	-1.0	0.6	1.1	0.1	1.1	0.1
				AITIANQTNCPLYITK	2	100.0%	1																									
				DIGAIAQVHAENGDIIAEEQQR	3	100.0%	2																									
				DNFTLIPEGTNGTEER	2	88.3%	1																									
				FQLTDCQIYEVLSVIR	2	96.3%	1																									
				FQLTDCQIYEVLSVIR	3	97.5%	1																									
				FQMPDQGMTSADDFFQGTK	2	100.0%	2																									
				GIQEEMEALVK	2	100.0%	2																									
				GLYDGPVCEVSVTPK	2	100.0%	2																									
				ILDLGITGPEGHVLSRPEEVEAEAVNR	3	100.0%	1																									
				IVNDDQSFYADIYMEDGLIK	2	100.0%	1																									
				MDENQFVAVTSTNAAK	2	98.9%	1																									
				NLHQSGFSLSGAQIDDNIPR	3	100.0%	1																									
				QIGENLIVPGGVK	2	99.9%	2																									
				RAGGEPSVESGR	2	88.3%	1																									
				SSAEVIAQAR	2	99.4%	2																									
IPI00883896	LIMA1	isoform 4 of LIM domain and actin-binding protein 1	100.0%	19.6	10	11	13	1	18,493,170	19,392,864	20,234,853	21,675,997	797,015	965,298	1,311,508	599,087	9.6	11.1	14.5	6.2	1.0	0.5	1.1	0.3	1.2	0.01	1.0	0.6	1.1	0.08	1.1	0.3
				IAWPPPTELGSSGSALEEGIK	2	99.9%	1																									
				ISANENSLAVR	2	100.0%	2																									
				NENEEILERPAQLANAR	3	100.0%	1																									
				QSSSTNYTNELK	2	99.9%	1																									
				SEVQQPVHPKPLSPDSR	3	87.4%	1																									
				SLNWSSFVDNTFAEEFTTQNQK	2	83.9%	1																									
				SLNWSSFVDNTFAEEFTTQNQK	3	100.0%	1																									
				SNTENLSQHFR	2	94.4%	1																									
				SPPEALVQGR	2	99.9%	1																									
				SQDVELWEGEVVK	2	100.0%	2																									
				STPAEDDSPGDSQVK	2	98.5%	1																									
IPI00883946	LASP1	Uncharacterized protein	100.0%	43.4	8	9	12	1	17,154,828	17,425,189	15,777,226	18,440,490	845,826	889,673	539,971	594,562	11.0	11.4	7.7	7.2	1.0	0.8	-1.1	0.2	1.1	0.2	-1.1	0.2	1.1	0.4	1.2	0.01
				GFSVVADTPELQR	2	100.0%	2																									
				KPYCNAHYPK	2	99.4%	1																									
				KPYCNAHYPK	3	99.4%	1																									
				LKQQSELQSQVR	3	95.4%	1																									
				MGPSGGEGMEPER	2	99.7%	1																									
				MGPSGGEGMEPERR	2	93.1%	1																									
				QQSELQSQVR	2	100.0%	2																									
				QSFTMVADTPENLR	2	100.0%	1																									
				TQDQISNIK	2	100.0%	2																									
IPI00884105	LAMP1	Lysosome-associated membrane glycoprotein 1	100.0%	5.0	2	2	2	1	2,828,015	3,218,030	3,502,125	3,851,905	454,659	215,295	350,858	246,682	36.0	15.0	22.4	14.3	1.1	0.5	1.2	0.3	1.4	0.08	1.1	0.5	1.2	0.09	1.1	0.4
				FFLQGIQLNTILPDAR	2	99.8%	1																									
				FFLQGIQLNTILPDARDPAFK	3	99.9%	1																									
IPI00884126	BTNL8	butyrophilin-like protein 8 isoform 3 precursor	91.0%	5.0	1	1	1	1	774,373	806,627	1,057,148	1,109,295	149,022	155,125	224,030	88,239	43.0	43.0	47.4	17.8	1.0	0.9	1.4	0.3	1.4	0.09	1.3	0.4	1.4	0.1	1.0	0.8
				LGSALGSVPLISITGYVDR	2	91.0%	1																									
IPI00884329	-	Similar to Protein cramped-like	100.0%	26.6	1	1	1	1	262,542	297,003	268,296	256,668	15,378	19,675	27,765	23,492	13.1	14.8	23.1	20.5	1.1	0.2	1.0	0.9	-1.0	0.8	-1.1	0.4	-1.2	0.2	-1.0	0.8
				MASNIFGPTEEPQNIPK	2	100.0%	1																									
IPI00885057	CHORDC1	isoform 2 of Cysteine and histidine-rich domain-containing protein 1	100.0%	9.6	2	2	2	1	1,369,169	1,396,999	1,477,377	1,533,361	168,552	70,332	171,093	59,631	27.5	11.3	25.9	8.7	1.0	0.9	1.1	0.7	1.1	0.4	1.1	0.7	1.1	0.2	1.0	0.8
				FQEHIIQAPKPVEAIK	3	95.0%	1																									
				RPSPDEPMTNLELK	2	99.9%	1																									
IPI00885081	HDGFRP2	isoform 2 of Hepatoma-derived growth factor-related protein 2	100.0%	3.4	2	2	2	1	3,428,100	3,339,952	3,410,245	3,919,807	192,234	200,035	198,613	268,873	12.5	13.4	13.0	15.3	-1.0	0.8	-1.0	1	1.1	0.2	1.0	0.8	1.2	0.1	1.1	0.2
				GYPHWPAR	2	99.0%	1																									
				LAGEELAGEEAPQEK	2	99.9%	1																									
IPI00885203	BAX	isoform Psi of Apoptosis regulator BAX	100.0%	13.9	2	2	3	1	2,015,088	2,014,736	2,152,786	2,564,300	254,764	128,476	181,812	126,707	28.3	14.3	18.9	11.1	-1.0	1	1.1	0.7	1.3	0.09	1.1	0.6	1.3	0.02	1.2	0.1
				IGDELDSNMELQR	2	100.0%	2																									
				MIAAVDTDSPR	2	99.0%	1																									
IPI00887249	EYS	isoform 1 of Protein eyes shut homolog	92.9%	0.9	1	1	1	4	1,060,168	971,788	1,123,038	1,349,008	191,571	80,688	132,303	103,912	40.4	18.6	26.3	17.2	-1.1	0.7	1.1	0.8	1.3	0.2	1.2	0.4	1.4	0.02	1.2	0.2
IPI00914000	EYS	Protein	92.9%	5.7	1	1	1	4	1,060,168	971,788	1,123,038	1,349,008	191,571	80,688	132,303	103,912	40.4	18.6	26.3	17.2	-1.1	0.7	1.1	0.8	1.3	0.2	1.2	0.4	1.4	0.02	1.2	0.2
IPI00923621	EYS	isoform 3 of Protein eyes shut homolog	92.9%	0.9	1	1	1	4	1,060,168	971,788	1,123,038	1,349,008	191,571	80,688	132,303	103,912	40.4	18.6	26.3	17.2	-1.1	0.7	1.1	0.8	1.3	0.2	1.2	0.4	1.4	0.02	1.2	0.2
IPI00953555	EYS	Uncharacterized protein	92.9%	0.9	1	1	1	4	1,060,168	971,788	1,123,038	1,349,008	191,571	80,688	132,303	103,912	40.4	18.6	26.3	17.2	-1.1	0.7	1.1	0.8	1.3	0.2	1.2	0.4	1.4	0.02	1.2	0.2
				GLGNPEGHPNAGRSVGQCHASPCSLMK	3	92.9%	1																									
IPI00887363	LOC100132707	Uncharacterized protein	92.7%	27.6	1	1	1	1	16,864,600	15,511,300	15,757,500	17,263,500	1,453,909	959,946	716,824	816,150	19.3	13.8	10.2	10.6	-1.1	0.5	-1.1	0.5	1.0	0.8	1.0	0.8	1.1	0.2	1.1	0.2
				FLGRRFMTAEFLLEDPSSGSLIPQESSWK	3	92.7%	1																									
IPI00887673	AKR1C2	aldo-keto reductase family 1 member C2 isoform 2	100.0%	15.8	1	1	1	1	1,110,581	1,049,113	947,796	1,225,583	159,667	78,789	83,983	35,991	32.2	16.8	19.8	6.6	-1.1	0.7	-1.2	0.4	1.1	0.5	-1.1	0.4	1.2	0.08	1.3	0.02
				LNDGHFMPVLGFGTYAPAEVPK	3	100.0%	1																									
IPI00887938	LOC389217	protein SET-like	100.0%	2.6	1	1	2	2	2,027,895	1,944,108	1,938,745	2,127,133	165,551	113,741	200,329	106,092	18.3	13.1	23.1	11.2	-1.0	0.7	-1.0	0.7	1.0	0.6	-1.0	1	1.1	0.3	1.1	0.4
IPI00888355	LOC389217	protein SET-like	100.0%	2.8	1	1	2	2	2,027,895	1,944,108	1,938,745	2,127,133	165,551	113,741	200,329	106,092	18.3	13.1	23.1	11.2	-1.0	0.7	-1.0	0.7	1.0	0.6	-1.0	1	1.1	0.3	1.1	0.4
				VEVTEFEDIK	2	100.0%	2																									
IPI00888280	LOC100133944	IgGFc-binding protein-like	100.0%	11.8	24	24	29	2	37,129,933	39,272,615	37,442,227	42,426,470	3,195,721	1,490,815	2,470,729	1,115,924	19.3	8.5	14.8	5.9	1.1	0.6	1.0	0.9	1.1	0.2	-1.0	0.5	1.1	0.1	1.1	0.1
IPI00936296	LOC100290309	IgGFc-binding protein-like	100.0%	11.8	24	24	29	2	37,129,933	39,272,615	37,442,227	42,426,470	3,195,721	1,490,815	2,470,729	1,115,924	19.3	8.5	14.8	5.9	1.1	0.6	1.0	0.9	1.1	0.2	-1.0	0.5	1.1	0.1	1.1	0.1
				AGCVAESTAVCR	2	100.0%	2																									
				AIGYATAADCGR	2	100.0%	1																									
				AISGLTIDGHAVGAK	2	100.0%	1																									
				APGWDPLCWDECR	2	100.0%	1																									
				ASQHGSDVVIETDFGLR	3	100.0%	1																									
				CLANGGIHYITLDGR	2	99.0%	1																									
				CPGLQNTIPWYR	2	100.0%	1																									
				EGCVCDAGFVLSGDTCVPVGQCGCLHDGR	3	92.9%	1																									
				GATTSPGVYELSSR	2	100.0%	1																									
				GEVGFVLVDNQR	2	100.0%	2																									
				LPVSLSEGR	2	95.8%	1																									
				LPVVLANGQIR	2	100.0%	2																									
				NPQGPFATCQAVLSPSEYFR	2	100.0%	1																									
				SPANCPLSCPANSR	2	99.8%	1																									
				SVPGCEGVALVVAQTK	2	100.0%	1																									
				TPDGSLLVR	2	99.9%	1																									
				TVLSPVEPSCEGMQCAAGQR	3	98.8%	1																									
				VAVIVSNDHAGK	2	99.4%	1																									
				VAYDLVYYVR	2	100.0%	1																									
				VNGVLTALPVSVADGR	2	100.0%	2																									
				VTLQPYNVAQLQSSVDLSGSK	3	99.9%	1																									
				VTVNGVDMK	2	100.0%	2																									
				YDLAFVVASQATK	2	100.0%	1																									
				YQKEEFCGLLSSPTGPLSSCHK	3	99.8%	1																									
IPI00888475	MAP4	isoform 6 of Microtubule-associated protein 4	100.0%	12.3	10	12	13	1	7,846,977	7,875,447	7,817,931	8,824,508	815,198	293,521	414,856	331,349	23.2	8.3	11.9	8.4	1.0	1	-1.0	1	1.1	0.3	-1.0	0.9	1.1	0.06	1.1	0.09
				DFIATLEAEAFDDVVGETVGK	2	100.0%	2																									
				DFIATLEAEAFDDVVGETVGK	3	100.0%	1																									
				DMSPLSETEMALGK	2	99.4%	1																									
				QPAPTTIGGLNK	2	99.1%	1																									

				SVPADLSRPK	2	86.6%	1																									
				TAGPIASAQK	2	99.8%	1																									
				TTTAAAVASTGPSSR	2	99.6%	1																									
				TTTLSGTAPAAGVVPSR	2	100.0%	1																									
				VALSSETEVALAR	2	98.0%	1																									
				VGSLDNVGHLPAGGAVK	2	99.7%	1																									
				VGSLDNVGHLPAGGAVK	3	100.0%	1																									
				WPTETDVSSAK	2	99.7%	1																									
IPI00888697	LOC100287294	equilibrative nucleoside transporter 4-like	96.1%	6.2	1	1	1	2	1,618,865	1,477,040	1,674,320	1,728,370	148,109	100,378	134,485	131,576	20.5	15.2	18.0	17.0	-1.1	0.5	1.0	0.8	1.1	0.6	1.1	0.3	1.2	0.2	1.0	0.8
IPI00973094	LOC402269	hypothetical protein LOC402269	96.1%	5.5	1	1	1	2	1,618,865	1,477,040	1,674,320	1,728,370	148,109	100,378	134,485	131,576	20.5	15.2	18.0	17.0	-1.1	0.5	1.0	0.8	1.1	0.6	1.1	0.3	1.2	0.2	1.0	0.8
				WPLSADVCSVLVGGPGK	2	96.1%	1																									
IPI00889133	HMCN2	LOW QUALITY PROTEIN: hemicentin-2	99.5%	0.8	1	1	1	1	899,530	953,110	1,060,073	1,143,563	121,003	58,637	94,642	77,080	30.1	13.8	20.0	15.1	1.1	0.7	1.2	0.3	1.3	0.1	1.1	0.4	1.2	0.08	1.1	0.5
				TETVSQVAGSPLVLTCDVSGVPAPTVTWLK	3	92.4%	1																									
IPI00889541	DDX17	isoform 4 of Probable ATP-dependent RNA helicase DDX17	100.0%	26.9	15	15	18	1	118,331,141	110,931,486	113,810,787	127,483,037	4,225,076	4,713,856	8,687,098	4,257,010	8.0	9.5	17.1	7.5	-1.1	0.3	-1.0	0.7	1.1	0.2	1.0	0.8	1.1	0.03	1.1	0.2
				APILIATDVASR	2	100.0%	2																									
				CTYLVLDEADR	2	99.1%	1																									
				DMVGIAQTGSGK	2	99.7%	1																									
				ESAAPAAAPTAEAPPPSVVTRPEPQALPSPAIR	3	100.0%	1																									
				FVINYDYPNSSEDYVHR	3	99.9%	1																									
				GDGPICLVLAPTR	2	99.3%	1																									
				LIDFLESGK	2	93.2%	1																									
				LIQLMEEIMAEK	2	100.0%	2																									
				LIQLMEEIMAEKENK	3	99.7%	1																									
				LMQLVDHR	2	95.4%	1																									
				NFYVEHPEVAR	2	99.9%	1																									
				SSQSSSQQFSGIGR	2	100.0%	2																									
				STCIYGGAPK	2	99.5%	1																									
				TTSSANNPNLMYQDECDRR	3	87.3%	1																									
				VLEEANQAINPK	2	99.9%	1																									
IPI00889791	XRCC6	cDNA FLJ31224 fis, clone KIDNE2004305, highly similar to ATP-dependent DNA he	100.0%	15.3	6	7	8	1	7,249,341	7,200,493	7,298,063	8,195,917	815,383	235,637	422,430	161,789	25.2	7.3	12.9	4.4	-1.0	1	1.0	1	1.1	0.3	1.0	0.8	1.1	0.008	1.1	0.1
				DIISIAEDEDLR	2	99.9%	1																									
				IQVTPPGFQLVFLPFADDKR	3	93.8%	1																									
				KQELLEALTK	2	99.8%	1																									
				LGSLVDEFK	2	99.5%	1																									
				NLEALALDLMEPEQAVDLTLPK	2	100.0%	2																									
				NLEALALDLMEPEQAVDLTLPK	3	100.0%	1																									
				QIILEKEETEELKR	3	90.2%	1																									
IPI00890829	MYEOV2	Uncharacterized protein	99.5%	25.6	1	1	2	1	871,813	839,448	944,028	933,002	69,141	23,237	87,779	32,693	17.7	6.2	20.8	7.8	-1.0	0.7	1.1	0.5	1.1	0.4	1.1	0.3	1.1	0.05	-1.0	0.9
				AVHADFFNDFEDLFDDDDIQ	2	99.5%	2																									
IPI00892518	2-Sep	Uncharacterized protein	100.0%	17.8	1	1	1	1	279,854	307,280	281,634	338,924	32,550	16,796	29,416	20,565	26.0	12.2	23.4	13.6	1.1	0.5	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.3	1.2	0.1
				MQAQMQMQMQGGDGDGGALGHHV	3	100.0%	1																									
IPI00892521	ST13	Protein	100.0%	28.8	3	3	5	1	4,702,381	5,253,452	4,406,650	5,146,058	342,538	543,637	127,595	201,251	16.3	23.1	6.5	8.7	1.1	0.4	-1.1	0.5	1.1	0.3	-1.2	0.2	-1.0	0.9	1.2	0.01
				AIEINPDSAQPYK	2	100.0%	2																									
				LDYDEDASAMLK	2	100.0%	2																									
				LLGHWEEAAHDLALACK	3	100.0%	1																									
IPI00892588	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	33.5	5	5	6	2	4,763,830	4,657,610	4,408,794	5,195,108	371,524	239,183	328,211	181,699	17.4	11.5	16.7	7.8	-1.0	0.8	-1.1	0.5	1.1	0.3	-1.1	0.6	1.1	0.1	1.2	0.07
IPI00985355	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	24.5	5	5	6	2	4,763,830	4,657,610	4,408,794	5,195,108	371,524	239,183	328,211	181,699	17.4	11.5	16.7	7.8	-1.0	0.8	-1.1	0.5	1.1	0.3	-1.1	0.6	1.1	0.1	1.2	0.07
				CIALAQLLVEQNFPAIAIHR	3	100.0%	2																									
				FMQDPMEIFVDDETK	2	99.8%	1																									
				HFILDECDK	2	99.7%	1																									
				MLEQLDMR	2	100.0%	1																									
				RDVQEIFR	2	98.1%	1																									
IPI00892657	NUCB1	Protein	100.0%	8.1	2	2	2	1	1,925,867	1,965,352	2,389,643	2,100,113	130,723	237,348	115,482	76,183	15.2	27.0	10.8	8.1	1.0	0.9	1.2	0.03	1.1	0.3	1.2	0.1	1.1	0.6	-1.1	0.07
				DLELLIQTATR	2	99.8%	1																									
				LVTLEEFLASTQR	2	99.4%	1																									
IPI00892668	PPP1CB	Serine/threonine-protein phosphatase	100.0%	21.0	2	2	2	2	3,168,073	3,640,330	3,243,457	3,811,628	217,146	490,699	360,898	287,951	15.3	30.1	24.9	16.9	1.1	0.4	1.0	0.9	1.2	0.1	-1.1	0.5	1.0	0.8	1.2	0.3
IPI00894333	PPP1CB	Serine/threonine-protein phosphatase	100.0%	23.2	2	2	2	2	3,168,073	3,640,330	3,243,457	3,811,628	217,146	490,699	360,898	287,951	15.3	30.1	24.9	16.9	1.1	0.4	1.0	0.9	1.2	0.1	-1.1	0.5	1.0	0.8	1.2	0.3
				IVQMTEAEVR	2	99.9%	1																									
				SREIFLSQPILLELEAPLK	3	98.3%	1																									
IPI00892782	NUCB1	Uncharacterized protein	100.0%	4.1	1	1	1	1	835,317	868,697	1,009,133	1,009,043	77,962	88,339	83,001	57,781	20.9	22.7	18.4	12.8	1.0	0.8	1.2	0.2	1.2	0.1	1.2	0.3	1.2	0.2	-1.0	1
				DLELLIQTATR	2	99.8%	1																									
IPI00892810	2-Sep	Uncharacterized protein	100.0%	19.1	2	2	3	6	679,523	750,115	751,757	855,426	81,621	24,485	96,245	46,438	26.9	7.3	28.6	12.1	1.1	0.4	1.1	0.6	1.3	0.1	1.0	1	1.1	0.08	1.1	0.4
IPI00893096	2-Sep	Uncharacterized protein	100.0%	18.9	2	2	3	6	679,523	750,115	751,757	855,426	81,621	24,485	96,245	46,438	26.9	7.3	28.6	12.1	1.1	0.4	1.1	0.6	1.3	0.1	1.0	1	1.1	0.08	1.1	0.4
IPI00894055	2-Sep	Protein	100.0%	17.4	2	2	3	6	679,523	750,115	751,757	855,426	81,621	24,485	96,245	46,438	26.9	7.3	28.6	12.1	1.1	0.4	1.1	0.6	1.3	0.1	1.0	1	1.1	0.08	1.1	0.4
IPI00894199	2-Sep	Uncharacterized protein	100.0%	16.2	2	2	3	6	679,523	750,115	751,757	855,426	81,621	24,485	96,245	46,438	26.9	7.3	28.6	12.1	1.1	0.4	1.1	0.6	1.3	0.1	1.0	1	1.1	0.08	1.1	0.4
IPI00894283	2-Sep	Uncharacterized protein	100.0%	23.1	2	2	3	6	679,523	750,115	751,757	855,426	81,621	24,485	96,245	46,438	26.9	7.3	28.6	12.1	1.1	0.4	1.1	0.6	1.3	0.1	1.0	1	1.1	0.08	1.1	0.4
IPI00894322	2-Sep	Uncharacterized protein	100.0%	21.4	2	2	3	6	679,523	750,115	751,757	855,426	81,621	24,485	96,245	46,438	26.9	7.3	28.6	12.1	1.1	0.4	1.1	0.6	1.3	0.1	1.0	1	1.1	0.08	1.1	0.4
				LTVVDTPGYGDAINCR	2	100.0%	1																									
				TIISYIDEQFER	2	100.0%	2																									
IPI00892872	FLOT1	cDNA FLJ54943, highly similar to Flotillin-1	99.4%	6.3	2	2	2	1	9,186,310	8,126,383	9,629,888	8,843,945	424,874	291,416	459,877	431,315	10.3	8.0	10.7	10.9	-1.1	0.07	1.0	0.5	-1.0	0.6	1.2	0.02	1.1	0.2	-1.1	0.2
				AQADLAYQLQVAK	2	96.2%	1																									
				VTGEVLDILTR	2	99.4%	1																									
IPI00892880	PNPT1	Protein	96.6%	13.0	1	1	1	2	469,802	442,145	557,466	534,390	62,837	47,973	79,904	45,366	29.9	24.3	32.1	19.0	-1.1	0.7	1.2	0.4	1.1	0.4	1.3	0.3	1.2	0.2	-1.0	0.8
IPI00894110	PNPT1	59 kDa protein	96.6%	3.4	1	1	1	2	469,802	442,145	557,466	534,390	62,837	47,973	79,904	45,366	29.9	24.3	32.1	19.0	-1.1	0.7	1.2	0.4	1.1	0.4	1.3	0.3	1.2	0.2	-1.0	0.8
				FPEADPYEIIESFNVVAK	2	96.6%	1																									
IPI00892906	SELENBP1	18 kDa protein	100.0%	17.6	2	2	2	2	2,735,327	3,046,212	2,568,117	3,657,975	339,336	213,132	331,164	298,275	27.7	15.6	28.8	18.2	1.1	0.5	-1.1	0.7	1.3	0.08	-1.2	0.3	1.2	0.1	1.4	0.04
IPI00965813	SELENBP1	Selenium binding protein 1 (Fragment)	100.0%	14.4	2	2	2	2	2,735,327	3,046,212	2,568,117	3,657,975	339,336	213,132	331,164	298,275	27.7	15.6	28.8	18.2	1.1	0.5	-1.1	0.7	1.3	0.08	-1.2	0.3	1.2	0.1	1.4	0.04
				IYVVDVGSEPR	2	99.7%	1																									
				NTGTEAPDYLATVDVDPK	2	100.0%	1																									
IPI00892935	XPO1	Uncharacterized protein	100.0%	9.1	1	1	2	6	399,967	449,854	479,957	468,881	30,996	15,500	44,286	26,952	17.3	7.7	20.6	12.9	1.1	0.2	1.2	0.2	1.2	0.1	1.1	0.5	1.0	0.6	-1.0	0.8
IPI00893403	XPO1	9 kDa protein	100.0%	16.7	1	1	2	6	399,967	449,854	479,957	468,881	30,996	15,500	44,286	26,952	17.3	7.7	20.6	12.9	1.1	0.2	1.2	0.2	1.2	0.1	1.1	0.5	1.0	0.6	-1.0	0.8
IPI00893771	XPO1	Uncharacterized protein	100.0%	12.0	1	1	2	6	399,967	449,854	479,957	468,881	30,996	15,500	44,286	26,952	17.3	7.7	20.6	12.9	1.1	0.2	1.2	0.2	1.2	0.1	1.1	0.5	1.0	0.6	-1.0	0.8
IPI00893889	XPO1	Uncharacterized protein	100.0%	12.6	1	1	2	6	399,967	449,854	479,957	468,881	30,996	15,500	44,286	26,952	17.3	7.7	20.6	12.9	1.1	0.2	1.2	0.2	1.2	0.1	1.1	0.5	1.0	0.6	-1.0	0.8
IPI00894059	XPO1	Uncharacterized protein	100.0%	12.8	1	1	2	6	399,967	449,854	479,957	468,881	30,996	15,500	44,286	26,952	17.3	7.7	20.6	12.9	1.1	0.2	1.2	0.2	1.2	0.1	1.1	0.5	1.0	0.6	-1.0	0.8
IPI00894253	XPO1	Uncharacterized protein	100.0%	6.7	1	1	2	6	399,967	449,854	479,957	468,881	30,996	15,500	44,286	26,952	17.3	7.7	20.6	12.9	1.1	0.2	1.2	0.2	1.2	0.1	1.1	0.5	1.0	0.6	-1.0	0.8
				YYGLQILENVIK	2	100.0%	2																									
IPI00892957	ITSN2	isoform 3 of Intersectin-2	98.8%	2.0	1	1	1	4	486,805	393,728	539,943	432,693	28,273	30,650	53,081	50,001	13.0	17.4	22.0	25.8	-1.2	0.06	1.1	0.4	-1.1	0.4	1.4	0.04	1.1	0.5	-1.2	0.2
IPI00937782	ITSN2	isoform 1 of Intersectin-2	98.8%	1.5	1	1	1	4	486,805	393,728	539,943	432,693	28,273	30,650	53,081	50,001	13.0	17.4	22.0	25.8	-1.2	0.06	1.1	0.4	-1.1	0.4	1.4	0.04	1.1	0.5	-1.2	0.2
IPI00941398	ITSN2	isoform 2 of Intersectin-2	98.8%	1.5	1	1	1	4	486,805	393,728	539,943	432,693	28,273	30,650	53,081	50,001	13.0	17.4	22.0	25.8	-1.2	0.06	1.1	0.4	-1.1	0.4	1.4	0.04	1.1	0.5	-1.2	0.2
IPI00943185	ITSN2	intersectin-2 isoform 2	98.8%	2.0	1	1	1	4	486,805	393,728	539,943	432,693	28,273	30,650	53,081	50,001	13.0	17.4	22.0	25.8	-1.2	0.06	1.1	0.4	-1.1	0.4	1.4	0.04	1.1	0.5	-1.2	0.2
				AQSLIDLGSSSSTSSTASLSGNSPK	2	98.8%	1																									
IPI00892994	CPNE1	Uncharacterized protein	100.0%	12.9	4	4	6	1	1,513,728	1,826,694	1,614,401	1,944,049	106,750	74,225	87,124	148,626	15.8	9.1	12.1	17.1	1.2	0.04	1.1	0.5	1.3	0.05	-1.1	0.1	1.1	0.5	1.2	0.09
				FGIYDIDNK	2	98.5%	1																									
				LYGPTNFAPIINHVAR	3	100.0%	1																									
				SDPFLEFFR	2	100.0%	2																									
				SDPLCVLLQDVGGGSWAELGR	2	100.0%	2																									
IPI00893062	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	100.0%	19.9	8	9	10	1	11,577,737	11,701,359	11,237,292	12,823,900	1,145,913	359,621	803,847	329,285	22.1	6.9	16.0	5.7	1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.6	1.1	0.05	1.1	0.1
				DIISIAEDEDLR	2	99.9%	1																									
				IMATPEQVGK	2	97.7%	1																									
				IQVTPPGFQLVFLPFADDKR	3	93.8%	1																									
				KQELLEALTK	2	99.8%	1																									
				LGSLVDEFK	2	99.5%	1																									
				NIYVLQELDNPGAK	2	100.0%	1																									
				NLEALALDLMEPEQAVDLTLPK	2	100.0%	2																									
				NLEALALDLMEPEQAVDLTLPK	3	100.0%	1																									
				QIILEKEETEELKR	3	90.2%	1																									
IPI00893078	-	Uncharacterized protein	93.1%	1.0	1	1	1	1	4,196,240	4,207,920	4,779,400	4,238,930	563,648	201,534	613,317	352,706	30.0	10.7	28.7	18.6	1.0	1	1.1	0.5	1.0	1	1.1	0.4	1.0	0.9	-1.1	0.5
				INVYFLDYGNTDSIPFFDVK	3	93.1%	1																									
IPI00893087	LUC7L2	Putative uncharacterized protein CGI-59	100.0%	22.9	1	1	2	2	3,671,730	2,851,683	2,595,967	2,934,253	570,657	165,421	245,776	126,820	34.8	13.0	21.2	9.7	-1.3	0.2	-1.4	0.1	-1.3	0.3	-1.1	0.4	1.0	0.7	1.1	0.3
IPI00893315	LUC7L2	9 kDa protein	100.0%	13.3	1	1	2	2	3,671,730	2,851,683	2,595,967	2,934,253	570,657	165,421	245,776	126,820	34.8	13.0	21.2	9.7	-1.3	0.2	-1.4	0.1	-1.3	0.3	-1.1	0.4	1.0	0.7	1.1	0.3
				AMLDQLMGTSR	2	100.0%	2																									
IPI00893108	HADHB	Uncharacterized protein	100.0%	6.0	2	2	2	1	2,601,498	2,436,470	2,548,024	2,354,371	212,672	207,012	108,222	116,273	18.3	19.0	9.5	11.0	-1.1	0.6	-1.0	0.8	-1.1	0.3	1.0	0.6	-1.0	0.7	-1.1	0.3
				DFMYVSQDPK	2	99.9%	1																									
				TPFLLSGTSYK	2	99.8%	1																									
IPI00893179	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	100.0%	13.8	5	6	7	1	5,939,463	6,053,656	6,305,065	6,623,599	695,084	111,431	496,546	197,192	26.2	4.1	17.6	6.7	1.0	0.9	1.1	0.7	1.1	0.4	1.0	0.6	1.1	0.04	1.1	0.6
				DIISIAEDEDLR	2	99.9%	1																									
				IQVTPPGFQLVFLPFADDKR	3	93.8%	1																									
				LGSLVDEFK	2	99.5%	1																									
				NIYVLQELDNPGAK	2	100.0%	1																									
				NLEALALDLMEPEQAVDLTLPK	2	100.0%	2																									
				NLEALALDLMEPEQAVDLTLPK	3	100.0%	1																									
IPI00893203	ACP1	9 kDa protein	100.0%	37.5	2	2	2	1	5,873,309	7,471,358	6,165,343	9,967,502	1,549,667	943,048	548,140	731,328	59.0	28.2	19.9	16.4	1.3	0.4	1.0	0.9	1.7	0.04	-1.2	0.3	1.3	0.07	1.6	0.003
				LVTDQNISENWR	2	100.0%	1																									
				VDSAATSGYEIGNPPDYR	2	100.0%	1																									
IPI00893301	EIF3B	Uncharacterized protein	100.0%	9.6	2	2	2	1	3,345,802	3,543,356	3,529,396	3,896,422	308,248	175,600	283,841	96,689	20.6	11.1	18.0	5.6	1.1	0.6	1.1	0.7	1.2	0.2	-1.0	1	1.1	0.1	1.1	0.3
				DQYSVIFESGDR	2	93.8%	1																									
				TSIFWNDVKDPVSIEER	3	100.0%	1																									
IPI00910759	-	cDNA, FLJ79368, highly similar to Spliceosome RNA helicase Bat1	100.0%	8.0	2	2	2	6	2,398,271	2,363,955	2,129,156	2,547,993	211,888	154,755	224,383	139,817	19.8	14.6	23.6	12.3	-1.0	0.9	-1.1	0.4	1.1	0.6	-1.1	0.4	1.1	0.4	1.2	0.2
IPI00893446	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	13.0	2	2	2	6	2,398,271	2,363,955	2,129,156	2,547,993	211,888	154,755	224,383	139,817	19.8	14.6	23.6	12.3	-1.0	0.9	-1.1	0.4	1.1	0.6	-1.1	0.4	1.1	0.4	1.2	0.2
IPI00893920	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	9.0	2	2	2	6	2,398,271	2,363,955	2,129,156	2,547,993	211,888	154,755	224,383	139,817	19.8	14.6	23.6	12.3	-1.0	0.9	-1.1	0.4	1.1	0.6	-1.1	0.4	1.1	0.4	1.2	0.2
IPI00893927	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	12.5	2	2	2	6	2,398,271	2,363,955	2,129,156	2,547,993	211,888	154,755	224,383	139,817	19.8	14.6	23.6	12.3	-1.0	0.9	-1.1	0.4	1.1	0.6	-1.1	0.4	1.1	0.4	1.2	0.2
IPI00894545	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	12.3	2	2	2	6	2,398,271	2,363,955	2,129,156	2,547,993	211,888	154,755	224,383	139,817	19.8	14.6	23.6	12.3	-1.0	0.9	-1.1	0.4	1.1	0.6	-1.1	0.4	1.1	0.4	1.2	0.2
IPI00910878	DDX39B;SNORD84	cDNA FLJ54033, highly similar to Spliceosome RNA helicase Bat1	100.0%	7.0	2	2	2	6	2,398,271	2,363,955	2,129,156	2,547,993	211,888	154,755	224,383	139,817	19.8	14.6	23.6	12.3	-1.0	0.9	-1.1	0.4	1.1	0.6	-1.1	0.4	1.1	0.4	1.2	0.2
				HFILDECDK	2	99.7%	1																									
				MLEQLDMR	2	100.0%	1																									
IPI00893477	2-Sep	Uncharacterized protein	100.0%	17.0	1	1	1	1	201,752	235,425	191,062	242,388	23,862	22,366	23,634	15,647	26.5	21.2	27.7	14.4	1.2	0.3	-1.1	0.8	1.2	0.2	-1.2	0.2	1.0	0.8	1.3	0.1
				LTVVDTPGYGDAINCR	2	100.0%	1																									
IPI00893487	VARS	cDNA FLJ50305, highly similar to Valyl-tRNA synthetase	92.4%	5.4	1	1	1	1	450,027	474,799	467,707	515,303	21,667	18,014	21,443	15,816	10.8	8.5	10.3	6.9	1.1	0.4	1.0	0.6	1.1	0.04	-1.0	0.8	1.1	0.1	1.1	0.1
				VQGSDSDEEVVVATTR	2	92.4%	1																									
IPI00893498	C2orf73	7 kDa protein	96.3%	27.1	1	1	1	1	4,221,260	4,870,420	3,945,290	4,766,960	310,229	254,692	537,295	366,052	16.4	11.7	30.5	17.2	1.2	0.1	-1.1	0.7	1.1	0.3	-1.2	0.2	-1.0	0.8	1.2	0.2
				HWNLSSYHLTTLRAPR	3	96.3%	1																									
IPI00893518	FLOT1	Flotillin 1	99.4%	12.2	1	1	1	2	8,405,650	7,267,575	8,872,675	8,049,750	400,521	317,056	528,616	408,367	10.7	9.8	13.3	11.3	-1.2	0.06	1.1	0.5	-1.0	0.6	1.2	0.03	1.1	0.2	-1.1	0.3
IPI00894029	FLOT1	Flotillin 1	99.4%	5.9	1	1	1	2	8,405,650	7,267,575	8,872,675	8,049,750	400,521	317,056	528,616	408,367	10.7	9.8	13.3	11.3	-1.2	0.06	1.1	0.5	-1.0	0.6	1.2	0.03	1.1	0.2	-1.1	0.3
				VTGEVLDILTR	2	99.4%	1																									
IPI00893542	FSCN1	Uncharacterized protein	100.0%	14.2	1	1	1	3	649,000	722,202	639,068	832,854	93,970	47,246	92,056	74,367	32.4	14.6	32.2	20.0	1.1	0.5	-1.0	0.9	1.3	0.2	-1.1	0.4	1.2	0.2	1.3	0.1
IPI00894286	FSCN1	cDNA FLJ38511 fis, clone HCHON2000417, highly similar to FASCIN	100.0%	7.9	1	1	1	3	649,000	722,202	639,068	832,854	93,970	47,246	92,056	74,367	32.4	14.6	32.2	20.0	1.1	0.5	-1.0	0.9	1.3	0.2	-1.1	0.4	1.2	0.2	1.3	0.1
IPI00894471	FSCN1	Uncharacterized protein	100.0%	12.9	1	1	1	3	649,000	722,202	639,068	832,854	93,970	47,246	92,056	74,367	32.4	14.6	32.2	20.0	1.1	0.5	-1.0	0.9	1.3	0.2	-1.1	0.4	1.2	0.2	1.3	0.1

				YWTLTATGGVQSTASSK	2	99.5%	1																									
IPI00893645	2-Sep	Uncharacterized protein	100.0%	21.2	3	3	4	1	1,203,845	1,197,611	1,279,077	1,415,724	154,364	86,299	145,129	62,620	28.7	16.1	25.4	9.9	-1.0	1	1.1	0.7	1.2	0.2	1.1	0.6	1.2	0.08	1.1	0.4
				ILDEIEEHNIK	2	100.0%	1																									
				LTVVDTPGYGDAINCR	2	100.0%	1																									
				TIISYIDEQFER	2	100.0%	2																									
IPI00893650	HDLBP	Protein	100.0%	9.9	3	3	5	1	9,784,300	10,493,847	8,714,293	12,605,710	1,176,249	697,394	1,000,951	711,332	26.9	14.9	25.7	12.6	1.1	0.6	-1.1	0.5	1.3	0.07	-1.2	0.2	1.2	0.07	1.4	0.01
				ICLEIMQR	2	92.7%	1																									
				LQTQASATVAIPK	2	100.0%	2																									
				LVGEIMQETGTR	2	100.0%	2																									
IPI00893658	2-Sep	22 kDa protein	100.0%	18.1	2	2	2	1	804,176	754,776	808,954	899,222	112,309	67,345	71,106	53,941	31.2	20.0	19.7	13.4	-1.1	0.7	1.0	1	1.1	0.5	1.1	0.6	1.2	0.1	1.1	0.3
				ILDEIEEHNIK	2	100.0%	1																									
				MQAQMQMQMQGGDGDGGALGHHV	3	100.0%	1																									
IPI00893703	RPS7	Uncharacterized protein	100.0%	12.3	2	3	3	1	4,025,447	3,691,786	4,395,175	4,739,865	497,203	233,645	409,958	200,852	27.6	14.2	20.9	9.5	-1.1	0.6	1.1	0.6	1.2	0.2	1.2	0.2	1.3	0.009	1.1	0.5
				TLTAVHDAILEDLVFPSEIVGK	2	100.0%	1																									
				TLTAVHDAILEDLVFPSEIVGK	3	99.8%	1																									
				TLTAVHDAILEDLVFPSEIVGKR	3	100.0%	1																									
IPI00893737	DDT	Protein	100.0%	22.0	1	1	2	1	2,574,123	2,603,637	2,487,770	2,817,897	187,907	104,413	207,134	41,902	16.3	9.0	18.6	3.3	1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.6	1.1	0.09	1.1	0.2
				FFPLESWQIGK	2	100.0%	2																									
IPI00893815	NIPSNAP1	Protein	100.0%	4.5	1	1	1	2	480,565	483,900	536,943	587,723	80,846	61,518	40,807	47,460	37.6	28.4	17.0	18.1	1.0	1	1.1	0.6	1.2	0.3	1.1	0.5	1.2	0.2	1.1	0.4
IPI00894014	NIPSNAP1	15 kDa protein	100.0%	7.8	1	1	1	2	480,565	483,900	536,943	587,723	80,846	61,518	40,807	47,460	37.6	28.4	17.0	18.1	1.0	1	1.1	0.6	1.2	0.3	1.1	0.5	1.2	0.2	1.1	0.4
				KDAHSTLLSK	2	99.9%	1																									
IPI00893886	AGR3	Protein	100.0%	38.8	3	4	6	2	16,405,427	16,066,973	15,853,670	18,330,530	1,118,822	722,028	994,746	871,839	15.3	10.1	14.0	10.6	-1.0	0.8	-1.0	0.7	1.1	0.2	-1.0	0.9	1.1	0.08	1.2	0.1
IPI00894341	AGR3	Uncharacterized protein	100.0%	30.7	3	4	6	2	16,405,427	16,066,973	15,853,670	18,330,530	1,118,822	722,028	994,746	871,839	15.3	10.1	14.0	10.6	-1.0	0.8	-1.0	0.7	1.1	0.2	-1.0	0.9	1.1	0.08	1.2	0.1
				FIMLNLMHETTDKNLSPDGQYVPR	3	99.5%	1																									
				IMFVDPSLTVR	2	100.0%	2																									
				VFAQNEEIQEMAQNK	2	100.0%	2																									
				VFAQNEEIQEMAQNK	3	100.0%	1																									
IPI00893928	EPCAM	Uncharacterized protein	100.0%	14.1	2	2	2	1	5,922,270	5,906,687	5,289,730	6,876,813	1,024,010	479,779	451,188	692,946	38.7	18.2	19.1	22.5	-1.0	1	-1.1	0.6	1.2	0.5	-1.1	0.4	1.2	0.3	1.3	0.09
				IGAELWSWAGLGGSGPR	3	81.2%	1																									
				LAVNCFVNNNR	2	100.0%	1																									
IPI00893935	EML4	27 kDa protein	100.0%	6.5	1	1	1	1	380,890	364,912	345,608	376,745	41,220	33,974	27,472	26,655	24.2	20.8	17.8	15.8	-1.0	0.8	-1.1	0.5	-1.0	0.9	-1.1	0.7	1.0	0.8	1.1	0.4
				LSLPQNETVADTTLTK	2	99.9%	1																									
IPI00894147	RPS18	Ribosomal protein S18	100.0%	26.5	1	1	1	1	3,854,843	3,739,075	3,554,750	4,393,225	214,052	132,135	232,229	344,085	12.4	7.9	14.6	17.5	-1.0	0.7	-1.1	0.4	1.1	0.2	-1.1	0.5	1.2	0.1	1.2	0.08
				VLNTNIDGR	2	99.7%	1																									
IPI00894160	PPP1CB	7 kDa protein	100.0%	29.7	2	2	3	1	312,733	315,315	355,087	365,076	41,011	5,477	41,913	23,062	29.3	3.9	26.4	14.1	1.0	1	1.1	0.5	1.2	0.3	1.1	0.4	1.2	0.1	1.0	0.8
				EIFLSQPILLELEAPLK	2	100.0%	2																									
				SREIFLSQPILLELEAPLK	3	98.3%	1																									
IPI00894161	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	28.0	7	7	8	1	7,451,845	7,514,173	7,352,600	8,590,399	705,408	323,518	439,993	221,144	21.2	9.6	13.4	5.8	1.0	0.9	-1.0	0.9	1.2	0.2	-1.0	0.8	1.1	0.03	1.2	0.04
				CIALAQLLVEQNFPAIAIHR	3	100.0%	2																									
				FMQDPMEIFVDDETK	2	99.8%	1																									
				HFILDECDK	2	99.7%	1																									
				MLEQLDMR	2	100.0%	1																									
				NCPHIVVGTPGR	2	99.8%	1																									
				RDVQEIFR	2	98.1%	1																									
				VNIAFNYDMPEDSDTYLHR	3	100.0%	1																									
IPI00894274	PPP1CB	Serine/threonine-protein phosphatase	100.0%	24.6	3	3	4	2	1,751,692	1,896,538	2,092,654	2,320,609	170,813	119,141	282,945	109,268	21.8	14.1	30.2	10.5	1.1	0.5	1.2	0.3	1.3	0.02	1.1	0.5	1.2	0.03	1.1	0.5
IPI00930380	PPP1CB	Serine/threonine-protein phosphatase	100.0%	26.0	3	3	4	2	1,751,692	1,896,538	2,092,654	2,320,609	170,813	119,141	282,945	109,268	21.8	14.1	30.2	10.5	1.1	0.5	1.2	0.3	1.3	0.02	1.1	0.5	1.2	0.03	1.1	0.5
				EIFLSQPILLELEAPLK	2	100.0%	2																									
				IYGFYDECK	2	99.2%	1																									
				TFTDCFNCLPIAAIVDEK	2	100.0%	1																									
IPI00894287	HDLBP	cDNA FLJ56889, moderately similar to Vigilin	100.0%	18.2	16	17	21	1	47,648,872	47,736,252	43,745,531	54,556,973	4,146,342	2,897,306	3,348,980	1,909,509	19.5	13.6	17.1	7.8	1.0	1	-1.1	0.5	1.1	0.2	-1.1	0.4	1.1	0.08	1.2	0.02
				AACLESAQEPAGAWGNK	2	100.0%	1																									
				APDMSSSEEFPSFGAQVAPK	2	90.1%	1																									
				ASVITQVFHVPLEER	2	97.2%	1																									
				DKFPEVIINFPDPAQK	3	98.9%	1																									
				DQGLSIMVSGK	2	99.8%	1																									
				EALEALVPVTIEVEVPFDLHR	3	100.0%	1																									
				EIAEEYGGVMVSFPR	2	100.0%	2																									
				FPEVIINFPDPAQKSDIVQLR	2	97.6%	1																									
				HEVLLISAEQDKR	3	99.3%	1																									
				ICLEIMQR	2	92.7%	1																									
				IDLPAENSNSETIIITGK	2	100.0%	1																									
				IVGELEQMVSEDVPLDHR	3	100.0%	2																									
				LQTQASATVAIPK	2	100.0%	2																									
				LVGEIMQETGTR	2	100.0%	2																									
				RCDIIIISGR	2	99.2%	1																									
				TGAHLELSLAK	2	99.4%	1																									
				TGAHLELSLAK	3	99.5%	1																									
IPI00894448	RAD50	Uncharacterized protein	98.4%	3.3	1	1	1	1	76,372	83,191	72,529	81,225	9,639	3,084	7,016	13,599	28.2	8.3	21.6	37.4	1.1	0.5	-1.1	0.8	1.1	0.8	-1.1	0.2	-1.0	0.9	1.1	0.6
				DSLIQSLATQLELDGFER	2	98.4%	1																									
IPI00895865	ETFA	electron transfer flavoprotein subunit alpha, mitochondrial isoform b	100.0%	37.0	7	7	8	1	9,689,462	10,229,897	10,075,933	11,120,508	845,829	463,031	727,858	432,266	19.5	10.1	16.2	8.7	1.1	0.6	1.0	0.7	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.3
				AAVDAGFVPNDMQVGQTGK	2	100.0%	2																									
				DPEAPIFQVADYGIVADLFK	2	100.0%	1																									
				GLLPEELTPLILATQK	2	100.0%	1																									
				GTSFDAAATSGGSASSEK	2	100.0%	1																									
				LEVAPISDIIAIK	2	99.9%	1																									
				TIVAINKDPEAPIFQVADYGIVADLFK	3	100.0%	1																									
				TIYAGNALCTVK	2	100.0%	1																									
IPI00895901	PSMC1	Similar to 26S protease regulatory subunit 4	100.0%	18.4	3	3	3	1	5,624,342	5,801,043	5,397,820	6,492,432	318,420	459,994	314,846	386,027	12.7	17.7	13.0	13.3	1.0	0.8	-1.0	0.6	1.2	0.1	-1.1	0.5	1.1	0.3	1.2	0.06
				AVANQTSATFLR	2	100.0%	1																									
				IKDYLLMEEEFIR	3	99.9%	1																									
				VHAVIGVLMDDTDPLVTVMK	3	100.0%	1																									
IPI00896393	SULT1A4;SULT1A3	Uncharacterized protein	94.0%	17.6	1	1	1	1	908,623	947,150	946,160	1,137,547	111,674	39,654	71,842	44,814	27.5	9.4	17.0	8.8	1.0	0.8	1.0	0.8	1.3	0.09	-1.0	1	1.2	0.01	1.2	0.05
				YFAEALGPLQSFQARPDDLLINTYPK	3	94.0%	1																									
IPI00900297	-	isoform 2 of Eukaryotic translation initiation factor 2 subunit 3-like protein	93.7%	3.4	1	1	1	1	2,241,863	2,114,987	2,183,613	2,138,500	52,935	180,105	151,587	101,583	5.3	19.0	15.5	10.6	-1.1	0.5	-1.0	0.7	-1.0	0.4	1.0	0.8	1.0	0.9	-1.0	0.8
				NEVLMVNIGSLSTGGR	2	92.7%	1																									
IPI00902463	ESYT1	cDNA FLJ46898 fis, clone UTERU3022168, highly similar to Protein FAM62A	97.7%	2.2	1	1	1	1	3,266,387	3,951,703	3,325,443	3,967,840	197,134	251,079	333,697	215,143	13.5	14.2	22.4	12.1	1.2	0.06	1.0	0.9	1.2	0.04	-1.2	0.2	1.0	1	1.2	0.1
				VLQASVLDDWFPLQGGQGQVHLR	3	97.7%	1																									
IPI00902652	SLC9A3R1	cDNA FLJ37148 fis, clone BRACE2025333, highly similar to Homo sapiens Na+/H+	100.0%	29.3	5	5	8	1	15,295,570	15,619,028	14,630,135	17,687,800	1,333,896	433,058	1,121,527	612,196	19.5	6.2	17.1	7.7	1.0	0.8	-1.0	0.7	1.2	0.1	-1.1	0.4	1.1	0.02	1.2	0.04
				AQEAPGQAEPPAAAEVQGAGNENEPR	3	100.0%	1																									
				IVEVNGVCMEGK	2	100.0%	2																									
				KGPSGYGFNLHSDK	3	100.0%	1																									
				LLVVDPETDEQLQK	2	100.0%	2																									
				SVDPDSPAEASGLR	2	100.0%	2																									
IPI00902654	LGALS3BP	cDNA FLJ54583, highly similar to Galectin-3-binding protein	100.0%	16.1	6	6	8	1	16,652,053	17,369,815	16,343,227	19,817,743	1,431,520	784,727	1,405,960	607,782	19.2	10.1	19.2	6.9	1.0	0.7	-1.0	0.9	1.2	0.08	-1.1	0.5	1.1	0.04	1.2	0.05
				ASHEEVEGLVEK	3	100.0%	1																									
				AVDTWSWGER	2	100.0%	2																									
				RIDITLSSVK	2	100.0%	2																									
				SDLAVPSELALLK	2	99.9%	1																									
				STSSFPCPAGHFNGFR	3	98.6%	1																									
				TLQALEFHTVPFQLLAR	3	99.1%	1																									
IPI00902660	RALGDS	isoform 2 of Ral guanine nucleotide dissociation stimulator	97.8%	3.5	2	2	2	1	11,410,460	11,361,910	11,663,400	11,921,510	740,080	425,504	447,395	353,783	14.5	8.4	8.6	6.6	-1.0	1	1.0	0.8	1.0	0.6	1.0	0.6	1.0	0.3	1.0	0.7
				ARVVEHWIEVARECR	2	83.8%	1																									
				HQLSLQQHLVLLSLHHAR	3	87.1%	1																									
IPI00902799	-	cDNA FLJ12779 fis, clone NT2RP2001748, moderately similar to FARNESYL PYR	100.0%	39.5	3	3	3	1	12,311,870	12,677,458	12,026,008	14,207,293	951,363	526,839	943,527	503,141	17.3	9.3	17.5	7.9	1.0	0.7	-1.0	0.8	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.08
				LKEVLEYNAIGGK	3	99.8%	1																									
				QDFVQHFSQIVR	3	93.5%	1																									
				VLTEDEMGHPEIGDAIAR	3	99.1%	1																									
IPI00902887	CAPN2	cDNA FLJ39928 fis, clone SPLEN2021273, highly similar to Calpain-2 catalytic subu	100.0%	13.1	2	4	4	1	644,457	570,414	761,861	725,590	71,441	34,000	134,362	28,962	24.8	13.3	39.4	8.9	-1.1	0.4	1.2	0.5	1.1	0.3	1.3	0.2	1.3	0.008	-1.0	0.8
				FADDQLIIDFDNFVR	2	100.0%	1																									
				FADDQLIIDFDNFVR	3	95.2%	1																									
				LFAQLAGEDAEISAFELQTILR	2	100.0%	1																									
				LFAQLAGEDAEISAFELQTILR	3	100.0%	1																									
IPI00902909	NAP1L1	cDNA FLJ16112 fis, clone 3NB692001853, highly similar to NUCLEOSOME ASSEM	100.0%	20.7	5	5	7	2	4,072,505	4,076,023	4,143,855	4,569,347	488,202	142,629	301,597	221,410	26.8	7.8	16.3	10.8	1.0	1	1.0	0.9	1.1	0.4	1.0	0.8	1.1	0.1	1.1	0.3
IPI01013371	NAP1L1	cDNA FLJ58569, highly similar to Nucleosome assembly protein 1-like 1	100.0%	19.2	5	5	7	2	4,072,505	4,076,023	4,143,855	4,569,347	488,202	142,629	301,597	221,410	26.8	7.8	16.3	10.8	1.0	1	1.0	0.9	1.1	0.4	1.0	0.8	1.1	0.1	1.1	0.3
				FYEEVHDLER	2	100.0%	1																									
				GIPEFWLTVFK	2	100.0%	2																									
				LDGLVETPTGYIESLPR	2	100.0%	2																									
				NVDLLSDMVQEHDEPILK	3	99.9%	1																									
				YAVLYQPLFDK	2	99.9%	1																									
IPI00903103	CAPZB	Capping protein (Actin filament) muscle Z-line, beta	100.0%	46.3	3	3	3	1	4,763,056	4,845,759	4,724,410	5,631,197	246,965	329,483	242,385	143,828	11.6	15.2	11.5	5.7	1.0	0.8	-1.0	0.9	1.2	0.02	-1.0	0.8	1.2	0.06	1.2	0.01
				LEVEANNAFDQYR	2	100.0%	1																									
				MLKVPSLCEDLLSSVDQPLKIAR	3	96.9%	1																									
				SPWSNKYDPPLEDGAMPSAR	3	100.0%	1																									
IPI00903129	ARFGAP2	cDNA FLJ41005 fis, clone UTERU2017613, highly similar to Homo sapiens zinc fing	100.0%	5.5	2	2	2	1	1,474,477	1,313,033	1,124,659	1,510,482	165,423	178,881	134,910	157,419	25.1	30.5	26.8	23.3	-1.1	0.5	-1.3	0.1	1.0	0.9	-1.2	0.4	1.2	0.4	1.3	0.1
				LAYQELQIDR	2	98.9%	1																									
				VSSQSFSEIER	2	99.9%	1																									
IPI00903143	-	cDNA FLJ44205 fis, clone THYMU3001379, highly similar to 116 kDa U5 small nucl	100.0%	15.8	7	9	10	1	9,071,160	8,918,265	8,916,354	10,190,972	837,002	442,854	680,554	354,240	20.6	11.1	17.1	7.8	-1.0	0.9	-1.0	0.9	1.1	0.3	-1.0	1	1.1	0.06	1.1	0.1
				DSIVQGFQWGTR	2	99.7%	1																									
				GLAEDIENEVVQITWNR	2	99.9%	1																									
				GLAEDIENEVVQITWNR	3	99.9%	1																									
				IAVEPVNPSELPK	2	100.0%	1																									
				ILAQVVGDVDTSLPR	2	100.0%	2																									
				ITMIAEPLEK	2	99.1%	1																									
				LGEFFQTK	2	99.7%	1																									
				SFVEFILEPLYK	2	100.0%	1																									
				SFVEFILEPLYK	3	94.5%	1																									
IPI00903190	GNPDA1	cDNA FLJ12717 fis, clone NT2RP1001253, highly similar to Glucosamine-6-phosph	95.4%	3.9	1	1	1	1	554,450	571,121	459,866	584,181	28,131	21,546	8,610	31,110	11.4	8.4	4.2	11.9	1.0	0.7	-1.2	0.03	1.1	0.5	-1.2	0.001	1.0	0.7	1.3	0.01
				IIQFNPGPEK	2	95.4%	1																									
IPI00903228	WDR20	Uncharacterized protein	90.3%	3.1	1	1	1	1	6,801,620	7,788,100	8,939,070	8,007,110	356,924	388,252	746,436	351,443	11.7	11.2	18.7	9.8	1.1	0.1	1.3	0.03	1.2	0.04	1.1	0.2	1.0	0.7	-1.1	0.3
				MNEIKTQFTTREGLYK	3	91.1%	1																									
IPI00903238	GGCT	cDNA FLJ11717 fis, clone HEMBA1005241	100.0%	29.9	3	3	3	1	5,962,580	6,542,172	5,896,500	7,465,483	854,582	377,729	496,748	247,791	32.1	12.9	18.8	7.4	1.1	0.6	-1.0	0.9	1.3	0.2	-1.1	0.3	1.1	0.08	1.3	0.02
				AIEPNDYTGK	2	97.2%	1																									
				SYLMTNYESAPPSPQYKK	2	86.6%	1																									
				VSEEIEDIIK	2	99.9%	1																									
IPI00903257	BZW1	cDNA FLJ39170 fis, clone OCBBF2003028, highly similar to Rattus norvegicus basi	99.7%	9.0	2	2	2	1	5,022,892	5,089,620	4,776,210	6,144,264	502,888	241,471	314,774	296,969	22.4	10.6	14.7	10.8	1.0	0.9	-1.1	0.7	1.2	0.09	-1.1	0.5	1.2	0.02	1.3	0.01
				EGVSAAFAVK	2	92.4%	1																									

				LMELFPANK	2	99.5%	1																									
IPI00903259	SUPT5H	cDNA FLJ54005, highly similar to Transcription elongation factor SPT5	98.7%	1.0	1	1	1	1	1,469,875	1,087,313	1,322,905	1,449,870	155,472	130,250	155,148	225,800	23.7	26.8	26.2	34.8	-1.4	0.1	-1.1	0.5	-1.0	0.9	1.2	0.3	1.3	0.2	1.1	0.7
				ILNLRFLGK	2	98.1%	1																									
IPI00903292	WDR1	isoform 2 of WD repeat-containing protein 1	100.0%	8.8	3	3	4	1	4,367,239	3,962,673	4,166,926	5,141,509	326,862	152,110	258,300	355,649	16.7	8.6	13.9	15.5	-1.1	0.3	-1.0	0.6	1.2	0.1	1.1	0.5	1.3	0.02	1.2	0.06
				DYSGQGVVK	2	99.8%	2																									
				GPVTDVAYSHDGAFLAVCDASK	3	100.0%	1																									
				VFASLPQVER	2	89.8%	1																									
IPI00908351	HADHA	cDNA FLJ52806, highly similar to Trifunctional enzyme subunit alpha, mitochondrial	100.0%	5.8	1	1	1	1	604,059	613,482	677,023	601,187	80,112	87,820	85,588	53,202	29.7	32.0	28.3	19.8	1.0	0.9	1.1	0.6	-1.0	1	1.1	0.6	-1.0	0.9	-1.1	0.5
				MVGVPAALDMMLTGR	2	100.0%	1																									
IPI00908365	AGT	cDNA FLJ52255, highly similar to Angiotensinogen	91.7%	2.2	1	1	1	1	6,234,045	6,216,985	6,401,720	6,975,600	817,116	378,228	522,307	237,447	29.3	13.6	18.2	7.6	-1.0	1	1.0	0.9	1.1	0.4	1.0	0.8	1.1	0.1	1.1	0.3
				FMQAVTGWK	2	91.8%	1																									
IPI00908375	SEC23A	cDNA FLJ52821, highly similar to Protein transport protein Sec23A	99.5%	5.4	1	1	1	1	277,828	305,794	335,946	320,186	15,706	22,629	14,158	23,235	12.6	16.6	9.4	16.2	1.1	0.3	1.2	0.03	1.2	0.2	1.1	0.3	1.0	0.7	-1.0	0.6
				IMMFIGGPATQGPGMVVGDELK	2	99.5%	1																									
IPI00908396	ACTR3	cDNA FLJ52216, highly similar to Actin-like protein 3	100.0%	13.5	2	2	2	1	1,316,597	1,518,790	1,517,112	1,552,825	78,504	109,568	42,546	80,762	13.3	16.1	6.3	11.6	1.2	0.2	1.2	0.05	1.2	0.07	-1.0	1	1.0	0.8	1.0	0.7
				LSEELSGGR	2	99.2%	1																									
				NIVLSGGSTMFR	2	100.0%	1																									
IPI00908400	CAPZA2	cDNA, FLJ78814, highly similar to F-actin capping protein alpha-2 subunit	100.0%	15.8	2	2	2	1	3,855,698	3,808,782	4,111,892	4,466,083	203,514	121,696	323,144	91,966	11.8	7.1	17.6	4.6	-1.0	0.8	1.1	0.5	1.2	0.03	1.1	0.4	1.2	0.003	1.1	0.3
				IVEAAENEYQTAISENYQTMSDTTFK	3	90.3%	1																									
				RQLPVTR	2	99.9%	1																									
IPI00908463	STIP1	cDNA FLJ54451, highly similar to Stress-induced-phosphoprotein 1	100.0%	43.0	19	21	24	1	59,093,523	60,712,660	59,843,073	67,178,273	4,612,659	2,451,373	3,322,253	1,622,769	17.5	9.0	12.4	5.4	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.8	1.1	0.06	1.1	0.08
				AAALEAMKDYTK	2	100.0%	1																									
				ALDLDSSCKEAADGYQR	3	99.8%	1																									
				ALSVGNIDDALQCYSEAIK	2	100.0%	2																									
				AMADPEVQQIMSDPAMR	2	100.0%	2																									
				AMADPEVQQIMSDPAMR	3	85.2%	1																									
				CMMAQYNR	2	99.5%	1																									
				DPQALSEHLK	2	100.0%	1																									
				DPQALSEHLKNPVIAQK	3	100.0%	2																									
				EGLQNMEAR	2	98.9%	1																									
				ELDPTNMTYITNQAAVYFEK	2	100.0%	1																									
				ELDPTNMTYITNQAAVYFEK	3	100.0%	1																									
				ETKPEPMEEDLPENKK	3	99.9%	1																									
				FMNPFNMPNLYQK	2	99.9%	1																									
				GDYPQAMK	2	99.8%	1																									
				HYTEAIK	2	99.6%	1																									
				IGNSYFKEEK	2	91.7%	1																									
				LAYINPDLALEEK	2	100.0%	1																									
				LILEQMQK	2	98.5%	1																									
				TLLSDPTYR	2	96.4%	1																									
				TVDLKPDWGK	2	99.2%	1																									
				YKDAIHFYNK	3	99.5%	1																									
IPI00908482	-	cDNA FLJ57081, moderately similar to WD repeat protein 1	100.0%	7.7	1	1	1	1	777,530	920,050	794,780	858,283	79,285	89,161	59,290	64,248	22.8	21.7	16.7	16.7	1.2	0.3	1.0	0.9	1.1	0.5	-1.2	0.3	-1.1	0.6	1.1	0.5
				YAPSGFYIASGDVSGK	2	100.0%	1																									
IPI00908503	PLS3	cDNA FLJ50605, moderately similar to Plastin-3	100.0%	5.5	1	1	1	1	199,990	174,470	227,585	229,959	30,114	21,213	6,944	9,299	33.7	27.2	6.8	9.0	-1.1	0.5	1.1	0.4	1.1	0.4	1.3	0.06	1.3	0.04	1.0	0.8
				ISFDEFVYIFQEVK	2	100.0%	1																									
IPI00908505	SCRN1	cDNA FLJ54276, highly similar to Secernin-1	100.0%	20.4	2	2	2	3	12,684,221	12,857,915	11,650,368	14,098,436	719,504	623,302	797,536	591,224	12.7	10.8	15.3	9.4	1.0	0.9	-1.1	0.4	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.04
IPI00917232	SCRN1	Uncharacterized protein	100.0%	20.6	2	2	2	3	12,684,221	12,857,915	11,650,368	14,098,436	719,504	623,302	797,536	591,224	12.7	10.8	15.3	9.4	1.0	0.9	-1.1	0.4	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.04
IPI00917382	SCRN1	Uncharacterized protein	100.0%	20.7	2	2	2	3	12,684,221	12,857,915	11,650,368	14,098,436	719,504	623,302	797,536	591,224	12.7	10.8	15.3	9.4	1.0	0.9	-1.1	0.4	1.1	0.2	-1.1	0.3	1.1	0.2	1.2	0.04
				EPAAEIEALLGMDLVR	2	99.7%	1																									
				VECTYISIDQVPR	2	95.8%	1																									
IPI00908516	ARL1	ADP-ribosylation factor-like protein 1	100.0%	10.7	1	1	1	1	46,956	40,543	50,216	71,631	962	5,888	6,916	6,088	4.6	32.5	30.8	19.0	-1.2	0.3	1.1	0.7	1.5	0.01	1.2	0.3	1.8	0.006	1.4	0.05
				GTGLDEAMEWLVETLK	3	100.0%	1																									
IPI00908532	LAMP1	cDNA FLJ57633, highly similar to Lysosome-associated membrane glycoprotein 1	100.0%	5.8	2	2	2	1	2,828,015	3,218,030	3,502,125	3,851,905	454,659	215,295	350,858	246,682	36.0	15.0	22.4	14.3	1.1	0.5	1.2	0.3	1.4	0.08	1.1	0.5	1.2	0.09	1.1	0.4
				FFLQGIQLNTILPDAR	2	99.8%	1																									
				FFLQGIQLNTILPDARDPAFK	3	99.9%	1																									
IPI00908533	SRRM1	Uncharacterized protein	98.2%	5.3	1	1	1	1	1,229,623	1,298,287	1,209,920	1,442,643	76,274	137,060	117,726	65,087	13.9	23.6	21.8	10.1	1.1	0.7	-1.0	0.9	1.2	0.07	-1.1	0.6	1.1	0.4	1.2	0.1
				VKEPSVQEATSTSDILK	3	98.2%	1																									
IPI00908543	PPP2R1A	cDNA FLJ56133, highly similar to Serine/threonine-protein phosphatase 2A 65 kDa	100.0%	34.4	16	20	23	1	18,966,268	22,348,204	19,514,850	25,360,260	2,742,965	1,258,403	1,621,630	907,385	32.3	12.6	18.6	8.0	1.2	0.3	1.0	0.9	1.3	0.08	-1.1	0.2	1.1	0.09	1.3	0.01
				DNTIEHLLPLFLAQLK	3	100.0%	1																									
				DNTIEHLLPLFLAQLKDECPEVR	3	100.0%	1																									
				ELVSDANQHVK	2	98.3%	1																									
				ENVIMSQILPCIK	2	100.0%	1																									
				LNIISNLDCVNEVIGIR	2	100.0%	1																									
				LNIISNLDCVNEVIGIR	3	99.8%	1																									
				LSTIALALGVER	2	100.0%	1																									
				LTQDQDVDVK	2	100.0%	2																									
				MAGDPVANVR	2	100.0%	1																									
				NLCSDDTPMVR	2	97.5%	1																									
				QLSQSLLPAIVELAEDAK	2	100.0%	2																									
				QLSQSLLPAIVELAEDAK	3	100.0%	1																									
				QLSQSLLPAIVELAEDAKWR	3	100.0%	1																									
				SEIIPMFSNLASDEQDSVR	2	100.0%	2																									
				TDLVPAFQNLMK	2	99.9%	1																									
				VLAMSGDPNYLHR	2	99.9%	1																									
				VLAMSGDPNYLHR	3	99.7%	1																									
				VLELDNVK	2	95.1%	1																									
				YMVADKFTELQK	2	99.9%	1																									
				YMVADKFTELQK	3	99.8%	1																									
IPI00908545	PDXDC1	cDNA FLJ59412	100.0%	13.3	6	6	6	2	47,795,149	49,491,753	51,417,653	56,535,595	4,720,745	2,936,862	3,912,437	1,981,281	22.1	13.3	17.0	7.8	1.0	0.8	1.1	0.6	1.2	0.1	1.0	0.7	1.1	0.08	1.1	0.3
IPI01011550	PDXDC1	85 kDa protein	100.0%	12.0	6	6	6	2	47,795,149	49,491,753	51,417,653	56,535,595	4,720,745	2,936,862	3,912,437	1,981,281	22.1	13.3	17.0	7.8	1.0	0.8	1.1	0.6	1.2	0.1	1.0	0.7	1.1	0.08	1.1	0.3
				FFQELPGSDPVFK	2	98.8%	1																									
				HDDPALTLVAGLTSNKPTDK	3	100.0%	1																									
				LLENMTEVVR	2	99.9%	1																									
				LNELESDLTFK	2	99.9%	1																									
				QIPVVGSVLNWFSPVQALQK	2	99.6%	1																									
				TFNLTAGSLESTEPIYVYK	2	100.0%	1																									
IPI00908553	TPT1	cDNA FLJ57738, highly similar to Translationally-controlled tumor protein	100.0%	23.9	3	3	4	1	3,752,052	3,989,915	3,613,518	4,304,041	402,917	167,613	229,198	174,405	24.0	9.4	14.2	9.1	1.1	0.6	-1.0	0.8	1.1	0.2	-1.1	0.2	1.1	0.2	1.2	0.04
				DLISHDEMFSDIYK	3	100.0%	1																									
				EIADGLCLEVEGK	2	100.0%	2																									
				HILANFK	2	94.9%	1																									
IPI00908564	-	cDNA FLJ57619, highly similar to Delta 3,5-delta 2,4-dienoyl-CoA isomerase, mitoch	100.0%	15.2	2	3	5	1	3,685,452	3,327,787	3,369,419	3,938,450	377,067	123,023	281,508	169,779	22.9	8.3	18.7	9.6	-1.1	0.4	-1.1	0.5	1.1	0.6	1.0	0.9	1.2	0.02	1.2	0.1
				MFTAGIDLMDMASDILQPK	2	100.0%	2																									
				MFTAGIDLMDMASDILQPK	3	100.0%	1																									
				YQETFNVIER	2	100.0%	2																									
IPI00908580	-	cDNA FLJ53349, highly similar to Transmembrane 9 superfamily protein member 4	99.3%	2.3	1	1	1	1	2,168,597	2,301,517	2,176,830	2,613,347	145,966	146,041	123,725	91,086	15.1	14.2	12.7	7.8	1.1	0.5	1.0	1	1.2	0.03	-1.1	0.5	1.1	0.1	1.2	0.02
				IVNTPFQVLMNSEK	2	99.3%	1																									
IPI00908612	VARS	cDNA FLJ54383, highly similar to Valyl-tRNA synthetase	100.0%	2.4	1	2	3	1	303,732	256,719	280,135	340,766	43,696	30,046	27,136	10,214	32.2	26.2	21.7	6.7	-1.2	0.4	-1.1	0.7	1.1	0.5	1.1	0.6	1.3	0.05	1.2	0.09
				LLSPFMPFVTEELFQR	2	100.0%	2																									
				LLSPFMPFVTEELFQR	3	100.0%	1																									
IPI00908618	SRSF4	cDNA FLJ50118, highly similar to Splicing factor, arginine/serine-rich 4	100.0%	13.3	2	2	2	1	3,765,478	4,253,680	4,052,943	4,788,933	606,234	433,784	357,549	349,421	36.0	22.8	19.7	16.3	1.1	0.5	1.1	0.7	1.3	0.2	-1.0	0.7	1.1	0.4	1.2	0.2
				LIVENLSSR	2	99.9%	1																									
				NGYGFVEFDDLR	2	91.9%	1																									
IPI00908657	HLA-DRA	cDNA FLJ52115, highly similar to HLA class II histocompatibility antigen, DRalpha c	97.4%	13.3	1	1	1	1	5,236,420	5,103,550	7,100,540	8,307,060	738,984	796,981	1,286,964	661,465	31.6	34.9	40.5	17.8	-1.0	0.9	1.4	0.2	1.6	0.01	1.4	0.2	1.6	0.01	1.2	0.4
				HTGVCLCYGMPHGASLVYLLFK	3	97.4%	1																									
IPI00908662	RPL4	Uncharacterized protein	100.0%	7.2	2	2	3	1	8,798,230	8,124,153	10,253,193	8,086,840	744,619	500,576	361,947	435,452	18.9	13.8	7.9	12.0	-1.1	0.5	1.2	0.1	-1.1	0.4	1.3	0.009	-1.0	1	-1.3	0.005
				FCIWTESAFR	2	100.0%	2																									
				MINTDLSR	2	95.8%	1																									
IPI00908669	OLA1	Uncharacterized protein	100.0%	22.4	2	2	3	1	1,234,348	1,328,568	1,241,883	1,493,920	168,299	62,299	114,718	126,956	30.5	10.5	20.7	19.0	1.1	0.6	1.0	1	1.2	0.3	-1.1	0.5	1.1	0.3	1.2	0.2
				IGIVGLPNVGK	2	99.9%	1																									
				IPAFLNVVDIAGLVK	2	100.0%	2																									
IPI00908691	AKR7A2	cDNA FLJ51420, highly similar to Aflatoxin B1 aldehyde reductase member 2	100.0%	14.3	2	2	3	1	1,593,738	1,629,737	1,837,752	1,860,766	148,515	162,270	110,426	48,680	20.8	22.3	13.4	5.9	1.0	0.9	1.2	0.2	1.2	0.2	1.1	0.3	1.1	0.2	1.0	0.9
				RMDAPASAAAVR	2	99.9%	1																									
				VASVLGTMEMGR	2	100.0%	2																									
IPI00908707	HMGCL	hydroxymethylglutaryl-CoA lyase, mitochondrial isoform 2 precursor	100.0%	11.4	2	2	2	2	1,625,103	1,746,273	1,592,137	1,744,495	125,192	104,703	131,201	89,913	17.2	13.4	18.4	11.5	1.1	0.5	-1.0	0.9	1.1	0.5	-1.1	0.4	-1.0	1	1.1	0.4
IPI01013953	HMGCL	Mitochondrial 3-hydroxy-3-methylglutaryl-CoA lyase	100.0%	17.5	2	2	2	2	1,625,103	1,746,273	1,592,137	1,744,495	125,192	104,703	131,201	89,913	17.2	13.4	18.4	11.5	1.1	0.5	-1.0	0.9	1.1	0.5	-1.1	0.4	-1.0	1	1.1	0.4
				IVEVGPR	2	94.4%	1																									
				LIDMLSEAGLSVIETTSFVSPK	2	99.9%	1																									
IPI00908715	FDFT1	cDNA FLJ50548, highly similar to Squalene synthetase	100.0%	14.2	4	4	4	1	2,289,848	2,410,497	2,440,173	2,811,615	154,846	153,383	200,037	147,926	15.1	14.2	18.3	11.8	1.1	0.6	1.1	0.6	1.2	0.04	1.0	0.9	1.2	0.1	1.2	0.2
				DYLEDQQGGR	2	100.0%	1																									
				LFSASEFEDPLVGEDTER	2	100.0%	1																									
				MDQDSLSSSLK	2	100.0%	1																									
				SFAAVIQALDGEMR	2	100.0%	1																									
IPI00908729	MCM6	cDNA FLJ51590, moderately similar to DNA replication licensing factor MCM6	99.1%	20.5	1	1	1	1	1,300,765	1,297,545	1,623,820	1,889,850	176,515	185,705	211,708	129,161	30.3	32.0	29.2	15.3	-1.0	1	1.2	0.3	1.5	0.03	1.3	0.3	1.5	0.03	1.2	0.3
				LFLDFLEEFQSSDGEIK	2	99.1%	1																									
IPI00908746	PEBP1	cDNA FLJ51535, highly similar to Phosphatidylethanolamine-binding protein 1	100.0%	12.9	1	2	3	1	7,562,380	7,766,925	7,024,980	8,254,020	885,814	465,610	704,235	459,497	26.2	13.4	22.4	12.5	1.0	0.8	-1.1	0.6	1.1	0.5	-1.1	0.4	1.1	0.5	1.2	0.2
				GNDISSGTVLSDYVGSGPPK	2	100.0%	2																									
				GNDISSGTVLSDYVGSGPPK	3	100.0%	1																									
IPI00908752	CMPK1	cDNA FLJ53966, moderately similar to Homo sapiens cytidylate kinase (CMPK), mR	100.0%	40.3	8	10	14	1	20,353,137	20,502,803	20,463,407	22,685,684	1,593,911	200,537	1,088,502	664,632	17.5	2.2	11.9	6.6	1.0	0.9	1.0	1	1.1	0.2	-1.0	1	1.1	0.03	1.1	0.1
				FLIDGFPR	2	92.4%	1																									
				IVPVEITISLLK	2	100.0%	1																									
				KNPDSQYGELIEK	2	100.0%	1																									
				NPDSQYGELIEK	2	98.9%	1																									
				NQDNLQGWNK	2	100.0%	2																									
				SVDEVFDEVVQIFDK	2	100.0%	2																									
				SVDEVFDEVVQIFDKEG	2	100.0%	2																									
				SVDEVFDEVVQIFDKEG	3	100.0%	1																									
				YGYTHLSAGELLR	2	100.0%	2																									
				YGYTHLSAGELLR	3	100.0%	1																									
IPI00908757	-	cDNA FLJ51345, highly similar to Histamine N-methyltransferase	100.0%	11.2	1	1	2	1	3,048,615	3,114,645	2,904,520	3,322,340	183,094	114,819	258,747	187,879	13.4	8.2	19.9	12.7	1.0	0.8	-1.0	0.7	1.1	0.3	-1.1	0.5	1.1	0.4	1.1	0.2
				ILSIGGGAGEIDLQILSK	2	99.8%	2																									
IPI00908762	LGALS3BP	Uncharacterized protein	100.0%	6.0	2	2	2	1	2,697,170	2,126,148	4,406,150	2,207,233	485,496	243,297	1,113,591	182,108	40.3	25.6	56.5	18.5	-1.3	0.3	1.6	0.2	-1.2	0.4	2.1	0.1	1.0	0.8	-2.0	0.1
				ASHEEVEGLVEK	2	99.8%	1																									
				YSSDYFQAPSDYR	2	100.0%	1																									
IPI00908779	HARS	cDNA FLJ58554, highly similar to Histidyl-tRNA synthetase	100.0%	18.3	7	7	7	2	5,826,926	6,134,825	5,655,779	6,738,061	516,226	267,275	399,675	176,698	19.8	9.7	15.8	5.9	1.1	0.6	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00965198	HARS	50 kDa protein	100.0%	19.2	7	7	7	2	5,826,926	6,134,825	5,655,779	6,738,061	516,226	267,275	399,675	176,698	19.8	9.7	15.8	5.9	1.1	0.6	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
				ASAELIEEEVAK	2	100.0%	1																									
				IFSIVEQR	2	90.1%	1																									

				IGDYVQQHGGVSLVEQLLQDPK	3	99.9%	1																										
				LLFEYLTLFGIDDK	2	89.3%	1																										
				QALEGLGDLK	2	96.4%	1																										
				YDGLVGMFDPK	2	98.9%	1																										
				YDLTVPFAR	2	86.3%	1																										
IPI00908791	LDHA	Uncharacterized protein	100.0%	32.0	8	13	16	1	55,819,137	56,217,032	55,612,640	64,784,586	5,191,721	2,480,877	5,740,817	2,979,410	20.8	9.9	23.1	10.3	1.0	0.9	-1.0	1	1.2	0.2	-1.0	0.9	1.2	0.06	1.2	0.2
				DDVFLSVPCILGQNGISDLVK	2	100.0%	1																										
				DYNVTANSK	1	100.0%	1																										
				DYNVTANSK	2	100.0%	1																										
				GLYGIKDDVFLSVPCILGQNGISDLVK	2	100.0%	1																										
				LLIVSNPVDILTYVAWK	2	97.6%	1																										
				LVIITAGAR	1	96.1%	1																										
				LVIITAGAR	2	99.7%	2																										
				SADTLWGIQK	1	100.0%	1																										
				SADTLWGIQK	2	100.0%	2																										
				TLHPDLGTDKDKEQWK	2	100.0%	1																										
				TLHPDLGTDKDKEQWK	3	99.7%	2																										
				VTLTSEEEAR	1	98.7%	1																										
				VTLTSEEEAR	2	100.0%	1																										
IPI00908804	ABCD3	cDNA FLJ53353, highly similar to ATP-binding cassette sub-family D member 3	100.0%	4.5	2	2	2	1	1,296,054	1,148,671	1,402,456	1,446,000	209,681	102,627	182,208	87,720	36.2	20.0	29.1	13.6	-1.1	0.5	1.1	0.7	1.1	0.5	1.2	0.3	1.3	0.06	1.0	0.8
				EGGWDSVQDWMDVLSGGEK	2	100.0%	1																										
				VLGELWPLFGGR	2	99.8%	1																										
IPI00908835	RAB5B	cDNA FLJ60627, highly similar to Ras-related protein Rab-5B	100.0%	8.1	1	1	1	1	1,051,860	1,239,000	1,305,535	1,388,675	61,498	114,333	91,285	55,358	13.1	20.6	15.6	8.9	1.2	0.2	1.2	0.05	1.3	0.004	1.1	0.7	1.1	0.3	1.1	0.5
				TAMNVNDLFLAIAK	2	99.9%	1																										
IPI00908873	NOLC1	isoform 3 of Nucleolar and coiled-body phosphoprotein 1	100.0%	3.6	2	3	4	1	2,511,851	2,196,322	2,100,041	2,730,379	465,817	150,866	174,946	324,615	41.5	15.4	18.6	26.6	-1.1	0.5	-1.2	0.4	1.1	0.7	-1.0	0.7	1.2	0.2	1.3	0.1
				DNQLSEVANK	2	99.4%	1																										
				VVPSDLYPLVLGFLR	2	100.0%	2																										
				VVPSDLYPLVLGFLR	3	100.0%	1																										
IPI00908881	GPI	Uncharacterized protein	100.0%	47.4	18	22	34	1	133,692,940	140,898,516	137,539,764	161,770,584	########	7,685,648	########	6,359,543	25.6	12.2	19.0	8.8	1.1	0.7	1.0	0.8	1.2	0.1	-1.0	0.8	1.1	0.07	1.2	0.1
				AVLHVALR	2	88.1%	1																										
				EWFLQAAK	2	99.9%	1																										
				FAAYFQQGDMESNGK	2	100.0%	2																										
				HFVALSTNTTK	2	100.0%	2																										
				IFVQGIIWDINSFDQWGVELGK	2	100.0%	1																										
				ILLANFLAQTEALMR	2	100.0%	2																										
				ILLANFLAQTEALMR	3	100.0%	2																										
				INYTEGR	2	96.5%	2																										
				KIEPELDGSAQVTSHDASTNGLINFIK	3	100.0%	2																										
				LQQWYR	2	99.8%	1																										
				SNTPILVDGK	2	99.8%	1																										
				SNTPILVDGKDVMPEVNK	2	100.0%	2																										
				SNTPILVDGKDVMPEVNK	3	100.0%	2																										
				TFTTQETITNAETAK	2	100.0%	2																										
				TFTTQETITNAETAKEWFLQAAK	3	100.0%	1																										
				TITDVINIGIGGSDLGPLMVTEALKPYSSGGPR	3	100.0%	1																										
				TLAQLNPESSLFIIASK	2	100.0%	1																										
				VFEGNRPTNSIVFTK	2	100.0%	2																										
				VFEGNRPTNSIVFTK	3	99.9%	1																										
				VKEFGIDPQNMFEFWDWVGGR	3	100.0%	1																										
				VWYVSNIDGTHIAK	2	100.0%	2																										
				VWYVSNIDGTHIAK	3	100.0%	2																										
IPI00908883	ACTR1A	Uncharacterized protein	100.0%	13.7	4	4	4	1	6,287,027	6,415,765	6,743,065	6,999,585	320,275	197,080	296,683	160,928	11.4	6.9	9.8	5.1	1.0	0.7	1.1	0.3	1.1	0.08	1.1	0.4	1.1	0.05	1.0	0.5
				AGFAGDQIPK	2	90.2%	1																										
				AQYYLPDGSTIEIGPSR	2	100.0%	1																										
				LYSTWIGGSILASLDTFK	2	86.9%	1																										
				LYSTWIGGSILASLDTFKK	3	100.0%	1																										
IPI00908884	LOC729658	cDNA FLJ58069	90.6%	11.6	1	1	1	1	3,365,750	3,435,410	3,556,780	4,054,610	296,963	58,882	290,606	247,421	19.7	3.8	18.3	13.6	1.0	0.8	1.1	0.7	1.2	0.1	1.0	0.7	1.2	0.07	1.1	0.2
				ILDNLGAEGRHGSEWEWRR	3	90.6%	1																										
IPI00908896	HNRNPH1	Uncharacterized protein	100.0%	7.7	2	2	3	1	2,726,569	1,990,662	2,238,070	2,673,159	523,988	171,533	225,719	305,723	43.0	19.3	22.6	25.6	-1.4	0.2	-1.2	0.4	-1.0	0.9	1.1	0.4	1.3	0.09	1.2	0.3
				ATENDIYNFFSPLNPVR	3	100.0%	1																										
				HTGPNSPDTANDGFVR	2	100.0%	2																										
IPI00908931	PDCD5	cDNA FLJ52456, moderately similar to Programmed cell death protein 5	100.0%	18.6	2	2	2	1	12,794,310	12,728,690	12,833,895	14,747,005	1,042,593	469,848	742,792	402,685	18.2	8.3	12.9	6.1	-1.0	1	1.0	1	1.2	0.1	1.0	0.9	1.2	0.01	1.1	0.05
				LSNLALVKPEK	2	91.9%	1																										
				NSILAQVLDQSAR	2	100.0%	1																										
IPI00908949	TARS	cDNA FLJ53464, highly similar to Threonyl-tRNA synthetase, cytoplasmic	100.0%	22.0	15	15	18	1	28,153,426	29,444,694	27,885,777	33,814,332	2,617,999	928,049	1,373,957	608,313	20.8	7.1	11.0	4.0	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.4	1.1	0.004	1.2	0.004
				AEHDSILAEK	2	99.5%	1																										
				AELNPWPEYIYTR	2	100.0%	1																										
				CGPLIDLCR	2	91.2%	1																										
				FLGDIEVWDQAEK	2	100.0%	2																										
				FMADIDLDPGCTLNK	2	99.6%	1																										
				FMADIDLDPGCTLNKK	3	99.0%	1																										
				GAYIYNALIEFIR	2	100.0%	2																										
				ISGTVNIR	2	81.4%	1																										
				IYGISFPDPK	2	99.9%	1																										
				LADFGVLHR	2	98.8%	1																										
				MIAILTENYGGK	2	99.7%	1																										
				NAQLAQYNFILVVGEK	2	99.3%	1																										
				NELSGALTGLTR	2	100.0%	2																										
				QVMVVPVGPTCDEYAQK	2	100.0%	1																										
				WPFWLSPR	2	100.0%	1																										
IPI00908950	RPL18	Ribosomal protein L18	100.0%	17.5	2	2	2	1	5,941,005	5,719,485	5,616,920	6,559,105	439,068	233,550	336,272	460,255	16.5	9.1	13.4	15.7	-1.0	0.7	-1.1	0.6	1.1	0.4	-1.0	0.8	1.1	0.1	1.2	0.1
				TAVVVGTITDDVR	2	100.0%	1																										
				TNSTFNQVVLK	2	99.9%	1																										
IPI00921469	-	Similar to Syntenin-2	100.0%	6.0	1	1	1	2	1,898,470	1,913,993	2,063,667	2,055,317	184,213	166,571	101,349	226,351	21.7	19.5	11.0	24.6	1.0	1	1.1	0.5	1.1	0.6	1.1	0.5	1.1	0.6	-1.0	1
IPI00908959	SDCBP2	cDNA FLJ58991, highly similar to Syntenin-2	100.0%	6.4	1	1	1	2	1,898,470	1,913,993	2,063,667	2,055,317	184,213	166,571	101,349	226,351	21.7	19.5	11.0	24.6	1.0	1	1.1	0.5	1.1	0.6	1.1	0.5	1.1	0.6	-1.0	1
				VDQAIQAQVR	2	100.0%	1																										
IPI00908963	ATP5A1	ATP synthase subunit alpha	100.0%	36.0	15	16	24	1	30,482,288	31,440,697	31,079,758	34,604,541	3,039,206	1,196,777	2,315,370	1,450,549	22.3	8.5	16.7	9.4	1.0	0.8	1.0	0.9	1.1	0.3	-1.0	0.9	1.1	0.1	1.1	0.2
				APGIIPR	2	99.6%	1																										
				AVDSLVPIGR	2	99.9%	1																										
				EIVTNFLAGFEA	2	100.0%	1																										
				EVAAFAQFGSDLDAATQQLLSR	2	100.0%	2																										
				EVAAFAQFGSDLDAATQQLLSR	3	100.0%	2																										
				FENAFLSHVVSQHQALLGTIR	3	100.0%	2																										
				GIRPAINVGLSVSR	2	97.9%	1																										
				GMSLNLEPDNVGVVVFGNDK	2	100.0%	2																										
				GYLDKLEPSK	3	99.9%	1																										
				HALIIYDDLSK	2	100.0%	2																										
				ILGADTSVDLEETGR	2	100.0%	2																										
				LKEIVTNFLAGFEA	2	100.0%	2																										
				NVQAEEMVEFSSGLK	2	100.0%	1																										
				RLTDADAMK	2	99.9%	1																										
				TGTAEMSSILEER	2	100.0%	2																										
				VLSIGDGIAR	2	100.0%	1																										
IPI00908988	HSPH1	cDNA FLJ52360, highly similar to Heat-shock protein 105 kDa	100.0%	12.9	6	7	8	1	3,651,205	3,807,720	4,278,607	4,489,948	274,947	212,866	306,457	121,030	16.8	12.5	16.0	6.0	1.0	0.7	1.2	0.2	1.2	0.02	1.1	0.2	1.2	0.02	1.0	0.5
				DLLNMYIETEGK	2	100.0%	2																										
				IEVPLYSLLEQTHLK	3	100.0%	1																										
				NAVEEYVYEFR	2	99.6%	1																										
				SQFEELCAELLQK	2	93.7%	1																										
				SVNEVMEWMNNVMNAQAK	2	100.0%	1																										
				VVNVELPIEANLVWQLGK	2	100.0%	1																										
				VVNVELPIEANLVWQLGK	3	99.9%	1																										
IPI00908994	HNRNPA1	cDNA FLJ51587, highly similar to Heterogeneous nuclear ribonucleoprotein A1	100.0%	43.8	8	8	11	1	5,429,856	5,692,294	5,557,055	5,974,659	328,717	176,112	281,268	62,407	13.5	6.9	11.3	2.3	1.0	0.5	1.0	0.8	1.1	0.2	-1.0	0.7	1.0	0.2	1.1	0.2
				EDSQRPGAHLTVK	2	90.2%	1																										
				GFGFVTYATVEEVDAAMNAR	3	100.0%	2																										
				KLFIGGLSFETTDESLR	2	100.0%	1																										
				LFIGGLSFETTDESLR	2	100.0%	3																										
				SESPKEPEQLRK	3	99.9%	1																										
				SHFEQWGTLTDCVVMR	2	100.0%	1																										
				SSGPYGGGGQYFAK	2	100.0%	1																										
				WGTLTDCVVMR	2	99.9%	1																										
IPI00909008	DDB1	cDNA FLJ51067, highly similar to DNA damage-binding protein 1	100.0%	2.8	3	3	3	2	2,472,159	2,616,905	2,335,706	2,950,794	201,390	84,564	200,527	173,528	18.2	7.2	19.2	13.2	1.1	0.5	-1.1	0.6	1.2	0.1	-1.1	0.2	1.1	0.1	1.3	0.05
IPI01015574	DDB1	27 kDa protein	100.0%	11.7	3	3	3	2	2,472,159	2,616,905	2,335,706	2,950,794	201,390	84,564	200,527	173,528	18.2	7.2	19.2	13.2	1.1	0.5	-1.1	0.6	1.2	0.1	-1.1	0.2	1.1	0.1	1.3	0.05
				EMLGGEIIPR	2	97.9%	1																										
				LPSFELLHK	3	96.8%	1																										
				LVFSNVNLK	2	99.8%	1																										
IPI00909058	BCCIP	cDNA FLJ54246, highly similar to Homo sapiens BRCA2 and CDKN1A interacting pr	100.0%	8.8	1	1	1	1	1,037,530	1,097,598	1,086,016	1,145,050	87,168	94,706	113,128	77,372	18.8	19.3	23.3	15.1	1.1	0.7	1.0	0.7	1.1	0.4	-1.0	0.9	1.0	0.7	1.1	0.7
				APVNTAELTDLLIQQNHIGSVIK	3	100.0%	1																										
IPI00909072	FADS6	cDNA FLJ59012, highly similar to Homo sapiens fatty acid desaturase domain family	93.8%	4.4	1	1	1	1	5,277,060	5,226,540	4,581,750	4,714,530	696,154	392,773	84,271	422,233	29.5	16.8	4.1	20.0	-1.0	1	-1.2	0.4	-1.1	0.5	-1.1	0.2	-1.1	0.4	1.0	0.8
				WGCSPGSQR	2	93.8%	1																										
IPI00909075	HARS	cDNA FLJ59476, highly similar to Histidyl-tRNA synthetase	100.0%	28.4	7	7	7	2	3,724,802	3,986,611	3,626,611	4,141,895	379,872	150,299	201,896	124,026	22.8	8.4	12.5	6.7	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.2	1.0	0.4	1.1	0.06
IPI00910697	HARS	cDNA FLJ53703, highly similar to Histidyl-tRNA synthetase	100.0%	20.9	7	7	7	2	3,724,802	3,986,611	3,626,611	4,141,895	379,872	150,299	201,896	124,026	22.8	8.4	12.5	6.7	1.1	0.5	-1.0	0.8	1.1	0.3	-1.1	0.2	1.0	0.4	1.1	0.06
				ASAELIEEEVAK	2	100.0%	1																										
				HGAEVIDTPVFELK	2	96.7%	1																										
				IFSIVEQR	2	90.1%	1																										
				IGDYVQQHGGVSLVEQLLQDPK	3	99.9%	1																										
				LLFEYLTLFGIDDK	2	89.3%	1																										
				QALEGLGDLK	2	96.4%	1																										
				YDGLVGMFDPK	2	98.9%	1																										
IPI00909083	GSPT1	eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform 2	100.0%	10.9	5	5	6	2	8,289,074	7,953,003	7,807,251	8,751,877	559,580	227,263	350,274	423,160	15.1	6.4	10.0	10.8	-1.0	0.6	-1.1	0.5	1.1	0.5	-1.0	0.7	1.1	0.1	1.1	0.1
IPI00910513	GSPT1	eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform 1	100.0%	10.8	5	5	6	2	8,289,074	7,953,003	7,807,251	8,751,877	559,580	227,263	350,274	423,160	15.1	6.4	10.0	10.8	-1.0	0.6	-1.1	0.5	1.1	0.5	-1.0	0.7	1.1	0.1	1.1	0.1
				GQQLVMMPNK	2	100.0%	1																										
				HFTILDAPGHK	3	99.2%	1																										
				HLIVLINK	2	95.5%	1																										
				PFVPNVHAAEFVPSFLR	3	100.0%	2																										
				SFVPNMIGGASQADLAVLVISAR	2	99.8%	1																										
IPI00909102	CDH17	cDNA FLJ53459, highly similar to Cadherin-17	100.0%	4.5	2	2	2	1	4,916,435	5,062,730	5,104,210	5,452,645	586,923	201,591	349,801	269,365	26.7	8.9	15.3	11.1	1.0	0.8	1.0	0.8	1.1	0.4	1.0	0.9	1.1	0.3	1.1	0.5
				KPLDFETAAVSNIVFK	2	100.0%	1																										

				VSEDVAIGTK	2	99.9%	1																									
IPI00909108	NEUROD6	cDNA FLJ56829, highly similar to Neurogenic differentiation factor 6	100.0%	9.5	4	4	5	1	6,796,719	7,049,679	6,403,817	7,475,513	937,673	450,901	520,520	221,244	30.9	14.3	18.2	6.6	1.0	0.8	-1.1	0.7	1.1	0.5	-1.1	0.4	1.1	0.4	1.2	0.09
				QLAGEDMEISVK	2	100.0%	2																									
				SGSMSAYEMR	2	99.9%	1																									
				SMVNLMDR	2	99.4%	1																									
				YSEPDLAVDFDNFVCCLVR	2	99.9%	1																									
IPI00909130	-	cDNA FLJ60052, highly similar to Aldo-keto reductase family 1 member C1	100.0%	33.6	3	3	3	2	2,023,524	1,955,966	1,822,512	2,328,492	245,452	118,935	116,514	76,865	27.1	13.6	14.3	7.4	-1.0	0.8	-1.1	0.5	1.2	0.3	-1.1	0.4	1.2	0.03	1.3	0.007
IPI00978772	LOC100508006	aldo-keto reductase family 1 member C2-like isoform 4	100.0%	35.3	3	3	3	2	2,023,524	1,955,966	1,822,512	2,328,492	245,452	118,935	116,514	76,865	27.1	13.6	14.3	7.4	-1.0	0.8	-1.1	0.5	1.2	0.3	-1.1	0.4	1.2	0.03	1.3	0.007
				HIDSAHLYNNEEQVGLAIR	3	100.0%	1																									
				LAIEAGFR	2	97.8%	1																									
				LNDGHFMPVLGFGTYAPAEVPK	3	100.0%	1																									
IPI00979841	LOC100508474	60S ribosomal protein L9-like, partial	100.0%	31.2	3	3	3	5	2,120,204	2,247,446	1,761,684	2,391,854	202,974	127,115	128,623	129,998	21.4	12.7	16.3	12.2	1.1	0.6	-1.2	0.2	1.1	0.3	-1.3	0.03	1.1	0.4	1.4	0.009
IPI00981834	LOC100510447	60S ribosomal protein L9-like, partial	100.0%	26.8	3	3	3	5	2,120,204	2,247,446	1,761,684	2,391,854	202,974	127,115	128,623	129,998	21.4	12.7	16.3	12.2	1.1	0.6	-1.2	0.2	1.1	0.3	-1.3	0.03	1.1	0.4	1.4	0.009
IPI00909133	RPL9	cDNA FLJ52179, highly similar to 60S ribosomal protein L9	100.0%	29.9	3	3	3	5	2,120,204	2,247,446	1,761,684	2,391,854	202,974	127,115	128,623	129,998	21.4	12.7	16.3	12.2	1.1	0.6	-1.2	0.2	1.1	0.3	-1.3	0.03	1.1	0.4	1.4	0.009
IPI00910195	RPL9	cDNA FLJ51990, highly similar to 60S ribosomal protein L9	100.0%	26.2	3	3	3	5	2,120,204	2,247,446	1,761,684	2,391,854	202,974	127,115	128,623	129,998	21.4	12.7	16.3	12.2	1.1	0.6	-1.2	0.2	1.1	0.3	-1.3	0.03	1.1	0.4	1.4	0.009
IPI00966707	RPL9	Uncharacterized protein	100.0%	26.5	3	3	3	5	2,120,204	2,247,446	1,761,684	2,391,854	202,974	127,115	128,623	129,998	21.4	12.7	16.3	12.2	1.1	0.6	-1.2	0.2	1.1	0.3	-1.3	0.03	1.1	0.4	1.4	0.009
				DFNHINVELSLLGK	2	99.9%	1																									
				TICSHVQNMIK	2	89.6%	1																									
				TILSNQTVDIPENVDITLK	2	100.0%	1																									
IPI00909140	TUBB	Tubulin beta chain	100.0%	39.0	10	13	22	1	71,510,111	70,941,215	72,119,157	82,892,590	7,684,526	2,935,646	6,002,388	2,018,075	24.0	9.3	18.6	5.4	-1.0	0.9	1.0	1	1.2	0.2	1.0	0.9	1.2	0.01	1.1	0.2
				AILVDLEPGTMDSVR	2	100.0%	2																									
				ALTVPELTQQVFDAK	2	100.0%	1																									
				EIVHIQAGQCGNQIGAK	2	99.5%	2																									
				FWEVISDEHGIDPTGTYHGDSDLQLDR	3	100.0%	1																									
				GHYTEGAELVDSVLDVVR	2	100.0%	2																									
				GHYTEGAELVDSVLDVVR	3	100.0%	2																									
				ISVYYNEATGGK	2	100.0%	2																									
				LTTPTYGDLNHLVSATMSGVTTCLR	2	100.0%	2																									
				MAVTFIGNSTAIQELFK	2	100.0%	2																									
				MAVTFIGNSTAIQELFK	3	100.0%	1																									
				MAVTFIGNSTAIQELFKR	3	100.0%	1																									
				SGPFGQIFRPDNFVFGQSGAGNNWAK	2	100.0%	2																									
				SGPFGQIFRPDNFVFGQSGAGNNWAK	3	100.0%	2																									
IPI00909143	DLD	Dihydrolipoyl dehydrogenase	100.0%	19.5	5	5	5	1	5,732,543	6,097,110	5,871,278	6,814,718	409,318	259,678	503,200	266,756	16.0	9.5	19.2	8.8	1.1	0.5	1.0	0.8	1.2	0.06	-1.0	0.7	1.1	0.09	1.2	0.1
				ALTGGIAHLFK	2	99.6%	1																									
				EANLAASFGK	2	99.3%	1																									
				IPNIYAIGDVVAGPMLAHK	3	100.0%	1																									
				NETLGGTCLNVGCIPSK	2	90.4%	1																									
				VLGAHILGPGAGEMVNEAALALEYGASCEDIAR	3	100.0%	1																									
IPI00909218	C22orf28	cDNA FLJ57752	100.0%	6.3	1	1	2	1	1,254,148	1,435,240	1,207,965	1,426,923	145,767	108,286	152,369	100,183	26.0	16.9	28.2	15.7	1.1	0.3	-1.0	0.8	1.1	0.4	-1.2	0.3	-1.0	1	1.2	0.3
				SYNDELQFLEK	2	100.0%	2																									
IPI00909241	PCDH8	cDNA FLJ60443, moderately similar to Protocadherin-8	93.2%	2.9	1	1	1	1	4,550,710	5,619,680	2,822,630	5,324,510	855,785	947,108	609,075	853,249	42.1	37.7	48.3	35.8	1.2	0.4	-1.6	0.1	1.2	0.5	-2.0	0.04	-1.1	0.8	1.9	0.04
				DVNDNAPDIAITPLAAPGAGNLTLRR	3	93.2%	1																									
IPI00909251	DDB1;LOC100290337	cDNA FLJ51165, highly similar to DNA damage-binding protein 1	100.0%	13.2	8	8	8	1	73,599,582	79,323,832	76,517,513	90,695,885	8,846,221	5,123,814	6,339,355	3,822,165	26.9	14.4	18.5	9.4	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.7	1.1	0.1	1.2	0.09
				DLLFILTAK	2	99.6%	1																									
				EMLGGEIIPR	2	97.9%	1																									
				GAVYSMVEFNGK	2	96.1%	1																									
				IEVQDTSGGTTALRPSASTQALSSSVSSSK	3	100.0%	1																									
				LPSFELLHK	3	96.8%	1																									
				LVFSNVNLK	2	99.8%	1																									
				SVLLLAYKPMEGNFEEIAR	3	100.0%	1																									
				VTLGTQPTVLR	2	92.6%	1																									
IPI00909276	-	cDNA FLJ56734, moderately similar to Sepiapterin reductase	100.0%	23.6	2	3	4	1	5,963,175	5,519,730	5,538,340	6,857,405	397,122	80,716	295,978	152,012	14.9	3.3	12.0	5.0	-1.1	0.3	-1.1	0.4	1.1	0.09	1.0	1	1.2	5.00E-05	1.2	0.004
				QLEAELGAER	2	98.1%	1																									
				VPADLGAEAGLQQLLGALR	2	100.0%	2																									
				VPADLGAEAGLQQLLGALR	3	99.4%	1																									
IPI00909288	-	cDNA FLJ51586, moderately similar to Heterogeneous nuclear ribonucleoprotein A1	100.0%	40.6	8	9	12	1	9,057,258	9,382,653	9,138,962	9,833,125	474,698	297,922	434,837	216,389	11.7	7.1	10.6	4.9	1.0	0.6	1.0	0.9	1.1	0.2	-1.0	0.7	1.0	0.3	1.1	0.2
				GFGFVTYATVEEVDAAMNAR	3	100.0%	2																									
				GGGFGGNDNFGR	2	98.0%	1																									
				KLFIGGLSFETTDESLR	2	100.0%	1																									
				KLFIGGLSFETTDESLR	3	99.5%	1																									
				LFIGGLSFETTDESLR	2	100.0%	3																									
				NQGGYGGSSSSSSYGSGR	2	100.0%	1																									
				SESPKEPEQLRK	3	99.9%	1																									
				SSGPYGGGGQYFAK	2	100.0%	1																									
				WGTLTDCVVMR	2	99.9%	1																									
IPI00909299	KIF5B	cDNA FLJ51288, highly similar to Kinesin heavy chain	100.0%	11.9	4	4	5	1	8,031,952	7,652,637	8,518,890	8,917,633	279,074	275,771	190,956	224,824	7.8	8.1	5.0	5.6	-1.0	0.4	1.1	0.2	1.1	0.04	1.1	0.03	1.2	0.007	1.0	0.2
				ISFLENNLEQLTK	2	100.0%	2																									
				LITDLQDQNQK	2	100.0%	1																									
				QAVEQQIQSHR	2	97.7%	1																									
				QLEESVDALSEELVQLR	2	100.0%	1																									
IPI00909336	-	cDNA FLJ59092	100.0%	30.3	6	6	7	1	11,685,445	12,411,849	11,785,062	13,790,662	1,234,092	608,804	1,055,039	512,795	23.6	11.0	20.0	8.3	1.1	0.6	1.0	1	1.2	0.2	-1.1	0.6	1.1	0.1	1.2	0.1
				GGVDHAAAFGR	3	87.5%	1																									
				ILTPLVSLDTPGK	2	100.0%	1																									
				LGNDFMGITLASSQAVSNAR	3	100.0%	1																									
				LLDDAMAADKSDEWFAK	3	99.9%	1																									
				SLNYWCNLLGMK	2	100.0%	1																									
				VTLAVSDLQK	2	99.9%	2																									
IPI00909338	SCARB2	lysosome membrane protein 2	98.3%	6.6	2	2	2	1	3,022,275	3,068,445	2,982,170	3,386,420	128,324	195,772	141,881	149,969	9.5	14.3	10.6	9.9	1.0	0.8	-1.0	0.8	1.1	0.1	-1.0	0.7	1.1	0.2	1.1	0.09
				KLDDFVETGDIR	2	96.2%	1																									
				VEEVGPYTYR	2	80.1%	1																									
IPI00909366	MYL6B	cDNA FLJ60058, highly similar to Myosin light chain 1, slow-twitch muscle A isoform	100.0%	9.4	2	2	3	1	10,176,200	10,577,778	10,233,410	11,586,230	951,707	433,364	679,261	412,659	20.9	9.2	14.8	8.0	1.0	0.7	1.0	1	1.1	0.2	-1.0	0.7	1.1	0.1	1.1	0.1
				ALGQNPTNAEVLK	2	100.0%	2																									
				EAFELFDR	2	99.9%	1																									
IPI00909383	EPRS	cDNA FLJ56021, highly similar to Bifunctional aminoacyl-tRNA synthetase[Includes:	100.0%	9.1	6	6	6	2	17,058,253	17,457,490	16,476,100	19,516,553	1,064,901	751,640	1,237,324	491,971	14.0	9.6	16.8	5.6	1.0	0.8	-1.0	0.7	1.1	0.07	-1.1	0.5	1.1	0.05	1.2	0.05
IPI01009785	EPRS	EPRS protein (Fragment)	100.0%	9.2	6	6	6	2	17,058,253	17,457,490	16,476,100	19,516,553	1,064,901	751,640	1,237,324	491,971	14.0	9.6	16.8	5.6	1.0	0.8	-1.0	0.7	1.1	0.07	-1.1	0.5	1.1	0.05	1.2	0.05
				HEELMLGDPCLK	2	99.7%	1																									
				INEAVECLLSLK	2	99.9%	1																									
				KGDIIQLQR	2	86.5%	1																									
				LNLNNTVLSK	2	99.8%	1																									
				TGQEYKPGNPPAEIGQNISSNSSASILESK	3	100.0%	1																									
				WFGFLEAQQAFQSVGTK	2	100.0%	1																									
IPI00909419	CMPK1	UMP-CMP kinase isoform b	100.0%	20.7	3	4	7	1	6,868,627	7,487,306	7,098,572	9,540,899	1,701,344	1,073,532	1,013,515	419,253	55.4	32.1	31.9	9.8	1.1	0.8	1.0	0.9	1.4	0.2	-1.1	0.8	1.3	0.1	1.3	0.06
				IQTYLQSTKPIIDLYEEMGK	3	100.0%	2																									
				SVDEVFDEVVQIFDK	2	100.0%	2																									
				SVDEVFDEVVQIFDKEG	2	100.0%	2																									
				SVDEVFDEVVQIFDKEG	3	100.0%	1																									
IPI00909433	-	cDNA FLJ54812, moderately similar to Mannose-6-phosphate isomerase	100.0%	7.0	1	1	1	1	618,894	641,312	679,510	743,192	41,089	29,840	43,369	58,120	14.9	10.4	14.3	17.5	1.0	0.7	1.1	0.3	1.2	0.1	1.1	0.5	1.2	0.2	1.1	0.4
				TLSQWIAENQDSLGSK	2	100.0%	1																									
IPI00909453	HSPB1	Uncharacterized protein	100.0%	43.9	4	4	4	1	6,381,090	7,085,215	6,774,100	7,850,375	535,739	231,411	517,784	387,121	18.8	7.3	17.1	11.0	1.1	0.3	1.1	0.6	1.2	0.06	-1.0	0.6	1.1	0.1	1.2	0.1
				KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	3	100.0%	1																									
				LATQSNEITIPVTFESR	2	100.0%	1																									
				TKDGVVEITGK	2	86.6%	1																									
				VSLDVNHFAPDELTVK	2	100.0%	1																									
IPI00909458	-	cDNA FLJ57908, moderately similar to Nuclear transport factor 2	93.9%	19.2	1	1	1	1	1,393,740	1,536,590	1,659,870	1,580,365	42,214	105,241	127,841	82,174	6.8	15.3	17.2	11.6	1.1	0.2	1.2	0.1	1.1	0.08	1.1	0.5	1.0	0.8	-1.1	0.6
				TQLGAIYIDASCLTWEGQQFQGK	3	93.9%	1																									
IPI00909481	LASP1	cDNA FLJ58065, highly similar to LIM and SH3 domain protein 1	100.0%	11.4	2	2	4	2	1,462,492	1,486,782	1,394,080	1,599,675	105,080	60,352	110,498	44,453	16.1	9.1	17.7	6.2	1.0	0.8	-1.0	0.7	1.1	0.3	-1.1	0.5	1.1	0.2	1.1	0.1
IPI00909939	LASP1	cDNA FLJ52195, highly similar to LIM and SH3 domain protein 1	100.0%	20.0	2	2	4	2	1,462,492	1,486,782	1,394,080	1,599,675	105,080	60,352	110,498	44,453	16.1	9.1	17.7	6.2	1.0	0.8	-1.0	0.7	1.1	0.3	-1.1	0.5	1.1	0.2	1.1	0.1
				GFSVVADTPELQR	2	100.0%	2																									
				LKQQSELQSQVR	2	99.6%	2																									
IPI00909513	PYGM	Phosphorylase	100.0%	5.7	2	2	3	1	6,284,320	6,304,857	6,595,372	6,746,955	368,409	272,807	127,532	233,306	13.1	9.7	4.3	7.7	1.0	1	1.0	0.5	1.1	0.3	1.0	0.4	1.1	0.3	1.0	0.6
				VIPAADLSEQISTAGTEASGTGNMK	3	100.0%	1																									
				YEFGIFNQK	2	100.0%	2																									
IPI00909534	EEF1G	cDNA FLJ59433, highly similar to Elongation factor 1-gamma	100.0%	16.5	4	4	4	1	6,821,263	6,824,093	6,493,760	7,641,483	568,602	196,241	593,988	297,924	18.6	6.4	20.5	8.7	1.0	1	-1.1	0.7	1.1	0.2	-1.1	0.6	1.1	0.05	1.2	0.1
				AKDPFAHLPK	3	99.9%	1																									
				KLDPGSEETQTLVR	2	100.0%	1																									
				LDPGSEETQTLVR	2	100.0%	1																									
				STFVLDEFKR	3	99.5%	1																									
IPI00909541	-	cDNA FLJ58390, highly similar to Aldo-keto reductase family 1 member C3homolog	100.0%	19.6	2	2	2	1	912,943	906,853	874,716	1,102,909	86,375	47,527	52,136	42,810	21.2	11.7	13.3	8.7	-1.0	1	-1.0	0.7	1.2	0.08	-1.0	0.7	1.2	0.02	1.3	0.01
				HIDSAHLYNNEEQVGLAIR	3	100.0%	1																									
				LAIEAGFR	2	97.8%	1																									
IPI00909570	EEF2	cDNA FLJ56548, highly similar to Elongation factor 2	100.0%	20.7	8	9	17	1	24,786,745	24,643,405	26,682,730	27,792,240	1,833,302	672,266	1,662,445	581,607	16.5	6.1	13.9	4.7	-1.0	0.9	1.1	0.5	1.1	0.2	1.1	0.3	1.1	0.008	1.0	0.6
				ALLELQLEPEELYQTFQR	2	100.0%	2																									
				ALLELQLEPEELYQTFQR	3	100.0%	2																									
				ARPFPDGLAEDIDKGEVSAR	3	100.0%	2																									
				EGIPALDNFLDKL	2	100.0%	3																									
				GEGQLGPAER	2	100.0%	2																									
				GHVFEESQVAGTPMFVVK	2	100.0%	1																									
				IWCFGPDGTGPNILTDITK	2	100.0%	2																									
				KVEDMMK	2	99.8%	2																									
				NMSVIAHVDHGK	2	100.0%	1																									
IPI00909581	TM9SF4	cDNA FLJ54711, highly similar to Transmembrane 9 superfamily protein member 4	99.6%	7.6	1	1	1	1	1,781,270	1,636,947	1,742,613	1,781,137	171,912	85,317	106,783	168,231	21.6	11.7	13.7	21.1	-1.1	0.5	-1.0	0.9	-1.0	1	1.1	0.5	1.1	0.5	1.0	0.9
				ITEDYYVHLIADNLPVATR	3	99.6%	1																									
IPI00909582	HSD17B4	peroxisomal multifunctional enzyme type 2 isoform 1	100.0%	7.4	4	4	5	3	3,071,462	3,649,774	3,633,496	3,944,238	299,320	206,677	378,158	228,233	21.8	12.7	23.3	12.9	1.2	0.2	1.2	0.3	1.3	0.05	-1.0	1	1.1	0.4	1.1	0.5
IPI00965117	HSD17B4	peroxisomal multifunctional enzyme type 2 isoform 3	100.0%	7.8	4	4	5	3	3,071,462	3,649,774	3,633,496	3,944,238	299,320	206,677	378,158	228,233	21.8	12.7	23.3	12.9	1.2	0.2	1.2	0.3	1.3	0.05	-1.0	1	1.1	0.4	1.1	0.5
IPI00965580	HSD17B4	Uncharacterized protein	100.0%	7.9	4	4	5	3	3,071,462	3,649,774	3,633,496	3,944,238	299,320	206,677	378,158	228,233	21.8	12.7	23.3	12.9	1.2	0.2	1.2	0.3	1.3	0.05	-1.0	1	1.1	0.4	1.1	0.5
				FAKPVYPGQTLQTEMWK	3	100.0%	1																									
				IDVVVNNAGILR	2	100.0%	1																									
				LGLLGLANSLAIEGR	2	100.0%	2																									
				VLQQFADNDVSR	2	100.0%	1																									
IPI00909600	GOLGB1	cDNA FLJ56563, highly similar to Golgin subfamily B member 1 (Fragment)	99.7%	4.4	2	2	2	2	1,850,345	2,206,290	2,021,950	2,287,355	92,192	70,324	192,141	37,564	11.1	7.1	21.3	3.7	1.2	0.02	1.1	0.4	1.2	0.002	-1.1	0.4	1.0	0.3	1.1	0.2
IPI00945169	GOLGB1	Uncharacterized protein	99.7%	2.6	2	2	2	2	1,850,345	2,206,290	2,021,950	2,287,355	92,192	70,324	192,141	37,564	11.1	7.1	21.3	3.7	1.2	0.02	1.1	0.4	1.2	0.002	-1.1	0.4	1.0	0.3	1.1	0.2
				AQVVDLLQQELTAAEQR	2	96.6%	1																									
				LLQDKNEQAVQSAQTIQQLEDQLQQK	3	99.7%	1																									
IPI00909626	TBCA	cDNA FLJ57496, moderately similar to Tubulin-specific chaperone A	100.0%	8.5	2	2	2	1	5,889,515	5,786,908	5,776,115	6,992,660	347,468	293,914	301,038	183,792	13.2	11.4	11.7	5.9	-1.0	0.8	-1.0	0.8	1.2	0.02	-1.0	1	1.2	0.008	1.2	0.009
				LEAAYLDLQR	2	98.9%	1																									
				RLEAAYLDLQR	2	99.9%	1																									

IPI00909674	EPS8L2	cDNA FLJ55025, highly similar to Epidermal growth factor receptor kinase substrate	100.0%	6.6	2	2	2	1	2,361,837	2,459,752	2,034,495	2,612,882	207,189	181,289	202,275	164,091	19.6	16.5	22.2	14.0	1.0	0.7	-1.2	0.3	1.1	0.4	-1.2	0.2	1.1	0.5	1.3	0.06
				IWTQEMLLQVNDQSLR	3	95.5%	1																									
				SEAITSVDDAIR	2	99.7%	1																									
IPI00909678	LASP1	cDNA FLJ51834, highly similar to LIM and SH3 domain protein 1	100.0%	10.7	2	2	4	1	2,936,978	3,040,963	2,936,967	3,270,457	214,879	105,383	174,389	41,000	16.4	7.8	13.3	2.8	1.0	0.7	-1.0	1	1.1	0.2	-1.0	0.6	1.1	0.1	1.1	0.1
				GFSVVADTPELQR	2	100.0%	2																									
				TQDQISNIK	2	100.0%	2																									
IPI00909681	-	Serine hydroxymethyltransferase	100.0%	28.8	8	8	11	1	5,625,977	5,428,854	6,072,201	6,311,316	515,820	214,938	386,121	379,589	20.5	8.9	14.2	13.5	-1.0	0.7	1.1	0.5	1.1	0.3	1.1	0.2	1.2	0.08	1.0	0.7
				AALEALGSCLNNK	2	100.0%	2																									
				AMADALLER	2	90.9%	1																									
				CGQLVRMAIRAQHSNAAQTQTGEANR	3	93.4%	1																									
				GLELIASENFCSR	2	96.9%	1																									
				IMGLDLPDGGHLTHGYMSDVKR	3	95.8%	1																									
				ISATSIFFESMPYK	2	100.0%	2																									
				VLELVSITANK	2	100.0%	2																									
				VVDFIDEGVNIGLEVK	2	100.0%	1																									
IPI00909685	SCP2	cDNA FLJ58965, highly similar to Nonspecific lipid-transfer protein	100.0%	39.7	5	6	8	1	6,430,287	6,690,386	7,494,021	6,782,316	266,810	493,523	548,316	750,050	9.3	16.5	16.4	24.7	1.0	0.7	1.2	0.1	1.1	0.7	1.1	0.3	1.0	0.9	-1.1	0.5
				ADCTITMADSDFLALMTGK	2	100.0%	1																									
				EATWVVDVK	2	99.9%	2																									
				IGGIFAFK	2	100.0%	1																									
				KLEEEGEQFVK	2	100.0%	2																									
				KLEEEGEQFVKK	2	100.0%	1																									
				KLEEEGEQFVKK	3	100.0%	1																									
IPI00909694	ALDH7A1	alpha-aminoadipic semialdehyde dehydrogenase isoform 3	100.0%	17.5	6	6	8	1	8,861,561	9,055,768	9,011,640	10,054,224	661,239	349,274	589,568	375,688	16.7	8.6	14.6	8.4	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	1	1.1	0.09	1.1	0.2
				ELGLREENEGVYNGSWGGR	3	100.0%	1																									
				GAPTTSLISVAVTK	2	100.0%	2																									
				GEVITTYCPANNEPIAR	2	100.0%	1																									
				IQVLGSLVSLEMGK	2	100.0%	1																									
				QGLSSSIFTK	2	99.9%	1																									
				VNLLSFTGSTQVGK	2	100.0%	2																									
IPI00909711	VCL	cDNA FLJ53006, highly similar to Vinculin	100.0%	19.0	3	3	4	1	1,236,659	1,399,341	1,591,012	1,572,082	64,032	54,826	264,078	86,316	11.6	8.8	37.1	12.3	1.1	0.09	1.3	0.3	1.3	0.01	1.1	0.5	1.1	0.1	-1.0	0.9
				AGEVINQPMMMAAR	2	99.0%	1																									
				AIPDLTAPVAAVQAAVSNLVR	2	100.0%	2																									
				TNISDEESEQATEMLVHNAQNLMQSVK	3	100.0%	1																									
IPI00909717	ARL6IP5	cDNA FLJ51702, moderately similar to PRA1 family protein 3	100.0%	8.1	1	1	1	3	2,543,302	2,439,556	2,322,208	2,801,500	216,651	182,678	154,301	184,482	19.1	16.7	14.9	14.7	-1.0	0.7	-1.1	0.4	1.1	0.4	-1.1	0.6	1.1	0.2	1.2	0.08
IPI00945943	ARL6IP5	10 kDa protein	100.0%	11.8	1	1	1	3	2,543,302	2,439,556	2,322,208	2,801,500	216,651	182,678	154,301	184,482	19.1	16.7	14.9	14.7	-1.0	0.7	-1.1	0.4	1.1	0.4	-1.1	0.6	1.1	0.2	1.2	0.08
IPI00946721	ARL6IP5	Uncharacterized protein	100.0%	12.5	1	1	1	3	2,543,302	2,439,556	2,322,208	2,801,500	216,651	182,678	154,301	184,482	19.1	16.7	14.9	14.7	-1.0	0.7	-1.1	0.4	1.1	0.4	-1.1	0.6	1.1	0.2	1.2	0.08
				AWDDFFPGSDR	2	99.9%	1																									
IPI00909721	PHB	cDNA FLJ51562, highly similar to Prohibitin	100.0%	14.2	2	2	3	1	1,972,822	1,945,910	2,140,315	2,045,162	83,523	54,243	55,959	34,835	9.5	6.2	5.9	3.8	-1.0	0.8	1.1	0.1	1.0	0.4	1.1	0.04	1.1	0.2	-1.0	0.2
				DLQNVNITLR	2	100.0%	2																									
				ILFRPVASQLPR	2	98.5%	1																									
IPI00909735	AP2B1	cDNA FLJ54516, highly similar to Adapter-relatedprotein complex 2 beta-1 subunit	100.0%	10.9	3	3	3	1	1,503,575	1,303,096	1,489,093	1,489,516	94,219	61,908	98,638	84,890	14.0	10.6	14.8	12.7	-1.2	0.1	-1.0	0.9	-1.0	0.9	1.1	0.1	1.1	0.1	1.0	1
				LTNGIWILAELR	2	100.0%	1																									
				MEPLNNLQVAVK	2	99.8%	1																									
				NVEGQDMLYQSLK	2	100.0%	1																									
IPI00909766	PSMD5	cDNA FLJ52877, highly similar to 26S proteasome non-ATPase regulatory subunit 5	100.0%	12.2	4	4	4	1	9,827,700	10,129,350	9,826,980	11,132,280	716,678	513,060	568,519	489,201	16.3	11.3	12.9	9.8	1.0	0.7	-1.0	1	1.1	0.2	-1.0	0.7	1.1	0.2	1.1	0.1
				ILTLSQIGR	2	96.9%	1																									
				IVENSDAVTEILNNAELLK	2	100.0%	1																									
				LMFNSPGFVEYVVDR	2	98.8%	1																									
				TIAEIFGNPNYLR	2	100.0%	1																									
IPI00909774	PRPF40A	Uncharacterized protein	100.0%	2.8	2	2	2	1	3,670,660	3,371,462	3,021,062	3,756,298	346,422	95,665	354,108	383,182	21.1	6.3	26.2	22.8	-1.1	0.4	-1.2	0.2	1.0	0.9	-1.1	0.4	1.1	0.4	1.2	0.2
				FVKEPAFEDITLESER	3	99.9%	1																									
				LAFNSLLEK	2	99.7%	1																									
IPI00909779	DEK	cDNA FLJ53031, highly similar to Protein DEK	100.0%	7.2	2	2	2	2	2,759,995	2,982,959	2,747,669	3,145,225	278,060	126,687	160,744	138,173	22.5	9.5	13.1	9.8	1.1	0.5	-1.0	1	1.1	0.2	-1.1	0.3	1.1	0.4	1.1	0.1
IPI00942944	DEK	protein DEK isoform 2	100.0%	7.3	2	2	2	2	2,759,995	2,982,959	2,747,669	3,145,225	278,060	126,687	160,744	138,173	22.5	9.5	13.1	9.8	1.1	0.5	-1.0	1	1.1	0.2	-1.1	0.3	1.1	0.4	1.1	0.1
				LLASANLEEVTMK	2	100.0%	1																									
				NVGQFSGFPFEK	2	99.0%	1																									
IPI00909783	SPINT2	kunitz-type protease inhibitor 2 isoform b precursor	99.5%	6.2	1	1	1	1	434,858	428,660	429,688	384,037	89,682	90,019	35,220	49,687	46.1	47.0	18.3	28.9	-1.0	1	-1.0	1	-1.1	0.6	1.0	1	-1.1	0.7	-1.1	0.5
				NAADSSVPSAPR	2	99.5%	1																									
IPI00909795	SMS	cDNA FLJ50114, highly similar to Spermine synthase	99.9%	8.4	1	2	2	1	743,381	727,109	721,579	866,630	68,058	60,707	93,781	19,383	20.5	18.7	29.1	5.0	-1.0	0.9	-1.0	0.9	1.2	0.1	-1.0	1	1.2	0.08	1.2	0.2
				YFTQGNCVNLTEALSLYEEQLGR	2	99.6%	1																									
				YFTQGNCVNLTEALSLYEEQLGR	3	99.7%	1																									
IPI00909914	HEXA	Uncharacterized protein	91.9%	3.4	1	1	1	1	3,152,590	3,704,775	3,672,190	3,688,980	473,670	273,910	317,961	130,686	33.6	16.5	19.4	7.9	1.2	0.3	1.2	0.4	1.2	0.3	-1.0	0.9	-1.0	1	1.0	1
				GYVVWQEVFDNK	2	91.9%	1																									
IPI00909925	RUVBL2	cDNA FLJ56743, highly similar to RuvB-like 2	100.0%	23.1	5	5	7	1	17,159,447	17,716,515	16,899,388	18,838,647	1,759,021	586,045	1,187,036	699,769	22.9	7.4	15.7	8.3	1.0	0.8	-1.0	0.9	1.1	0.4	-1.0	0.6	1.1	0.3	1.1	0.2
				AAGVVLEMIR	2	99.3%	1																									
				AVLIAGQPGTGK	2	100.0%	1																									
				GLGLDDALEPR	2	99.9%	1																									
				QASQGMVGQLAAR	2	100.0%	2																									
				TTEMETIYDLGTK	2	100.0%	2																									
IPI00909942	KIAA1217	Uncharacterized protein	100.0%	3.4	3	3	3	1	5,805,609	6,209,392	6,305,063	7,103,839	750,472	297,504	277,586	540,598	28.9	10.7	9.8	17.0	1.1	0.6	1.1	0.6	1.2	0.2	1.0	0.8	1.1	0.2	1.1	0.2
				GDAPVDKVELSEDSPNSEQDLEK	3	99.5%	1																									
				SMVVPGNATIPR	2	100.0%	1																									
				SQPEDTPPPTSIPSASR	3	88.5%	1																									
IPI00909956	-	cDNA FLJ59103, highly similar to T-complex protein 1 subunit epsilon	100.0%	35.0	7	7	9	1	5,402,847	5,802,687	5,712,866	6,495,849	715,251	339,578	476,774	420,043	29.6	13.1	18.7	14.5	1.1	0.6	1.1	0.7	1.2	0.2	-1.0	0.9	1.1	0.2	1.1	0.3
				EKFEEMIQQIK	2	98.5%	1																									
				ETGANLAICQWGFDDEANHLLLQNNLPAVR	3	100.0%	1																									
				FEEMIQQIK	2	99.5%	1																									
				GVIVDKDFSHPQMPK	3	88.5%	1																									
				LDVTSVEDYK	2	100.0%	1																									
				LGFAGLVQEISFGTTK	2	100.0%	2																									
				WVGGPEIELIAIATGGR	2	100.0%	2																									
IPI00909961	TPM3	cDNA FLJ50720, highly similar to Homo sapiens tropomyosin 3 (TPM3), transcript va	100.0%	12.3	2	2	3	1	2,888,724	2,909,005	2,855,741	3,329,598	227,736	132,638	216,079	148,647	17.6	10.2	16.9	10.0	1.0	0.9	-1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.07	1.2	0.1
				IQVLQQQADDAEER	2	100.0%	2																									
				KLVIIEGDLER	3	99.9%	1																									
IPI00909973	FDFT1	cDNA FLJ33164 fis, clone UTERU2000542, highly similar to Squalene synthetase	100.0%	12.8	3	3	3	2	1,797,231	1,813,534	1,851,459	2,053,176	117,128	44,915	74,403	112,961	14.6	5.5	9.0	12.3	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.7	1.1	0.08	1.1	0.2
IPI01012882	FDFT1	cDNA, FLJ79433, highly similar to Squalene synthetase	100.0%	11.8	3	3	3	2	1,797,231	1,813,534	1,851,459	2,053,176	117,128	44,915	74,403	112,961	14.6	5.5	9.0	12.3	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.7	1.1	0.08	1.1	0.2
				DYLEDQQGGR	2	100.0%	1																									
				LFSASEFEDPLVGEDTER	2	100.0%	1																									
				MGIGMAEFLDK	2	100.0%	1																									
IPI00910005	PTGES3	cDNA FLJ59832, moderately similar to Prostaglandin E synthase 3	100.0%	17.7	2	2	3	1	1,141,985	1,120,553	1,115,395	1,259,442	23,185	94,263	69,013	76,592	4.5	18.8	13.8	13.6	-1.0	0.8	-1.0	0.7	1.1	0.2	-1.0	1	1.1	0.3	1.1	0.2
				KGESGQSWPR	2	100.0%	2																									
				LNWLSVDFNNWK	2	100.0%	1																									
IPI00910019	MVP	Uncharacterized protein	100.0%	30.0	18	19	20	1	62,667,895	65,660,945	60,249,767	71,143,459	4,259,395	3,752,221	3,236,815	3,688,196	15.2	12.8	12.0	11.6	1.0	0.6	-1.0	0.7	1.1	0.2	-1.1	0.3	1.1	0.3	1.2	0.06
				AQLELEVSK	2	98.8%	1																									
				AQQLAEVEVK	2	99.3%	1																									
				AQQLAEVEVKK	2	99.5%	1																									
				DAQGLVLFDVTGQVR	2	100.0%	1																									
				DLAVAGPEMQVK	2	99.9%	2																									
				ELLELEALSMAVESTGTAK	3	100.0%	1																									
				GAVASVTFDDFHK	2	100.0%	1																									
				GPLEYVPSAK	2	99.9%	1																									
				HYCTVANPVSR	2	100.0%	1																									
				IEGEGSVLQAK	2	99.9%	1																									
				ILDQSEAEK	2	99.6%	1																									
				IPPYHYIHVLDQNSNVSR	3	100.0%	1																									
				LFSVPDFVGDACK	2	86.8%	1																									
				QAIPLDENEGIYVQDVK	2	100.0%	1																									
				QAIPLDENEGIYVQDVK	3	99.9%	1																									
				QMTEAIGPSTIR	2	99.7%	1																									
				TAVFGFETSEAK	2	100.0%	1																									
				VASGPSPGEGISPQSAQAPQAPGDNHVVPVLR	3	100.0%	1																									
				VPHNAAVQVYDYR	3	94.7%	1																									
IPI00910113	GDI1	cDNA FLJ52902, highly similar to Rab GDP dissociation inhibitor alpha	100.0%	5.5	2	2	2	1	5,263,815	5,228,615	4,730,565	5,765,085	384,686	362,456	394,035	283,978	16.3	15.5	18.6	11.0	-1.0	0.9	-1.1	0.4	1.1	0.3	-1.1	0.4	1.1	0.3	1.2	0.07
				KQNDVFGEAEQ	2	99.5%	1																									
				QLICDPSYIPDR	2	97.9%	1																									
IPI00910126	REEP6	cDNA FLJ59119, highly similar to Receptor expression-enhancing protein 6	100.0%	8.6	1	1	1	1	199,008	190,968	216,216	220,574	30,012	16,563	19,534	8,599	33.7	19.4	20.2	8.7	-1.0	0.8	1.1	0.6	1.1	0.5	1.1	0.4	1.2	0.2	1.0	0.8
				NLVTEVLGALEAK	2	100.0%	1																									
IPI00910169	-	cDNA FLJ54122, highly similar to Cytosol aminopeptidase	100.0%	7.8	2	2	2	1	1,909,344	1,895,663	1,785,045	2,101,773	192,452	89,848	90,559	63,284	22.5	10.6	11.3	6.7	-1.0	1	-1.1	0.6	1.1	0.4	-1.1	0.4	1.1	0.1	1.2	0.02
				GITFDSGGISIK	2	99.9%	1																									
				SWIEEQAMGSFLSVAK	2	100.0%	1																									
IPI00910220	ASNA1	cDNA FLJ60230, highly similar to Arsenical pump-driving ATPase	100.0%	5.0	1	1	1	1	1,633,570	1,414,535	1,710,910	1,318,595	79,389	98,632	141,695	73,326	10.9	15.6	18.5	12.4	-1.2	0.1	1.0	0.6	-1.2	0.02	1.2	0.1	-1.1	0.5	-1.3	0.04
				YLDQMEDLYEDFHIVK	3	99.6%	1																									
IPI00910237	PSMB5	proteasome subunit beta type-5 isoform 2	100.0%	7.5	1	1	1	1	4,835,745	3,343,915	3,447,410	4,175,130	571,748	409,039	295,539	629,111	26.4	27.4	19.2	33.7	-1.4	0.07	-1.4	0.06	-1.2	0.5	1.0	0.8	1.2	0.3	1.2	0.3
				VSSDNVADLHEK	3	99.0%	1																									
IPI00910259	C22orf28	cDNA FLJ57223	100.0%	21.8	2	2	3	1	4,508,538	3,667,690	5,749,195	4,634,033	443,124	181,655	1,039,375	301,206	22.0	11.1	40.4	14.5	-1.2	0.1	1.3	0.3	1.0	0.8	1.6	0.1	1.3	0.03	-1.2	0.4
				SYNDELQFLEK	2	100.0%	2																									
				TNLDECQRLGGGLGDGGGLVLKR	3	90.3%	1																									
IPI00910267	GOT2	Aspartate aminotransferase	100.0%	14.5	4	4	5	1	15,080,105	14,922,535	14,157,185	16,564,320	1,053,383	702,787	869,006	724,003	15.6	10.5	13.7	9.8	-1.0	0.9	-1.1	0.5	1.1	0.3	-1.1	0.5	1.1	0.1	1.2	0.07
				DAGMQLQGYR	2	100.0%	1																									
				FVTVQTISGTGALR	2	100.0%	1																									
				IAAAILNTPDLR	2	100.0%	2																									
				VLPGIAAAFHPGLAAAASAR	2	93.1%	1																									
IPI00910272	CNN2	cDNA FLJ52701, highly similar to Calponin-2	100.0%	10.4	2	2	2	1	2,460,057	2,323,150	2,335,950	2,558,433	388,246	199,198	172,904	161,943	35.3	19.2	16.6	14.2	-1.1	0.8	-1.1	0.8	1.0	0.8	1.0	1	1.1	0.4	1.1	0.4
				AGQCVIGLQMGTNK	2	100.0%	1																									
				SMQNWHQLENLSNFIK	3	98.8%	1																									
IPI00910275	LAD1	Uncharacterized protein	100.0%	26.9	9	9	11	1	25,998,180	26,377,115	28,244,100	30,277,995	1,866,309	689,791	614,384	1,366,376	16.1	5.9	4.9	10.1	1.0	0.9	1.1	0.3	1.2	0.1	1.1	0.08	1.1	0.03	1.1	0.2
				GLPCTELFVAPVGVASK	2	100.0%	2																									
				GPWALEEESLVGREPEER	3	100.0%	2																									
				IPSKEEEADMSSPTQR	3	99.7%	1																									
				LSGVVTSR	2	97.6%	1																									
				NLPSLAKQGASDPPTVASR	2	100.0%	1																									
				NSLSPVQATQKPLVSK	2	99.9%	1																									
				QVVEAAQAPIQER	2	100.0%	1																									
				RATASEQPLAQEPPASGGSPATTK	3	100.0%	1																									
				SLAPGMALGSGR	2	80.5%	1																									
IPI00910322	TPM4	cDNA FLJ52936, weakly similar to Tropomyosin alpha-4 chain	100.0%	31.8	6	6	9	1	5,364,272	5,258,984	5,216,095	5,783,654	460,320	164,219	347,096	273,805	19.2	7.0	14.9	10.6	-1.0	0.8	-1.0	0.8	1.1	0.5	-1.0	0.9	1.1	0.1	1.1	0.2
				IQALQQQADEAEDR	2	100.0%	1																									

				IQLVEEELDR	2	100.0%	2																									
				LATALQK	1	96.5%	2																									
				RIQLVEEELDR	2	100.0%	2																									
				RIQLVEEELDRAQER	3	99.2%	1																									
				YSEKEDKYEEEIK	3	99.2%	1																									
IPI00910325	ARFIP1	cDNA FLJ60846, highly similar to Arfaptin-1	100.0%	13.5	2	2	3	1	1,884,113	1,905,065	1,795,548	2,094,368	208,908	169,080	129,051	61,328	24.8	19.9	16.1	6.6	1.0	0.9	-1.0	0.7	1.1	0.4	-1.1	0.6	1.1	0.3	1.2	0.07
				LKTPGVDAPSWLEEQ	2	99.2%	1																									
				TDLEELNLGPR	2	99.9%	2																									
IPI00910350	MAPRE1	cDNA FLJ52068, highly similar to Microtubule-associated protein RP/EB family mem	100.0%	29.8	5	6	7	1	13,902,015	15,023,540	13,845,115	16,588,330	1,352,363	595,141	829,359	698,648	21.8	8.9	13.4	9.4	1.1	0.5	-1.0	1	1.2	0.1	-1.1	0.3	1.1	0.1	1.2	0.04
				FQDNFEFVQWFK	2	100.0%	2																									
				LEHEYIQNFK	2	99.9%	1																									
				LEHEYIQNFK	3	98.0%	1																									
				LTVEDLEKER	3	80.4%	1																									
				NIELICQENEGENDPVLQR	3	99.9%	1																									
				QGQETAVAPSLVAPALNKPK	3	100.0%	1																									
IPI00910355	TARDBP	cDNA FLJ58188, highly similar to TAR DNA-binding protein 43	100.0%	17.1	3	3	4	1	2,616,798	2,645,347	2,459,299	3,141,757	276,488	190,329	232,450	211,907	23.6	16.1	21.1	15.1	1.0	0.9	-1.1	0.7	1.2	0.2	-1.1	0.6	1.2	0.1	1.3	0.06
				AFAFVTFADDQIAQSLCGEDLIIK	2	100.0%	1																									
				FGGNPGGFGNQGGFGNSR	2	100.0%	2																									
				FTEYETQVK	2	85.2%	1																									
IPI00910407	PPIA	Peptidyl-prolyl cis-trans isomerase	100.0%	33.3	6	7	11	1	41,450,885	45,024,375	40,585,650	50,697,315	4,521,563	2,073,922	3,659,543	1,855,775	24.4	10.3	20.2	8.2	1.1	0.5	-1.0	0.9	1.2	0.1	-1.1	0.3	1.1	0.08	1.2	0.04
				EGMNIVEAMER	2	98.7%	1																									
				KITIADCGQLE	2	100.0%	2																									
				TEWLDGK	1	98.8%	1																									
				VKEGMNIVEAMER	2	99.2%	1																									
				VSFELFADK	2	100.0%	2																									
				VSFELFADKVPK	2	100.0%	2																									
				VSFELFADKVPK	3	100.0%	2																									
IPI00910408	PSMA1	proteasome subunit alpha type-1 isoform 3	100.0%	16.5	2	2	3	2	1,802,023	1,901,033	1,827,505	1,894,440	166,677	52,542	82,540	60,068	20.7	6.2	10.1	7.1	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.5	-1.0	0.9	1.0	0.5
IPI00978506	PSMA1	Uncharacterized protein	100.0%	18.5	2	2	3	2	1,802,023	1,901,033	1,827,505	1,894,440	166,677	52,542	82,540	60,068	20.7	6.2	10.1	7.1	1.1	0.6	1.0	0.9	1.1	0.6	-1.0	0.5	-1.0	0.9	1.0	0.5
				IHQIEYAMEAVK	2	99.9%	1																									
				NQYDNDVTVWSPQGR	2	100.0%	2																									
IPI00910420	ALDH7A1	isoform 3 of Alpha-aminoadipic semialdehyde dehydrogenase	100.0%	4.0	1	1	2	1	1,342,355	1,125,208	1,183,183	1,559,733	113,218	70,995	99,423	144,433	18.9	14.1	18.8	20.7	-1.2	0.1	-1.1	0.3	1.2	0.3	1.1	0.6	1.4	0.03	1.3	0.06
				VNLLSFTGSTQVGK	2	100.0%	2																									
IPI00910433	DDX3X	cDNA FLJ60675, highly similar to ATP-dependent RNA helicase DDX3X	100.0%	7.3	2	2	2	1	699,888	578,741	605,698	628,309	43,664	47,199	63,279	47,022	14.0	18.2	23.4	16.7	-1.2	0.1	-1.2	0.3	-1.1	0.3	1.0	0.7	1.1	0.5	1.0	0.8
				LEQELFSGGNTGINFEK	2	92.8%	1																									
				TAAFLLPILSQIYSDGPGEALR	3	100.0%	1																									
IPI00910438	SND1	cDNA FLJ54574, highly similar to Staphylococcal nuclease domain-containing protei	100.0%	26.3	17	18	19	1	28,593,584	30,074,112	29,597,096	33,709,003	1,497,954	1,596,532	1,861,103	521,551	11.7	11.9	14.1	3.5	1.1	0.5	1.0	0.7	1.2	0.02	-1.0	0.9	1.1	0.08	1.1	0.09
				ADDADEFGYSR	2	99.9%	1																									
				DYVAPTANLDQK	2	100.0%	1																									
				EADGSETPEPFAAEAK	2	100.0%	1																									
				ETCLITFLLAGIECPR	2	99.9%	1																									
				EVEVEVESMDK	2	99.8%	1																									
				GDVGLGLVK	2	94.0%	1																									
				LGTLSPAFSTR	2	97.3%	1																									
				LRPLYDIPYMFEAR	2	96.8%	1																									
				MVLSGCAIIVR	2	100.0%	2																									
				NDIASHPPVEGSYAPR	2	99.9%	1																									
				NDIASHPPVEGSYAPR	3	99.9%	1																									
				NLPGLVQEGEPFSEEATLFTK	2	100.0%	1																									
				SEAVVEYVFSGSR	2	100.0%	1																									
				SSHYDELLAAEAR	2	99.9%	1																									
				VADISGDTQK	2	99.9%	1																									
				VITEYLNAQESAK	2	100.0%	1																									
				VMQVLDADAIVVK	2	100.0%	1																									
				VNVTVDYIRPASPATETVPAFSER	3	99.6%	1																									
IPI00910461	LOC729020;RPE	cDNA FLJ52962, highly similar to Ribulose-phosphate 3-epimerase	95.5%	9.6	1	1	1	2	836,227	787,827	772,127	946,409	69,691	44,672	92,451	46,761	18.6	12.7	26.8	11.1	-1.1	0.6	-1.1	0.6	1.1	0.2	-1.0	0.9	1.2	0.04	1.2	0.1
IPI00927442	LOC729020;RPE	6 kDa protein	95.5%	31.7	1	1	1	2	836,227	787,827	772,127	946,409	69,691	44,672	92,451	46,761	18.6	12.7	26.8	11.1	-1.1	0.6	-1.1	0.6	1.1	0.2	-1.0	0.9	1.2	0.04	1.2	0.1
				IGPSILNSDLANLGAECLR	2	95.5%	1																									
IPI00910463	ALDH1A1	cDNA FLJ50286, highly similar to Retinal dehydrogenase 1	100.0%	19.2	5	5	7	1	16,362,870	17,121,475	16,380,630	19,417,470	1,605,218	555,939	1,566,811	798,922	21.9	7.3	21.4	9.2	1.0	0.7	1.0	1	1.2	0.1	-1.0	0.7	1.1	0.05	1.2	0.1
				GYFVQPTVFSNVTDEMR	2	100.0%	1																									
				IFVEESIYDEFVR	2	100.0%	1																									
				LECGGGPWGNK	2	99.2%	1																									
				QAFQIGSPWR	2	99.9%	2																									
				YILGNPLTPGVTQGPQIDKEQYDK	3	99.9%	2																									
IPI00910473	CDC42	cDNA FLJ55107, highly similar to Cell division control protein 42 homolog	100.0%	25.3	5	6	8	1	11,598,083	12,987,871	13,123,645	13,583,253	853,831	451,756	1,044,932	329,943	16.5	7.8	17.8	5.4	1.1	0.2	1.1	0.3	1.2	0.08	1.0	0.9	1.0	0.3	1.0	0.7
				NVFDEAILAALEPPEPK	2	97.4%	1																									
				NVFDEAILAALEPPEPK	3	100.0%	1																									
				QKPITPETAEK	3	84.6%	1																									
				TPFLLVGTQIDLR	2	100.0%	2																									
				TPFLLVGTQIDLRDDPSTIEK	3	92.4%	1																									
				YVECSALTQK	2	100.0%	2																									
IPI00910487	SERPINH1	cDNA FLJ52569, highly similar to Collagen-binding protein 2	100.0%	22.9	6	8	12	1	14,490,395	14,402,974	15,530,133	15,949,060	211,552	380,708	522,441	452,017	3.3	5.9	7.5	6.3	-1.0	0.8	1.1	0.1	1.1	0.02	1.1	0.1	1.1	0.03	1.0	0.6
				DQAVENILVSPVVVASSLGLVSLGGK	2	100.0%	2																									
				DQAVENILVSPVVVASSLGLVSLGGK	3	100.0%	2																									
				GVVEVTHDLQK	2	100.0%	2																									
				HLAGLGLTEAIDKNK	3	100.0%	1																									
				LFYADHPFIFLVR	2	99.9%	1																									
				LQIVEMPLAHK	2	99.9%	1																									
				LQIVEMPLAHK	3	99.1%	1																									
				LYGPSSVSFADDFVR	2	100.0%	2																									
IPI00910496	VCL	cDNA FLJ55698, highly similar to Vinculin	100.0%	14.9	4	4	4	1	3,009,512	3,187,068	3,061,979	3,418,111	193,514	72,609	194,402	142,684	14.4	5.1	14.2	9.3	1.1	0.4	1.0	0.9	1.1	0.1	-1.0	0.6	1.1	0.2	1.1	0.2
				AGEVINQPMMMAAR	2	99.0%	1																									
				MTGLVDEAIDTK	2	100.0%	1																									
				TNISDEESEQATEMLVHNAQNLMQSVK	3	100.0%	1																									
				VAMANIQPQMLVAGATSIAR	2	100.0%	1																									
IPI00910509	PPA2	cDNA FLJ59863, highly similar to Inorganic pyrophosphatase 2, mitochondrial	100.0%	14.4	2	2	2	1	548,307	496,034	577,120	555,721	70,292	13,438	59,950	28,207	28.7	6.1	23.2	11.4	-1.1	0.5	1.1	0.8	1.0	0.9	1.2	0.3	1.1	0.09	-1.0	0.8
				ILGILALIDEGETDWK	2	100.0%	1																									
				LIAINANDPEASK	2	100.0%	1																									
IPI00910544	SERPINB5	cDNA FLJ57640, highly similar to Serpin B5	100.0%	13.2	2	2	2	1	5,652,457	5,990,715	5,222,458	6,786,683	466,862	392,186	188,624	310,677	18.5	14.6	8.1	10.2	1.1	0.6	-1.1	0.4	1.2	0.08	-1.1	0.1	1.1	0.2	1.3	0.003
				DLTDGHFENILADNSVNDQTK	3	99.8%	1																									
				HIFSEDTSDFSGMSETK	3	100.0%	1																									
IPI00910547	CAPN1	calpain-1 catalytic subunit isoform b	100.0%	25.5	12	12	14	1	26,644,760	28,246,308	26,613,465	30,674,928	2,963,108	921,760	1,991,288	247,907	24.9	7.3	16.7	1.8	1.1	0.6	-1.0	1	1.2	0.2	-1.1	0.5	1.1	0.06	1.2	0.1
				FRLPPGEYVVVPSTFEPNKEGDFVLR	3	99.6%	1																									
				LEICNLTPDALK	2	99.9%	2																									
				LGLVEFNILWNR	2	100.0%	1																									
				LPPGEYVVVPSTFEPNKEGDFVLR	3	92.5%	1																									
				LVFVHSAEGNEFWSALLEK	3	100.0%	1																									
				LYELIITR	2	98.8%	1																									
				QLAGEDMEISVK	2	100.0%	2																									
				SAGTVELDDQIQANLPDEQVLSEEEIDENFK	3	100.0%	1																									
				SGSMSAYEMR	2	99.9%	1																									
				SMVNLMDR	2	99.4%	1																									
				WNTTLYEGTWR	2	98.1%	1																									
				YSEPDLAVDFDNFVCCLVR	2	99.9%	1																									
IPI00910548	QARS	cDNA FLJ54881, highly similar to Glutaminyl-tRNA synthetase	100.0%	10.9	1	1	1	2	183,049	191,127	179,619	207,893	21,378	11,656	16,133	6,546	26.1	13.6	20.1	7.0	1.0	0.7	-1.0	0.9	1.1	0.3	-1.1	0.6	1.1	0.2	1.2	0.1
IPI00925735	QARS	11 kDa protein	100.0%	16.0	1	1	1	2	183,049	191,127	179,619	207,893	21,378	11,656	16,133	6,546	26.1	13.6	20.1	7.0	1.0	0.7	-1.0	0.9	1.1	0.3	-1.1	0.6	1.1	0.2	1.2	0.1
				EAATQAQQTLGSTIDK	2	100.0%	1																									
IPI00910575	PTGES3	cDNA FLJ59888, moderately similar to Prostaglandin E synthase 3	100.0%	10.2	1	1	1	1	1,243,286	1,208,312	1,157,294	1,252,122	135,011	98,667	64,808	55,280	24.3	18.3	12.5	9.9	-1.0	0.8	-1.1	0.6	1.0	1	-1.0	0.7	1.0	0.7	1.1	0.3
				LTFSCLGGSDNFK	2	100.0%	1																									
IPI00910647	AIMP1	cDNA FLJ52127, highly similar to Multisynthetase complex auxiliary component p43	100.0%	19.0	3	3	3	1	8,604,473	8,223,723	9,589,916	8,708,500	420,305	432,375	481,230	323,044	10.9	11.8	11.2	8.3	-1.0	0.5	1.1	0.2	1.0	0.8	1.2	0.07	1.1	0.4	-1.1	0.2
				EIEELKQELIQAEIQNGVK	3	100.0%	1																									
				GAEADQIIEYLK	2	100.0%	1																									
				IWEQIQPDLHTNDECVATYK	3	97.9%	1																									
IPI00910662	DNM1L	cDNA FLJ59504, highly similar to Dynamin-1-like protein	100.0%	9.6	3	3	3	1	4,361,286	5,007,103	4,769,803	5,046,733	1,003,550	1,022,143	527,763	534,627	51.5	45.7	24.7	23.7	1.1	0.7	1.1	0.7	1.2	0.6	-1.0	0.8	1.0	1	1.1	0.7
				ALQGASQIIAEIR	2	94.7%	1																									
				SSLLDDLLTESEDMAQR	2	99.8%	1																									
				TLESVDPLGGLNTIDILTAIR	2	100.0%	1																									
IPI00910664	API5	cDNA FLJ52148, highly similar to Apoptosis inhibitor 5	100.0%	3.9	1	1	2	1	843,427	1,004,054	943,686	987,670	125,142	178,563	150,056	143,857	33.2	39.8	35.6	32.6	1.2	0.5	1.1	0.6	1.2	0.5	-1.1	0.8	-1.0	0.9	1.0	0.8
				ELPQFATGENLPR	2	99.9%	2																									
IPI00910687	MARS	cDNA FLJ53309, highly similar to Methionyl-tRNA synthetase	100.0%	6.6	3	3	4	1	2,277,810	2,239,757	2,522,614	2,600,761	175,706	106,720	140,266	127,783	17.3	10.7	12.4	11.0	-1.0	0.9	1.1	0.3	1.1	0.2	1.1	0.1	1.2	0.06	1.0	0.7
				GVGVFGDMAQDTGIPADIWR	2	100.0%	1																									
				ITQDIFQQLLK	2	99.9%	2																									
				WFNISFDIFGR	2	87.4%	1																									
IPI00910701	AARS	cDNA FLJ61339, highly similar to Alanyl-tRNA synthetase	100.0%	32.2	19	21	27	1	36,245,989	36,615,152	34,796,947	40,250,659	3,013,133	1,232,775	2,154,362	1,090,444	18.6	7.5	13.8	6.1	1.0	0.9	-1.0	0.7	1.1	0.3	-1.1	0.5	1.1	0.06	1.2	0.05
				ASEWVQQVSGLMDGK	2	100.0%	2																									
				AVFDETYPDPVR	2	100.0%	2																									
				AVYTQDCPLAAAK	2	100.0%	1																									
				DAAHLVNQDDPNVLEIWNLVFIQYNR	3	92.0%	1																									
				EIADLGEALATAVIPQWQK	2	100.0%	2																									
				EIADLGEALATAVIPQWQK	3	100.0%	1																									
				GAGGEDLIMLDIYAIEELR	2	100.0%	1																									
				GLEVTDDSPK	2	99.4%	1																									
				GLVVDMDGFEEER	2	100.0%	2																									
				KAEEIANEMIEAAK	2	100.0%	1																									
				KDPDMVKDIINEEEVQFLK	3	99.5%	1																									
				MALELLTQEFGIPIER	2	99.8%	1																									
				MSNYDTDLFVPYFEAIQK	2	100.0%	2																									
				MSNYDTDLFVPYFEAIQK	3	99.4%	1																									
				NVGCLQEALQLATSFAQLR	3	100.0%	1																									
				QFIDSNPNQPLVILEMESGASAK	2	100.0%	1																									
				RIVAVTGAEAQK	2	99.9%	1																									
				SIDTGMGLER	2	99.8%	1																									
				VGAEDADGIDMAYR	2	100.0%	2																									
				VGDQVWLFIDEPR	2	100.0%	1																									
				VVSIGVPVSELLDDPSGPAGSLTSVEFCGGTHLR	3	98.8%	1																									
IPI00910712	TPM2	cDNA FLJ57036, highly similar to Homo sapiens tropomyosin 2 (beta) (TPM2), trans	100.0%	10.6	3	3	4	1	2,207,775	2,213,051	1,954,082	2,392,902	284,711	105,690	174,808	209,809	28.8	10.7	20.0	19.6	1.0	1	-1.1	0.5	1.1	0.6	-1.1	0.2	1.1	0.5	1.2	0.1
				IQLVEEELDR	2	100.0%	2																									

				KLVILEGELER	2	99.9%	1																									
				QLEEEQQALQK	2	99.7%	1																									
IPI00910719	TARS	cDNA FLJ55705, highly similar to Threonyl-tRNA synthetase, cytoplasmic	100.0%	23.8	13	13	16	1	25,672,377	26,908,745	25,299,445	31,150,621	2,552,710	1,047,753	1,271,058	683,989	22.2	8.7	11.2	4.9	1.0	0.7	-1.0	0.9	1.2	0.1	-1.1	0.4	1.2	0.009	1.2	0.004
				CGPLIDLCR	2	91.2%	1																									
				FLGDIEVWDQAEK	2	100.0%	2																									
				FMADIDLDPGCTLNK	2	99.6%	1																									
				FMADIDLDPGCTLNKK	3	99.0%	1																									
				GAYIYNALIEFIR	2	100.0%	2																									
				ISGTVNIR	2	81.4%	1																									
				IYGISFPDPK	2	99.9%	1																									
				LADFGVLHR	2	98.8%	1																									
				MIAILTENYGGK	2	99.7%	1																									
				NAQLAQYNFILVVGEK	2	99.3%	1																									
				NELSGALTGLTR	2	100.0%	2																									
				QVMVVPVGPTCDEYAQK	2	100.0%	1																									
				WPFWLSPR	2	100.0%	1																									
IPI00910732	PPP2R1A	cDNA FLJ56053, highly similar to Serine/threonine-protein phosphatase 2A 65 kDa	100.0%	35.0	15	18	20	1	16,653,382	19,491,228	16,910,680	23,037,603	2,487,113	1,315,158	1,464,615	956,051	33.4	15.1	19.4	9.3	1.2	0.3	1.0	0.9	1.4	0.06	-1.2	0.2	1.2	0.06	1.4	0.008
				DNTIEHLLPLFLAQLK	3	100.0%	1																									
				DNTIEHLLPLFLAQLKDECPEVR	3	100.0%	1																									
				ELVSDANQHVK	2	98.3%	1																									
				ENVIMSQILPCIK	2	100.0%	1																									
				LNIISNLDCVNEVIGIR	2	100.0%	1																									
				LNIISNLDCVNEVIGIR	3	99.8%	1																									
				LTQDQDVDVK	2	100.0%	2																									
				MAGDPVANVR	2	100.0%	1																									
				NLCSDDTPMVR	2	97.5%	1																									
				QLSQSLLPAIVELAEDAK	3	100.0%	1																									
				QLSQSLLPAIVELAEDAKWR	3	100.0%	1																									
				SALASVIMGLSPILGK	2	95.3%	1																									
				SEIIPMFSNLASDEQDSVR	2	100.0%	2																									
				TDLVPAFQNLMK	2	99.9%	1																									
				VLAMSGDPNYLHR	2	99.9%	1																									
				VLAMSGDPNYLHR	3	99.7%	1																									
				YMVADKFTELQK	2	99.9%	1																									
				YMVADKFTELQK	3	99.8%	1																									
IPI00910737	CSE1L	cDNA FLJ54022, highly similar to Exportin-2	100.0%	2.8	1	1	2	1	309,163	368,357	295,720	352,498	33,929	27,402	41,264	28,935	24.5	16.6	31.2	18.4	1.2	0.2	-1.0	0.8	1.1	0.4	-1.2	0.2	-1.0	0.7	1.2	0.3
				FLESVEGNQNYPLLLLTLLEK	3	100.0%	2																									
IPI00910745	CAPN2	cDNA FLJ58224, highly similar to Calpain-2 catalytic subunit	100.0%	17.4	6	8	9	1	6,168,599	6,337,701	6,253,330	7,331,888	820,061	249,981	599,372	172,253	29.7	8.8	21.4	5.3	1.0	0.9	1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.01	1.2	0.1
				FADDQLIIDFDNFVR	2	100.0%	1																									
				FADDQLIIDFDNFVR	3	95.2%	1																									
				LEICNLTPDTLTSDTYKK	3	99.9%	1																									
				LFAQLAGEDAEISAFELQTILR	2	100.0%	1																									
				LFAQLAGEDAEISAFELQTILR	3	100.0%	1																									
				NPWGEVEWTGR	2	100.0%	1																									
				NYPNTFWMNPQYLIK	2	100.0%	2																									
				YLNQDYEALR	2	99.8%	1																									
IPI00910754	LDHA	L-lactate dehydrogenase A chain isoform 2	100.0%	40.5	10	14	19	1	61,586,753	63,419,577	62,865,981	70,463,009	4,495,351	2,060,941	5,357,628	2,357,984	16.3	7.3	19.1	7.5	1.0	0.7	1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.05	1.1	0.2
				DDVFLSVPCILGQNGISDLVK	2	100.0%	1																									
				DLADELALVDVIEDK	2	100.0%	1																									
				DLADELALVDVIEDK	3	100.0%	1																									
				DLADELALVDVIEDKLK	3	99.9%	2																									
				DQLIYNLLKEEQTPQNK	2	99.9%	2																									
				GEMMDLQHGSLFLR	2	100.0%	2																									
				GLYGIKDDVFLSVPCILGQNGISDLVK	2	100.0%	1																									
				LKGEMMDLQHGSLFLR	3	99.0%	1																									
				SADTLWGIQK	1	100.0%	1																									
				SADTLWGIQK	2	100.0%	2																									
				TLHPDLGTDKDKEQWK	2	100.0%	1																									
				TLHPDLGTDKDKEQWK	3	99.7%	2																									
				VTLTSEEEAR	1	98.7%	1																									
				VTLTSEEEAR	2	100.0%	1																									
IPI00910755	HSPH1	cDNA FLJ51707, highly similar to Heat-shock protein 105 kDa	100.0%	6.7	3	3	3	1	12,612,815	13,138,131	13,728,351	15,628,785	836,395	596,897	1,253,345	400,287	14.8	10.2	20.4	5.7	1.0	0.6	1.1	0.5	1.2	0.01	1.0	0.7	1.2	0.008	1.1	0.2
				IEVPLYSLLEQTHLK	3	100.0%	1																									
				QAGGIETIANEFSDR	2	98.6%	1																									
				SQFEELCAELLQK	2	93.7%	1																									
IPI00910763	CAPRIN1	Uncharacterized protein	100.0%	2.8	1	1	2	3	2,178,130	2,214,143	2,242,952	2,219,278	114,609	91,991	51,532	69,070	11.8	9.3	5.1	7.0	1.0	0.8	1.0	0.6	1.0	0.8	1.0	0.8	1.0	1	-1.0	0.8
IPI00975644	CAPRIN1	Uncharacterized protein	100.0%	6.2	1	1	2	3	2,178,130	2,214,143	2,242,952	2,219,278	114,609	91,991	51,532	69,070	11.8	9.3	5.1	7.0	1.0	0.8	1.0	0.6	1.0	0.8	1.0	0.8	1.0	1	-1.0	0.8
IPI00978969	CAPRIN1	Uncharacterized protein	100.0%	5.9	1	1	2	3	2,178,130	2,214,143	2,242,952	2,219,278	114,609	91,991	51,532	69,070	11.8	9.3	5.1	7.0	1.0	0.8	1.0	0.6	1.0	0.8	1.0	0.8	1.0	1	-1.0	0.8
				LNQDQLDAVSK	2	100.0%	2																									
IPI00910779	YWHAG	cDNA FLJ52141, highly similar to 14-3-3 protein gamma	100.0%	50.7	7	8	10	1	14,134,838	14,447,427	14,134,584	15,919,454	847,743	532,630	838,053	439,147	13.4	8.2	13.3	6.2	1.0	0.8	-1.0	1	1.1	0.1	-1.0	0.8	1.1	0.07	1.1	0.1
				DNLTLWTSDQQDDDGGEGNN	2	100.0%	2																									
				EHMQPTHPIR	3	99.1%	1																									
				LAEQAERYDDMAAAMK	3	99.6%	1																									
				LGLALNYSVFYYEIQNAPEQACHLAK	3	100.0%	1																									
				NVTELNEPLSNEER	2	100.0%	2																									
				TAFDDAIAELDTLNEDSYK	2	100.0%	1																									
				TAFDDAIAELDTLNEDSYK	3	100.0%	1																									
				YDDMAAAMK	2	100.0%	1																									
IPI00910781	GPI	glucose-6-phosphate isomerase isoform 1	100.0%	33.2	15	19	31	1	126,423,390	134,039,430	130,786,117	153,465,037	########	7,516,406	########	6,096,869	25.8	12.5	19.0	8.9	1.1	0.7	1.0	0.8	1.2	0.1	-1.0	0.8	1.1	0.08	1.2	0.1
				EWFLQAAK	2	99.9%	1																									
				FAAYFQQGDMESNGK	2	100.0%	2																									
				HFVALSTNTTK	2	100.0%	2																									
				ILLANFLAQTEALMR	2	100.0%	2																									
				ILLANFLAQTEALMR	3	100.0%	2																									
				INYTEGR	2	96.5%	2																									
				KIEPELDGSAQVTSHDASTNGLINFIK	3	100.0%	2																									
				LQQWYR	2	99.8%	1																									
				SNTPILVDGK	2	99.8%	1																									
				SNTPILVDGKDVMPEVNK	2	100.0%	2																									
				SNTPILVDGKDVMPEVNK	3	100.0%	2																									
				TFTTQETITNAETAK	2	100.0%	2																									
				TFTTQETITNAETAKEWFLQAAK	3	100.0%	1																									
				TLAQLNPESSLFIIASK	2	100.0%	1																									
				VFEGNRPTNSIVFTK	2	100.0%	2																									
				VFEGNRPTNSIVFTK	3	99.9%	1																									
				VKEFGIDPQNMFEFWDWVGGR	3	100.0%	1																									
				VWYVSNIDGTHIAK	2	100.0%	2																									
				VWYVSNIDGTHIAK	3	100.0%	2																									
IPI00910786	AIFM1	Apoptosis-inducing factor short isoform 3	99.0%	13.5	2	2	2	2	1,826,510	1,849,630	1,796,133	2,015,070	129,545	85,619	54,565	190,076	15.9	10.4	6.8	21.1	1.0	0.9	-1.0	0.8	1.1	0.4	-1.0	0.6	1.1	0.5	1.1	0.3
IPI01015707	AIFM1	apoptosis-inducing factor 1, mitochondrial isoform 5 precursor	99.0%	9.9	2	2	2	2	1,826,510	1,849,630	1,796,133	2,015,070	129,545	85,619	54,565	190,076	15.9	10.4	6.8	21.1	1.0	0.9	-1.0	0.8	1.1	0.4	-1.0	0.6	1.1	0.5	1.1	0.3
				ISGLGLTPEQK	2	99.0%	1																									
				SITIIGGGFLGSELACALGRK	2	95.4%	1																									
IPI00910829	PSMC6	cDNA FLJ57570, highly similar to 26S protease regulatory subunit S10B	100.0%	22.6	2	2	2	1	1,937,990	1,936,837	2,151,187	2,246,107	222,539	112,162	191,843	125,580	25.7	13.0	19.9	12.5	-1.0	1	1.1	0.5	1.2	0.3	1.1	0.4	1.2	0.1	1.0	0.7
				AVASQLDCNFLK	2	99.9%	1																									
				EVDPLVYNMSHEDPGNVSYSEIGGLSEQIR	3	100.0%	1																									
IPI00910830	VDAC1	cDNA FLJ57715, highly similar to Voltage-dependent anion-selective channel protei	100.0%	29.5	3	3	4	1	4,663,717	5,387,133	4,405,670	5,615,420	616,650	228,171	344,229	265,800	29.6	9.5	17.5	10.6	1.2	0.3	-1.1	0.7	1.2	0.2	-1.2	0.04	1.0	0.5	1.3	0.02
				TDEFQLHTNVNDGTEFGGSIYQK	3	100.0%	2																									
				VTQSNFAVGYK	2	99.8%	1																									
				YQIDPDACFSAK	2	98.9%	1																									
IPI00910864	MIR1279;CPSF6	Uncharacterized protein	100.0%	4.7	1	1	2	1	2,248,235	1,825,535	2,799,090	2,028,428	282,566	163,365	187,221	197,514	28.1	20.0	15.0	21.8	-1.2	0.2	1.2	0.1	-1.1	0.5	1.5	0.004	1.1	0.5	-1.4	0.02
				TPLSEAEFEEIMNR	2	100.0%	2																									
IPI00910875	ABHD14B	cDNA FLJ52723, highly similar to Abhydrolase domain-containing protein 14B	100.0%	19.7	3	3	3	1	2,742,327	2,887,673	2,840,150	3,344,464	289,155	108,002	251,219	170,998	23.6	8.4	19.8	11.4	1.1	0.7	1.0	0.8	1.2	0.1	-1.0	0.9	1.2	0.05	1.2	0.1
				AVAIDLPGLGHSK	2	99.2%	1																									
				EGTIQVQGQALFFR	2	98.0%	1																									
				FSVLLLHGIR	3	93.5%	1																									
IPI00910936	-	cDNA FLJ61101, highly similar to Eukaryotic translation initiation factor 5	100.0%	7.8	1	1	2	1	1,454,385	1,369,980	1,473,200	1,609,555	85,687	91,292	103,267	61,090	13.2	14.9	15.7	8.5	-1.1	0.5	1.0	0.9	1.1	0.2	1.1	0.5	1.2	0.06	1.1	0.3
				AMGPLVLTEVLFNEK	2	100.0%	2																									
IPI00910949	DBNL	cDNA FLJ52531, highly similar to Drebrin-like protein	100.0%	19.9	5	5	7	1	2,717,788	2,874,629	2,628,084	3,067,705	291,711	217,986	206,545	171,473	24.0	17.0	17.6	12.5	1.1	0.7	-1.0	0.8	1.1	0.3	-1.1	0.4	1.1	0.5	1.2	0.1
				AMSTTSISSPQPGK	2	100.0%	1																									
				GYGPDGHFGMFPANYVELIE	2	100.0%	1																									
				NGPALQEAYVR	2	99.9%	2																									
				TWEQQQEVVSR	2	100.0%	2																									
				VAGTGEGGLEEMVEELNSGK	2	100.0%	1																									
IPI00910980	IARS	IARS protein	100.0%	14.0	11	11	12	1	21,789,313	22,150,999	22,376,370	25,654,114	1,919,368	1,243,022	1,939,711	858,216	19.7	12.6	19.4	7.5	1.0	0.9	1.0	0.8	1.2	0.1	1.0	0.9	1.2	0.05	1.1	0.2
				EFEDAFPADFIAEGIDQTR	2	100.0%	1																									
				FVDILTNWYVR	2	100.0%	1																									
				GSELEITLTR	2	99.8%	1																									
				LFLNETQTQEITEDIPVK	2	90.9%	1																									
				LQKEEEIEFLYNENTVR	3	89.2%	1																									
				NNDLCYWVPELVR	2	85.9%	1																									
				NVIVNGLVLASDGQK	2	98.8%	1																									
				QLSSEELEQFQK	2	99.7%	2																									
				TESAVSQMQSVIELGR	2	100.0%	1																									
				VENMVDQLLR	2	96.6%	1																									
				YGADALR	2	91.4%	1																									
IPI00910990	AKR1C2	cDNA FLJ52680, highly similar to Aldo-keto reductase family 1 member C2	100.0%	15.5	3	3	4	1	2,783,573	2,767,395	2,615,028	3,024,638	322,024	93,350	224,241	89,592	25.9	7.5	19.2	6.6	-1.0	1	-1.1	0.7	1.1	0.5	-1.1	0.5	1.1	0.08	1.2	0.1
				LNDGHFMPVLGFGTYAPAEVPK	3	100.0%	1																									
				QNVQVFEFQLTSEEMK	2	98.0%	1																									
				TPALIALR	2	99.8%	2																									
IPI00911023	HARS	cDNA FLJ58562, highly similar to Histidyl-tRNA synthetase	100.0%	29.4	8	8	8	1	20,583,366	20,348,205	19,434,385	22,097,809	1,512,805	1,040,961	1,277,056	731,866	16.4	11.4	14.7	7.4	-1.0	0.9	-1.1	0.6	1.1	0.4	-1.0	0.6	1.1	0.2	1.1	0.1
				ASAELIEEEVAK	2	100.0%	1																									
				FVLKTPKDFDIAGNFDPMIPDAECLK	3	90.9%	1																									
				IFSIVEQR	2	90.1%	1																									
				IGDYVQQHGGVSLVEQLLQDPK	3	99.9%	1																									
				LLFEYLTLFGIDDK	2	89.3%	1																									
				QALEGLGDLK	2	96.4%	1																									
				TTETQVLVASAQK	2	99.7%	1																									

				YDGLVGMFDPK	2	98.9%	1																										
IPI00911039	HSPA1A;HSPA1B	cDNA FLJ54408, highly similar to Heat shock 70 kDa protein 1	100.0%	20.5	9	9	12	1	31,115,478	32,212,348	30,478,664	36,832,776	3,272,615	1,059,639	2,676,338	1,600,314	23.5	7.4	19.6	9.7	1.0	0.8	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.04	1.2	0.08
				AAAIGIDLGTTYSCVGVFQHGK	3	90.7%	1																										
				ATAGDTHLGGEDFDNR	2	100.0%	2																										
				CQEVISWLDANTLAEKDEFEHK	3	99.9%	1																										
				DAGVIAGLNVLR	2	100.0%	1																										
				GGSGSGPTIEEVD	1	88.5%	1																										
				LLQDFFDGR	2	100.0%	1																										
				LVNHFVEEFK	2	100.0%	2																										
				LVNHFVEEFKR	3	100.0%	1																										
				NQVALNPQNTVFDAK	2	100.0%	2																										
IPI00911085	-	cDNA FLJ53754, highly similar to Transmembrane emp24 domain-containing protei	100.0%	13.0	2	2	2	1	5,720,060	5,460,490	5,973,930	6,383,645	307,803	261,586	335,804	256,732	12.0	10.7	12.6	9.0	-1.0	0.5	1.0	0.6	1.1	0.1	1.1	0.3	1.2	0.04	1.1	0.4
				IPDQLVILDMK	2	100.0%	1																										
				ITDSAGHILYSK	2	99.5%	1																										
IPI00914059	-	Uridine monophosphate synthetase isoform G	99.2%	4.6	1	1	1	4	787,375	841,778	800,428	1,054,303	86,433	34,450	101,506	89,909	24.6	9.2	28.4	19.1	1.1	0.6	1.0	0.9	1.3	0.06	-1.1	0.7	1.3	0.08	1.3	0.1
IPI00945051	UMPS	7 kDa protein	99.2%	25.8	1	1	1	4	787,375	841,778	800,428	1,054,303	86,433	34,450	101,506	89,909	24.6	9.2	28.4	19.1	1.1	0.6	1.0	0.9	1.3	0.06	-1.1	0.7	1.3	0.08	1.3	0.1
IPI00945224	UMPS	15 kDa protein	99.2%	12.0	1	1	1	4	787,375	841,778	800,428	1,054,303	86,433	34,450	101,506	89,909	24.6	9.2	28.4	19.1	1.1	0.6	1.0	0.9	1.3	0.06	-1.1	0.7	1.3	0.08	1.3	0.1
IPI00945920	UMPS	6 kDa protein	99.2%	29.8	1	1	1	4	787,375	841,778	800,428	1,054,303	86,433	34,450	101,506	89,909	24.6	9.2	28.4	19.1	1.1	0.6	1.0	0.9	1.3	0.06	-1.1	0.7	1.3	0.08	1.3	0.1
				AALGPLVTGLYDVQAFK	2	99.2%	1																										
IPI00914566	FDPS	Farnesyl pyrophosphate synthase	100.0%	10.3	3	3	3	2	12,311,870	12,677,458	12,026,008	14,207,293	951,363	526,839	943,527	503,141	17.3	9.3	17.5	7.9	1.0	0.7	-1.0	0.8	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.08
IPI00914971	FDPS	farnesyl pyrophosphate synthase isoform b	100.0%	12.2	3	3	3	2	12,311,870	12,677,458	12,026,008	14,207,293	951,363	526,839	943,527	503,141	17.3	9.3	17.5	7.9	1.0	0.7	-1.0	0.8	1.2	0.1	-1.1	0.6	1.1	0.07	1.2	0.08
				LKEVLEYNAIGGK	3	99.8%	1																										
				QDFVQHFSQIVR	3	93.5%	1																										
				VLTEDEMGHPEIGDAIAR	3	99.1%	1																										
IPI00914952	AP2A2	isoform 3 of AP-2 complex subunit alpha-2	100.0%	8.1	4	4	4	1	3,983,488	3,660,932	3,783,307	4,288,853	289,700	177,808	201,910	84,563	16.3	10.9	11.9	4.4	-1.1	0.4	-1.1	0.6	1.1	0.4	1.0	0.7	1.2	0.01	1.1	0.05
				EMAEAFAGEIPK	2	96.0%	1																										
				EMAEAFAGEIPKVLVAGDTMDSVK	3	97.3%	1																										
				THIETVINALK	2	86.0%	1																										
				VGGYILGEFGNLIAGDPR	2	100.0%	1																										
IPI00914989	GLI2	isoform 5 of Zinc finger protein GLI2	97.3%	0.9	1	1	1	1	1,985,910	1,996,105	2,175,453	2,294,644	211,836	280,848	147,225	139,484	23.9	31.5	15.1	13.6	1.0	1	1.1	0.5	1.2	0.3	1.1	0.6	1.1	0.4	1.1	0.6
				TSPNSLVAYINNSR	3	97.3%	1																										
IPI00915302	GSS	Glutathione synthetase	100.0%	24.0	7	7	8	1	20,184,598	20,587,080	19,101,878	22,932,282	1,977,797	1,002,243	1,214,083	478,685	21.9	10.9	14.2	4.7	1.0	0.9	-1.1	0.7	1.1	0.2	-1.1	0.4	1.1	0.07	1.2	0.03
				AIEHADGGVAAGVAVLDNPYPV	2	100.0%	1																										
				AIENELLAR	2	99.9%	1																										
				ALAEGVLLR	2	99.3%	1																										
				ASYILMEK	2	99.3%	1																										
				CPDIATQLAGTK	2	90.1%	1																										
				EGGGNNLYGEEMVQALK	2	99.9%	1																										
				QYSLQNWEAR	2	98.1%	2																										
IPI00915422	ARCN1	coatomer subunit delta isoform 2	100.0%	10.6	4	4	4	1	11,643,736	12,578,965	11,659,527	13,011,604	626,683	359,009	722,750	291,307	12.0	6.4	13.9	5.0	1.1	0.2	1.0	1	1.1	0.08	-1.1	0.3	1.0	0.4	1.1	0.1
				ENVNLAQIR	2	98.4%	1																										
				SEGETIMSSSMGK	2	99.4%	1																										
				SFPVNSDVGVLK	2	99.5%	1																										
				TFTEMDSHEEK	2	99.9%	1																										
IPI00915789	GPD2	GPD2 protein	99.9%	6.6	2	2	2	1	1,890,125	1,766,217	1,831,567	1,911,347	50,862	41,294	151,214	143,011	6.0	5.2	18.5	16.7	-1.1	0.1	-1.0	0.7	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.7
				VIFFLPWQK	2	92.9%	1																										
				YGAATANYMEVVSLLK	2	99.8%	1																										
IPI00915844	SPATS2L	Uncharacterized protein	99.6%	9.3	1	1	1	8	90,644	88,305	104,526	120,324	9,721	4,501	13,096	20,307	24.0	11.4	28.0	37.7	-1.0	0.8	1.2	0.4	1.3	0.2	1.2	0.3	1.4	0.2	1.2	0.5
IPI00916544	SPATS2L	Uncharacterized protein	99.6%	11.7	1	1	1	8	90,644	88,305	104,526	120,324	9,721	4,501	13,096	20,307	24.0	11.4	28.0	37.7	-1.0	0.8	1.2	0.4	1.3	0.2	1.2	0.3	1.4	0.2	1.2	0.5
IPI00916902	SPATS2L	Uncharacterized protein	99.6%	19.2	1	1	1	8	90,644	88,305	104,526	120,324	9,721	4,501	13,096	20,307	24.0	11.4	28.0	37.7	-1.0	0.8	1.2	0.4	1.3	0.2	1.2	0.3	1.4	0.2	1.2	0.5
IPI00917360	SPATS2L	Uncharacterized protein	99.6%	15.7	1	1	1	8	90,644	88,305	104,526	120,324	9,721	4,501	13,096	20,307	24.0	11.4	28.0	37.7	-1.0	0.8	1.2	0.4	1.3	0.2	1.2	0.3	1.4	0.2	1.2	0.5
IPI00917531	SPATS2L	21 kDa protein	99.6%	9.6	1	1	1	8	90,644	88,305	104,526	120,324	9,721	4,501	13,096	20,307	24.0	11.4	28.0	37.7	-1.0	0.8	1.2	0.4	1.3	0.2	1.2	0.3	1.4	0.2	1.2	0.5
IPI00917948	SPATS2L	16 kDa protein	99.6%	12.9	1	1	1	8	90,644	88,305	104,526	120,324	9,721	4,501	13,096	20,307	24.0	11.4	28.0	37.7	-1.0	0.8	1.2	0.4	1.3	0.2	1.2	0.3	1.4	0.2	1.2	0.5
IPI00925916	SPATS2L	Uncharacterized protein	99.6%	7.6	1	1	1	8	90,644	88,305	104,526	120,324	9,721	4,501	13,096	20,307	24.0	11.4	28.0	37.7	-1.0	0.8	1.2	0.4	1.3	0.2	1.2	0.3	1.4	0.2	1.2	0.5
IPI01013077	SPATS2L	19 kDa protein	99.6%	10.4	1	1	1	8	90,644	88,305	104,526	120,324	9,721	4,501	13,096	20,307	24.0	11.4	28.0	37.7	-1.0	0.8	1.2	0.4	1.3	0.2	1.2	0.3	1.4	0.2	1.2	0.5
				SNNEIVLVLQQFDFNVDK	2	99.6%	1																										
IPI00915850	HIBADH	Protein	99.5%	8.7	1	1	1	1	1,491,885	1,272,265	1,398,930	1,423,515	142,461	63,639	148,524	68,377	21.4	11.2	23.7	10.7	-1.2	0.2	-1.1	0.7	-1.0	0.7	1.1	0.5	1.1	0.1	1.0	0.9
				MGAVFMDAPVSGGVGAAR	2	99.5%	1																										
IPI00915869	MDH1	malate dehydrogenase, cytoplasmic isoform 3	100.0%	30.6	5	5	8	1	12,149,230	12,785,613	11,836,563	13,603,937	1,065,114	475,583	806,856	514,791	19.6	8.3	15.2	8.5	1.1	0.6	-1.0	0.8	1.1	0.3	-1.1	0.3	1.1	0.3	1.1	0.1
				ELTEEKESAFEFLSSA	2	99.9%	1																										
				FVEGLPINDFSR	2	100.0%	2																										
				GEFVTTVQQR	2	100.0%	2																										
				NVIIWGNHSSTQYPDVNHAK	3	100.0%	1																										
				VIVVGNPANTNCLTASK	2	100.0%	2																										
IPI00915917	MTAP	5 kDa protein	100.0%	36.0	1	1	1	1	1,002,950	1,161,315	901,928	1,149,678	92,637	48,474	140,826	86,741	20.7	9.3	34.9	16.9	1.2	0.2	-1.1	0.6	1.1	0.3	-1.3	0.1	-1.0	0.9	1.3	0.2
				IGIIGGTGLDDPEILEGR	2	100.0%	1																										
IPI00915960	RANBP2	Uncharacterized protein	100.0%	1.7	3	3	3	1	7,595,548	8,070,442	7,637,708	8,637,887	691,822	408,113	641,892	334,226	20.4	11.3	18.8	8.7	1.1	0.6	1.0	1	1.1	0.2	-1.1	0.6	1.1	0.3	1.1	0.2
				AWMWLASDFSDGDAK	2	100.0%	1																										
				EQLLDCEGEDGWNK	3	99.4%	1																										
				FVFGSESVK	2	96.6%	1																										
IPI00915974	ITGA6	30 kDa protein	100.0%	5.4	1	1	1	1	273,528	273,227	346,058	332,988	19,831	23,913	19,383	21,446	16.2	19.6	12.5	14.4	-1.0	1	1.3	0.03	1.2	0.08	1.3	0.05	1.2	0.1	-1.0	0.7
				SEDEVGSLIEYEFR	2	100.0%	1																										
IPI00916030	COPS8	Uncharacterized protein	100.0%	6.3	1	1	1	1	811,330	666,702	773,919	922,728	90,268	81,796	145,020	33,489	24.9	27.4	41.9	8.1	-1.2	0.3	-1.0	0.8	1.1	0.3	1.2	0.5	1.4	0.02	1.2	0.4
				KPVAGALDVSFNK	2	98.4%	1																										
IPI00916040	-	16 kDa protein	97.0%	6.4	1	1	1	2	7,099,685	6,551,020	6,854,470	7,926,550	680,254	329,662	498,866	292,462	21.4	11.3	16.3	8.3	-1.1	0.5	-1.0	0.8	1.1	0.3	1.0	0.6	1.2	0.01	1.2	0.1
IPI00916178	-	Protein	97.0%	7.4	1	1	1	2	7,099,685	6,551,020	6,854,470	7,926,550	680,254	329,662	498,866	292,462	21.4	11.3	16.3	8.3	-1.1	0.5	-1.0	0.8	1.1	0.3	1.0	0.6	1.2	0.01	1.2	0.1
				FACELEGNR	2	97.0%	1																										
IPI00916111	MDH1	Malate dehydrogenase, cytoplasmic	100.0%	35.9	8	8	11	2	17,865,461	18,451,889	17,417,870	19,754,974	1,736,715	728,504	1,174,868	739,154	21.7	8.8	15.1	8.4	1.0	0.8	-1.0	0.8	1.1	0.3	-1.1	0.5	1.1	0.2	1.1	0.1
IPI00952583	MDH1	malate dehydrogenase, cytoplasmic isoform 1	100.0%	34.1	8	8	11	2	17,865,461	18,451,889	17,417,870	19,754,974	1,736,715	728,504	1,174,868	739,154	21.7	8.8	15.1	8.4	1.0	0.8	-1.0	0.8	1.1	0.3	-1.1	0.5	1.1	0.2	1.1	0.1
				ELTEEKESAFEFLSSA	2	99.9%	1																										
				FVEGLPINDFSR	2	100.0%	2																										
				GEFVTTVQQR	2	100.0%	2																										
				KLSSAMSAAK	2	100.0%	1																										
				LGVTANDVK	2	99.9%	1																										
				NVIIWGNHSSTQYPDVNHAK	3	100.0%	1																										
				VIVVGNPANTNCLTASK	2	100.0%	2																										
				VLVTGAAGQIAYSLLYSIGNGSVFGK	3	100.0%	1																										
IPI00916188	NCL	32 kDa protein	100.0%	29.3	7	10	19	1	27,220,253	26,943,340	28,143,883	29,866,730	2,218,731	951,110	1,584,627	1,076,882	18.2	7.9	12.6	8.1	-1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.5	1.1	0.08	1.1	0.4
				EVFEDAAEIR	2	100.0%	2																										
				GFGFVDFNSEEDAK	2	100.0%	3																										
				GLSEDTTEETLK	2	100.0%	1																										
				GLSEDTTEETLKESFDGSVR	2	100.0%	2																										
				GLSEDTTEETLKESFDGSVR	3	100.0%	2																										
				GYAFIEFASFEDAK	2	100.0%	2																										
				TLVLSNLSYSATEETLQEVFEK	2	100.0%	2																										
				TLVLSNLSYSATEETLQEVFEK	3	100.0%	1																										
				VTQDELKEVFEDAAEIR	2	100.0%	2																										
				VTQDELKEVFEDAAEIR	3	100.0%	2																										
IPI00916229	MAT2A	S-adenosylmethionine synthase	100.0%	8.7	2	2	2	1	3,167,735	3,138,185	3,165,450	3,609,615	200,941	144,539	175,907	79,130	14.2	10.3	12.4	4.9	-1.0	0.9	-1.0	1	1.1	0.09	1.0	0.9	1.2	0.02	1.1	0.05
				FVIGGPQGDAGLTGR	2	100.0%	1																										
				TQVTVQYMQDR	2	100.0%	1																										
IPI00916263	PPM1B	Uncharacterized protein	99.9%	11.2	2	2	2	1	8,006,929	8,982,216	8,177,545	8,633,662	1,037,317	567,513	798,269	636,619	29.0	14.1	21.8	16.5	1.1	0.4	1.0	0.9	1.1	0.6	-1.1	0.4	-1.0	0.7	1.1	0.7
				CVDGKGPTEQLVSPEPEVSDEAVK	3	88.5%	1																										
				YGLSSMQGWR	2	99.7%	1																										
IPI00916306	DYNC1I2	Uncharacterized protein	99.4%	11.6	1	1	1	1	89,947	93,417	75,748	102,102	8,530	6,597	5,777	11,732	21.2	15.8	17.1	25.7	1.0	0.8	-1.2	0.2	1.1	0.4	-1.2	0.08	1.1	0.5	1.3	0.08
				EAVAPVQEESDLEK	2	99.4%	1																										
IPI00916345	HSPE1	Uncharacterized protein	100.0%	14.9	1	2	4	1	2,761,836	2,998,980	2,605,416	3,210,754	499,857	436,685	182,768	299,057	40.5	32.6	15.7	20.8	1.1	0.7	-1.1	0.8	1.2	0.5	-1.2	0.4	1.1	0.7	1.2	0.1
				DGDILGK	1	98.5%	2																										
				DGDILGK	2	99.6%	2																										
IPI00916418	MCFD2	10 kDa protein	97.1%	13.3	1	1	1	1	6,378,680	6,144,600	4,917,690	5,971,380	1,095,397	425,426	404,852	289,083	38.4	15.5	18.4	10.8	-1.0	0.8	-1.3	0.3	-1.1	0.7	-1.2	0.07	-1.0	0.7	1.2	0.07
				EANLCTELTLRR	3	97.1%	1																										
IPI00916612	GGCT	gamma-glutamylcyclotransferase isoform 4	100.0%	21.3	2	2	2	1	4,249,750	4,485,647	3,977,090	5,087,613	453,875	245,313	285,365	165,422	23.9	12.2	16.0	7.3	1.1	0.7	-1.1	0.6	1.2	0.1	-1.1	0.2	1.1	0.08	1.3	0.01
				AIEPNDYTGK	2	97.2%	1																										
				VSEEIEDIIK	2	99.9%	1																										
IPI00916632	PSMD1	Uncharacterized protein	100.0%	9.9	1	1	1	2	545,345	595,890	657,605	638,153	76,629	33,696	62,109	36,689	31.4	12.6	21.1	12.9	1.1	0.6	1.2	0.3	1.2	0.3	1.1	0.4	1.1	0.4	-1.0	0.8
IPI00916965	PSMD1	5 kDa protein	100.0%	41.7	1	1	1	2	545,345	595,890	657,605	638,153	76,629	33,696	62,109	36,689	31.4	12.6	21.1	12.9	1.1	0.6	1.2	0.3	1.2	0.3	1.1	0.4	1.1	0.4	-1.0	0.8
				MITSAAGIISLLDEDEPQLK	2	98.7%	1																										
IPI00916763	HSPE1	Uncharacterized protein	100.0%	21.8	2	2	3	1	15,719,370	16,320,230	15,554,365	17,393,450	1,261,033	573,646	1,182,889	278,168	17.9	7.9	17.0	3.6	1.0	0.7	-1.0	0.9	1.1	0.3	-1.0	0.6	1.1	0.1	1.1	0.2
				KFLPLFDR	2	99.1%	1																										
				VLQATVVAVGSGSK	2	100.0%	2																										
IPI00916783	CAPG	Uncharacterized protein	100.0%	19.8	7	8	11	1	23,223,283	22,744,797	20,358,408	25,177,200	2,615,471	1,518,386	1,538,295	2,037,743	25.2	14.9	16.9	18.1	-1.0	0.9	-1.1	0.4	1.1	0.6	-1.1	0.3	1.1	0.4	1.2	0.1
				ANAQAAALYK	2	99.5%	1																										
				DLALAIR	2	95.0%	1																										
				EGNPEEDLTADK	2	99.9%	1																										
				EGNPEEDLTADKANAQAAALYK	3	99.9%	2																										
				QAALQVAEGFISR	2	100.0%	2																										
				VSDATGQMNLTK	2	100.0%	1																										
				YQEGGVESAFHK	2	100.0%	2																										
				YQEGGVESAFHK	3	98.9%	1																										
IPI00916786	LILRA2	53 kDa protein	96.6%	5.1	1	1	1	1	1,347,358	1,279,570	1,261,837	1,452,160	110,956	63,264	108,203	25,121	18.4	11.1	19.2	3.9	-1.1	0.6	-1.1	0.6	1.1	0.4	-1.0	0.9	1.1	0.03	1.2	0.2
				STPAVGAAHTAPPVLTWRPLCSGHP	2	96.6%	1																										
IPI00916922	SSB	Uncharacterized protein	100.0%	42.9	6	7	10	1	5,866,286	6,119,754	6,219,714	6,924,035	468,756	206,387	467,166	220,149	17.9	7.5	16.8	7.1	1.0	0.6	1.1	0.6	1.2	0.08	1.0	0.8	1.1	0.03	1.1	0.2
				EQIKLDEGWVPLEIMIK	3	99.4%	1																										
				GSIFVVFDSIESAK	2	100.0%	2																										
				ICHQIEYYFGDFNLPR	2	100.0%	1																										
				ICHQIEYYFGDFNLPR	3	99.6%	1																										
				LDEGWVPLEIMIK	2	100.0%	2																										
				LTTDFNVIVEALSK	2	100.0%	2																										
				SPSKPLPEVTDEYKNDVK	3	100.0%	1																										
IPI00917040	SPATS2L	Uncharacterized protein	97.0%	3.4	1	1	1	1	305,327	328,627	353,060	327,803	40,467	9,166	22,305	15,963	29.6	6.2	14.1	10.9	1.1	0.6	1.2	0.3	1.1	0.6	1.1	0.3	-1.0	1	-1.1	0.4
				LTDLASQMAEMQLAELR	2	97.0%	1																										
IPI00917108	SF1	Uncharacterized protein	100.0%	21.0	1	1	1	1	466,639	452,016	418,968	508,481	47,991	29,216	37,069	73,585	23.0	14.5	19.8	32.4	-1.0	0.8	-1.1	0.5	1.1	0.6	-1.1	0.5	1.1	0.5	1.2	0.3
				AYIVQLQIEDLTR	2	99.9%	1																										
IPI00917117	FAM129B	FAM129B protein (Fragment)	100.0%	3.4	1	1	1	1	790,988	802,545	782,598	876,460	64,767	86,492	159,235	74,674	18.3	24.1	45.5	19.1	1.0	0.9	-1.0	1	1.1	0.4	-1.0	0.9	1.1	0.5	1.1	0.6
				FQELIFEDFAR	2	100.0%	1																										
IPI00917205	SSB	Uncharacterized protein	100.0%	45.5	4	5	7	1	4,234,030	4,429,244	4,359,150	4,967,229	373,265	138,004	349,001	192,077	19.7	7.0	17.9	8.7	1.0	0.6	1.0	0.8	1.2	0.1	-1.0	0.9	1.1	0.05	1.1	0.2
				ICHQIEYYFGDFNLPR	2	100.0%	1																										

				ICHQIEYYFGDFNLPR	3	99.6%	1																									
				LDEGWVPLEIMIK	2	100.0%	2																									
				LTTDFNVIVEALSK	2	100.0%	2																									
				SPSKPLPEVTDEYKNDVK	3	100.0%	1																									
IPI00917237	GALM	21 kDa protein	100.0%	13.9	2	2	2	1	4,917,580	5,379,528	4,635,290	5,206,855	292,959	405,297	321,059	245,169	13.3	16.9	15.5	10.5	1.1	0.4	-1.1	0.5	1.1	0.5	-1.2	0.2	-1.0	0.7	1.1	0.2
				ASDVVLGFAELEGYLQK	2	100.0%	1																									
				VLSNGVQFSR	2	98.1%	1																									
IPI00917299	GGCT	Uncharacterized protein	100.0%	7.8	1	1	1	2	841,373	791,323	821,653	845,757	94,211	49,530	43,960	31,781	25.0	14.0	12.0	8.4	-1.1	0.7	-1.0	0.9	1.0	1	1.0	0.7	1.1	0.4	1.0	0.7
IPI00917449	GGCT	Protein	100.0%	10.9	1	1	1	2	841,373	791,323	821,653	845,757	94,211	49,530	43,960	31,781	25.0	14.0	12.0	8.4	-1.1	0.7	-1.0	0.9	1.0	1	1.0	0.7	1.1	0.4	1.0	0.7
				SNLNSLDEQEGVK	2	100.0%	1																									
IPI00917386	SSB	Uncharacterized protein	100.0%	38.3	3	3	5	1	2,461,690	2,509,816	2,503,488	2,729,986	71,214	76,233	195,932	79,914	6.5	6.8	17.5	6.6	1.0	0.7	1.0	0.8	1.1	0.04	-1.0	1	1.1	0.08	1.1	0.3
				GSIFVVFDSIESAK	2	100.0%	2																									
				LTTDFNVIVEALSK	2	100.0%	2																									
				SPSKPLPEVTDEYKNDVK	3	100.0%	1																									
IPI00917399	DARS	Uncharacterized protein	100.0%	11.4	1	1	1	2	1,231,650	1,405,370	1,170,565	1,338,108	94,333	32,837	83,201	51,975	17.1	5.2	15.9	8.7	1.1	0.1	-1.1	0.6	1.1	0.4	-1.2	0.04	-1.1	0.3	1.1	0.1
IPI00917492	DARS	Uncharacterized protein	100.0%	11.0	1	1	1	2	1,231,650	1,405,370	1,170,565	1,338,108	94,333	32,837	83,201	51,975	17.1	5.2	15.9	8.7	1.1	0.1	-1.1	0.6	1.1	0.4	-1.2	0.04	-1.1	0.3	1.1	0.1
				LPLQLDDAVRPEAEGEEEGR	3	99.9%	1																									
IPI00917430	SF3B1	Protein	99.1%	5.0	1	1	1	1	1,086,960	1,106,850	1,193,360	1,090,690	84,847	103,176	133,406	54,315	17.5	20.8	25.0	11.1	1.0	0.9	1.1	0.5	1.0	1	1.1	0.6	-1.0	0.9	-1.1	0.5
				VPELNVQNGVLK	2	99.1%	1																									
IPI00917473	GALM	Uncharacterized protein	100.0%	7.7	1	1	2	1	578,070	460,308	536,335	564,415	61,949	41,833	53,503	30,189	24.0	20.3	22.3	12.0	-1.3	0.2	-1.1	0.6	-1.0	0.8	1.2	0.3	1.2	0.08	1.1	0.7
				AVFGELPSGGGTVEK	2	99.3%	2																									
IPI00917509	CBX3	Uncharacterized protein	100.0%	13.9	1	1	1	2	488,172	515,893	432,561	589,458	72,695	60,938	56,792	60,739	33.3	26.4	29.4	23.0	1.1	0.8	-1.1	0.6	1.2	0.3	-1.2	0.3	1.1	0.4	1.4	0.1
IPI00917646	CBX3	Uncharacterized protein	100.0%	22.6	1	1	1	2	488,172	515,893	432,561	589,458	72,695	60,938	56,792	60,739	33.3	26.4	29.4	23.0	1.1	0.8	-1.1	0.6	1.2	0.3	-1.2	0.3	1.1	0.4	1.4	0.1
				KVEEAEPEEFVVEK	2	100.0%	1																									
IPI00917593	ITGA6	Uncharacterized protein	100.0%	10.8	2	2	2	1	525,390	513,692	478,638	511,681	45,750	39,769	34,120	46,235	19.5	17.3	15.9	20.2	-1.0	0.9	-1.1	0.4	-1.0	0.8	-1.1	0.5	-1.0	1	1.1	0.6
				DEITFVSGAPR	2	98.3%	1																									
				FGSCQQGVAATFTK	2	100.0%	1																									
IPI00917594	PSMD1	Protein	100.0%	10.9	1	1	1	1	1,733,927	1,723,123	1,665,313	1,895,130	189,693	106,882	185,670	122,238	24.5	13.9	24.9	14.4	-1.0	1	-1.0	0.8	1.1	0.5	-1.0	0.8	1.1	0.3	1.1	0.3
				TPEQCPSVVSLLSESYNPHVR	3	100.0%	1																									
IPI00917682	ACTR1B	17 kDa protein	92.4%	10.2	1	1	1	1	1,720,660	1,863,085	1,816,715	2,246,450	170,772	107,896	202,366	230,602	22.2	13.0	24.9	23.0	1.1	0.5	1.1	0.7	1.3	0.1	-1.0	0.8	1.2	0.2	1.2	0.2
				VMAGALEGDLFIGPK	2	86.4%	1																									
IPI00917920	DARS	Protein	100.0%	14.5	2	2	2	1	4,336,693	4,641,688	4,362,753	5,133,317	579,042	162,449	401,106	221,570	29.9	7.8	20.6	9.7	1.1	0.6	1.0	1	1.2	0.3	-1.1	0.5	1.1	0.1	1.2	0.1
				ESIVDVEGVVR	2	99.9%	1																									
				YGISSMIQSQEKPDR	3	100.0%	1																									
IPI00917990	VAMP8	Uncharacterized protein	93.1%	9.1	1	1	1	1	2,583,640	2,521,650	2,633,735	2,839,245	296,607	118,762	122,804	180,165	25.7	10.5	10.4	14.2	-1.0	0.9	1.0	0.9	1.1	0.5	1.0	0.5	1.1	0.2	1.1	0.4
				NIMTQNVER	2	93.2%	1																									
IPI00918002	MUC5B	Mucin 5AC, oligomeric mucus/gel-forming	100.0%	4.0	16	16	19	1	47,143,400	49,587,735	46,494,810	52,824,184	4,906,141	2,221,661	3,534,130	1,349,792	23.3	10.0	17.0	5.7	1.1	0.7	-1.0	0.9	1.1	0.3	-1.1	0.5	1.1	0.2	1.1	0.2
				AAGGAVCEQPLGLECR	2	100.0%	1																									
				CGLTDSETCLK	2	100.0%	1																									
				DPCTANPFRK	2	99.9%	1																									
				GPDFCPQK	2	100.0%	1																									
				GQTCGLCGNFNSIQADDFR	2	100.0%	2																									
				GSVLVNGHPVLLPFSQSGVLIQQSSSYTK	3	100.0%	1																									
				LTPLQFGNLQK	2	96.1%	1																									
				LTPMEFGNLQK	2	100.0%	1																									
				NWEQEGVFK	2	95.3%	1																									
				QCTHAGGLPQDWR	2	100.0%	1																									
				SALPGTTGSLGTWRPSQPPTLAPTTMATSR	3	90.7%	1																									
				TCGLCGDFNGMPVVSELLSHNTK	3	100.0%	1																									
				TGLLVEQSGDYIK	2	99.9%	1																									
				TQAACPNIR	2	99.9%	2																									
				VDGVVIQLTK	2	100.0%	2																									
				WSCQEVPCPGTCSVLGGAHFSTFDGK	3	99.9%	1																									
IPI00920959	C2orf81	HCG40743	95.9%	4.4	1	1	1	1	23,187,700	24,103,000	23,356,000	27,612,300	1,449,099	1,189,903	1,809,407	1,172,377	14.0	11.0	17.3	9.5	1.0	0.6	1.0	0.9	1.2	0.04	-1.0	0.7	1.1	0.07	1.2	0.08
				GHPLGFHLSLEDLYCCMPQLDAAGDR	3	94.3%	1																									
IPI00921062	HAAO	isoform 2 of 3-hydroxyanthranilate 3,4-dioxygenase	100.0%	8.8	1	1	1	1	1,164,027	1,057,453	1,130,843	1,159,973	115,081	34,734	131,527	84,684	22.1	7.3	26.0	16.3	-1.1	0.4	-1.0	0.9	-1.0	1	1.1	0.6	1.1	0.3	1.0	0.9
				YYVGDTMDVLFEK	2	99.8%	1																									
IPI00921414	-	Chaperonin Cpn60/TCP-1 family protein	100.0%	24.5	10	12	12	1	12,857,237	14,381,575	13,524,113	14,784,157	878,835	538,455	1,324,654	574,051	15.3	8.4	21.9	8.7	1.1	0.2	1.1	0.7	1.1	0.1	-1.1	0.6	1.0	0.6	1.1	0.4
				DALSDLALHFLNK	2	100.0%	1																									
				DALSDLALHFLNK	3	88.5%	1																									
				FSNISAAK	2	99.6%	1																									
				GDVTITNDGATILK	2	95.2%	1																									
				KLGGTIDDCELVEGLVLTQKVSNSGITR	3	98.0%	1																									
				LGGTIDDCELVEGLVLTQK	2	100.0%	1																									
				LGGTIDDCELVEGLVLTQK	3	99.3%	1																									
				MIQDGKGDVTITNDGATILK	3	100.0%	1																									
				QMQVLHPAAR	2	98.6%	1																									
				TGCNVLLIQK	2	99.8%	1																									
				VIDPATATSVDLR	2	100.0%	1																									
				VVSQYSSLLSPMSVNAVMK	2	100.0%	1																									
IPI00921812	TBC1D8	cDNA FLJ58691, highly similar to Mus musculus TBC1 domain family, member 8 (T	94.6%	2.0	1	1	1	3	1,001,228	1,075,616	1,162,087	1,124,790	362,187	347,100	228,315	274,744	80.9	72.2	43.9	54.6	1.1	0.9	1.2	0.7	1.1	0.8	1.1	0.8	1.0	0.9	-1.0	0.9
IPI00952866	TBC1D8	isoform 1 of TBC1 domain family member 8	94.6%	1.1	1	1	1	3	1,001,228	1,075,616	1,162,087	1,124,790	362,187	347,100	228,315	274,744	80.9	72.2	43.9	54.6	1.1	0.9	1.2	0.7	1.1	0.8	1.1	0.8	1.0	0.9	-1.0	0.9
IPI01014112	TBC1D8	132 kDa protein	94.6%	1.1	1	1	1	3	1,001,228	1,075,616	1,162,087	1,124,790	362,187	347,100	228,315	274,744	80.9	72.2	43.9	54.6	1.1	0.9	1.2	0.7	1.1	0.8	1.1	0.8	1.0	0.9	-1.0	0.9
				DFSMFLNLDEVFK	2	94.6%	1																									
IPI00921826	CHCHD3	cDNA FLJ53726, highly similar to Coiled-coil-helix-coiled-coil-helixdomain-containing	100.0%	10.9	1	1	1	1	636,725	592,110	562,610	624,868	37,701	38,617	85,868	67,650	13.2	14.6	34.1	24.2	-1.1	0.4	-1.1	0.5	-1.0	0.9	-1.1	0.8	1.1	0.7	1.1	0.6
				YSGAYGASVSDEELK	2	100.0%	1																									
IPI00921849	-	cDNA FLJ57046, highly similar to Lysosomal alpha-glucosidase	99.4%	3.3	1	1	1	1	3,312,900	3,115,780	3,041,040	3,478,120	312,237	156,627	350,076	76,085	21.1	11.2	25.7	4.9	-1.1	0.6	-1.1	0.6	1.0	0.6	-1.0	0.9	1.1	0.07	1.1	0.3
				APSPLYSVEFSEEPFGVIVHR	3	99.4%	1																									
IPI00921858	10-Sep	cDNA FLJ59501, highly similar to Septin-10	100.0%	11.3	2	2	2	1	1,751,040	1,653,024	1,798,512	1,847,671	139,830	118,882	133,348	58,888	17.9	16.1	16.6	7.1	-1.1	0.6	1.0	0.8	1.1	0.5	1.1	0.4	1.1	0.2	1.0	0.7
				LLEEEIIAFSK	2	100.0%	1																									
				VNAAMNGQLPFAVVGSMDEVK	2	98.5%	1																									
IPI00921861	CPD	cDNA FLJ59794, highly similar to Carboxypeptidase D	100.0%	2.7	2	2	2	2	1,783,561	1,741,565	1,825,013	2,015,102	96,769	82,846	19,804	85,165	12.1	10.6	2.4	9.5	-1.0	0.8	1.0	0.7	1.1	0.1	1.0	0.4	1.2	0.05	1.1	0.09
IPI00979354	CPD	carboxypeptidase D isoform 2	100.0%	2.1	2	2	2	2	1,783,561	1,741,565	1,825,013	2,015,102	96,769	82,846	19,804	85,165	12.1	10.6	2.4	9.5	-1.0	0.8	1.0	0.7	1.1	0.1	1.0	0.4	1.2	0.05	1.1	0.09
				ELLLNLIEYLCK	2	99.9%	1																									
				SQEGDSISVIGR	2	98.1%	1																									
IPI00921866	CKMT1B;CKMT1A	cDNA FLJ52454, highly similar to Creatine kinase, ubiquitous mitochondrial	100.0%	9.5	2	2	2	2	201,574	231,931	244,082	216,309	17,474	11,124	16,348	10,639	19.4	10.7	15.0	11.0	1.2	0.2	1.2	0.1	1.1	0.5	1.1	0.6	-1.1	0.3	-1.1	0.2
IPI01009935	CKMT1B;CKMT1A	cDNA FLJ52442, highly similar to Creatine kinase, ubiquitous mitochondrial	100.0%	10.7	2	2	2	2	201,574	231,931	244,082	216,309	17,474	11,124	16,348	10,639	19.4	10.7	15.0	11.0	1.2	0.2	1.2	0.1	1.1	0.5	1.1	0.6	-1.1	0.3	-1.1	0.2
				TVGMVAGDEETYEVFADLFDPVIQER	2	100.0%	1																									
				VISMEK	1	100.0%	1																									
IPI00921893	MAT2B	cDNA FLJ55836, highly similar to Homo sapiens methionine adenosyltransferase II,	100.0%	15.4	2	2	2	1	3,062,211	3,290,910	3,248,815	3,606,201	303,628	180,771	265,743	172,555	22.2	12.3	18.3	10.7	1.1	0.5	1.1	0.7	1.2	0.2	-1.0	0.9	1.1	0.2	1.1	0.3
				AVLENNLGAAVLR	2	100.0%	1																									
				IPILYGEVEKLEESAVTVMFDK	3	100.0%	1																									
IPI00921911	CRIP2	Uncharacterized protein	100.0%	5.6	1	1	1	1	590,749	707,296	599,116	798,400	69,132	92,095	58,366	67,329	26.2	29.1	21.8	18.9	1.2	0.3	1.0	0.9	1.4	0.06	-1.2	0.4	1.1	0.4	1.3	0.06
				ASSVTTFTGEPNTCPR	2	100.0%	1																									
IPI00921920	CAST	cDNA FLJ53909, moderately similar to Calpastatin	100.0%	8.9	2	2	2	1	276,374	286,598	276,034	316,468	17,926	21,362	23,923	11,942	14.5	16.7	19.4	8.4	1.0	0.7	-1.0	1	1.1	0.1	-1.0	0.8	1.1	0.3	1.1	0.2
				EQLPPMSEDFLLDALSEDFSGPQNASSLK	3	99.8%	1																									
				LAAAISEVVSQTPASTTQAGAPPR	3	99.3%	1																									
IPI00921931	SUCLG2	cDNA FLJ50080, highly similar to Succinyl-CoA ligase (GDP-forming) beta-chain, mi	100.0%	15.3	5	5	6	2	6,044,133	6,172,279	5,641,171	6,667,635	671,192	340,948	371,054	318,080	24.8	12.4	14.7	10.7	1.0	0.9	-1.1	0.6	1.1	0.4	-1.1	0.3	1.1	0.3	1.2	0.07
IPI00945507	SUCLG2	succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial isoform 1 precursor	100.0%	13.2	5	5	6	2	6,044,133	6,172,279	5,641,171	6,667,635	671,192	340,948	371,054	318,080	24.8	12.4	14.7	10.7	1.0	0.9	-1.1	0.6	1.1	0.4	-1.1	0.3	1.1	0.3	1.2	0.07
				ETYLAILMDR	2	99.9%	1																									
				FFVADTANEALEAAK	2	99.9%	1																									
				INFDDNAEFR	2	99.9%	1																									
				MAENLGFVGPLK	2	100.0%	1																									
				VMVAEALDISR	2	100.0%	2																									
IPI00921934	GOLGA2	Golgi autoantigen, golgin subfamily a, 2	95.7%	2.5	1	1	1	2	2,563,365	2,776,195	2,433,440	2,483,345	265,923	210,937	325,137	185,564	23.2	17.0	29.9	16.7	1.1	0.5	-1.1	0.8	-1.0	0.8	-1.1	0.4	-1.1	0.3	1.0	0.9
IPI00943357	GOLGA2	isoform 1 of Golgin subfamily A member 2	95.7%	1.2	1	1	1	2	2,563,365	2,776,195	2,433,440	2,483,345	265,923	210,937	325,137	185,564	23.2	17.0	29.9	16.7	1.1	0.5	-1.1	0.8	-1.0	0.8	-1.1	0.4	-1.1	0.3	1.0	0.9
				VQELETSLAELR	2	81.3%	1																									
IPI00921953	C12orf49	cDNA FLJ52021	99.2%	13.1	1	1	1	1	3,240,680	3,275,240	3,060,720	3,518,030	339,089	184,232	246,057	209,226	23.4	12.6	18.0	13.3	1.0	0.9	-1.1	0.7	1.1	0.5	-1.1	0.5	1.1	0.4	1.1	0.2
				PRRDGEPGGHGVAPASAEEVGAR	3	99.2%	1																									
IPI00921960	AK2	isoform 6 of Adenylate kinase 2, mitochondrial	100.0%	49.5	7	7	9	1	5,991,497	5,893,210	7,324,574	6,594,367	496,789	555,277	438,403	306,403	18.5	21.1	13.4	10.4	-1.0	0.9	1.2	0.08	1.1	0.3	1.2	0.08	1.1	0.3	-1.1	0.2
				AMVASGSELGKK	2	99.9%	1																									
				EKLDSVIEFSIPDSLLIR	2	98.9%	1																									
				GIHSAIDASQTPDVVFASILAAFSK	3	100.0%	1																									
				LDSVIEFSIPDSLLIR	2	99.9%	1																									
				LQAYHTQTTPLIEYYR	3	100.0%	1																									
				LVSDEMVVELIEK	2	100.0%	2																									
				QAEMLDDLMEK	2	100.0%	2																									
IPI00921979	TACC2	Uncharacterized protein	100.0%	3.4	1	1	1	2	170,732	184,153	181,073	185,164	16,589	20,165	20,542	9,749	21.7	24.5	25.4	11.8	1.1	0.6	1.1	0.7	1.1	0.5	-1.0	0.9	1.0	1	1.0	0.9
IPI00967285	TACC2	45 kDa protein	100.0%	5.6	1	1	1	2	170,732	184,153	181,073	185,164	16,589	20,165	20,542	9,749	21.7	24.5	25.4	11.8	1.1	0.6	1.1	0.7	1.1	0.5	-1.0	0.9	1.0	1	1.0	0.9
				GTYTFDIDKWDDPNFNPFSSTSK	3	99.4%	1																									
IPI00922028	-	cDNA FLJ60546, highly similar to Homo sapiens bridging integrator 1 (BIN1), transc	100.0%	11.3	3	4	5	1	2,504,928	2,740,659	2,790,046	3,067,560	196,593	193,887	192,004	185,316	17.6	15.8	15.4	13.5	1.1	0.4	1.1	0.3	1.2	0.07	1.0	0.9	1.1	0.3	1.1	0.3
				LNQNLNDVLVGLEK	2	99.9%	2																									
				LVDQALLTMDTYLGQFPDIK	2	100.0%	1																									
				LVDQALLTMDTYLGQFPDIK	3	100.0%	1																									
				VNHEPEPAGGATPGATLPK	3	100.0%	1																									
IPI00922032	HDGF	cDNA FLJ55039, moderately similar to Hepatoma-derived growth factor	100.0%	24.4	3	3	3	1	6,836,035	7,077,770	6,999,072	8,113,248	986,529	417,447	937,679	397,319	32.3	13.2	30.0	11.0	1.0	0.8	1.0	0.9	1.2	0.3	-1.0	0.9	1.1	0.1	1.2	0.3
				EAENPEGEEKEAATLEVERPLPMEVEK	3	100.0%	1																									
				GPPQEEEEEEDEEEEATKEDAEAPGIR	3	100.0%	1																									
				IDEMPEAAVK	2	99.1%	1																									
IPI00922094	-	cDNA FLJ59160, highly similar to Testin	100.0%	8.2	1	1	1	1	900,264	922,472	775,124	941,608	164,222	114,218	73,335	56,725	40.8	27.7	21.2	13.5	1.0	0.9	-1.2	0.5	1.0	0.8	-1.2	0.3	1.0	0.9	1.2	0.1
				NVMILTNPVAAK	2	100.0%	1																									
IPI00922127	HYOU1	cDNA FLJ54708, highly similar to 150 kDa oxygen-regulated protein	100.0%	14.3	5	5	6	2	2,682,036	2,674,743	2,603,168	2,925,363	291,787	164,479	247,987	111,816	24.3	13.8	21.3	8.6	-1.0	1	-1.0	0.8	1.1	0.5	-1.0	0.8	1.1	0.2	1.1	0.3
IPI00977915	HYOU1	HYOU1 protein	100.0%	11.8	5	5	6	2	2,682,036	2,674,743	2,603,168	2,925,363	291,787	164,479	247,987	111,816	24.3	13.8	21.3	8.6	-1.0	1	-1.0	0.8	1.1	0.5	-1.0	0.8	1.1	0.2	1.1	0.3
				DAVVYPILVEFTR	2	100.0%	2																									
				TLGGLEMELR	2	99.8%	1																									
				TVLSANADHMAQIEGLMDDVDFK	3	100.0%	1																									
				VEFEELCADLFER	2	100.0%	1																									
				VESVFETLVEDSAEEESTLTK	2	100.0%	1																									
IPI00922165	AK2	isoform 5 of Adenylate kinase 2, mitochondrial	100.0%	39.3	6	6	8	1	5,253,707	5,647,237	5,427,463	6,201,367	427,673	266,589	390,247	308,932	18.2	10.6	16.1	11.1	1.1	0.5	1.0	0.8	1.2	0.1	-1.0	0.7	1.1	0.2	1.1	0.2
				AMVASGSELGKK	2	99.9%	1																									
				AVLLGPPGAGK	2	99.8%	1																									
				GIHSAIDASQTPDVVFASILAAFSK	3	100.0%	1																									
				LQAYHTQTTPLIEYYR	3	100.0%	1																									
				LVSDEMVVELIEK	2	100.0%	2																									
				QAEMLDDLMEK	2	100.0%	2																									
IPI00922322	NAP1L1	cDNA FLJ54129, highly similar to Nucleosome assembly protein 1-like 1	100.0%	37.0	4	5	6	1	4,389,589	4,184,585	4,545,822	4,657,348	261,251	175,528	239,376	202,750	13.3	9.4	11.8	9.7	-1.0	0.5	1.0	0.7	1.1	0.4	1.1	0.3	1.1	0.1	1.0	0.7
				FYEEVHDLER	2	100.0%	1																									

				LDGLVETPTGYIESLPR	2	100.0%	2																									
				QLTVQMMQNPQILAALQER	2	100.0%	1																									
				QLTVQMMQNPQILAALQER	3	100.0%	1																									
				YAVLYQPLFDK	2	99.9%	1																									
IPI00922333	SMC1A	cDNA FLJ50250, highly similar to Structural maintenance of chromosome 1-like 1 pr	100.0%	5.2	2	2	2	1	6,733,630	5,909,915	6,301,625	6,986,825	404,661	364,836	412,166	441,236	13.4	13.8	14.6	14.1	-1.1	0.2	-1.1	0.5	1.0	0.7	1.1	0.5	1.2	0.1	1.1	0.3
				NMDAIIVDSEK	2	99.4%	1																									
				SGVISGGASDLKAKAR	2	87.9%	1																									
IPI00922359	PCMT1	Protein-L-isoaspartate O-methyltransferase	100.0%	37.0	5	5	5	1	10,937,383	12,387,150	10,950,578	12,314,338	777,115	858,799	531,520	308,266	15.9	15.5	10.9	5.6	1.1	0.2	1.0	1	1.1	0.1	-1.1	0.2	-1.0	0.9	1.1	0.06
				ELVDDSVNNVR	2	99.9%	1																									
				KDDPTLLSSGR	2	99.8%	1																									
				LILPVGPAGGNQMLEQYDKLQDGSIK	3	94.8%	1																									
				SGGASHSELIHNLR	3	97.6%	1																									
				VQLVVGDGR	2	99.9%	1																									
IPI00922361	SRSF1	cDNA FLJ53078, highly similar to Splicing factor, arginine/serine-rich 1	100.0%	22.4	3	3	7	1	3,205,933	3,429,920	3,176,616	3,859,575	230,374	103,379	246,273	181,677	16.1	6.7	17.3	10.5	1.1	0.4	-1.0	0.9	1.2	0.06	-1.1	0.4	1.1	0.07	1.2	0.06
				DGTGVVEFVR	2	99.9%	2																									
				EAGDVCYADVYR	2	100.0%	2																									
				SHEGETAYIR	2	100.0%	3																									
IPI00922367	NONO	non-POU domain-containing octamer-binding protein isoform 2	100.0%	31.7	10	11	14	1	37,661,253	38,483,196	36,389,620	42,487,821	3,436,140	1,335,062	2,213,284	1,412,012	20.4	7.8	13.6	7.4	1.0	0.8	-1.0	0.8	1.1	0.2	-1.1	0.4	1.1	0.07	1.2	0.05
				AAPGAEFAPNKR	2	100.0%	2																									
				AGEVFIHK	2	99.7%	1																									
				EKLEMEMEAAR	2	99.9%	1																									
				FACHSASLTVR	3	100.0%	1																									
				FAQPGSFEYEYAMR	2	100.0%	2																									
				FGQAATMEGIGAIGGTPPAFNR	2	100.0%	1																									
				FGQAATMEGIGAIGGTPPAFNR	3	100.0%	1																									
				MGQMAMGGAMGINNR	2	94.2%	1																									
				RMEELHNQEVQK	3	100.0%	1																									
				TLAEIAK	1	98.8%	1																									
				VELDNMPLR	2	100.0%	2																									
IPI00922379	-	cDNA FLJ59030	93.8%	9.6	1	1	1	1	643,407	677,007	645,441	985,298	71,263	192,423	62,432	269,736	24.8	63.6	21.6	61.2	1.1	0.9	1.0	1	1.5	0.3	-1.0	0.9	1.5	0.4	1.5	0.3
				GSEAIQTLTTAGSCYHNK	3	93.8%	1																									
IPI00922399	-	cDNA FLJ57937, highly similar to DNA-directed RNA polymerase II 33 kDa polypept	93.8%	9.7	1	1	1	1	3,625,147	3,650,633	3,577,923	3,836,183	240,487	181,611	277,892	172,732	14.8	11.1	17.4	10.1	1.0	0.9	-1.0	0.9	1.1	0.5	-1.0	0.8	1.1	0.5	1.1	0.5
				FIIENTDLAVANSIR	2	93.8%	1																									
IPI00922413	-	cDNA FLJ61560, highly similar to Tight junction protein ZO-2	100.0%	7.5	6	6	6	1	8,908,407	9,293,452	8,135,733	10,070,325	720,445	220,568	659,826	512,850	18.1	5.3	18.1	11.4	1.0	0.6	-1.1	0.5	1.1	0.2	-1.1	0.2	1.1	0.2	1.2	0.05
				AEQMASVQNAQR	2	99.9%	1																									
				AFEVMDEFDGR	2	100.0%	1																									
				GEMVTILAQSR	2	99.9%	1																									
				MEELIWEQYTVTLQK	2	89.8%	1																									
				RPVVLFGPIADIAMEK	2	85.0%	1																									
				TFLRPSPEDEAIYGPNTK	3	100.0%	1																									
IPI00922415	SSBP1	cDNA FLJ51825, highly similar to Single-stranded DNA-binding protein, mitochondri	100.0%	14.5	2	2	3	3	2,841,336	2,745,609	2,632,395	2,840,250	349,738	138,317	139,651	136,616	27.5	11.3	11.9	10.8	-1.0	0.8	-1.1	0.6	-1.0	1	-1.0	0.6	1.0	0.6	1.1	0.3
IPI00947310	SSBP1	Uncharacterized protein	100.0%	19.0	2	2	3	3	2,841,336	2,745,609	2,632,395	2,840,250	349,738	138,317	139,651	136,616	27.5	11.3	11.9	10.8	-1.0	0.8	-1.1	0.6	-1.0	1	-1.0	0.6	1.0	0.6	1.1	0.3
IPI01014556	SSBP1	Uncharacterized protein	100.0%	17.0	2	2	3	3	2,841,336	2,745,609	2,632,395	2,840,250	349,738	138,317	139,651	136,616	27.5	11.3	11.9	10.8	-1.0	0.8	-1.1	0.6	-1.0	1	-1.0	0.6	1.0	0.6	1.1	0.3
				SGDSEVYQLGDVSQK	2	100.0%	2																									
				VGQDPVLR	2	99.8%	1																									
IPI00922421	GOT1	Aspartate aminotransferase	100.0%	35.0	11	13	16	1	30,159,758	30,313,982	29,866,401	34,717,099	2,524,241	1,109,504	1,993,431	689,864	18.7	8.2	14.9	4.4	1.0	1	-1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.01	1.2	0.07
				FLFPFFDSAYQGFASGNLER	2	100.0%	2																									
				FLFPFFDSAYQGFASGNLER	3	100.0%	1																									
				HIYLLPSGR	2	97.6%	1																									
				IGADFLAR	2	99.9%	1																									
				INVSGLTTK	2	83.5%	1																									
				ITWSNPPAQGAR	2	99.7%	1																									
				IVASTLSNPELFEEWTGNVK	2	100.0%	2																									
				IVASTLSNPELFEEWTGNVK	3	100.0%	1																									
				KVNLGVGAYR	2	89.6%	1																									
				QVEYLVNEK	2	98.1%	1																									
				VGNLTVVGKEPESILQVLSQMEK	3	93.8%	1																									
				VNLGVGAYR	2	98.1%	1																									
				WYNGTNNK	2	99.8%	2																									
IPI00922487	SLC1A5	neutral amino acid transporter B(0) isoform 2	100.0%	11.5	2	2	3	2	1,237,871	1,315,510	1,158,734	1,465,943	118,805	65,372	120,697	62,272	21.5	11.1	23.3	9.5	1.1	0.6	-1.1	0.7	1.2	0.1	-1.1	0.3	1.1	0.1	1.3	0.05
IPI00922776	SLC1A5	neutral amino acid transporter B(0) isoform 3	100.0%	10.6	2	2	3	2	1,237,871	1,315,510	1,158,734	1,465,943	118,805	65,372	120,697	62,272	21.5	11.1	23.3	9.5	1.1	0.6	-1.1	0.7	1.2	0.1	-1.1	0.3	1.1	0.1	1.3	0.05
				GPAGDATVASEKESVM	2	100.0%	1																									
				SELPLDPLPVPTEEGNPLLK	2	100.0%	2																									
IPI00922510	-	cDNA FLJ50165, moderately similar to Sorbitol dehydrogenase	100.0%	17.0	1	1	2	1	2,046,400	1,978,215	1,939,765	2,254,725	393,017	169,984	155,067	173,893	42.9	19.2	17.9	17.3	-1.0	0.9	-1.1	0.8	1.1	0.6	-1.0	0.9	1.1	0.3	1.2	0.2
				LENYPIPEPGPNEVLLR	2	100.0%	2																									
IPI00922549	F11R	cDNA FLJ59609, highly similar to Junctional adhesion molecule A	93.8%	5.2	1	1	1	1	2,540,430	2,567,774	2,246,384	3,023,418	268,933	171,618	146,325	204,386	23.7	14.9	14.6	15.1	1.0	0.9	-1.1	0.4	1.2	0.2	-1.1	0.2	1.2	0.1	1.3	0.01
				NGYGTPMTSNAVR	2	93.8%	1																									
IPI00922562	GNPDA1	cDNA FLJ55085, highly similar to Glucosamine-6-phosphate isomerase	95.4%	12.7	2	2	2	1	1,732,878	1,677,136	1,641,199	1,748,175	92,310	73,713	68,156	71,448	11.9	9.8	9.3	9.1	-1.0	0.6	-1.1	0.4	1.0	0.9	-1.0	0.7	1.0	0.5	1.1	0.3
				IIQFNPGPEK	2	95.4%	1																									
				YFTLGLPTGSTPLGCYK	2	94.5%	1																									
IPI00922576	-	cDNA FLJ57032, moderately similar to Tubulin-specific chaperone E	95.5%	8.6	1	1	1	1	203,721	241,942	297,595	260,466	31,918	30,410	59,840	34,427	35.0	28.1	45.0	29.6	1.2	0.4	1.5	0.2	1.3	0.3	1.2	0.4	1.1	0.7	-1.1	0.6
				NLLSSWDEVIHIADQLR	3	95.5%	1																									
IPI00922618	SNX5	cDNA FLJ55170, highly similar to Sorting nexin-5	99.5%	2.6	1	1	1	1	4,429,960	4,527,833	4,087,233	4,812,733	320,002	174,744	249,006	197,251	16.2	8.6	13.6	9.2	1.0	0.8	-1.1	0.4	1.1	0.3	-1.1	0.2	1.1	0.3	1.2	0.05
				YYMLNIEAAK	2	99.5%	1																									
IPI00922647	PPL	cDNA FLJ51206, moderately similar to Periplakin	96.9%	7.8	1	1	1	1	2,935,850	2,926,060	2,977,965	3,574,865	241,347	145,116	229,345	101,390	18.4	11.1	17.2	6.3	-1.0	1	1.0	0.9	1.2	0.04	1.0	0.9	1.2	0.006	1.2	0.04
				LLYVLEADAAIAK	2	96.9%	1																									
IPI00922656	PIK3C2G	Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing gamma polypeptid	100.0%	2.1	3	3	4	2	4,584,490	4,827,960	4,857,280	5,389,680	166,582	297,991	316,618	213,278	8.1	13.8	14.6	8.9	1.1	0.5	1.1	0.5	1.2	0.02	1.0	0.9	1.1	0.2	1.1	0.2
IPI01015248	PIK3C2G	PIK3C2G protein	100.0%	2.1	3	3	4	2	4,584,490	4,827,960	4,857,280	5,389,680	166,582	297,991	316,618	213,278	8.1	13.8	14.6	8.9	1.1	0.5	1.1	0.5	1.2	0.02	1.0	0.9	1.1	0.2	1.1	0.2
				FEWNLESPLVQLLLHR	3	93.5%	1																									
				QCLLTLIRK	2	99.9%	2																									
				QEVLKK	1	96.4%	1																									
IPI00922694	HSPA9	cDNA FLJ51903, highly similar to Stress-70 protein, mitochondrial	100.0%	16.5	8	9	15	1	19,505,389	19,869,796	19,091,233	22,169,196	1,500,264	881,372	1,288,517	773,257	17.2	9.9	15.1	7.8	1.0	0.8	-1.0	0.8	1.1	0.2	-1.0	0.6	1.1	0.09	1.2	0.07
				AQFEGIVTDLIR	2	100.0%	2																									
				DAGQISGLNVLR	2	100.0%	2																									
				LFEMAYK	2	99.7%	1																									
				MKETAENYLGHTAK	3	98.1%	1																									
				NAVITVPAYFNDSQR	2	99.9%	1																									
				SDIGEVILVGGMTR	2	100.0%	2																									
				STNGDTFLGGEDFDQALLR	2	100.0%	3																									
				STNGDTFLGGEDFDQALLR	3	100.0%	1																									
				VQQTVQDLFGR	2	100.0%	2																									
IPI00922808	-	cDNA FLJ54409, highly similar to Bullous pemphigoid antigen 1 isoforms 1/2/3/4/5/8	99.1%	1.1	1	1	1	1	7,227,260	7,107,010	6,508,980	8,673,260	923,192	456,800	707,183	973,318	28.6	14.4	24.3	25.1	-1.0	0.9	-1.1	0.6	1.2	0.3	-1.1	0.5	1.2	0.2	1.3	0.1
				LESVMVLVEY	2	99.1%	1																									
IPI00922815	LOC100287837	cDNA FLJ56880	97.2%	5.4	2	2	2	1	27,499,270	26,423,250	23,269,220	31,081,750	3,254,368	780,782	2,097,265	1,276,494	26.5	6.6	20.2	9.2	-1.0	0.8	-1.2	0.3	1.1	0.4	-1.1	0.2	1.2	0.01	1.3	0.01
				MEEEEQEAR	2	85.1%	1																									
				SLPSVSGPVRGRAER	3	80.9%	1																									
IPI00922851	AKR7L	aflatoxin B1 aldehyde reductase member 4 isoform 2	100.0%	10.4	2	2	2	1	859,708	818,914	819,913	910,091	47,103	75,832	48,019	50,926	12.3	20.7	13.1	12.5	-1.0	0.7	-1.0	0.6	1.1	0.5	1.0	1	1.1	0.3	1.1	0.2
				ARPATVLGAMEMGR	2	99.8%	1																									
				RMDAPTSAAVTR	2	100.0%	1																									
IPI00922903	ARFGAP2	Uncharacterized protein	100.0%	6.4	2	2	2	1	1,474,477	1,313,033	1,124,659	1,510,482	165,423	178,881	134,910	157,419	25.1	30.5	26.8	23.3	-1.1	0.5	-1.3	0.1	1.0	0.9	-1.2	0.4	1.2	0.4	1.3	0.1
				LAYQELQIDR	2	98.9%	1																									
				VSSQSFSEIER	2	99.9%	1																									
IPI00922910	USP7	cDNA FLJ52374, highly similar to Ubiquitin carboxyl-terminal hydrolase 7	100.0%	2.4	1	1	1	1	1,218,396	1,386,428	1,040,846	1,226,346	161,318	133,133	80,321	102,939	29.6	21.5	17.3	18.8	1.1	0.4	-1.2	0.4	1.0	1	-1.3	0.06	-1.1	0.4	1.2	0.2
				FMYDPQTDQNIK	2	99.8%	1																									
IPI00923470	RBMXL3	Conserved hypothetical protein	92.2%	2.4	1	1	1	1	8,180,050	9,777,330	8,268,540	9,496,860	771,717	511,005	604,298	534,564	21.1	11.7	16.3	12.6	1.2	0.1	1.0	0.9	1.2	0.2	-1.2	0.09	-1.0	0.7	1.1	0.2
				ATAMEEAAATR	2	92.2%	1																									
IPI00923539	-	cDNA FLJ58205, highly similar to Heterogeneous nuclear ribonucleoprotein H'	100.0%	10.7	2	2	3	1	3,151,187	3,496,885	2,690,907	3,441,547	537,098	239,654	221,226	165,125	38.1	15.3	18.4	10.7	1.1	0.6	-1.2	0.5	1.1	0.6	-1.3	0.04	-1.0	0.9	1.3	0.03
				ATENDIYNFFSPLNPMR	2	100.0%	2																									
				VTGEADVEFATHEDAVAAMAK	3	97.6%	1																									
IPI00924435	LRRFIP2	Uncharacterized protein	98.3%	19.1	1	1	1	3	519,183	554,160	483,086	631,561	44,467	35,761	56,783	37,030	19.2	14.4	26.3	13.1	1.1	0.6	-1.1	0.6	1.2	0.09	-1.1	0.3	1.1	0.2	1.3	0.06
IPI00925387	LRRFIP2	Uncharacterized protein	98.3%	5.8	1	1	1	3	519,183	554,160	483,086	631,561	44,467	35,761	56,783	37,030	19.2	14.4	26.3	13.1	1.1	0.6	-1.1	0.6	1.2	0.09	-1.1	0.3	1.1	0.2	1.3	0.06
IPI00925984	LRRFIP2	Uncharacterized protein	98.3%	22.0	1	1	1	3	519,183	554,160	483,086	631,561	44,467	35,761	56,783	37,030	19.2	14.4	26.3	13.1	1.1	0.6	-1.1	0.6	1.2	0.09	-1.1	0.3	1.1	0.2	1.3	0.06
				FSAEDEALSNIAR	2	98.3%	1																									
IPI00924436	HSPB1	20 kDa protein	100.0%	8.6	1	1	1	1	5,784,700	5,535,267	6,104,367	5,641,567	595,251	492,208	468,632	344,417	23.0	19.9	17.2	13.7	-1.0	0.8	1.1	0.7	-1.0	0.8	1.1	0.4	1.0	0.9	-1.1	0.4
				VSLDVNHFAPDELTVK	3	99.9%	1																									
IPI00924475	DBNL	cDNA FLJ54071, highly similar to Drebrin-like protein	100.0%	23.1	6	6	8	1	4,373,325	4,672,179	4,275,955	5,001,475	472,695	245,032	398,148	239,916	24.2	11.7	20.8	10.7	1.1	0.6	-1.0	0.9	1.1	0.3	-1.1	0.4	1.1	0.4	1.2	0.2
				AEEDVEPECIMEK	2	96.0%	1																									
				AMSTTSISSPQPGK	2	100.0%	1																									
				FQDVGPQAPVGSVYQK	2	100.0%	1																									
				GYGPDGHFGMFPANYVELIE	2	100.0%	1																									
				NGPALQEAYVR	2	99.9%	2																									
				TWEQQQEVVSR	2	100.0%	2																									
IPI00924490	DBNL	6 kDa protein	100.0%	22.0	1	1	2	8	623,608	713,336	566,832	787,911	112,646	53,647	72,938	54,232	40.4	16.8	28.8	15.4	1.1	0.5	-1.1	0.7	1.3	0.2	-1.3	0.1	1.1	0.4	1.4	0.04
IPI00924873	DBNL	9 kDa protein	100.0%	12.6	1	1	2	8	623,608	713,336	566,832	787,911	112,646	53,647	72,938	54,232	40.4	16.8	28.8	15.4	1.1	0.5	-1.1	0.7	1.3	0.2	-1.3	0.1	1.1	0.4	1.4	0.04
IPI00925506	DBNL	6 kDa protein	100.0%	17.7	1	1	2	8	623,608	713,336	566,832	787,911	112,646	53,647	72,938	54,232	40.4	16.8	28.8	15.4	1.1	0.5	-1.1	0.7	1.3	0.2	-1.3	0.1	1.1	0.4	1.4	0.04
IPI00926516	DBNL	5 kDa protein	100.0%	22.9	1	1	2	8	623,608	713,336	566,832	787,911	112,646	53,647	72,938	54,232	40.4	16.8	28.8	15.4	1.1	0.5	-1.1	0.7	1.3	0.2	-1.3	0.1	1.1	0.4	1.4	0.04
IPI00926741	DBNL	3 kDa protein	100.0%	35.5	1	1	2	8	623,608	713,336	566,832	787,911	112,646	53,647	72,938	54,232	40.4	16.8	28.8	15.4	1.1	0.5	-1.1	0.7	1.3	0.2	-1.3	0.1	1.1	0.4	1.4	0.04
IPI00947133	DBNL	14 kDa protein	100.0%	8.6	1	1	2	8	623,608	713,336	566,832	787,911	112,646	53,647	72,938	54,232	40.4	16.8	28.8	15.4	1.1	0.5	-1.1	0.7	1.3	0.2	-1.3	0.1	1.1	0.4	1.4	0.04
IPI01012501	DBNL	5 kDa protein	100.0%	27.5	1	1	2	8	623,608	713,336	566,832	787,911	112,646	53,647	72,938	54,232	40.4	16.8	28.8	15.4	1.1	0.5	-1.1	0.7	1.3	0.2	-1.3	0.1	1.1	0.4	1.4	0.04
IPI01012957	DBNL	cDNA FLJ59941, highly similar to Drebrin-like protein	100.0%	7.9	1	1	2	8	623,608	713,336	566,832	787,911	112,646	53,647	72,938	54,232	40.4	16.8	28.8	15.4	1.1	0.5	-1.1	0.7	1.3	0.2	-1.3	0.1	1.1	0.4	1.4	0.04
				NGPALQEAYVR	2	99.9%	2																									
IPI00924522	PSMA2	4 kDa protein	100.0%	58.3	1	2	2	1	2,184,133	2,145,417	2,011,977	2,554,810	224,958	92,421	237,208	124,784	23.0	9.6	26.4	10.9	-1.0	0.9	-1.1	0.6	1.2	0.2	-1.1	0.6	1.2	0.03	1.3	0.08
				LVQIEYALAAVAGGAPSVGIK	2	99.9%	1																									
				LVQIEYALAAVAGGAPSVGIK	3	100.0%	1																									
IPI00924536	1;SNORA4;SNORD2	Uncharacterized protein	100.0%	20.2	4	5	8	1	7,911,378	8,877,939	7,986,623	9,903,311	1,096,701	933,047	783,711	694,777	31.0	23.5	21.9	15.7	1.1	0.5	1.0	1	1.3	0.2	-1.1	0.5	1.1	0.4	1.2	0.1
				EHGGPEGMDPDGVIESNWNEIVDNFDDMNLK	3	100.0%	2																									
				GYDVIAQAQSGTGK	2	100.0%	2																									
				LQAEAPHIVVGTPGR	2	99.3%	1																									
				LQAEAPHIVVGTPGR	3	99.9%	1																									
				MFVLDEADEMLSR	2	100.0%	2																									
IPI00924544	APEH	35 kDa protein	100.0%	9.4	2	2	2	1	1,697,350	1,454,555	1,686,378	1,810,765	54,689	63,536	104,486	49,158	7.2	9.8	13.9	6.1	-1.2	0.02	-1.0	0.9	1.1	0.2	1.2	0.09	1.2	0.002	1.1	0.3
				GDQFVFYEDWGENMVSK	2	100.0%	1																									
				SALYYVDLIGGK	2	100.0%	1																									
IPI00924593	MDH2	cDNA FLJ52880, highly similar to Malate dehydrogenase, mitochondrial	100.0%	45.6	10	12	19	1	47,047,150	48,816,965	46,024,595	51,916,440	4,341,082	1,437,884	3,142,140	1,464,157	20.6	6.6	15.3	6.3	1.0	0.7	-1.0	0.9	1.1	0.3	-1.1	0.4	1.1	0.2	1.1	0.1
				EGVVECSFVK	2	100.0%	1																									
				GCDVVVIPAGVPR	2	100.0%	2																									
				GYLGPEQLPDCLK	2	100.0%	2																									

				IQEAGTEVVK	2	100.0%	2																									
				LTLYDIAHTPGVAADLSHIETK	3	100.0%	1																									
				MISDAIPELK	2	99.8%	1																									
				TIIPLISQCTPK	2	100.0%	2																									
				VAVLGASGGIGQPLSLLLK	2	100.0%	2																									
				VAVLGASGGIGQPLSLLLK	3	100.0%	1																									
				VDFPQDQLTALTGR	2	100.0%	3																									
				VNVPVIGGHAGK	2	100.0%	1																									
				VNVPVIGGHAGK	3	100.0%	1																									
IPI00924714	PRKAR2A	Protein	98.6%	13.1	1	1	1	1	524,649	575,815	588,053	610,578	96,397	62,130	49,147	29,496	41.1	24.1	18.7	10.8	1.1	0.7	1.1	0.6	1.2	0.4	1.0	0.9	1.1	0.6	1.0	0.7
				MFESFIESVPLLK	2	98.6%	1																									
IPI00924720	VAMP8	Uncharacterized protein	99.9%	29.7	2	2	2	1	5,496,835	5,223,330	5,195,955	5,803,270	372,023	297,722	331,048	304,212	15.1	12.8	14.3	11.7	-1.1	0.6	-1.1	0.6	1.1	0.5	-1.0	1	1.1	0.2	1.1	0.2
				GENLEHLR	2	83.8%	1																									
				NKTEDLEATSEHFK	3	99.2%	1																									
IPI00924758	GNB2	cDNA FLJ32188 fis, clone PLACE6002056, highly similar to Guanine nucleotide-bin	100.0%	39.6	5	6	8	1	7,306,378	7,715,878	7,772,923	8,393,684	645,129	229,434	600,982	245,254	19.7	6.7	17.3	6.5	1.1	0.6	1.1	0.6	1.1	0.2	1.0	0.9	1.1	0.08	1.1	0.4
				AGVLAGHDNR	2	100.0%	1																									
				LLLAGYDDFNCNIWDAMK	2	100.0%	2																									
				QTFIGHESDINAVAFFPNGYAFTTGSDDATCR	3	100.0%	1																									
				TFVSGACDASIK	2	100.0%	1																									
				VSCLGVTDDGMAVATGSWDSFLK	2	100.0%	2																									
				VSCLGVTDDGMAVATGSWDSFLK	3	100.0%	1																									
IPI00924782	LOC729020;RPE	Uncharacterized protein	99.4%	13.2	1	1	1	6	1,659,800	1,630,746	1,559,700	1,820,991	112,847	49,831	76,806	57,019	15.2	6.8	11.0	7.0	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.0	0.5	1.1	0.04	1.2	0.03
IPI00926040	LOC729020;RPE	Uncharacterized protein	99.4%	14.9	1	1	1	6	1,659,800	1,630,746	1,559,700	1,820,991	112,847	49,831	76,806	57,019	15.2	6.8	11.0	7.0	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.0	0.5	1.1	0.04	1.2	0.03
IPI00926433	LOC729020;RPE	Uncharacterized protein	99.4%	13.4	1	1	1	6	1,659,800	1,630,746	1,559,700	1,820,991	112,847	49,831	76,806	57,019	15.2	6.8	11.0	7.0	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.0	0.5	1.1	0.04	1.2	0.03
IPI00927218	LOC729020;RPE	Uncharacterized protein	99.4%	13.1	1	1	1	6	1,659,800	1,630,746	1,559,700	1,820,991	112,847	49,831	76,806	57,019	15.2	6.8	11.0	7.0	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.0	0.5	1.1	0.04	1.2	0.03
IPI00927626	LOC729020;RPE	Uncharacterized protein	99.4%	14.3	1	1	1	6	1,659,800	1,630,746	1,559,700	1,820,991	112,847	49,831	76,806	57,019	15.2	6.8	11.0	7.0	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.0	0.5	1.1	0.04	1.2	0.03
IPI00939663	LOC729020;RPE	Ribulose-5-phosphate-3-epimerase, isoform CRA_b	99.4%	11.8	1	1	1	6	1,659,800	1,630,746	1,559,700	1,820,991	112,847	49,831	76,806	57,019	15.2	6.8	11.0	7.0	-1.0	0.8	-1.1	0.5	1.1	0.2	-1.0	0.5	1.1	0.04	1.2	0.03
				TQFPSLDIEVDGGVGPDTVHK	3	99.4%	1																									
IPI00924795	GUSB	17 kDa protein	100.0%	23.6	2	2	3	2	2,539,738	2,450,598	2,719,100	2,733,878	64,341	113,276	184,690	112,348	5.7	10.3	15.2	9.2	-1.0	0.5	1.1	0.4	1.1	0.2	1.1	0.3	1.1	0.1	1.0	0.9
IPI01012614	GUSB	16 kDa protein	100.0%	25.4	2	2	3	2	2,539,738	2,450,598	2,719,100	2,733,878	64,341	113,276	184,690	112,348	5.7	10.3	15.2	9.2	-1.0	0.5	1.1	0.4	1.1	0.2	1.1	0.3	1.1	0.1	1.0	0.9
				GFEEQWYR	2	94.6%	1																									
				RPLWESGPTVDMPVPSSFNDISQDWR	3	100.0%	2																									
IPI00924816	LUZP6;MTPN	Myotrophin	100.0%	30.5	3	3	5	1	14,913,875	13,342,785	14,256,795	15,568,340	830,705	363,899	679,875	336,720	12.5	6.1	10.7	4.8	-1.1	0.1	-1.0	0.6	1.0	0.5	1.1	0.3	1.2	0.002	1.1	0.1
				GPDGLTAFEATDNQAIK	2	100.0%	2																									
				NGDLDEVKDYVAK	2	100.0%	2																									
				NGDLDEVKDYVAKGEDVNR	3	99.9%	1																									
IPI00924866	NOP58	21 kDa protein	100.0%	15.5	2	2	2	1	4,907,470	4,717,475	6,305,710	5,728,845	516,822	571,578	430,038	438,237	23.6	27.1	15.3	17.1	-1.0	0.8	1.3	0.07	1.2	0.3	1.3	0.06	1.2	0.2	-1.1	0.4
				MMAIAPNVTVMVGELVGAR	2	100.0%	1																									
				TQLYEYLQNR	2	99.3%	1																									
IPI00924874	SRRT	17 kDa protein	100.0%	8.7	1	1	1	1	243,561	321,083	289,016	361,634	19,985	27,697	23,667	18,069	18.4	19.3	18.3	11.2	1.3	0.05	1.2	0.2	1.5	0.002	-1.1	0.4	1.1	0.3	1.3	0.04
				EVAFFNNFLTDAK	2	100.0%	1																									
IPI00924885	FAM136A	Uncharacterized protein	100.0%	9.5	1	1	1	1	2,296,337	2,171,717	2,012,937	2,287,250	278,360	65,549	117,224	80,870	27.1	6.8	13.0	7.9	-1.1	0.7	-1.1	0.4	-1.0	1	-1.1	0.3	1.1	0.3	1.1	0.09
				VQEAVESMVK	2	99.1%	1																									
IPI00924931	ZYX	Uncharacterized protein	99.9%	12.2	1	1	1	2	144,771	132,902	185,750	128,148	22,361	14,318	17,122	9,877	34.5	24.1	20.6	17.2	-1.1	0.7	1.3	0.2	-1.1	0.5	1.4	0.05	-1.0	0.8	-1.4	0.02
IPI00925876	ZYX	19 kDa protein	99.9%	11.2	1	1	1	2	144,771	132,902	185,750	128,148	22,361	14,318	17,122	9,877	34.5	24.1	20.6	17.2	-1.1	0.7	1.3	0.2	-1.1	0.5	1.4	0.05	-1.0	0.8	-1.4	0.02
				VSSIDLEIDSLSSLLDDMTK	2	100.0%	1																									
IPI00924935	TFRC	cDNA FLJ57106, highly similar to Transferrin receptor protein 1	100.0%	23.6	13	13	15	1	43,081,438	43,494,279	45,430,727	50,339,492	4,569,563	2,722,560	3,133,468	1,648,235	23.7	14.0	15.4	7.3	1.0	0.9	1.1	0.7	1.2	0.2	1.0	0.7	1.2	0.06	1.1	0.2
				AAAEVAGQFVIK	2	100.0%	1																									
				AFTYINLDK	2	96.5%	1																									
				DSAQNSVIIVDK	2	100.0%	1																									
				HPVTGQFLYQDSNWASK	3	100.0%	1																									
				ILNIFGVIK	2	99.8%	1																									
				IPELNK	1	86.7%	1																									
				LAQMFSDMVLK	2	100.0%	2																									
				LFGNMEGDCPSDWK	2	100.0%	1																									
				LVYLVENPGGYVAYSK	2	82.1%	1																									
				SGVGTALLLK	2	83.0%	1																									
				SSGLPNIPVQTISR	2	99.5%	2																									
				VANAESLNAIGVLIYMDQTK	3	99.9%	1																									
				YNSQLLSFVR	2	100.0%	1																									
IPI00924946	PRKAR2A	Uncharacterized protein	100.0%	10.5	1	1	1	1	2,815,310	3,363,620	3,138,197	3,856,120	145,731	237,261	339,554	236,155	11.6	15.8	24.2	13.7	1.2	0.08	1.1	0.4	1.4	0.006	-1.1	0.6	1.1	0.2	1.2	0.1
				APASVLPAATPR	2	99.9%	1																									
IPI00924999	IMPDH2	Uncharacterized protein	100.0%	20.8	4	4	4	1	4,431,022	4,908,447	4,620,014	5,075,237	403,316	119,283	266,420	233,286	20.4	5.4	12.9	10.3	1.1	0.3	1.0	0.7	1.1	0.2	-1.1	0.4	1.0	0.5	1.1	0.2
				HGFCGIPITDTGR	2	99.8%	1																									
				LPIVNEDDELVAIIAR	2	100.0%	1																									
				REDLVVAPAGITLK	2	96.1%	1																									
				YEQGFITDPVVLSPK	2	100.0%	1																									
IPI00925016	APEH	32 kDa protein	100.0%	4.6	1	1	1	1	604,328	639,228	660,094	685,044	39,578	21,755	38,565	26,814	14.6	7.6	13.1	8.8	1.1	0.5	1.1	0.3	1.1	0.1	1.0	0.7	1.1	0.2	1.0	0.6
				ALDVSASDDEIAR	2	100.0%	1																									
IPI00925046	QARS	Glutaminyl-tRNA synthetase	100.0%	8.7	4	4	4	2	1,825,522	2,144,755	2,312,859	2,189,845	90,724	170,700	318,073	113,234	11.1	17.8	30.8	11.6	1.2	0.1	1.3	0.2	1.2	0.04	1.1	0.7	1.0	0.8	-1.1	0.7
IPI00925511	QARS	cDNA FLJ54314, highly similar to Glutaminyl-tRNA synthetase	100.0%	8.8	4	4	4	2	1,825,522	2,144,755	2,312,859	2,189,845	90,724	170,700	318,073	113,234	11.1	17.8	30.8	11.6	1.2	0.1	1.3	0.2	1.2	0.04	1.1	0.7	1.0	0.8	-1.1	0.7
				DRPMEESLLLFEAMR	3	87.4%	1																									
				EAATQAQQTLGSTIDK	2	100.0%	1																									
				ECGVGVIVTPEQIEEAVEAAINR	3	100.0%	1																									
				HTGYVIELQHVVK	2	81.9%	1																									
IPI00925057	EIF4G1	Uncharacterized protein	100.0%	10.2	5	5	6	4	1,131,316	1,197,154	1,125,082	1,324,920	137,311	69,205	119,404	37,381	27.1	12.9	23.7	6.3	1.1	0.7	-1.0	1	1.2	0.2	-1.1	0.6	1.1	0.1	1.2	0.2
IPI00925434	EIF4G1	Uncharacterized protein	100.0%	9.8	5	5	6	4	1,131,316	1,197,154	1,125,082	1,324,920	137,311	69,205	119,404	37,381	27.1	12.9	23.7	6.3	1.1	0.7	-1.0	1	1.2	0.2	-1.1	0.6	1.1	0.1	1.2	0.2
IPI00926013	EIF4G1	Uncharacterized protein	100.0%	9.4	5	5	6	4	1,131,316	1,197,154	1,125,082	1,324,920	137,311	69,205	119,404	37,381	27.1	12.9	23.7	6.3	1.1	0.7	-1.0	1	1.2	0.2	-1.1	0.6	1.1	0.1	1.2	0.2
IPI00926917	EIF4G1	Uncharacterized protein	100.0%	11.2	5	5	6	4	1,131,316	1,197,154	1,125,082	1,324,920	137,311	69,205	119,404	37,381	27.1	12.9	23.7	6.3	1.1	0.7	-1.0	1	1.2	0.2	-1.1	0.6	1.1	0.1	1.2	0.2
				EAVGDLLDAFK	2	100.0%	1																									
				GGPGGELPR	2	87.6%	1																									
				LQGINCGPDFTPSFANLGR	2	99.8%	1																									
				QVTQLAIDTEER	2	100.0%	2																									
				TASTPTPPQTGGGLEPQANGETPQVAVIVRPDDR	3	100.0%	1																									
IPI00925058	RPL15	Ribosomal protein L15	100.0%	17.3	2	2	3	1	2,822,140	3,275,262	3,078,723	3,572,377	216,419	192,993	209,263	164,841	17.2	13.2	15.2	10.3	1.2	0.2	1.1	0.4	1.3	0.02	-1.1	0.5	1.1	0.3	1.2	0.1
				SLQSVAEER	2	99.4%	1																									
				VLNSYWVGEDSTYK	2	100.0%	2																									
IPI00925083	CTNNB1	Uncharacterized protein	100.0%	19.3	1	1	1	1	2,654,490	3,063,250	1,860,553	2,707,757	440,729	273,733	366,861	422,338	37.1	20.0	44.1	34.9	1.2	0.5	-1.4	0.2	1.0	0.9	-1.6	0.03	-1.1	0.5	1.5	0.2
				AAMFPETLDEGMQIPSTQFDAAHPTNVQR	3	100.0%	1																									
IPI00925098	DBNL	cDNA FLJ59450, highly similar to Drebrin-like protein	100.0%	25.9	7	7	9	1	5,164,809	5,479,659	5,088,665	5,888,075	544,394	299,990	429,334	256,265	23.6	12.2	18.9	9.7	1.1	0.6	-1.0	0.9	1.1	0.3	-1.1	0.5	1.1	0.3	1.2	0.1
				AEEDVEPECIMEK	2	96.0%	1																									
				AMSTTSISSPQPGK	2	100.0%	1																									
				FQDVGPQAPVGSVYQK	2	100.0%	1																									
				GYGPDGHFGMFPANYVELIE	2	100.0%	1																									
				NGPALQEAYVR	2	99.9%	2																									
				TWEQQQEVVSR	2	100.0%	2																									
				VAGTGEGGLEEMVEELNSGK	2	100.0%	1																									
IPI00925162	TFRC	9 kDa protein	100.0%	19.8	1	1	1	1	3,257,970	3,471,485	4,389,110	3,919,960	317,849	263,827	499,622	279,886	21.8	17.0	25.5	16.0	1.1	0.6	1.3	0.09	1.2	0.2	1.3	0.1	1.1	0.3	-1.1	0.4
				SAFSNLFGGEPLSYTR	2	100.0%	1																									
IPI00925196	IMPDH2	IMP dehydrogenase 2	100.0%	21.9	5	5	5	1	7,136,402	7,659,512	7,047,489	8,315,102	808,428	341,868	348,475	246,815	25.3	10.0	11.1	6.6	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.2	1.1	0.2	1.2	0.02
				DKYPNLQVIGGNVVTAAQAK	3	97.6%	1																									
				HGFCGIPITDTGR	2	99.8%	1																									
				LPIVNEDDELVAIIAR	2	100.0%	1																									
				REDLVVAPAGITLK	2	96.1%	1																									
				YEQGFITDPVVLSPK	2	100.0%	1																									
IPI00925298	ASNS	Uncharacterized protein	99.9%	6.5	1	1	1	4	970,949	1,007,886	970,544	1,042,926	82,059	68,827	69,597	83,726	18.9	15.3	16.0	18.0	1.0	0.7	-1.0	1	1.1	0.6	-1.0	0.7	1.0	0.8	1.1	0.5
IPI00925986	ASNS	Uncharacterized protein	99.9%	22.2	1	1	1	4	970,949	1,007,886	970,544	1,042,926	82,059	68,827	69,597	83,726	18.9	15.3	16.0	18.0	1.0	0.7	-1.0	1	1.1	0.6	-1.0	0.7	1.0	0.8	1.1	0.5
IPI00926760	ASNS	Uncharacterized protein	99.9%	11.8	1	1	1	4	970,949	1,007,886	970,544	1,042,926	82,059	68,827	69,597	83,726	18.9	15.3	16.0	18.0	1.0	0.7	-1.0	1	1.1	0.6	-1.0	0.7	1.0	0.8	1.1	0.5
IPI00926959	ASNS	Uncharacterized protein	99.9%	8.6	1	1	1	4	970,949	1,007,886	970,544	1,042,926	82,059	68,827	69,597	83,726	18.9	15.3	16.0	18.0	1.0	0.7	-1.0	1	1.1	0.6	-1.0	0.7	1.0	0.8	1.1	0.5
				LAVVDPLFGMQPIR	2	99.1%	1																									
IPI00925317	RCC1	Uncharacterized protein	100.0%	26.1	4	4	4	4	2,039,435	2,275,245	2,017,716	2,320,401	176,922	104,351	126,646	107,244	19.4	10.3	14.0	10.3	1.1	0.3	-1.0	0.9	1.1	0.2	-1.1	0.2	1.0	0.8	1.2	0.1
IPI00925791	RCC1	Uncharacterized protein	100.0%	25.1	4	4	4	4	2,039,435	2,275,245	2,017,716	2,320,401	176,922	104,351	126,646	107,244	19.4	10.3	14.0	10.3	1.1	0.3	-1.0	0.9	1.1	0.2	-1.1	0.2	1.0	0.8	1.2	0.1
IPI00926548	RCC1	Uncharacterized protein	100.0%	26.0	4	4	4	4	2,039,435	2,275,245	2,017,716	2,320,401	176,922	104,351	126,646	107,244	19.4	10.3	14.0	10.3	1.1	0.3	-1.0	0.9	1.1	0.2	-1.1	0.2	1.0	0.8	1.2	0.1
IPI00927389	RCC1	Uncharacterized protein	100.0%	30.9	4	4	4	4	2,039,435	2,275,245	2,017,716	2,320,401	176,922	104,351	126,646	107,244	19.4	10.3	14.0	10.3	1.1	0.3	-1.0	0.9	1.1	0.2	-1.1	0.2	1.0	0.8	1.2	0.1
				SHSTEPGLVLTLGQGDVGQLGLGENVMER	3	100.0%	1																									
				SMVPVQVQLDVPVVK	2	100.0%	1																									
				VPELFANR	2	92.5%	1																									
				VVQVSAGDSHTAALTDDGR	3	98.2%	1																									
IPI00925327	PRKAR2A	Protein	100.0%	19.5	3	3	4	1	2,921,054	2,928,091	2,976,716	3,507,247	366,694	148,070	209,762	60,530	28.1	11.3	15.8	3.9	1.0	1	1.0	0.9	1.2	0.2	1.0	0.9	1.2	0.007	1.2	0.06
				GTYDILVTK	2	91.2%	1																									
				MFESFIESVPLLK	2	98.6%	1																									
				NLDQEQLSQVLDAMFER	2	100.0%	2																									
IPI00925520	PFKL	Similar to Phosphofructokinase	100.0%	1.8	1	1	2	2	662,667	680,357	887,647	670,293	29,909	61,597	93,496	42,651	10.1	20.2	23.6	14.2	1.0	0.8	1.3	0.07	1.0	0.9	1.3	0.1	-1.0	0.9	-1.3	0.07
IPI01015709	PFKL	27 kDa protein	100.0%	5.9	1	1	2	2	662,667	680,357	887,647	670,293	29,909	61,597	93,496	42,651	10.1	20.2	23.6	14.2	1.0	0.8	1.3	0.07	1.0	0.9	1.3	0.1	-1.0	0.9	-1.3	0.07
				SEWGSLLEELVAEGK	2	100.0%	2																									
IPI00925530	GNB2	Uncharacterized protein	100.0%	39.5	7	8	11	1	15,588,878	15,937,128	15,555,846	17,729,464	1,192,343	693,392	1,272,087	583,522	17.1	9.7	18.3	7.4	1.0	0.8	-1.0	1	1.1	0.1	-1.0	0.8	1.1	0.08	1.1	0.2
				AGVLAGHDNR	2	100.0%	1																									
				IYAMHWGTDSR	2	100.0%	1																									
				LIIWDSYTTNK	2	100.0%	2																									
				LLLAGYDDFNCNIWDAMK	2	100.0%	2																									
				QTFIGHESDINAVAFFPNGYAFTTGSDDATCR	3	100.0%	1																									
				TFVSGACDASIK	2	100.0%	1																									
				VSCLGVTDDGMAVATGSWDSFLK	2	100.0%	2																									
				VSCLGVTDDGMAVATGSWDSFLK	3	100.0%	1																									
IPI00925564	PCYOX1	Uncharacterized protein	100.0%	8.2	2	2	2	1	3,349,285	3,564,368	3,383,568	3,809,331	242,106	99,294	226,118	191,467	16.2	6.2	14.9	11.2	1.1	0.4	1.0	0.9	1.1	0.2	-1.1	0.5	1.1	0.3	1.1	0.2
				LVCSGLLQASK	2	99.2%	1																									
				YQSHDYAFSSVEK	3	99.6%	1																									
IPI00925567	AKR1B15	Putative aldo-keto reductase family 1 member B15	100.0%	4.7	1	1	1	3	477,613	449,001	560,970	684,995	67,838	74,266	97,329	28,333	31.8	37.0	38.8	9.3	-1.1	0.8	1.2	0.5	1.4	0.02	1.2	0.4	1.5	0.03	1.2	0.3
IPI00942692	AKR1B15	Putative uncharacterized protein	100.0%	4.4	1	1	1	3	477,613	449,001	560,970	684,995	67,838	74,266	97,329	28,333	31.8	37.0	38.8	9.3	-1.1	0.8	1.2	0.5	1.4	0.02	1.2	0.4	1.5	0.03	1.2	0.3
IPI01010749	AKR1B15	Uncharacterized protein	100.0%	5.1	1	1	1	3	477,613	449,001	560,970	684,995	67,838	74,266	97,329	28,333	31.8	37.0	38.8	9.3	-1.1	0.8	1.2	0.5	1.4	0.02	1.2	0.4	1.5	0.03	1.2	0.3
				LSYLDVYLIHWPQGFK	3	100.0%	1																									
IPI00925570	RCC1	Protein	100.0%	26.6	3	3	3	1	1,467,438	1,617,138	1,413,640	1,631,505	113,412	61,080	90,775	38,677	17.3	8.5	14.4	5.3	1.1	0.3	-1.0	0.7	1.1	0.2	-1.1	0.1	1.0	0.8	1.2	0.06
				SMVPVQVQLDVPVVK	2	100.0%	1																									
				VPELFANR	2	92.5%	1																									
				VVQVSAGDSHTAALTDDGR	3	98.2%	1																									
IPI00925574	COPS6	14 kDa protein	99.9%	10.6	1	1	1	1	1,120,443	1,093,723	1,006,860	1,160,843	40,280	94,124	76,771	43,086	8.0	19.2	17.1	8.3	-1.0	0.8	-1.1	0.2	1.0	0.5	-1.1	0.5	1.1	0.5	1.2	0.1
				QVCEIIESPLFLK	2	99.4%	1																									

IPI00925736	NOSTRIN	11 kDa protein	91.7%	18.6	1	1	1	1	1,445,722	1,250,538	1,662,373	1,607,021	167,293	72,519	184,565	228,534	25.9	13.0	24.8	31.8	-1.2	0.3	1.1	0.4	1.1	0.6	1.3	0.09	1.3	0.2	-1.0	0.9
				QVTSVLQQRDGVLILLLR	3	91.7%	1																									
IPI00925799	PSMA2	5 kDa protein	100.0%	72.9	2	3	3	1	12,324,733	15,428,517	15,433,227	19,479,160	1,718,444	1,505,911	1,257,953	1,417,168	31.2	21.8	18.2	16.3	1.3	0.2	1.3	0.2	1.6	0.01	1.0	1	1.3	0.09	1.3	0.07
				GYSFSLTTFSPSGK	2	100.0%	1																									
				LVQIEYALAAVAGGAPSVGIK	2	99.9%	1																									
				LVQIEYALAAVAGGAPSVGIK	3	100.0%	1																									
IPI00925804	AIP	Non-functional aryl hydrocarbon receptor interacting protein (Fragment)	100.0%	12.2	4	4	4	2	20,678,604	24,198,662	23,608,395	28,231,270	3,549,534	1,642,280	1,677,368	1,550,684	38.4	15.2	15.9	12.3	1.2	0.4	1.1	0.5	1.4	0.09	-1.0	0.8	1.2	0.1	1.2	0.08
IPI00953925	AIP	Aryl hydrocarbon receptor interacting protein	100.0%	13.4	4	4	4	2	20,678,604	24,198,662	23,608,395	28,231,270	3,549,534	1,642,280	1,677,368	1,550,684	38.4	15.2	15.9	12.3	1.2	0.4	1.1	0.5	1.4	0.09	-1.0	0.8	1.2	0.1	1.2	0.08
				EGEIAQFLCDIK	2	100.0%	1																									
				HVVLYPLVAK	2	99.5%	1																									
				VLELDPALAPVVSR	2	99.9%	1																									
				YYDAIACLK	2	99.9%	1																									
IPI00925920	ARPC2	10 kDa protein	93.3%	13.2	1	1	1	2	662,963	642,343	679,673	802,455	47,816	38,366	38,189	54,916	16.1	13.4	12.6	15.3	-1.0	0.7	1.0	0.8	1.2	0.09	1.1	0.5	1.2	0.04	1.2	0.1
IPI00926315	ARPC2	Uncharacterized protein	93.3%	13.3	1	1	1	2	662,963	642,343	679,673	802,455	47,816	38,366	38,189	54,916	16.1	13.4	12.6	15.3	-1.0	0.7	1.0	0.8	1.2	0.09	1.1	0.5	1.2	0.04	1.2	0.1
				ELQAHGADELLK	2	93.3%	1																									
IPI00925997	SRI	cDNA FLJ54267, moderately similar to Sorcin	100.0%	34.2	5	5	6	1	7,268,805	8,580,122	8,700,562	10,243,352	938,351	529,636	558,435	574,715	28.9	13.8	14.4	12.6	1.2	0.3	1.2	0.2	1.4	0.03	1.0	0.9	1.2	0.07	1.2	0.09
				DMSGTMGFNEFK	2	98.9%	1																									
				DTAQQGVVNFPYDDFIQCVMSV	2	90.1%	1																									
				ITFDDYIACCVK	2	100.0%	2																									
				LMVSMLDR	2	99.9%	1																									
				LMVSMLDRDMSGTMGFNEFK	3	99.9%	1																									
IPI00926027	GLB1	Uncharacterized protein	91.5%	17.5	1	1	1	1	72,170	69,224	64,026	88,035	10,833	7,268	8,130	7,396	33.6	23.5	28.4	18.8	-1.0	0.8	-1.1	0.6	1.2	0.3	-1.1	0.6	1.3	0.1	1.4	0.06
				SSDPDYLAAVDKWLGVLLPK	3	91.5%	1																									
IPI00926178	LUZP6	Uncharacterized protein	100.0%	57.7	2	2	4	1	4,656,365	4,751,655	4,489,585	5,185,690	423,780	255,112	358,613	99,340	20.4	12.0	17.9	4.3	1.0	0.9	-1.0	0.8	1.1	0.3	-1.1	0.6	1.1	0.2	1.2	0.1
				GPDGLTAFEATDNQAIK	2	100.0%	2																									
				NGDLDEVKDYVAK	2	100.0%	2																									
IPI00926202	RPL15	Ribosomal protein L15	100.0%	18.9	3	4	5	1	4,889,743	5,709,832	5,694,563	6,221,687	494,380	218,525	602,452	172,064	22.6	8.6	23.7	6.2	1.2	0.2	1.2	0.3	1.3	0.05	-1.0	1	1.1	0.1	1.1	0.4
				FFEVILIDPFHK	2	84.1%	1																									
				FFEVILIDPFHK	3	100.0%	1																									
				VLNSYWVGEDSTYK	2	100.0%	2																									
				YIQELWR	2	99.3%	1																									
IPI00926258	PSMD2	Uncharacterized protein	100.0%	18.3	10	11	11	2	12,908,339	14,205,413	13,451,525	15,362,605	1,010,880	316,534	930,454	348,529	17.5	5.0	15.5	5.1	1.1	0.3	1.0	0.7	1.2	0.07	-1.1	0.5	1.1	0.04	1.1	0.1
IPI00926410	PSMD2	Uncharacterized protein	100.0%	19.0	10	11	11	2	12,908,339	14,205,413	13,451,525	15,362,605	1,010,880	316,534	930,454	348,529	17.5	5.0	15.5	5.1	1.1	0.3	1.0	0.7	1.2	0.07	-1.1	0.5	1.1	0.04	1.1	0.1
				AVPLALALISVSNPR	2	98.6%	1																									
				LAQGLTHLGK	2	81.0%	1																									
				MLVTFDEELRPLPVSVR	3	97.3%	1																									
				MNLASSFVNGFVNAAFGQDK	2	100.0%	1																									
				MNLASSFVNGFVNAAFGQDK	3	98.4%	1																									
				NECDPALALLSDYVLHNSNTMR	3	99.7%	1																									
				SETELKDTYAR	2	91.6%	1																									
				SGALLACGIVNSGVR	2	100.0%	1																									
				VGQAVDVVGQAGKPK	3	99.9%	1																									
				YGEPTLR	2	88.6%	1																									
				YLYSSEDYIK	2	99.5%	1																									
IPI00926319	DLD	cDNA FLJ56112, highly similar to Dihydrolipoyl dehydrogenase, mitochondrial	100.0%	15.0	4	4	4	2	3,833,550	4,116,167	3,911,398	4,610,288	257,237	142,067	345,886	206,311	15.0	7.7	19.8	10.0	1.1	0.4	1.0	0.9	1.2	0.05	-1.1	0.6	1.1	0.08	1.2	0.1
IPI01011882	DLD	cDNA FLJ50515, highly similar to Dihydrolipoyl dehydrogenase, mitochondrial	100.0%	17.8	4	4	4	2	3,833,550	4,116,167	3,911,398	4,610,288	257,237	142,067	345,886	206,311	15.0	7.7	19.8	10.0	1.1	0.4	1.0	0.9	1.2	0.05	-1.1	0.6	1.1	0.08	1.2	0.1
				ALTGGIAHLFK	2	99.6%	1																									
				EANLAASFGK	2	99.3%	1																									
				IPNIYAIGDVVAGPMLAHK	3	100.0%	1																									
				VLGAHILGPGAGEMVNEAALALEYGASCEDIAR	3	100.0%	1																									
IPI00926442	ACAA1	Protein	100.0%	37.2	6	7	7	2	15,349,190	16,112,759	17,110,113	18,637,413	1,917,886	1,059,841	1,554,741	636,254	27.9	14.7	20.3	7.6	1.0	0.7	1.1	0.5	1.2	0.2	1.1	0.6	1.2	0.08	1.1	0.4
IPI01010885	ACAA1	3-oxoacyl-CoA thiolase	100.0%	30.3	6	7	7	2	15,349,190	16,112,759	17,110,113	18,637,413	1,917,886	1,059,841	1,554,741	636,254	27.9	14.7	20.3	7.6	1.0	0.7	1.1	0.5	1.2	0.2	1.1	0.6	1.2	0.08	1.1	0.4
				AEELGLPILGVLR	2	99.9%	1																									
				DGSTTAGNSSQVSDGAAAILLAR	2	100.0%	1																									
				DGSTTAGNSSQVSDGAAAILLAR	3	100.0%	1																									
				IAQFLSDIPETVPLSTVNR	2	98.2%	1																									
				QCSSGLQAVASIAGGIR	2	100.0%	1																									
				QVITLLNELK	2	96.5%	1																									
				SYAVVGVPPDIMGIGPAYAIPVALQK	3	99.9%	1																									
IPI00926466	RHOA	Uncharacterized protein	100.0%	38.4	2	2	3	2	333,792	345,423	321,705	335,933	38,801	15,507	25,889	10,628	26.0	10.0	18.0	7.1	1.0	0.8	-1.0	0.8	1.0	1	-1.1	0.5	-1.0	0.6	1.0	0.6
IPI00926881	RHOA	Uncharacterized protein	100.0%	36.7	2	2	3	2	333,792	345,423	321,705	335,933	38,801	15,507	25,889	10,628	26.0	10.0	18.0	7.1	1.0	0.8	-1.0	0.8	1.0	1	-1.1	0.5	-1.0	0.6	1.0	0.6
				DQFPEVYVPTVFENYVADIEVDGK	2	94.7%	2																									
				TCLLIVFSK	2	95.7%	1																									
IPI00926601	PLOD3	Protein	100.0%	40.9	2	2	4	1	3,822,107	3,612,443	4,489,852	4,192,410	320,452	275,483	173,295	194,229	18.8	17.1	8.6	10.4	-1.1	0.6	1.2	0.1	1.1	0.4	1.2	0.03	1.2	0.1	-1.1	0.3
				LWSNFWGALSPDEYYAR	2	100.0%	2																									
				SEDYVELVQR	2	100.0%	2																									
IPI00926625	ZYX	Zyxin	99.9%	5.4	2	2	2	1	2,190,283	2,169,186	2,101,416	2,369,318	280,387	107,545	172,371	87,797	28.6	11.1	18.3	8.3	-1.0	0.9	-1.0	0.8	1.1	0.6	-1.0	0.7	1.1	0.2	1.1	0.2
				SPGAPGPLTLK	2	96.9%	1																									
				VSSIDLEIDSLSSLLDDMTK	2	100.0%	1																									
IPI00926659	ASL	Uncharacterized protein	100.0%	18.2	3	3	3	1	1,936,280	1,900,652	1,853,549	2,314,732	210,723	37,668	157,149	87,312	24.3	4.4	19.0	8.4	-1.0	0.9	-1.0	0.8	1.2	0.1	-1.0	0.8	1.2	0.002	1.2	0.03
				INVLPLGSGAIAGNPLGVDR	2	99.3%	1																									
				NPDSLELIR	2	93.8%	1																									
				QTCSTLSGLLWELIR	2	99.9%	1																									
IPI00926695	PAK2;LOC646214	Protein	100.0%	5.9	1	1	1	1	5,676,190	6,046,245	5,835,570	5,986,640	459,329	285,694	302,828	361,154	18.1	10.6	11.6	13.5	1.1	0.5	1.0	0.8	1.1	0.6	-1.0	0.6	-1.0	0.9	1.0	0.8
				SDNVLLGMEGSVK	2	99.6%	1																									
IPI00926710	RHOA	Uncharacterized protein	100.0%	29.5	2	2	3	2	650,863	709,822	714,037	759,775	68,211	32,130	44,957	38,563	23.4	10.1	14.1	11.4	1.1	0.5	1.1	0.5	1.2	0.2	1.0	0.9	1.1	0.3	1.1	0.5
IPI00927114	RHOA	Uncharacterized protein	100.0%	20.3	2	2	3	2	650,863	709,822	714,037	759,775	68,211	32,130	44,957	38,563	23.4	10.1	14.1	11.4	1.1	0.5	1.1	0.5	1.2	0.2	1.0	0.9	1.1	0.3	1.1	0.5
				DQFPEVYVPTVFENYVADIEVDGK	2	94.7%	2																									
				HFCPNVPIILVGNK	2	99.4%	1																									
IPI00926796	PLOD3	Protein	100.0%	15.2	3	3	5	1	5,093,272	4,679,708	5,755,232	5,480,815	321,210	293,146	266,214	160,858	14.1	14.0	10.3	6.6	-1.1	0.4	1.1	0.2	1.1	0.3	1.2	0.03	1.2	0.04	-1.1	0.4
				LVGPEEALSPGEAR	2	100.0%	1																									
				LWSNFWGALSPDEYYAR	2	100.0%	2																									
				SEDYVELVQR	2	100.0%	2																									
IPI00926839	CYP51A1	isoform 2 of Lanosterol 14-alpha demethylase	99.9%	6.7	2	2	2	1	3,494,997	3,881,426	3,569,610	3,936,450	365,480	210,466	283,260	170,078	23.4	12.1	17.7	9.7	1.1	0.4	1.0	0.9	1.1	0.3	-1.1	0.4	1.0	0.8	1.1	0.3
				GVAYDVPNPVFLEQK	2	99.2%	1																									
				NEDLNAEDVYSR	2	99.8%	1																									
IPI00926864	APEH	Uncharacterized protein	100.0%	10.8	2	2	2	1	1,460,041	1,528,386	1,593,579	1,731,872	92,882	61,349	64,311	55,308	14.2	9.0	9.0	7.1	1.0	0.6	1.1	0.3	1.2	0.04	1.0	0.5	1.1	0.04	1.1	0.1
				ALDVSASDDEIAR	2	100.0%	1																									
				SALYYVDLIGGK	2	100.0%	1																									
IPI00926874	PLOD3	Protein	100.0%	9.9	2	2	3	1	3,448,835	3,498,958	3,323,190	3,859,440	311,934	102,570	179,528	100,170	20.2	6.6	12.1	5.8	1.0	0.9	-1.0	0.7	1.1	0.3	-1.1	0.4	1.1	0.04	1.2	0.03
				DVFSGSDTDPDMAFCK	2	99.8%	1																									
				SEDYVELVQR	2	100.0%	2																									
IPI00926884	PDAP1	4 kDa protein	100.0%	41.0	1	1	2	1	1,712,480	1,747,325	1,628,980	1,848,495	133,753	75,412	97,502	74,951	17.5	9.7	13.4	9.1	1.0	0.8	-1.1	0.6	1.1	0.4	-1.1	0.4	1.1	0.4	1.1	0.1
				QYTSPEEIDAQLQAEK	2	100.0%	2																									
IPI00926984	MAP4	Protein	100.0%	7.2	1	1	2	2	83,958	86,356	90,279	97,600	7,391	8,196	6,751	4,989	19.7	21.2	16.7	11.4	1.0	0.8	1.1	0.5	1.2	0.2	1.0	0.7	1.1	0.3	1.1	0.4
IPI01011707	MAP4	microtubule-associated protein 4 isoform 3	100.0%	21.2	1	1	2	2	83,958	86,356	90,279	97,600	7,391	8,196	6,751	4,989	19.7	21.2	16.7	11.4	1.0	0.8	1.1	0.5	1.2	0.2	1.0	0.7	1.1	0.3	1.1	0.4
				DFIATLEAEAFDDVVGETVGK	2	100.0%	2																									
IPI00927028	DDC	cDNA FLJ51517, moderately similar to Aromatic-L-amino-acid decarboxylase	90.8%	3.9	1	1	1	1	6,459,260	7,382,860	7,334,470	7,881,390	777,744	506,532	551,980	195,391	26.9	15.3	16.8	5.5	1.1	0.3	1.1	0.4	1.2	0.1	-1.0	1	1.1	0.4	1.1	0.4
				EMVDYVANYMEGIEGR	2	90.8%	1																									
IPI00927053	PSMC2	26S protease regulatory subunit 7 2	100.0%	17.0	2	2	2	1	5,040,695	5,269,565	5,001,990	5,863,920	693,024	296,305	465,672	247,886	30.7	12.6	20.8	9.5	1.0	0.8	-1.0	1	1.2	0.3	-1.1	0.6	1.1	0.2	1.2	0.1
				QTLQSEQPLQVAR	2	99.7%	1																									
				QVEDDIQQLLK	2	100.0%	1																									
IPI00927271	TRA2B	Protein	100.0%	11.0	1	1	1	1	1,029,423	1,079,363	1,129,420	1,241,293	117,015	93,086	103,530	37,012	25.4	19.3	20.5	6.7	1.0	0.7	1.1	0.5	1.2	0.1	1.0	0.7	1.2	0.1	1.1	0.4
				GFAFVYFENVDDAK	2	100.0%	1																									
IPI00927297	DNAJB11	Protein	100.0%	6.6	1	1	1	1	2,239,230	1,981,180	2,136,805	2,720,575	264,288	106,602	298,698	317,719	26.4	12.0	31.3	26.1	-1.1	0.4	-1.0	0.8	1.2	0.3	1.1	0.6	1.4	0.08	1.3	0.2
				TLEVEIEPGVR	2	99.9%	1																									
IPI00927496	ACAA1	Uncharacterized protein	100.0%	11.5	2	3	3	1	2,637,759	2,870,756	2,673,890	3,068,483	190,466	115,276	213,828	81,754	16.2	9.0	17.9	6.0	1.1	0.3	1.0	0.9	1.2	0.07	-1.1	0.4	1.1	0.2	1.1	0.1
				DGSTTAGNSSQVSDGAAAILLAR	2	100.0%	1																									
				DGSTTAGNSSQVSDGAAAILLAR	3	100.0%	1																									
				GGFKDTTPDELLSAVMTAVLK	3	100.0%	1																									
IPI00927606	GPX1	Glutathione peroxidase 1	100.0%	16.3	3	3	3	1	7,956,960	8,391,785	7,809,920	9,533,160	723,510	435,196	578,436	196,579	20.3	11.6	16.6	4.6	1.1	0.6	-1.0	0.9	1.2	0.09	-1.1	0.4	1.1	0.04	1.2	0.04
				DYTQMNELQR	2	99.6%	1																									
				NDVAWNFEK	2	91.9%	1																									
				PLAGGEPVSLGSLR	2	99.7%	1																									
IPI00927689	PCYOX1	Uncharacterized protein	100.0%	10.0	1	1	1	1	1,287,585	1,283,218	1,167,330	1,532,058	213,253	90,882	158,522	236,808	37.0	15.8	30.4	34.6	-1.0	1	-1.1	0.7	1.2	0.5	-1.1	0.5	1.2	0.4	1.3	0.2
				YQSHDYAFSSVEK	3	99.6%	1																									
IPI00927819	MAP4	80 kDa protein	100.0%	7.8	4	5	6	1	3,144,316	3,301,285	3,307,347	3,596,356	254,962	254,822	197,959	140,031	18.1	17.3	13.4	8.7	1.0	0.7	1.1	0.6	1.1	0.2	1.0	1	1.1	0.3	1.1	0.3
				DFIATLEAEAFDDVVGETVGK	2	100.0%	2																									
				DFIATLEAEAFDDVVGETVGK	3	100.0%	1																									
				DMSPLSETEMALGK	2	99.4%	1																									
				QPAPTTIGGLNK	2	99.1%	1																									
				WPTETDVSSAK	2	99.7%	1																									
IPI00927825	FLNA	65 kDa protein	100.0%	6.6	4	4	5	1	1,013,332	979,929	1,102,952	1,122,629	66,777	36,149	63,293	8,991	14.7	8.3	12.8	1.8	-1.0	0.7	1.1	0.4	1.1	0.2	1.1	0.1	1.1	0.01	1.0	0.8
				LIALLEVLSQK	2	100.0%	2																									
				LLGWIQNK	2	98.6%	1																									
				QMQLENVSVALEFLDR	2	100.0%	1																									
				QMQLENVSVALEFLDRESIK	3	99.2%	1																									
IPI00927830	PSMA2	Uncharacterized protein	99.5%	11.6	1	1	1	1	323,834	339,342	352,754	392,559	55,941	36,224	33,769	14,268	38.6	23.9	21.4	8.1	1.0	0.8	1.1	0.7	1.2	0.3	1.0	0.8	1.2	0.2	1.1	0.3
				YNEDLELEDAIHTAILTLK	3	99.5%	1																									
IPI00927939	PCYOX1	Uncharacterized protein	100.0%	15.6	2	2	3	1	4,194,865	3,862,518	3,913,310	4,357,778	363,480	108,799	271,703	253,450	19.4	6.3	15.5	13.0	-1.1	0.4	-1.1	0.6	1.0	0.7	1.0	0.9	1.1	0.1	1.1	0.3
				FLNEMIAPVMR	2	99.7%	2																									
				YQSHDYAFSSVEK	3	99.6%	1																									
IPI00929107	-	Seipin isoform 1	100.0%	22.9	13	13	13	1	33,808,355	34,466,350	34,614,235	37,793,510	2,635,156	884,408	2,327,579	1,925,435	17.4	5.7	15.0	11.4	1.0	0.8	1.0	0.8	1.1	0.3	1.0	1	1.1	0.2	1.1	0.3
				ANFSLPEK	2	86.7%	1																									
				DLLVQQASQCLSK	2	100.0%	1																									
				EEPFFPPPEEFVFIHAVPVEER	3	95.8%	1																									
				EGCTEVSLLR	2	99.8%	1																									
				FPTLWSGAR	2	97.6%	1																									
				GLEEPEMDPK	2	96.8%	1																									
				KEVEGDDVPESIMLEMK	2	99.9%	1																									
				KVVVVVPNEEDWKK	3	100.0%	1																									
				NCVVELNFGQK	2	99.9%	1																									
				NFILDQCNVYNSGQR	2	100.0%	1																									
				VGWSVDFSRPQLGEDEFSYGFDGR	3	100.0%	1																									
				VTQNLPMKEGCTEVSLLR	3	99.9%	1																									
				YGGQPLFSEK	2	100.0%	1																									
IPI00929313	C13orf40	hypothetical protein LOC643677	97.8%	0.5	2	2	2	1	6,196,660	6,644,280	6,298,340	7,484,100	700,572	350,430	728,221	204,871	25.3	11.8	25.9	6.1	1.1	0.6	1.0	0.9	1.2	0.1	-1.1	0.7	1.1	0.07	1.2	0.2

				LEMQWNMTDK	3	94.4%	1																									
				LTSHLESKALEIQLNLIPEMARK	3	89.0%	1																									
IPI00929635	CGN	isoform 2 of Cingulin	100.0%	4.5	3	3	4	1	4,114,885	3,493,333	3,792,770	3,844,550	152,109	194,505	136,262	145,360	8.3	12.5	8.0	8.5	-1.2	0.04	-1.1	0.2	-1.1	0.2	1.1	0.2	1.1	0.2	1.0	0.8
				AVAGQGELTR	2	99.9%	2																									
				FITEPVSGAEMGTLR	2	100.0%	1																									
				GPVDHGVQIR	3	88.9%	1																									
IPI00930068	B2M	Beta-2-microglobulin	100.0%	17.7	1	1	1	1	1,240,797	1,429,637	1,430,550	1,630,710	133,199	15,373	156,143	119,081	24.0	2.4	24.4	16.3	1.2	0.2	1.2	0.4	1.3	0.06	1.0	1	1.1	0.2	1.1	0.3
				SNFLNCYVSGFHPSDIEVDLLK	3	99.8%	1																									
IPI00930130	TUBB6	cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain	100.0%	29.5	8	10	16	1	52,624,770	56,418,084	49,651,634	61,843,353	5,628,498	3,122,238	4,425,169	1,990,853	23.9	12.4	19.9	7.2	1.1	0.6	-1.1	0.7	1.2	0.2	-1.1	0.2	1.1	0.2	1.2	0.04
				ALTVPELTQQMFDAK	2	100.0%	3																									
				AVLVDLEPGTMDSVR	2	100.0%	2																									
				ENVHLQAGQCGNQIGAK	2	100.0%	1																									
				ENVHLQAGQCGNQIGAK	3	100.0%	1																									
				FWEVISDEHGIDPTGTYHGDSDLQLER	3	100.0%	2																									
				IMNTFSVVPSPK	2	100.0%	2																									
				INVYYNEATGGK	2	100.0%	2																									
				MRENVHLQAGQCGNQIGAK	3	100.0%	1																									
				MSATFIGNSTAIQELFK	2	99.2%	1																									
				MSATFIGNSTAIQELFK	3	90.7%	1																									
IPI00930562	SUB1	Activated RNA polymerase II transcription cofactor 4 (Fragment)	100.0%	15.1	1	1	2	1	2,592,120	2,601,995	2,365,755	3,097,165	158,075	218,354	143,605	109,897	13.6	18.8	13.6	7.9	1.0	1	-1.1	0.3	1.2	0.03	-1.1	0.4	1.2	0.08	1.3	0.004
				EQISDIDDAVR	2	100.0%	2																									
IPI00930694	IGF2BP1	insulin-like growth factor 2 mRNA-binding protein 1 isoform 2	100.0%	15.8	5	5	7	1	10,755,047	11,431,323	11,290,487	12,314,698	1,115,889	222,795	719,798	236,810	23.2	4.4	14.3	4.3	1.1	0.6	1.0	0.7	1.1	0.2	-1.0	0.9	1.1	0.03	1.1	0.2
				DQTPDENDQVIVK	2	100.0%	2																									
				ISYSGQFLVK	2	96.7%	1																									
				LYIGNLNESVTPADLEK	2	100.0%	1																									
				MVIITGPPEAQFK	2	100.0%	2																									
				SGYAFVDCPDEHWAMK	3	82.7%	1																									
IPI00935307	DIAPH1	Uncharacterized protein	100.0%	3.4	2	2	2	1	1,746,425	1,519,913	2,124,523	1,855,859	49,891	85,308	144,492	122,722	6.4	12.6	15.2	14.8	-1.1	0.05	1.2	0.06	1.1	0.4	1.4	0.007	1.2	0.05	-1.1	0.2
				FENNELFAK	2	97.7%	1																									
				VGCLQLINALITPAEELDFR	2	100.0%	1																									
IPI00935456	ACLY	cDNA FLJ55447, highly similar to ATP-citrate synthase	100.0%	12.3	7	7	7	1	7,788,234	7,502,957	8,551,859	8,308,076	594,164	291,429	639,164	257,725	17.1	8.7	16.7	6.9	-1.0	0.7	1.1	0.4	1.1	0.4	1.1	0.2	1.1	0.07	-1.0	0.7
				AFDSGIIPMEFVNK	2	100.0%	1																									
				DLVSSLTSGLLTIGDR	2	99.6%	1																									
				FICTTSAIQNR	2	100.0%	1																									
				IGNTGGMLDNILASK	2	100.0%	1																									
				LGLVGVNLTLDGVK	2	99.9%	1																									
				QHFPATPLLDYALEVEK	3	98.5%	1																									
				TIAIIAEGIPEALTR	2	100.0%	1																									
IPI00935516	HSBP1	Heat shock factor-binding protein 1	100.0%	25.0	1	2	3	1	1,682,044	1,874,240	1,872,846	2,131,735	117,174	170,642	297,291	126,640	15.6	20.4	35.5	13.3	1.1	0.4	1.1	0.6	1.3	0.03	-1.0	1	1.1	0.3	1.1	0.4
				TVQDLTSVVQTLLQQMQDK	2	100.0%	2																									
				TVQDLTSVVQTLLQQMQDK	3	100.0%	1																									
IPI00935729	HBXIP	hepatitis B virus X-interacting protein	99.6%	11.6	1	1	2	2	2,421,910	2,552,530	2,683,695	3,065,890	196,150	145,301	159,202	282,068	18.1	12.7	13.3	20.6	1.1	0.6	1.1	0.3	1.3	0.1	1.1	0.6	1.2	0.1	1.1	0.3
IPI00976097	HBXIP	Uncharacterized protein	99.6%	22.2	1	1	2	2	2,421,910	2,552,530	2,683,695	3,065,890	196,150	145,301	159,202	282,068	18.1	12.7	13.3	20.6	1.1	0.6	1.1	0.3	1.3	0.1	1.1	0.6	1.2	0.1	1.1	0.3
				GTLSDEHAGVISVLAQQAAK	3	99.6%	2																									
IPI00935818	AHCY	adenosylhomocysteinase isoform 2	100.0%	31.7	9	10	14	1	59,351,877	60,113,996	56,482,458	66,237,725	4,373,685	2,000,291	3,893,286	2,753,123	16.5	7.4	15.4	9.3	1.0	0.9	-1.1	0.6	1.1	0.2	-1.1	0.4	1.1	0.1	1.2	0.07
				DGPLNMILDDGGDLTNLIHTK	3	100.0%	2																									
				GETDEEYLWCIEQTLYFK	2	100.0%	1																									
				GISEETTTGVHNLYK	2	100.0%	2																									
				KLDEAVAEAHLGK	3	100.0%	1																									
				QAQYLGMSCDGPFKPDHYR	3	86.7%	1																									
				RIILLAEGR	2	99.9%	1																									
				VAVVAGYGDVGK	2	100.0%	2																									
				VNIKPQVDR	2	99.6%	1																									
				VNIKPQVDR	3	97.9%	1																									
				VPAINVNDSVTK	2	100.0%	2																									
IPI00936387	RPN2	Ribophorin II, isoform CRA_d	100.0%	8.4	2	2	3	2	1,283,379	1,658,372	1,141,080	1,645,719	166,347	115,990	197,756	102,771	29.0	15.6	38.8	14.0	1.3	0.1	-1.1	0.6	1.3	0.1	-1.5	0.05	-1.0	0.9	1.4	0.05
IPI00941764	RPN2	Ribophorin II	100.0%	17.4	2	2	3	2	1,283,379	1,658,372	1,141,080	1,645,719	166,347	115,990	197,756	102,771	29.0	15.6	38.8	14.0	1.3	0.1	-1.1	0.6	1.3	0.1	-1.5	0.05	-1.0	0.9	1.4	0.05
				LQVTNVLSQPLTQATVK	2	99.7%	1																									
				SIVEEIEDLVAR	2	100.0%	2																									
IPI00936845	00289959;LOC10029	ankyrin repeat domain-containing protein 30B-like	90.6%	14.4	1	1	1	1	4,439,830	4,304,320	4,123,760	5,010,510	521,170	485,510	249,692	377,170	26.3	25.2	13.5	16.8	-1.0	0.9	-1.1	0.6	1.1	0.4	-1.0	0.7	1.2	0.3	1.2	0.09
				IEVLEEGTAKMITCPTK	3	90.6%	1																									
IPI00937735	ACADVL	cDNA FLJ55801, highly similar to Very-long-chain specific acyl-CoAdehydrogenase,	100.0%	15.5	8	8	9	1	11,501,016	12,333,416	12,131,514	14,163,736	1,426,693	592,085	1,204,087	492,751	27.7	10.7	22.2	7.8	1.1	0.6	1.1	0.7	1.2	0.1	-1.0	0.9	1.1	0.04	1.2	0.2
				AGLGSGLSLSGLVHPELSR	3	100.0%	1																									
				ASNTAEVFFDGVR	2	100.0%	1																									
				FGMAAALAGTMR	2	100.0%	1																									
				GIVNEQFLLQR	2	99.9%	1																									
				IFEGTNDILR	2	99.4%	1																									
				IHNFGLIQEK	2	99.8%	1																									
				NPFGNAGLLLGEAGK	2	99.9%	2																									
				VPSENVLGEVGSGFK	2	100.0%	1																									
IPI00938042	LOC100292290	10 kDa heat shock protein, mitochondrial-like	100.0%	19.6	2	2	3	1	19,304,830	18,059,633	17,637,928	18,762,550	945,351	601,828	1,261,710	855,518	11.0	7.5	16.0	10.2	-1.1	0.3	-1.1	0.3	-1.0	0.7	-1.0	0.8	1.0	0.5	1.1	0.5
				GGIMLPEK	2	98.0%	1																									
				VVLDDKDYFLFR	3	100.0%	2																									
IPI00938328	DTYMK	Protein	97.7%	5.9	1	1	1	1	1,423,663	1,549,938	1,541,975	1,620,778	104,016	92,409	96,796	53,218	16.3	13.3	14.0	7.3	1.1	0.4	1.1	0.4	1.1	0.1	-1.0	1	1.0	0.5	1.1	0.5
				SIEAVHEDIR	2	97.7%	1																									
IPI00939159	CAP1	Adenylyl cyclase-associated protein	100.0%	10.9	3	5	6	1	14,173,909	15,384,839	13,825,428	17,393,656	2,102,333	799,112	1,254,398	1,045,022	33.2	11.6	20.3	13.4	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.3	1.1	0.2	1.3	0.06
				KEPAVLELEGK	2	99.9%	1																									
				KEPAVLELEGK	3	99.2%	1																									
				SALFAQINQGESITHALK	2	92.8%	1																									
				SALFAQINQGESITHALK	3	99.7%	1																									
				VENQENVSNLVIEDTELK	2	100.0%	2																									
IPI00939172	MAP7	isoform 1 of Ensconsin	98.0%	4.1	2	2	2	1	2,654,848	2,951,208	3,217,585	3,037,612	227,572	133,484	210,100	203,872	19.2	10.1	14.6	15.0	1.1	0.3	1.2	0.1	1.1	0.2	1.1	0.3	1.0	0.7	-1.1	0.6
				GGDGAVRSETAPDSYK	3	90.8%	1																									
				RLSSSSATLLNSPDR	2	94.8%	1																									
IPI00939221	DDX39B;SNORD84	HLA-B associated transcript 1	100.0%	18.2	2	2	3	1	1,560,467	1,482,256	1,503,160	1,986,905	234,326	74,850	116,546	267,861	33.6	11.3	17.3	30.2	-1.1	0.8	-1.0	0.8	1.3	0.3	1.0	0.9	1.3	0.1	1.3	0.1
				CIALAQLLVEQNFPAIAIHR	3	100.0%	2																									
				GLAITFVSDENDAK	2	100.0%	1																									
IPI00939283	EIF2A	isoform 2 of Eukaryotic translation initiation factor 2A	99.4%	8.1	2	2	2	2	1,535,400	1,496,654	1,467,562	1,693,689	106,955	59,320	90,964	91,105	15.6	8.9	13.9	12.0	-1.0	0.8	-1.0	0.6	1.1	0.3	-1.0	0.8	1.1	0.1	1.2	0.1
IPI00945560	EIF2A	Protein	99.4%	9.5	2	2	2	2	1,535,400	1,496,654	1,467,562	1,693,689	106,955	59,320	90,964	91,105	15.6	8.9	13.9	12.0	-1.0	0.8	-1.0	0.6	1.1	0.3	-1.0	0.8	1.1	0.1	1.2	0.1
				ETALLQELEDLELGI	2	98.4%	1																									
				KATAVLVIASTDVDK	2	87.9%	1																									
IPI00939442	HSPA1L	Heat shock 70 kDa protein 1-like	100.0%	7.3	3	3	5	1	6,052,937	6,251,357	5,900,395	6,766,221	345,904	239,182	296,981	315,799	12.8	8.6	11.3	10.4	1.0	0.6	-1.0	0.7	1.1	0.2	-1.1	0.4	1.1	0.2	1.1	0.08
				AFYPEEISSMVLTK	2	100.0%	2																									
				ATAGDTHLGGEDFDNR	2	100.0%	2																									
				MDKAKIHDIVLVGGSTR	3	97.4%	1																									
IPI00939558	RBMX	cDNA FLJ38696 fis, clone KIDNE2001931, highly similar to HETEROGENEOUS NU	100.0%	26.5	10	11	12	1	24,710,136	26,442,392	26,828,931	30,508,982	1,978,605	1,492,307	1,613,380	1,322,143	17.9	12.6	13.5	9.7	1.1	0.5	1.1	0.4	1.2	0.04	1.0	0.9	1.2	0.08	1.1	0.1
				ALEAVFGK	2	99.9%	1																									
				DRDYSDHPSGGSYR	3	97.3%	1																									
				DSYESYGNSR	2	100.0%	1																									
				GPPPSYGGSSR	2	100.0%	1																									
				IVEVLLMK	2	99.5%	1																									
				LFIGGLNTETNEK	2	100.0%	2																									
				REPLPSR	2	92.6%	1																									
				SDLYSSGR	2	99.3%	1																									
				VEQATKPSFESGR	2	100.0%	1																									
				VEQATKPSFESGR	3	99.9%	1																									
				YDDYSSSR	2	98.5%	1																									
IPI00939578	PLOD2	cDNA FLJ43712 fis, clone TESOP2004114, highly similar to Homo sapiens procollag	100.0%	6.7	2	2	3	1	3,461,660	3,373,465	3,414,320	3,505,943	396,012	233,253	171,807	162,490	25.6	15.5	11.3	10.4	-1.0	0.9	-1.0	0.9	1.0	0.9	1.0	0.9	1.0	0.7	1.0	0.7
				ISGGYENVPTDDIHMK	3	100.0%	1																									
				SEDYVDIVQGNR	2	100.0%	2																									
IPI00939854	WDR1	Uncharacterized protein	100.0%	10.0	5	5	6	1	14,399,474	13,754,138	13,016,991	16,237,933	1,105,547	390,930	644,677	930,093	17.2	6.4	11.1	12.8	-1.0	0.6	-1.1	0.3	1.1	0.2	-1.1	0.4	1.2	0.04	1.2	0.02
				DYSGQGVVK	2	99.8%	2																									
				GPVTDVAYSHDGAFLAVCDASK	3	100.0%	1																									
				IAVVGEGR	2	99.8%	1																									
				VCALGGSK	1	91.5%	1																									
				VFASLPQVER	2	89.8%	1																									
IPI00939930	SUMF2	sulfatase-modifying factor 2 isoform d precursor	100.0%	6.4	1	1	1	2	723,536	661,476	661,174	686,654	49,034	107,547	66,727	44,836	15.2	36.4	22.6	14.6	-1.1	0.6	-1.1	0.5	-1.1	0.6	-1.0	1	1.0	0.8	1.0	0.8
IPI00942954	SUMF2	sulfatase-modifying factor 2 isoform c precursor	100.0%	4.9	1	1	1	2	723,536	661,476	661,174	686,654	49,034	107,547	66,727	44,836	15.2	36.4	22.6	14.6	-1.1	0.6	-1.1	0.5	-1.1	0.6	-1.0	1	1.0	0.8	1.0	0.8
				MGNTPDSASDNLGFR	2	99.5%	1																									
IPI00940257	CCT5	cDNA FLJ52362, highly similar to T-complex protein 1 subunit epsilon	100.0%	51.6	16	16	18	1	15,693,173	16,931,152	15,941,400	18,648,143	1,751,246	779,592	1,164,335	882,577	25.0	10.3	16.3	10.6	1.1	0.5	1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.2	1.2	0.1
				AFADALEVIPMALSENSGMNPIQTMTEVR	2	97.8%	1																									
				DVDFELIKVEGK	2	90.8%	1																									
				EKFEEMIQQIK	2	98.5%	1																									
				ETGANLAICQWGFDDEANHLLLQNNLPAVR	3	100.0%	1																									
				FEEMIQQIK	2	99.5%	1																									
				FSELTAEK	2	98.2%	1																									
				GVIVDKDFSHPQMPK	3	88.5%	1																									
				HKLDVTSVEDYK	3	94.2%	1																									
				IADGYEQAAR	2	100.0%	1																									
				ISDSVLVDIKDTEPLIQTAK	3	100.0%	1																									
				LDVTSVEDYK	2	100.0%	1																									
				LGFAGLVQEISFGTTK	2	100.0%	2																									
				QMAEIAVNAVLTVADMER	3	99.8%	1																									
				QQISLATQMVR	2	98.4%	1																									
				VVYGGGAAEISCALAVSQEADK	3	92.9%	1																									
				WVGGPEIELIAIATGGR	2	100.0%	2																									
IPI00940393	EEF1A1	Elongation factor 1-alpha	100.0%	41.7	14	18	26	1	70,652,416	72,993,682	73,080,058	83,148,501	6,669,071	2,596,884	6,730,948	2,484,480	21.1	8.0	20.6	6.7	1.0	0.8	1.0	0.8	1.2	0.1	1.0	1	1.1	0.02	1.1	0.2
				DGNASGTTLLEALDCILPPTRPTDKPLR	3	100.0%	1																									
				EHALLAYSQKR	3	87.7%	1																									
				EVSTYIK	1	96.3%	1																									
				EVSTYIKK	2	98.6%	1																									
				IGGIGTVPVGR	2	100.0%	3																									
				LPLQDVYK	2	99.9%	1																									
				NMITGTSQADCAVLIVAAGVGEFEAGISK	2	100.0%	2																									
				NMITGTSQADCAVLIVAAGVGEFEAGISK	3	100.0%	1																									
				QTVAVGVIK	1	92.1%	1																									
				QTVAVGVIK	2	100.0%	2																									

				SGDAAIVDMVPGKPMCVESFSDYPPLGR	3	100.0%	1																									
				STTTGHLIYK	2	100.0%	2																									
				VETGVLKPGMVVTFAPVNVTTEVK	3	100.0%	1																									
				YEEIVK	1	97.5%	1																									
				YEEIVK	2	93.9%	2																									
				YEEIVKEVSTYIK	2	91.5%	1																									
				YYVTIIDAPGHR	2	100.0%	2																									
				YYVTIIDAPGHR	3	100.0%	2																									
IPI00940549	HARS	Uncharacterized protein	100.0%	20.7	5	5	5	1	2,585,744	2,777,049	2,577,743	2,938,493	244,047	113,718	145,814	79,942	21.1	9.2	12.7	6.1	1.1	0.5	-1.0	1	1.1	0.2	-1.1	0.3	1.1	0.3	1.1	0.06
				IFSIVEQR	2	90.1%	1																									
				IGDYVQQHGGVSLVEQLLQDPK	3	99.9%	1																									
				LLFEYLTLFGIDDK	2	89.3%	1																									
				QALEGLGDLK	2	96.4%	1																									
				YDGLVGMFDPK	2	98.9%	1																									
IPI00940673	TKT	cDNA FLJ53217, highly similar to Transketolase	100.0%	40.0	14	18	25	1	31,123,796	31,190,820	30,657,168	36,191,170	2,346,818	1,067,019	2,020,339	1,270,080	16.9	7.7	14.7	7.9	1.0	1	-1.0	0.9	1.2	0.09	-1.0	0.8	1.2	0.02	1.2	0.05
				AVELAANTK	1	100.0%	1																									
				AVELAANTK	2	100.0%	2																									
				GITGVEDKESWHGKPLPK	3	81.1%	1																									
				IIALDGDTK	2	99.9%	1																									
				ILATPPQEDAPSVDIANIR	2	100.0%	2																									
				ILATPPQEDAPSVDIANIR	3	100.0%	1																									
				LGQSDPAPLQHQMDIYQK	3	100.0%	1																									
				MFGIDR	2	99.8%	1																									
				MFGIDRDAIAQAVR	2	99.8%	1																									
				MFGIDRDAIAQAVR	3	100.0%	1																									
				MPSLPSYK	2	100.0%	2																									
				NMAEQIIQEIYSQIQSK	2	100.0%	2																									
				NMAEQIIQEIYSQIQSK	3	100.0%	1																									
				NSTFSEIFKK	2	99.8%	1																									
				SGKPAELLK	2	96.8%	1																									
				SVPTSTVFYPSDGVATEK	2	100.0%	2																									
				TSRPENAIIYNNNEDFQVGQAK	3	100.0%	2																									
				VLDPFTIKPLDR	2	100.0%	2																									
IPI00940720	PARP1	PARP1 protein (Fragment)	100.0%	9.6	2	2	2	1	2,667,023	2,957,919	2,521,232	3,104,339	272,446	73,844	222,079	118,111	22.8	5.6	19.7	8.5	1.1	0.4	-1.1	0.7	1.2	0.2	-1.2	0.1	1.0	0.3	1.2	0.05
				MAIMVQSPMFDGK	2	99.9%	1																									
				TLGDFAAEYAK	2	98.4%	1																									
IPI00940730	ENOPH1	MasA	98.7%	5.5	1	1	1	1	1,407,567	1,362,117	1,230,377	1,202,497	171,277	101,752	60,570	88,353	27.2	16.7	11.0	16.4	-1.0	0.8	-1.1	0.4	-1.2	0.3	-1.1	0.3	-1.1	0.3	-1.0	0.8
				AEFFADVVPAVR	2	98.7%	1																									
IPI00940872	TTN	Titin, isoform CRA_a	99.8%	0.4	10	10	10	1	6,896,660	6,811,064	7,880,054	7,965,456	613,931	296,005	603,873	215,133	19.9	9.7	17.1	6.0	-1.0	0.9	1.1	0.3	1.2	0.2	1.2	0.2	1.2	0.01	1.0	0.9
				AEDLSATVTDVVEGQEYSFR	3	97.1%	1																									
				DSCSAQLGVQEPPRFIKK	2	88.8%	1																									
				ITQFLKAEASKEIAK	2	84.0%	1																									
				LEADVSGRPPPTMEWSK	3	84.9%	1																									
				MPDDDGGDR	1	92.2%	1																									
				STVTIVDSKR	2	89.8%	1																									
				VLDTPGPPVNVTVK	2	90.2%	1																									
				VNTEDHQGEYVCEALNDSGK	3	87.7%	1																									
				VTGLSEGCEYFFR	3	94.3%	1																									
				YLISTEEVSYFNVQSR	3	85.6%	1																									
IPI00940955	HNRNPH2	cDNA FLJ57964, highly similar to Heterogeneous nuclear ribonucleoprotein H'	100.0%	20.1	5	5	8	1	9,395,692	9,867,275	8,609,935	10,209,499	1,080,281	377,033	625,291	201,866	25.7	8.5	16.2	4.4	1.1	0.7	-1.1	0.5	1.1	0.5	-1.1	0.1	1.0	0.4	1.2	0.06
				ATENDIYNFFSPLNPMR	2	100.0%	2																									
				DLNYCFSGMSDHR	2	99.8%	1																									
				GLPWSCSADEVMR	2	100.0%	2																									
				STGEAFVQFASQEIAEK	2	100.0%	2																									
				VTGEADVEFATHEDAVAAMAK	3	97.6%	1																									
IPI00941031	KIAA1967	cDNA FLJ12599 fis, clone NT2RM4001410	100.0%	2.7	1	1	1	1	4,899,463	6,856,400	5,629,767	8,357,400	1,157,937	840,329	564,408	524,577	52.9	27.4	22.4	14.0	1.4	0.2	1.1	0.6	1.7	0.03	-1.2	0.3	1.2	0.2	1.5	0.008
				TLAAEMQELR	2	99.4%	1																									
IPI00941379	-	Uncharacterized protein	100.0%	4.3	1	1	2	1	109,508	106,702	116,186	122,741	14,415	6,732	22,241	12,561	29.4	14.1	42.8	22.9	-1.0	0.9	1.1	0.8	1.1	0.5	1.1	0.7	1.2	0.3	1.1	0.8
				LATALQK	1	96.5%	2																									
IPI00941730	ARHGAP1	Uncharacterized protein	98.2%	5.7	1	1	1	2	236,282	255,579	380,372	333,007	9,193	35,832	59,837	19,140	8.7	31.4	35.2	12.9	1.1	0.6	1.6	0.07	1.4	0.002	1.5	0.1	1.3	0.09	-1.1	0.5
IPI00980090	ARHGAP1	Protein	98.2%	7.8	1	1	1	2	236,282	255,579	380,372	333,007	9,193	35,832	59,837	19,140	8.7	31.4	35.2	12.9	1.1	0.6	1.6	0.07	1.4	0.002	1.5	0.1	1.3	0.09	-1.1	0.5
				ELPEPLLTFDLYPHVVGFLNIDESQR	3	98.2%	1																									
IPI00942141	SRSF12	Serine/arginine-rich splicing factor 12	100.0%	8.4	2	2	2	1	1,734,956	1,619,591	1,545,840	1,928,590	159,637	115,192	84,111	66,793	20.6	15.9	12.2	7.7	-1.1	0.6	-1.1	0.3	1.1	0.3	-1.0	0.6	1.2	0.05	1.2	0.007
				GFAYVQFEDVR	2	100.0%	1																									
				QIEIQFAQGDR	2	99.8%	1																									
IPI00942143	MSH2	Uncharacterized protein	99.6%	4.3	2	2	2	1	137,752	131,042	122,137	143,856	13,795	6,710	10,465	7,227	22.4	11.5	19.2	11.2	-1.1	0.7	-1.1	0.4	1.0	0.7	-1.1	0.5	1.1	0.2	1.2	0.1
				GVSTFMAEMLETASILR	2	98.4%	1																									
				LNLVEAFVEDAELR	2	99.6%	1																									
IPI00942344	VAT1	cDNA FLJ54106, moderately similar to Synaptic vesicle membrane protein VAT-1 ho	100.0%	7.7	2	2	3	1	2,981,237	2,773,473	2,795,917	3,182,157	373,397	154,457	256,125	208,752	28.0	12.5	20.5	14.7	-1.1	0.6	-1.1	0.7	1.1	0.7	1.0	0.9	1.1	0.2	1.1	0.3
				VLLVPGPEKEN	2	100.0%	2																									
				VVTYGMANLLTGPK	2	99.9%	1																									
IPI00942368	SELENBP1	cDNA FLJ61035, highly similar to Selenium-binding protein 1	100.0%	14.9	4	4	5	1	3,805,096	4,021,467	4,096,943	4,317,963	266,093	111,557	254,153	139,688	15.6	6.2	13.9	7.2	1.1	0.5	1.1	0.5	1.1	0.1	1.0	0.8	1.1	0.1	1.1	0.5
				GGFVLLDGETFEVK	2	99.9%	1																									
				HNVMISTEWAAPNVLR	2	99.8%	1																									
				LTGQLFLGGSIVK	2	99.5%	2																									
				NTGTEAPDYLATVDVDPK	2	100.0%	1																									
IPI00942853	RBM39	RNA binding motif protein 39	100.0%	10.7	3	3	3	1	1,798,324	1,617,278	1,985,914	1,746,122	125,024	84,878	125,722	48,892	15.6	11.7	14.2	6.3	-1.1	0.3	1.1	0.3	-1.0	0.7	1.2	0.04	1.1	0.2	-1.1	0.1
				DLEEFFSTVGK	2	94.2%	1																									
				NSAQGNVYVK	2	99.7%	1																									
				VLGVPIIVQASQAEK	2	98.5%	1																									
IPI00943181	PSME2	Uncharacterized protein	100.0%	19.3	3	3	4	1	11,523,826	11,191,731	10,503,400	12,909,317	1,635,785	749,119	649,322	938,094	31.7	15.0	13.8	16.3	-1.0	0.9	-1.1	0.6	1.1	0.5	-1.1	0.5	1.2	0.2	1.2	0.07
				ALVHERDEAAYGELR	3	99.9%	1																									
				IIYLNQLLQEDSLNVADLTSLR	2	100.0%	2																									
				TKVEAFQTTISK	2	99.1%	1																									
IPI00943550	PLIN3	isoform 3 of Perilipin-3	100.0%	48.5	12	13	18	1	17,854,062	18,973,063	18,197,833	21,715,639	1,677,364	912,179	1,276,062	728,007	21.0	10.8	15.7	7.5	1.1	0.6	1.0	0.9	1.2	0.07	-1.0	0.6	1.1	0.05	1.2	0.04
				DIAQQLQATCTSLGSSIQGLPTNVKDQVQQAR	3	100.0%	1																									
				DTVATQLSEAVDATR	2	100.0%	1																									
				EALDHMVEYVAQNTPVTWLVGPFAPGITEK	3	100.0%	1																									
				ELVSSKVSGAQEMVSSAKDTVATQLSEAVDATR	3	95.6%	1																									
				IATSLDGFDVASVQQQR	2	100.0%	2																									
				IATSLDGFDVASVQQQR	3	95.3%	1																									
				LGQMVLSGVDTVLGK	2	100.0%	2																									
				QEQSYFVR	2	99.9%	2																									
				QVEDLQATFSSIHSFQDLSSSILAQSR	3	94.0%	1																									
				SEEWADNHLPLTDAELAR	3	100.0%	1																									
				SVVTGGVQSVMGSR	2	100.0%	1																									
				TLTAAAVSGAQPILSK	2	100.0%	2																									
				VSGAQEMVSSAK	2	100.0%	2																									
IPI00944907	ACTL6A	Uncharacterized protein	100.0%	28.0	1	1	1	1	1,220,368	1,370,513	1,280,423	1,307,373	187,754	170,845	70,246	204,294	34.4	27.9	12.3	34.9	1.1	0.6	1.0	0.8	1.1	0.8	-1.1	0.6	-1.0	0.8	1.0	0.9
				QGGPTYYIDTNALR	2	99.9%	1																									
IPI00945024	SND1	26 kDa protein	100.0%	11.3	2	2	2	1	3,396,230	4,422,376	3,281,190	4,814,453	489,335	455,654	475,084	145,095	32.2	23.0	32.4	6.7	1.3	0.2	-1.0	0.9	1.4	0.04	-1.3	0.1	1.1	0.5	1.5	0.03
				SEAVVEYVFSGSR	2	100.0%	1																									
				SSHYDELLAAEAR	2	99.9%	1																									
IPI00945037	ITGB1	Integrin beta	99.9%	11.2	1	1	1	6	353,626	361,481	324,347	374,528	22,188	32,538	30,795	26,007	14.0	20.1	21.2	15.5	1.0	0.8	-1.1	0.5	1.1	0.6	-1.1	0.4	1.0	0.8	1.2	0.2
IPI00945878	ITGB1	Integrin beta	99.9%	10.4	1	1	1	6	353,626	361,481	324,347	374,528	22,188	32,538	30,795	26,007	14.0	20.1	21.2	15.5	1.0	0.8	-1.1	0.5	1.1	0.6	-1.1	0.4	1.0	0.8	1.2	0.2
IPI00946209	ITGB1	Integrin beta	99.9%	17.4	1	1	1	6	353,626	361,481	324,347	374,528	22,188	32,538	30,795	26,007	14.0	20.1	21.2	15.5	1.0	0.8	-1.1	0.5	1.1	0.6	-1.1	0.4	1.0	0.8	1.2	0.2
IPI00947385	ITGB1	Integrin beta	99.9%	13.6	1	1	1	6	353,626	361,481	324,347	374,528	22,188	32,538	30,795	26,007	14.0	20.1	21.2	15.5	1.0	0.8	-1.1	0.5	1.1	0.6	-1.1	0.4	1.0	0.8	1.2	0.2
IPI00979111	ITGB1	Integrin beta	99.9%	12.5	1	1	1	6	353,626	361,481	324,347	374,528	22,188	32,538	30,795	26,007	14.0	20.1	21.2	15.5	1.0	0.8	-1.1	0.5	1.1	0.6	-1.1	0.4	1.0	0.8	1.2	0.2
IPI01013133	ITGB1	Uncharacterized protein	99.9%	11.9	1	1	1	6	353,626	361,481	324,347	374,528	22,188	32,538	30,795	26,007	14.0	20.1	21.2	15.5	1.0	0.8	-1.1	0.5	1.1	0.6	-1.1	0.4	1.0	0.8	1.2	0.2
				LKPEDITQIQPQQLVLR	3	99.1%	1																									
IPI00945241	MUC13	Uncharacterized protein	100.0%	7.6	1	1	1	1	1,939,410	1,890,290	1,985,855	2,236,635	72,688	144,239	160,400	147,840	8.4	17.1	18.1	14.8	-1.0	0.8	1.0	0.8	1.2	0.1	1.1	0.7	1.2	0.1	1.1	0.3
				ISVTVSETFDPEEK	2	100.0%	1																									
IPI00945251	CUTA	Uncharacterized protein	100.0%	11.6	1	1	1	1	437,108	414,366	426,632	528,774	56,853	32,928	42,109	60,579	29.1	17.8	22.1	25.6	-1.1	0.7	-1.0	0.9	1.2	0.3	1.0	0.8	1.3	0.1	1.2	0.2
				LAACVNLIPQITSIYEWK	2	100.0%	1																									
IPI00945375	CUTA	Uncharacterized protein	100.0%	23.7	2	2	3	1	2,017,761	1,956,456	2,053,097	1,953,597	133,531	79,201	131,709	115,068	14.8	9.1	14.3	13.2	-1.0	0.7	1.0	0.9	-1.0	0.7	1.0	0.5	-1.0	1	-1.1	0.6
				LAACVNLIPQITSIYEWK	2	100.0%	1																									
				TQSSLVPALTDFVR	2	100.0%	2																									
IPI00945447	UGP2	Uncharacterized protein	100.0%	25.7	3	4	6	4	7,831,777	7,749,421	7,626,085	9,043,331	568,627	340,845	539,873	258,864	16.2	9.8	15.8	6.4	-1.0	0.9	-1.0	0.8	1.2	0.09	-1.0	0.9	1.2	0.02	1.2	0.05
IPI00945711	UGP2	Uncharacterized protein	100.0%	29.3	3	4	6	4	7,831,777	7,749,421	7,626,085	9,043,331	568,627	340,845	539,873	258,864	16.2	9.8	15.8	6.4	-1.0	0.9	-1.0	0.8	1.2	0.09	-1.0	0.9	1.2	0.02	1.2	0.05
IPI00946647	UGP2	Uncharacterized protein	100.0%	20.7	3	4	6	4	7,831,777	7,749,421	7,626,085	9,043,331	568,627	340,845	539,873	258,864	16.2	9.8	15.8	6.4	-1.0	0.9	-1.0	0.8	1.2	0.09	-1.0	0.9	1.2	0.02	1.2	0.05
IPI00946873	UGP2	Uncharacterized protein	100.0%	25.1	3	4	6	4	7,831,777	7,749,421	7,626,085	9,043,331	568,627	340,845	539,873	258,864	16.2	9.8	15.8	6.4	-1.0	0.9	-1.0	0.8	1.2	0.09	-1.0	0.9	1.2	0.02	1.2	0.05
				GLPDNISSVLNK	2	99.8%	2																									
				IQRPPEDSIQPYEK	3	99.7%	1																									
				NENTFLDLTVQQIEHLNK	2	99.8%	1																									
				NENTFLDLTVQQIEHLNK	3	100.0%	2																									
IPI00945538	UBA5	Uncharacterized protein	94.0%	20.3	1	1	1	2	1,312,114	1,094,066	1,432,279	1,270,070	70,957	174,363	204,360	99,542	12.1	35.6	31.9	17.5	-1.2	0.3	1.1	0.6	-1.0	0.7	1.3	0.2	1.2	0.4	-1.1	0.5
IPI00945700	UBA5	Uncharacterized protein	94.0%	14.8	1	1	1	2	1,312,114	1,094,066	1,432,279	1,270,070	70,957	174,363	204,360	99,542	12.1	35.6	31.9	17.5	-1.2	0.3	1.1	0.6	-1.0	0.7	1.3	0.2	1.2	0.4	-1.1	0.5
				LLLFDYDKVELANMNR	3	94.0%	1																									
IPI00945574	RAB7A	Uncharacterized protein	100.0%	21.3	3	3	4	1	11,542,558	11,305,342	11,951,077	12,708,667	559,664	302,165	500,386	345,522	10.8	6.0	9.4	6.1	-1.0	0.7	1.0	0.6	1.1	0.1	1.1	0.3	1.1	0.02	1.1	0.2
				ATIGADFLTK	2	98.3%	1																									
				EAINVEQAFQTIAR	2	100.0%	1																									
				FQSLGVAFYR	2	98.5%	2																									
IPI00945620	GMPS	Uncharacterized protein	100.0%	12.0	4	4	4	2	7,928,685	10,338,943	7,056,196	10,565,394	1,242,149	668,074	1,091,772	948,180	35.0	14.5	34.6	20.1	1.3	0.1	-1.1	0.6	1.3	0.1	-1.5	0.03	1.0	0.9	1.5	0.04
IPI01013391	GMPS	cDNA FLJ57604, highly similar to GMP synthase	100.0%	11.1	4	4	4	2	7,928,685	10,338,943	7,056,196	10,565,394	1,242,149	668,074	1,091,772	948,180	35.0	14.5	34.6	20.1	1.3	0.1	-1.1	0.6	1.3	0.1	-1.5	0.03	1.0	0.9	1.5	0.04
				ELGLPEELVSR	2	96.4%	1																									
				GLQKEEVVLLTHGDSVDK	3	100.0%	1																									
				IMYDLTSKPPGTTEWE	2	99.4%	1																									
				TFITSDFMTGIPATPGNEIPVEVVLK	2	99.5%	1																									
IPI00945689	PSMD6	Uncharacterized protein	100.0%	11.5	2	2	2	1	2,155,069	2,403,160	2,141,160	2,447,044	206,947	81,889	210,506	40,597	21.5	7.6	22.0	3.7	1.1	0.3	-1.0	1	1.1	0.2	-1.1	0.3	1.0	0.6	1.1	0.2
				IGLFYMDNDLITR	2	99.7%	1																									
				SLDWQIDVDLLNK	2	99.9%	1																									
IPI00945735	RAB7A	Uncharacterized protein	100.0%	31.3	4	4	7	1	12,606,778	11,866,609	13,396,672	12,406,742	442,248	453,611	672,846	403,765	7.8	8.6	11.2	7.3	-1.1	0.3	1.1	0.4	-1.0	0.7	1.1	0.1	1.0	0.4	-1.1	0.2
				ATIGADFLTK	2	98.3%	1																									
				DPENFPFVVLGNK	2	100.0%	2																									
				FQSLGVAFYR	2	98.5%	2																									
				LVTMQIWDTAGQER	2	100.0%	2																									
IPI00945760	HMGCS2	hydroxymethylglutaryl-CoA synthase, mitochondrial isoform 2 precursor	100.0%	4.1	1	1	1	1	985,595	1,167,320	952,790	1,120,365	127,945	92,320	144,144	93,347	29.0	17.7	33.8	18.6	1.2	0.3	-1.0	0.9	1.1	0.4	-1.2	0.2	-1.0	0.7	1.2	0.4

				LMFNDFLSASSDTQTSLYK	2	100.0%	1																									
IPI00945851	RPN1	13 kDa protein	100.0%	12.4	1	1	1	1	2,665,650	2,687,060	2,792,465	3,231,445	273,863	237,361	466,504	186,976	23.0	19.8	37.4	12.9	1.0	1	1.0	0.8	1.2	0.1	1.0	0.8	1.2	0.1	1.2	0.4
				ATSFLLALEPELEAR	2	100.0%	1																									
IPI00945858	METTL2B	26 kDa protein	98.6%	3.8	1	1	1	1	3,024,520	3,333,560	3,091,920	3,436,930	214,047	161,723	171,234	121,410	15.8	10.9	12.4	7.9	1.1	0.3	1.0	0.8	1.1	0.1	-1.1	0.3	1.0	0.6	1.1	0.1
				CFAFVHDLC	2	99.5%	1																									
IPI00946012	UGP2	Uncharacterized protein	100.0%	13.3	1	1	1	2	6,047,822	5,891,511	5,679,411	6,871,133	545,672	393,708	460,635	215,332	20.2	14.9	18.1	7.0	-1.0	0.8	-1.1	0.6	1.1	0.2	-1.0	0.7	1.2	0.06	1.2	0.05
IPI00946068	UGP2	Uncharacterized protein	100.0%	10.4	1	1	1	2	6,047,822	5,891,511	5,679,411	6,871,133	545,672	393,708	460,635	215,332	20.2	14.9	18.1	7.0	-1.0	0.8	-1.1	0.6	1.1	0.2	-1.0	0.7	1.2	0.06	1.2	0.05
				IQRPPEDSIQPYEK	3	99.7%	1																									
IPI00946029	KLC4	Uncharacterized protein	100.0%	11.0	3	3	3	1	1,728,703	1,680,111	1,692,658	1,972,657	172,087	89,585	115,854	97,967	22.3	11.9	15.3	11.1	-1.0	0.8	-1.0	0.9	1.1	0.3	1.0	0.9	1.2	0.06	1.2	0.1
				HLEFLGQLR	2	99.6%	1																									
				LSQEEILGSTR	2	100.0%	1																									
				LVSQGLEALR	2	99.7%	1																									
IPI00946087	PLS1	Uncharacterized protein	100.0%	11.8	1	1	2	2	419,706	372,805	476,359	484,473	19,888	39,234	33,486	35,211	10.6	23.5	15.7	16.3	-1.1	0.3	1.1	0.2	1.2	0.1	1.3	0.08	1.3	0.07	1.0	0.9
IPI00947477	PLS1	Uncharacterized protein	100.0%	11.7	1	1	2	2	419,706	372,805	476,359	484,473	19,888	39,234	33,486	35,211	10.6	23.5	15.7	16.3	-1.1	0.3	1.1	0.2	1.2	0.1	1.3	0.08	1.3	0.07	1.0	0.9
				ISFEEFVSLMQELK	2	100.0%	2																									
IPI00946092	CALU	calumenin isoform f	100.0%	29.9	3	3	3	1	4,197,580	3,791,951	3,735,301	4,550,537	302,196	99,818	206,663	167,648	16.1	5.9	12.4	8.2	-1.1	0.3	-1.1	0.2	1.1	0.3	-1.0	0.8	1.2	0.005	1.2	0.02
				EEIVDKYDLFVGSQATDFGEALVR	3	100.0%	1																									
				HLVYESDQNKDGK	3	100.0%	1																									
				MADKDGDLIATK	2	99.1%	1																									
IPI00946103	NDUFA5	Uncharacterized protein	95.5%	9.7	1	1	1	2	129,309	114,714	130,771	140,657	16,229	11,648	20,238	12,950	28.1	22.7	34.6	20.6	-1.1	0.5	1.0	1	1.1	0.6	1.1	0.5	1.2	0.2	1.1	0.7
IPI00946474	NDUFA5	8 kDa protein	95.5%	12.9	1	1	1	2	129,309	114,714	130,771	140,657	16,229	11,648	20,238	12,950	28.1	22.7	34.6	20.6	-1.1	0.5	1.0	1	1.1	0.6	1.1	0.5	1.2	0.2	1.1	0.7
				YTEQITNEK	2	95.5%	1																									
IPI00946316	KPNA4	19 kDa protein	100.0%	20.6	2	2	2	1	2,855,655	2,854,840	2,751,605	2,766,460	348,447	232,923	94,289	63,646	27.3	18.2	7.7	5.1	-1.0	1	-1.0	0.8	-1.0	0.8	-1.0	0.7	-1.0	0.7	1.0	0.9
				IEQLQNHENEDIYK	3	98.5%	1																									
				MAEDEAETIGNLIEECGGLEK	2	99.7%	1																									
IPI00946351	AP1B1	Uncharacterized protein	100.0%	13.0	6	6	8	1	2,691,871	3,046,438	2,716,847	3,133,329	265,748	157,995	239,852	105,353	22.1	11.6	19.7	7.5	1.1	0.3	1.0	0.9	1.2	0.2	-1.1	0.3	1.0	0.7	1.2	0.2
				AAMIWIVGEYAER	2	100.0%	2																									
				CVSTLLDLIQTK	2	100.0%	1																									
				LASQANIAQVLAELK	2	100.0%	2																									
				LASQANIAQVLAELKEYATEVDVDFVR	3	100.0%	1																									
				SQPDMAIMAVNTFVK	2	100.0%	1																									
				YNDPIYVK	2	99.7%	1																									
IPI00946377	CCDC58	Uncharacterized protein	99.6%	28.3	1	1	1	1	992,938	1,070,690	995,108	1,143,673	67,135	44,121	144,297	104,263	15.1	9.2	32.4	20.4	1.1	0.4	1.0	1	1.2	0.3	-1.1	0.6	1.1	0.5	1.1	0.4
				WMQSELNVEEVVNDR	2	99.6%	1																									
IPI00946476	ATP6V1A	Uncharacterized protein	100.0%	4.5	1	1	2	1	2,243,560	2,444,623	2,339,237	2,473,953	145,165	131,546	234,190	98,211	14.5	12.0	22.4	8.9	1.1	0.3	1.0	0.7	1.1	0.2	-1.0	0.7	1.0	0.9	1.1	0.6
				FTMVQVWPVR	2	100.0%	2																									
IPI00946483	PFN2	Profilin	100.0%	31.2	2	2	2	1	324,714	296,613	285,929	370,219	44,370	18,919	22,725	7,826	30.6	14.3	17.8	4.7	-1.1	0.6	-1.1	0.5	1.1	0.4	-1.0	0.7	1.2	0.007	1.3	0.02
				DSLYVDGDCTMDIR	2	97.4%	1																									
				YVWAATAGGVFQSITPIEIDMIVGK	2	100.0%	1																									
IPI00946493	TRIM59	Uncharacterized protein	91.4%	10.6	1	1	1	1	3,545,530	2,923,210	3,634,990	3,588,610	173,987	264,349	435,770	395,764	11.0	20.2	26.8	24.7	-1.2	0.08	1.0	0.9	1.0	0.9	1.2	0.2	1.2	0.2	-1.0	0.9
				DSGGVGEECIQPPNHEINK	3	91.4%	1																									
IPI00946712	FAM166A	Uncharacterized protein	95.4%	8.5	1	1	1	1	4,536,428	5,456,259	5,517,370	5,472,420	1,473,246	1,698,307	756,457	978,314	72.6	69.6	30.7	40.0	1.2	0.7	1.2	0.6	1.2	0.6	1.0	1	1.0	1	-1.0	1
				LPVPALTGCPVGTGLKPSK	2	95.4%	1																									
IPI00946911	RAB7A	Uncharacterized protein	100.0%	20.7	2	2	4	1	7,052,430	7,007,438	7,402,050	7,534,985	253,097	257,357	281,474	427,364	8.0	8.2	8.5	12.7	-1.0	0.9	1.0	0.4	1.1	0.4	1.1	0.3	1.1	0.3	1.0	0.8
				FQSLGVAFYR	2	98.5%	2																									
				LVTMQIWDTAGQER	2	100.0%	2																									
IPI00946929	ARF4	Uncharacterized protein	94.7%	5.2	1	1	1	1	1,829,050	1,888,400	1,867,190	2,114,200	208,417	104,841	138,839	105,474	25.5	12.4	16.6	11.2	1.0	0.8	1.0	0.9	1.2	0.3	-1.0	0.9	1.1	0.2	1.1	0.2
				MLLVDELR	2	94.7%	1																									
IPI00947129	PDHB	Uncharacterized protein	100.0%	12.3	3	3	3	1	4,692,954	5,611,299	4,421,569	6,904,988	934,438	540,585	691,860	500,366	44.5	21.5	35.0	16.2	1.2	0.4	-1.1	0.8	1.5	0.07	-1.3	0.2	1.2	0.1	1.6	0.02
				EGVECEVINMR	2	99.4%	1																									
				TIRPMDMETIEASVMK	2	100.0%	1																									
				VFLLGEEVAQYDGAYK	2	95.3%	1																									
IPI00947227	PLS3	plastin-3 isoform 2	100.0%	17.7	7	7	8	1	7,637,480	7,425,794	7,975,810	8,472,858	738,650	314,358	607,318	379,436	21.6	9.5	17.0	10.0	-1.0	0.8	1.0	0.7	1.1	0.3	1.1	0.4	1.1	0.07	1.1	0.5
				ANDDIIVNWVNR	2	99.9%	1																									
				LNLAFVANLFNK	2	100.0%	1																									
				QFVTPADVVSGNPK	2	100.0%	2																									
				VDLNSNGFICDYELHELFK	2	99.3%	1																									
				VYALPEDLVEVKPK	3	96.0%	1																									
				YPALTKPENQDIDWTLLEGETR	3	100.0%	1																									
				YTLNVLEDLGDGQK	2	100.0%	1																									
IPI00947319	PDHB	28 kDa protein	96.9%	6.4	1	1	1	1	542,856	578,316	582,184	621,018	49,944	58,398	38,196	44,104	20.6	22.6	14.7	15.9	1.1	0.7	1.1	0.5	1.1	0.3	1.0	1	1.1	0.6	1.1	0.5
				VFLLGEEVAQYDGAYK	2	95.3%	1																									
IPI00947393	RBBP7	Uncharacterized protein	100.0%	31.0	1	1	2	1	1,191,490	1,234,781	1,059,602	1,410,690	132,700	57,903	105,230	89,824	24.9	10.5	22.2	14.2	1.0	0.8	-1.1	0.5	1.2	0.2	-1.2	0.2	1.1	0.1	1.3	0.03
				TPSSDVLVFDYTK	2	100.0%	2																									
IPI00947396	PSMD6	Uncharacterized protein	100.0%	15.3	2	2	2	1	1,526,525	1,659,506	1,524,419	1,769,728	144,710	77,454	138,047	55,297	21.2	10.4	20.3	7.0	1.1	0.4	-1.0	1	1.2	0.2	-1.1	0.4	1.1	0.3	1.2	0.1
				FLLSLPEHR	3	96.6%	1																									
				SLDWQIDVDLLNK	2	99.9%	1																									
IPI00947447	ACY1	aminoacylase-1 isoform c	100.0%	23.3	6	7	8	1	11,291,896	11,870,023	11,573,525	12,572,526	1,196,014	751,598	906,376	413,119	23.7	14.2	17.5	7.4	1.1	0.7	1.0	0.9	1.1	0.4	-1.0	0.8	1.1	0.4	1.1	0.3
				AVGVPALGFSPMNR	2	99.9%	2																									
				DMNLTLEPEIMPAATDNR	2	100.0%	1																									
				GPEEEHPSVTLFR	3	99.3%	1																									
				LLPALASVPALPSDS	2	93.1%	1																									
				PDYGAAVAFFEETAR	2	90.9%	1																									
				TVQPKPDYGAAVAFFEETAR	2	100.0%	1																									
				TVQPKPDYGAAVAFFEETAR	3	100.0%	1																									
IPI00947454	PLS3	Protein	100.0%	13.7	2	2	3	1	1,239,912	1,102,698	1,185,961	1,318,393	145,339	56,681	56,639	96,448	26.2	11.5	10.7	16.4	-1.1	0.4	-1.0	0.7	1.1	0.7	1.1	0.3	1.2	0.09	1.1	0.3
				LNLAFVANLFNK	2	100.0%	1																									
				QFVTPADVVSGNPK	2	100.0%	2																									
IPI00947554	MST4	cDNA FLJ90669 fis, clone PLACE1005519, moderately similar to Homo sapiens STI	100.0%	6.1	2	2	2	1	7,578,669	8,089,230	8,462,837	9,046,133	339,895	580,737	372,602	263,247	10.0	16.1	9.8	6.5	1.1	0.5	1.1	0.1	1.2	0.009	1.0	0.6	1.1	0.2	1.1	0.2
				KVQNGAQDENNASR	2	91.3%	1																									
				TSYLTELIDR	2	99.8%	1																									
IPI00952671	CCT7	T-complex protein 1 subunit eta isoform c	100.0%	29.6	9	9	10	2	14,172,367	14,022,306	13,595,969	15,812,332	1,144,915	641,133	1,045,390	757,005	18.1	10.2	17.2	10.7	-1.0	0.9	-1.0	0.7	1.1	0.3	-1.0	0.7	1.1	0.1	1.2	0.1
IPI01015939	CCT7	cDNA FLJ54568, highly similar to T-complex protein 1 subunit eta	100.0%	30.5	9	9	10	2	14,172,367	14,022,306	13,595,969	15,812,332	1,144,915	641,133	1,045,390	757,005	18.1	10.2	17.2	10.7	-1.0	0.9	-1.0	0.7	1.1	0.3	-1.0	0.7	1.1	0.1	1.2	0.1
				CAMTALSSK	2	99.3%	1																									
				GGAEQFMEETER	2	100.0%	1																									
				INALTAASEAACLIVSVDETIKNPR	3	100.0%	1																									
				QLCDNAGFDATNILNK	2	100.0%	1																									
				SLHDAIMIVR	2	96.7%	1																									
				TATQLAVNK	2	99.9%	1																									
				TFSYAGFEMQPK	2	100.0%	2																									
				VHTVEDYQAIVDAEWNILYDKLEK	3	97.4%	1																									
				VQGGALEDSQLVAGVAFK	2	100.0%	1																									
IPI00952872	TFG	Uncharacterized protein	100.0%	7.8	1	1	1	1	1,139,384	1,073,360	1,124,036	1,148,572	95,170	56,768	94,486	51,739	18.7	11.8	18.8	10.1	-1.1	0.6	-1.0	0.9	1.0	0.9	1.0	0.7	1.1	0.4	1.0	0.8
				LLSNDEVTIK	2	100.0%	1																									
IPI00953321	STAM	Uncharacterized protein	100.0%	10.2	1	1	2	1	1,018,800	1,135,617	1,189,000	1,132,327	47,313	97,108	57,370	36,769	10.4	19.1	10.8	7.3	1.1	0.3	1.2	0.05	1.1	0.09	1.0	0.6	-1.0	1	-1.1	0.4
				DFASEVSNVLNK	2	99.9%	2																									
IPI00953536	CDHR5	Uncharacterized protein	99.4%	3.7	1	1	1	1	3,802,950	4,210,850	4,068,375	4,590,375	238,748	279,985	403,629	220,916	14.0	14.9	22.2	10.8	1.1	0.3	1.1	0.6	1.2	0.04	-1.0	0.8	1.1	0.3	1.1	0.3
				VFVSVLDVNDNAPEFPFK	2	99.4%	1																									
IPI00953668	IGF2BP3	9 kDa protein	100.0%	37.0	2	2	3	1	4,778,875	4,822,575	4,261,045	5,144,155	263,778	361,383	162,086	194,608	12.3	16.8	8.5	8.5	1.0	0.9	-1.1	0.1	1.1	0.3	-1.1	0.2	1.1	0.5	1.2	0.008
				IPVSGPFLVK	2	89.1%	1																									
				LYIGNLSENAAPSDLESIFK	2	100.0%	2																									
IPI00953696	GSR	glutathione reductase, mitochondrial isoform 4 precursor	100.0%	22.3	6	6	7	2	9,515,285	9,496,659	9,276,141	10,865,942	479,314	385,605	422,360	346,639	11.3	9.1	10.2	7.1	-1.0	1	-1.0	0.7	1.1	0.05	-1.0	0.7	1.1	0.03	1.2	0.02
IPI00978634	GSR	glutathione reductase, mitochondrial isoform 3 precursor	100.0%	20.9	6	6	7	2	9,515,285	9,496,659	9,276,141	10,865,942	479,314	385,605	422,360	346,639	11.3	9.1	10.2	7.1	-1.0	1	-1.0	0.7	1.1	0.05	-1.0	0.7	1.1	0.03	1.2	0.02
				ADFDNTVAIHPTSSEELVTLR	3	100.0%	1																									
				ALLTPVAIAAGR	2	85.6%	1																									
				LGGTCVNVGCVPK	2	100.0%	1																									
				LNAIYQNNLTK	2	100.0%	2																									
				QEPQPQGPPPAAGAVASYDYLVIGGGSGGLASAR	3	98.8%	1																									
				YGIENVK	2	88.7%	1																									
IPI00954180	SELENBP1	isoform 2 of Selenium-binding protein 1	100.0%	13.2	4	4	5	1	6,134,998	6,605,684	6,242,740	7,446,531	521,277	225,568	521,328	385,660	19.0	7.6	18.7	11.6	1.1	0.4	1.0	0.9	1.2	0.08	-1.1	0.5	1.1	0.1	1.2	0.1
				GGFVLLDGETFEVK	2	99.9%	1																									
				HNVMISTEWAAPNVLR	2	99.8%	1																									
				IYVVDVGSEPR	2	99.7%	1																									
				LTGQLFLGGSIVK	2	99.5%	2																									
IPI00954849	FCAMR	high affinity immunoglobulin alpha and immunoglobulin mu Fc receptor isoform b	98.8%	3.1	1	1	1	1	2,911,680	3,271,870	3,213,390	4,026,030	380,277	345,203	301,491	214,244	29.2	23.6	21.0	11.9	1.1	0.5	1.1	0.6	1.4	0.03	-1.0	0.9	1.2	0.1	1.3	0.06
				MLQDDSLPAGASLTAPER	2	95.0%	1																									
IPI00954850	STARD9	stAR-related lipid transfer protein 9	92.9%	0.5	1	1	1	1	8,782,680	9,249,500	11,352,560	10,885,170	267,275	761,073	422,660	719,088	6.8	18.4	8.3	14.8	1.1	0.6	1.3	0.0009	1.2	0.04	1.2	0.04	1.2	0.2	-1.0	0.6
				DWTQKWNDWQALMEHYSVDINR	3	90.5%	1																									
IPI00955490	OAT	ornithine aminotransferase, mitochondrial isoform 2	100.0%	3.3	1	1	1	1	6,135,770	7,172,450	6,006,780	7,007,270	573,621	355,025	515,424	378,354	20.9	11.1	19.2	12.1	1.2	0.2	-1.0	0.9	1.1	0.2	-1.2	0.1	-1.0	0.8	1.2	0.2
				LPSDVVTAVR	2	99.9%	1																									
IPI00955780	-	Hydroxysteroid (17-beta) dehydrogenase 12, isoform CRA_a	96.8%	11.9	3	3	3	1	13,102,930	13,424,955	15,013,790	15,677,570	1,576,252	816,229	1,970,370	1,749,259	26.9	13.6	29.4	25.0	1.0	0.9	1.1	0.5	1.2	0.3	1.1	0.5	1.2	0.3	1.0	0.8
				GVFVQSVLPYFVATK	2	81.2%	1																									
				LNPGGGGCSEPR	2	83.4%	1																									
				TFVDFFSQCLHEEYR	2	93.9%	1																									
IPI00955977	PGM1	phosphoglucomutase-1 isoform 3	100.0%	10.7	3	3	5	1	5,775,850	5,769,602	5,808,757	7,208,113	661,841	723,133	989,015	307,572	25.6	28.0	38.1	9.5	-1.0	1	1.0	1	1.2	0.09	1.0	1	1.2	0.1	1.2	0.2
				ADNFEYSDPVDGSISR	2	100.0%	1																									
				IALYETPTGWK	2	100.0%	2																									
				LSGTGSAGATIR	2	100.0%	2																									
IPI00956097	-	HCG2036932, isoform CRA_a	95.4%	39.0	1	1	1	1	9,909,200	9,623,880	10,118,730	9,734,910	801,186	125,210	301,214	323,324	18.1	2.9	6.7	7.4	-1.0	0.7	1.0	0.8	-1.0	0.8	1.1	0.2	1.0	0.8	-1.0	0.4
				MINQHSSICIQCSRSR	3	95.4%	1																									
IPI00956389	BBS1	cDNA FLJ53282, highly similar to Dipeptidyl-peptidase 3	100.0%	12.1	4	4	4	3	1,048,649	993,270	1,085,759	1,181,016	86,583	54,529	56,744	54,144	18.5	12.3	11.7	10.3	-1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.04	1.1	0.3
IPI00956436	BBS1	Dipeptidylpeptidase III isoform 1 variant (Fragment)	100.0%	10.5	4	4	4	3	1,048,649	993,270	1,085,759	1,181,016	86,583	54,529	56,744	54,144	18.5	12.3	11.7	10.3	-1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.04	1.1	0.3
IPI00956642	BBS1	Dipeptidylpeptidase III isoform 1 variant (Fragment)	100.0%	10.5	4	4	4	3	1,048,649	993,270	1,085,759	1,181,016	86,583	54,529	56,744	54,144	18.5	12.3	11.7	10.3	-1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.3	1.2	0.04	1.1	0.3
				AGLLALEFYTPEAFNWR	2	100.0%	1																									
				GPIVESYIGFIESYR	2	99.6%	1																									
				LEGSDVQLLEYEASAAGLIR	2	100.0%	1																									
				VLLEAGEGLVTITPTTGSDGRPDAR	3	100.0%	1																									
IPI00956392	HMGCS2	Mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase	99.2%	5.8	1	1	1	1	13,393,400	13,221,750	13,386,500	16,378,400	1,067,974	398,396	1,171,117	583,817	17.8	6.7	19.6	8.0	-1.0	0.9	-1.0	1	1.2	0.04	1.0	0.9	1.2	0.002	1.2	0.05
				PTGGAGAVAMLIGPK	2	99.2%	1																									
IPI00956475	SEBOX	cDNA FLJ51266, highly similar to Vitronectin	100.0%	12.6	2	2	3	1	3,978,030	4,598,210	4,078,505	5,308,200	290,973	361,857	245,043	338,851	16.4	17.6	13.4	14.3	1.2	0.2	1.0	0.8	1.3	0.02	-1.1	0.3	1.2	0.2	1.3	0.02
				DVWGIEGPIDAAFTR	2	100.0%	2																									
				FEDGVLDPDYPR	2	98.1%	1																									
IPI00956601	UGDH	UDP-glucose 6-dehydrogenase isoform 2	100.0%	47.3	14	16	19	1	25,668,150	25,337,186	26,337,627	28,757,991	1,913,394	928,225	1,608,535	762,693	16.7	8.2	13.7	5.9	-1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.6	1.1	0.02	1.1	0.2
				AVQALCAVYEHWVPR	3	99.7%	1																									
				DVLNLVYLCEALNLPEVAR	2	100.0%	1																									
				DVLNLVYLCEALNLPEVAR	3	100.0%	1																									
				EQIVVDLSHPGVSEDDQVSR	3	99.9%	2																									

				IAILGFAFK	2	100.0%	1																									
				IIDSLFNTVTDKK	2	98.9%	1																									
				ILTTNTWSSELSK	2	100.0%	1																									
				INAWNSPTLPIYEPGLK	2	100.0%	2																									
				ISSINSISALCEATGADVEEVATAIGMDQR	3	100.0%	1																									
				LAANAFLAQR	2	100.0%	1																									
				MLKPAFIFDGR	3	100.0%	1																									
				VLDGLHNELQTIGFQIETIGK	2	100.0%	1																									
				VLDGLHNELQTIGFQIETIGK	3	100.0%	1																									
				VLDGLHNELQTIGFQIETIGKK	3	99.9%	1																									
				VTVVDVNESR	2	100.0%	1																									
				YWQQVIDMNDYQR	2	100.0%	2																									
IPI00963816	PAICS	Uncharacterized protein	100.0%	13.2	4	4	4	1	8,243,880	7,985,603	8,161,536	8,845,188	711,538	306,199	756,025	476,023	19.3	8.6	20.7	12.0	-1.0	0.7	-1.0	0.9	1.1	0.5	1.0	0.8	1.1	0.2	1.1	0.5
				ASILNTWISLK	2	100.0%	1																									
				EIVLADVIDNDSWR	2	99.7%	1																									
				EVTPEGLQMVK	2	98.5%	1																									
				NFEWVAER	2	99.9%	1																									
IPI00963822	11-Sep	Uncharacterized protein	100.0%	5.7	2	2	2	3	1,289,451	1,239,419	1,269,696	1,143,059	114,261	24,898	55,823	83,000	19.8	4.5	9.8	16.2	-1.0	0.7	-1.0	0.9	-1.1	0.3	1.0	0.6	-1.1	0.3	-1.1	0.2
IPI00964658	11-Sep	Uncharacterized protein	100.0%	16.7	2	2	2	3	1,289,451	1,239,419	1,269,696	1,143,059	114,261	24,898	55,823	83,000	19.8	4.5	9.8	16.2	-1.0	0.7	-1.0	0.9	-1.1	0.3	1.0	0.6	-1.1	0.3	-1.1	0.2
IPI00964663	11-Sep	Uncharacterized protein	100.0%	15.4	2	2	2	3	1,289,451	1,239,419	1,269,696	1,143,059	114,261	24,898	55,823	83,000	19.8	4.5	9.8	16.2	-1.0	0.7	-1.0	0.9	-1.1	0.3	1.0	0.6	-1.1	0.3	-1.1	0.2
				STLMDTLFNTK	2	97.9%	1																									
				SYELQESNVR	2	98.9%	1																									
IPI00963851	LAP3	23 kDa protein	100.0%	11.5	2	2	2	1	2,618,816	2,794,243	2,452,142	2,915,801	194,143	165,213	82,141	102,086	16.6	13.2	7.5	7.8	1.1	0.5	-1.1	0.5	1.1	0.2	-1.1	0.1	1.0	0.5	1.2	0.008
				GITFDSGGISIK	2	99.9%	1																									
				LYGSGDQEAWQK	2	99.5%	1																									
IPI00963877	DBN1	Uncharacterized protein	99.5%	16.1	1	1	1	1	795,182	764,057	963,437	960,717	92,906	62,517	71,146	74,542	26.1	18.3	16.5	17.4	-1.0	0.8	1.2	0.2	1.2	0.2	1.3	0.07	1.3	0.08	-1.0	1
				YVLINWVGEDVPDAR	2	99.5%	1																									
IPI00963908	GNPDA1	Uncharacterized protein	98.0%	7.6	2	2	2	1	2,112,436	2,192,055	2,215,211	2,257,537	209,621	150,678	139,446	83,099	22.2	15.4	14.1	8.2	1.0	0.8	1.0	0.7	1.1	0.5	1.0	0.9	1.0	0.7	1.0	0.8
				IIQFNPGPEK	2	95.4%	1																									
				TFNMDEYVGLPR	2	98.0%	1																									
IPI00963912	RPS3A;SNORD73A	Uncharacterized protein	100.0%	17.8	2	2	2	6	663,975	681,225	671,176	669,036	40,076	23,235	47,977	29,795	13.5	7.6	16.0	10.0	1.0	0.7	1.0	0.9	1.0	0.9	-1.0	0.9	-1.0	0.8	-1.0	1
IPI00965481	RPS3A;SNORD73A	Uncharacterized protein	100.0%	27.7	2	2	2	6	663,975	681,225	671,176	669,036	40,076	23,235	47,977	29,795	13.5	7.6	16.0	10.0	1.0	0.7	1.0	0.9	1.0	0.9	-1.0	0.9	-1.0	0.8	-1.0	1
IPI00965772	RPS3A;SNORD73A	22 kDa protein	100.0%	9.5	2	2	2	6	663,975	681,225	671,176	669,036	40,076	23,235	47,977	29,795	13.5	7.6	16.0	10.0	1.0	0.7	1.0	0.9	1.0	0.9	-1.0	0.9	-1.0	0.8	-1.0	1
IPI00966860	RPS3A;SNORD73A	Uncharacterized protein	100.0%	8.8	2	2	2	6	663,975	681,225	671,176	669,036	40,076	23,235	47,977	29,795	13.5	7.6	16.0	10.0	1.0	0.7	1.0	0.9	1.0	0.9	-1.0	0.9	-1.0	0.8	-1.0	1
IPI00967388	RPS3A;SNORD73A	Uncharacterized protein	100.0%	14.4	2	2	2	6	663,975	681,225	671,176	669,036	40,076	23,235	47,977	29,795	13.5	7.6	16.0	10.0	1.0	0.7	1.0	0.9	1.0	0.9	-1.0	0.9	-1.0	0.8	-1.0	1
IPI00967897	RPS3A;SNORD73A	Uncharacterized protein	100.0%	19.0	2	2	2	6	663,975	681,225	671,176	669,036	40,076	23,235	47,977	29,795	13.5	7.6	16.0	10.0	1.0	0.7	1.0	0.9	1.0	0.9	-1.0	0.9	-1.0	0.8	-1.0	1
				VFEVSLADLQNDEVAFR	2	100.0%	1																									
				VFEVSLADLQNDEVAFRK	3	99.9%	1																									
IPI00963963	SFXN1	Uncharacterized protein	100.0%	23.2	1	1	2	1	1,400,615	1,535,125	1,278,275	1,677,578	230,113	60,626	116,392	67,012	36.7	8.8	20.4	8.9	1.1	0.6	-1.1	0.6	1.2	0.3	-1.2	0.09	1.1	0.2	1.3	0.02
				NILLTNEQLESAR	2	100.0%	2																									
IPI00963980	HNRNPD	Uncharacterized protein	100.0%	21.3	4	4	8	1	1,710,625	1,859,307	1,641,053	2,056,215	160,814	78,716	96,978	59,557	21.0	9.5	13.2	6.5	1.1	0.4	-1.0	0.7	1.2	0.1	-1.1	0.1	1.1	0.08	1.3	0.007
				ESESVDKVMDQK	2	99.9%	2																									
				GFGFVLFK	2	100.0%	2																									
				MFIGGLSWDTTK	2	100.0%	2																									
				MFIGGLSWDTTKK	2	100.0%	2																									
IPI00964062	PARP8	Uncharacterized protein	99.1%	2.6	2	2	2	5	1,330,680	1,602,816	1,770,462	1,636,900	109,217	99,162	154,060	46,262	18.4	13.8	19.5	6.3	1.2	0.1	1.3	0.05	1.2	0.03	1.1	0.4	1.0	0.8	-1.1	0.4
IPI00964299	PARP8	Uncharacterized protein	99.1%	2.6	2	2	2	5	1,330,680	1,602,816	1,770,462	1,636,900	109,217	99,162	154,060	46,262	18.4	13.8	19.5	6.3	1.2	0.1	1.3	0.05	1.2	0.03	1.1	0.4	1.0	0.8	-1.1	0.4
IPI00964996	PARP8	Uncharacterized protein	99.1%	2.7	2	2	2	5	1,330,680	1,602,816	1,770,462	1,636,900	109,217	99,162	154,060	46,262	18.4	13.8	19.5	6.3	1.2	0.1	1.3	0.05	1.2	0.03	1.1	0.4	1.0	0.8	-1.1	0.4
IPI00966012	PARP8	PARP8 protein	99.1%	4.2	2	2	2	5	1,330,680	1,602,816	1,770,462	1,636,900	109,217	99,162	154,060	46,262	18.4	13.8	19.5	6.3	1.2	0.1	1.3	0.05	1.2	0.03	1.1	0.4	1.0	0.8	-1.1	0.4
IPI01009901	PARP8	55 kDa protein	99.1%	4.5	2	2	2	5	1,330,680	1,602,816	1,770,462	1,636,900	109,217	99,162	154,060	46,262	18.4	13.8	19.5	6.3	1.2	0.1	1.3	0.05	1.2	0.03	1.1	0.4	1.0	0.8	-1.1	0.4
				RSPSYPPPGCGKSK	2	93.7%	1																									
				TDDVCVTK	2	86.3%	1																									
IPI00964070	ANXA3	Uncharacterized protein	100.0%	24.7	5	5	9	1	13,917,219	14,236,715	12,391,260	15,081,115	1,482,302	670,453	1,102,266	388,227	23.8	10.5	19.9	5.8	1.0	0.8	-1.1	0.4	1.1	0.5	-1.1	0.2	1.1	0.3	1.2	0.07
				GAGTNEDALIEILTTR	2	100.0%	2																									
				GIGTDEFTLNR	2	100.0%	2																									
				SDTSGDYEITLLK	2	100.0%	2																									
				SLGDDISSETSGDFR	2	100.0%	2																									
				WGTDEDKFTEILCLR	3	100.0%	1																									
IPI00964078	CTBP1	Protein	99.9%	20.0	2	2	2	1	4,844,882	4,202,000	4,108,010	4,580,538	603,355	883,394	841,631	875,577	27.9	47.0	45.8	42.7	-1.2	0.6	-1.2	0.5	-1.1	0.8	-1.0	0.9	1.1	0.8	1.1	0.7
				AFGFNVLFYDPYLSDGVER	2	100.0%	1																									
				QGAFLVNTAR	2	90.2%	1																									
IPI00964079	CCT5	Uncharacterized protein	100.0%	50.2	17	17	19	2	16,425,143	17,570,349	16,616,707	19,387,093	1,791,178	811,503	1,225,717	863,132	24.4	10.3	16.5	10.0	1.1	0.6	1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00965269	CCT5	cDNA, FLJ79275, highly similar to T-complex protein 1 subunit epsilon	100.0%	51.9	17	17	19	2	16,425,143	17,570,349	16,616,707	19,387,093	1,791,178	811,503	1,225,717	863,132	24.4	10.3	16.5	10.0	1.1	0.6	1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.2	1.2	0.1
				AFADALEVIPMALSENSGMNPIQTMTEVR	2	97.8%	1																									
				DVDFELIKVEGK	2	90.8%	1																									
				EKFEEMIQQIK	2	98.5%	1																									
				ETGANLAICQWGFDDEANHLLLQNNLPAVR	3	100.0%	1																									
				FEEMIQQIK	2	99.5%	1																									
				FSELTAEK	2	98.2%	1																									
				GVIVDKDFSHPQMPK	3	88.5%	1																									
				HKLDVTSVEDYK	3	94.2%	1																									
				IADGYEQAAR	2	100.0%	1																									
				ISDSVLVDIKDTEPLIQTAK	3	100.0%	1																									
				LDVTSVEDYK	2	100.0%	1																									
				LGFAGLVQEISFGTTK	2	100.0%	2																									
				MMVDKDGDVTVTNDGATILSMMDVDHQIAK	3	99.8%	1																									
				QMAEIAVNAVLTVADMER	3	99.8%	1																									
				QQISLATQMVR	2	98.4%	1																									
				VVYGGGAAEISCALAVSQEADK	3	92.9%	1																									
				WVGGPEIELIAIATGGR	2	100.0%	2																									
IPI00964123	PAICS	Uncharacterized protein	100.0%	8.2	3	3	3	1	2,710,871	2,815,262	2,868,816	3,159,310	286,381	141,380	264,707	85,169	23.6	11.2	20.6	6.0	1.0	0.8	1.1	0.7	1.2	0.2	1.0	0.9	1.1	0.07	1.1	0.3
				EVTPEGLQMVK	2	98.5%	1																									
				ITSCIFQLLQEAGIK	2	100.0%	1																									
				NFEWVAER	2	99.9%	1																									
IPI00964151	ADD1	Uncharacterized protein	100.0%	16.0	7	7	9	1	16,417,490	17,650,097	15,194,870	16,966,805	1,552,110	922,821	1,073,617	1,324,440	21.1	11.7	15.8	17.5	1.1	0.5	-1.1	0.5	1.0	0.8	-1.2	0.1	-1.0	0.7	1.1	0.3
				INLQGDIVDR	2	99.9%	1																									
				LEEAGDGCAREYLLP	3	81.7%	1																									
				NMAPDLRQDFNMMEQKK	3	97.6%	1																									
				SLVQGELVTASK	2	99.7%	2																									
				TAGPQSQVLCGVVMDR	2	99.9%	1																									
				TLASAGGPDNLVLLNPEK	2	100.0%	1																									
				WQIGEQEFEALMR	2	100.0%	2																									
IPI00964204	ADD1	Uncharacterized protein	100.0%	17.5	1	1	1	1	110,264	105,114	130,655	136,436	24,587	13,928	25,497	4,137	49.9	29.6	43.6	6.8	-1.0	0.9	1.2	0.6	1.2	0.4	1.2	0.4	1.3	0.09	1.0	0.8
				VSMILQSPAFCEELESMIQEQFKK	3	100.0%	1																									
IPI00964232	SUB1	cDNA FLJ51816, highly similar to Activated RNA polymerase II transcriptional coacti	100.0%	17.9	2	2	4	1	6,764,425	7,080,405	6,657,915	7,243,210	503,098	399,932	415,132	159,770	16.6	12.6	13.9	4.9	1.0	0.6	-1.0	0.9	1.1	0.4	-1.1	0.5	1.0	0.7	1.1	0.2
				DDNMFQIGK	2	100.0%	2																									
				GISLNPEQWSQLK	2	100.0%	2																									
IPI00964254	ACSL1	33 kDa protein	92.3%	3.7	1	1	1	1	457,491	485,279	444,542	450,285	35,291	58,848	55,167	33,884	17.3	27.1	27.8	16.8	1.1	0.7	-1.0	0.8	-1.0	0.9	-1.1	0.6	-1.1	0.6	1.0	0.9
				LAQGEYIAPEK	2	92.3%	1																									
IPI00964267	SFXN1	Uncharacterized protein	100.0%	32.0	3	3	4	1	2,429,634	2,669,160	2,394,735	2,933,206	324,614	85,369	205,974	151,751	29.9	7.2	19.2	11.6	1.1	0.5	-1.0	0.9	1.2	0.2	-1.1	0.3	1.1	0.2	1.2	0.07
				NILLTNEQLESAR	2	100.0%	2																									
				QGIVPPGLTENELWR	2	100.0%	1																									
				SGDAPLTVNELGTAYVSATTGAVATALGLNALTK	3	100.0%	1																									
IPI00964308	CANX	Protein	100.0%	30.6	4	5	6	1	4,670,625	4,967,906	5,089,554	5,701,979	353,609	290,191	391,008	223,544	16.9	13.1	17.2	8.8	1.1	0.5	1.1	0.4	1.2	0.04	1.0	0.8	1.1	0.08	1.1	0.2
				APVPTGEVYFADSFDR	2	100.0%	2																									
				GTLSGWILSK	2	100.0%	1																									
				TPELNLDQFHDK	2	99.9%	1																									
				TPELNLDQFHDK	3	100.0%	1																									
				YDGKWEVEEMKESK	3	99.6%	1																									
IPI00964334	CTBP1	Uncharacterized protein	100.0%	20.8	2	2	2	4	628,952	646,088	623,105	717,661	56,798	35,379	49,847	43,372	20.2	12.2	17.9	13.5	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.2	0.2
IPI00964612	CTBP1	Uncharacterized protein	100.0%	24.6	2	2	2	4	628,952	646,088	623,105	717,661	56,798	35,379	49,847	43,372	20.2	12.2	17.9	13.5	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.2	0.2
IPI00966719	CTBP1	Uncharacterized protein	100.0%	29.0	2	2	2	4	628,952	646,088	623,105	717,661	56,798	35,379	49,847	43,372	20.2	12.2	17.9	13.5	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.2	0.2
IPI00968298	CTBP1	Uncharacterized protein	100.0%	22.5	2	2	2	4	628,952	646,088	623,105	717,661	56,798	35,379	49,847	43,372	20.2	12.2	17.9	13.5	1.0	0.8	-1.0	0.9	1.1	0.2	-1.0	0.7	1.1	0.2	1.2	0.2
				PLVALLDGR	2	99.9%	1																									
				SAGDLGIAVCNVPAASVEETADSTLCHILNLYR	3	96.3%	1																									
IPI00964335	ETF1	Uncharacterized protein	100.0%	13.7	1	1	2	2	1,341,940	1,358,106	1,312,340	1,760,508	121,677	103,453	155,711	48,354	20.3	17.0	26.5	6.1	1.0	0.9	-1.0	0.9	1.3	0.01	-1.0	0.8	1.3	0.008	1.3	0.04
IPI00967974	ETF1	Uncharacterized protein	100.0%	10.8	1	1	2	2	1,341,940	1,358,106	1,312,340	1,760,508	121,677	103,453	155,711	48,354	20.3	17.0	26.5	6.1	1.0	0.9	-1.0	0.9	1.3	0.01	-1.0	0.8	1.3	0.008	1.3	0.04
				LSVLGAITSVQQR	2	99.9%	2																									
IPI00964504	SNHG4;MATR3	Uncharacterized protein	100.0%	43.6	2	2	3	6	1,006,075	934,139	923,735	1,040,460	65,913	35,893	44,233	54,727	14.7	8.6	10.7	11.8	-1.1	0.4	-1.1	0.3	1.0	0.7	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00965961	SNHG4;MATR3	Uncharacterized protein	100.0%	72.3	2	2	3	6	1,006,075	934,139	923,735	1,040,460	65,913	35,893	44,233	54,727	14.7	8.6	10.7	11.8	-1.1	0.4	-1.1	0.3	1.0	0.7	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00966123	SNHG4;MATR3	Uncharacterized protein	100.0%	39.1	2	2	3	6	1,006,075	934,139	923,735	1,040,460	65,913	35,893	44,233	54,727	14.7	8.6	10.7	11.8	-1.1	0.4	-1.1	0.3	1.0	0.7	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00967777	SNHG4;MATR3	Uncharacterized protein	100.0%	31.8	2	2	3	6	1,006,075	934,139	923,735	1,040,460	65,913	35,893	44,233	54,727	14.7	8.6	10.7	11.8	-1.1	0.4	-1.1	0.3	1.0	0.7	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00968041	SNHG4;MATR3	Uncharacterized protein	100.0%	34.0	2	2	3	6	1,006,075	934,139	923,735	1,040,460	65,913	35,893	44,233	54,727	14.7	8.6	10.7	11.8	-1.1	0.4	-1.1	0.3	1.0	0.7	-1.0	0.9	1.1	0.1	1.1	0.1
IPI00968288	SNHG4;MATR3	Uncharacterized protein	100.0%	34.3	2	2	3	6	1,006,075	934,139	923,735	1,040,460	65,913	35,893	44,233	54,727	14.7	8.6	10.7	11.8	-1.1	0.4	-1.1	0.3	1.0	0.7	-1.0	0.9	1.1	0.1	1.1	0.1
				DLSAAGIGLLAAATQSLSMPASLGR	2	100.0%	2																									
				SFQQSSLSR	2	100.0%	1																									
IPI00964515	GNB2L1	Protein	100.0%	27.8	4	5	6	1	4,341,265	4,811,509	4,631,209	5,345,291	477,681	281,066	347,465	160,510	24.6	13.1	16.8	6.7	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.7	1.1	0.1	1.2	0.1
				DGQAMLWDLNEGK	2	100.0%	2																									
				FSPNSSNPIIVSCGWDK	2	100.0%	1																									
				IIVDELKQEVISTSSK	2	100.0%	1																									
				IIVDELKQEVISTSSK	3	99.9%	1																									
				VWQVTIGTR	2	100.0%	1																									
IPI00964535	HNRNPH1	Uncharacterized protein	100.0%	15.6	2	2	4	4	1,747,321	1,681,442	1,629,394	1,847,729	98,622	23,786	112,766	77,841	12.6	3.2	15.5	9.4	-1.0	0.5	-1.1	0.5	1.1	0.4	-1.0	0.7	1.1	0.1	1.1	0.1
IPI00967216	HNRNPH1	Uncharacterized protein	100.0%	19.6	2	2	4	4	1,747,321	1,681,442	1,629,394	1,847,729	98,622	23,786	112,766	77,841	12.6	3.2	15.5	9.4	-1.0	0.5	-1.1	0.5	1.1	0.4	-1.0	0.7	1.1	0.1	1.1	0.1
IPI00974526	HNRNPH1	Uncharacterized protein	100.0%	21.3	2	2	4	4	1,747,321	1,681,442	1,629,394	1,847,729	98,622	23,786	112,766	77,841	12.6	3.2	15.5	9.4	-1.0	0.5	-1.1	0.5	1.1	0.4	-1.0	0.7	1.1	0.1	1.1	0.1
IPI00982782	HNRNPH1	Uncharacterized protein	100.0%	33.0	2	2	4	4	1,747,321	1,681,442	1,629,394	1,847,729	98,622	23,786	112,766	77,841	12.6	3.2	15.5	9.4	-1.0	0.5	-1.1	0.5	1.1	0.4	-1.0	0.7	1.1	0.1	1.1	0.1
				HTGPNSPDTANDGFVR	2	100.0%	2																									
				STGEAFVQFASQEIAEK	2	100.0%	2																									
IPI00964598	COPB2	20 kDa protein	100.0%	9.6	1	1	1	1	1,021,957	1,048,033	986,617	1,049,523	27,456	44,840	79,697	43,351	6.0	9.6	18.1	9.2	1.0	0.6	-1.0	0.7	1.0	0.6	-1.1	0.5	1.0	1	1.1	0.5
				SVNGLAFYDWDNTELIR	2	100.0%	1																									
IPI00964643	SFXN1	Uncharacterized protein	100.0%	19.4	2	2	3	1	2,237,272	2,453,392	2,136,462	2,671,591	292,121	73,148	189,842	126,865	29.2	6.7	19.9	10.6	1.1	0.5	-1.0	0.8	1.2	0.2	-1.1	0.2	1.1	0.2	1.3	0.05
				NILLTNEQLESAR	2	100.0%	2																									
				QGIVPPGLTENELWR	2	100.0%	1																									
IPI00964725	SDHA	Protein	100.0%	11.1	1	1	2	1	253,995	229,726	275,431	321,456	28,167	19,941	23,069	6,355	24.8	19.4	18.7	4.4	-1.1	0.5	1.1	0.6	1.3	0.07	1.2	0.2	1.4	0.008	1.2	0.1
				LGANSLLDLVVFGR	2	100.0%	2																									
IPI00964764	SDHA	cDNA FLJ55072, highly similar to Succinate dehydrogenase (ubiquinone) flavoprote	100.0%	14.6	6	6	7	1	9,464,451	8,474,632	9,129,243	10,094,001	694,066	244,026	486,923	240,809	16.4	6.4	11.9	5.3	-1.1	0.2	-1.0	0.7	1.1	0.4	1.1	0.3	1.2	0.001	1.1	0.1
				GEGGILINSQGER	2	100.0%	1																									

				HTLSYVDVGTGK	2	100.0%	1																									
				LGANSLLDLVVFGR	2	100.0%	2																									
				NTVVATGGYGR	2	100.0%	1																									
				VGSVLQEGCGK	2	99.9%	1																									
				VSDSISAQYPVVDHEFDAVVVGAGGAGLR	3	93.8%	1																									
IPI00964790	GNB2L1	Protein	100.0%	18.6	3	4	5	2	3,435,365	3,618,833	3,550,627	3,981,133	301,304	157,329	258,278	76,158	19.6	9.7	16.3	4.3	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.8	1.1	0.07	1.1	0.2
IPI00964877	GNB2L1	Protein	100.0%	16.8	3	4	5	2	3,435,365	3,618,833	3,550,627	3,981,133	301,304	157,329	258,278	76,158	19.6	9.7	16.3	4.3	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.8	1.1	0.07	1.1	0.2
				DGQAMLWDLNEGK	2	100.0%	2																									
				FSPNSSNPIIVSCGWDK	2	100.0%	1																									
				IIVDELKQEVISTSSK	2	100.0%	1																									
				IIVDELKQEVISTSSK	3	99.9%	1																									
IPI00964854	SNHG4;MATR3	cDNA FLJ10526 fis, clone NT2RP2000931, highly similar to Matrin-3	100.0%	9.8	3	3	4	2	2,374,533	2,343,608	2,250,324	2,678,580	277,508	212,544	224,099	143,164	26.1	20.3	22.3	12.0	-1.0	0.9	-1.1	0.7	1.1	0.4	-1.0	0.8	1.1	0.2	1.2	0.1
IPI00965324	SNHG4;MATR3	matrin-3 isoform b	100.0%	8.9	3	3	4	2	2,374,533	2,343,608	2,250,324	2,678,580	277,508	212,544	224,099	143,164	26.1	20.3	22.3	12.0	-1.0	0.9	-1.1	0.7	1.1	0.4	-1.0	0.8	1.1	0.2	1.2	0.1
				SQAFIEMETR	2	100.0%	2																									
				VIHLSNLPHSGYSDSAVLK	3	100.0%	1																									
				YQLLQLVEPFGVISNHLILNK	3	100.0%	1																									
IPI00964855	CCT5	Uncharacterized protein	100.0%	47.6	17	17	19	2	16,947,453	18,520,315	17,491,727	20,312,287	1,819,877	798,962	1,322,051	899,040	24.0	9.7	16.9	9.9	1.1	0.5	1.0	0.8	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.1
IPI00965722	CCT5	cDNA FLJ52361, highly similar to T-complex protein 1 subunit epsilon	100.0%	50.4	17	17	19	2	16,947,453	18,520,315	17,491,727	20,312,287	1,819,877	798,962	1,322,051	899,040	24.0	9.7	16.9	9.9	1.1	0.5	1.0	0.8	1.2	0.1	-1.1	0.5	1.1	0.2	1.2	0.1
				AFADALEVIPMALSENSGMNPIQTMTEVR	2	97.8%	1																									
				DVDFELIKVEGK	2	90.8%	1																									
				EKFEEMIQQIK	2	98.5%	1																									
				ETGANLAICQWGFDDEANHLLLQNNLPAVR	3	100.0%	1																									
				FEEMIQQIK	2	99.5%	1																									
				FSELTAEK	2	98.2%	1																									
				GVIVDKDFSHPQMPK	3	88.5%	1																									
				HKLDVTSVEDYK	3	94.2%	1																									
				IADGYEQAAR	2	100.0%	1																									
				IAILTCPFEPPKPK	3	99.9%	1																									
				ISDSVLVDIKDTEPLIQTAK	3	100.0%	1																									
				LDVTSVEDYK	2	100.0%	1																									
				LGFAGLVQEISFGTTK	2	100.0%	2																									
				QMAEIAVNAVLTVADMER	3	99.8%	1																									
				QQISLATQMVR	2	98.4%	1																									
				VVYGGGAAEISCALAVSQEADK	3	92.9%	1																									
				WVGGPEIELIAIATGGR	2	100.0%	2																									
IPI00964862	SNHG4;MATR3	Protein	100.0%	9.3	2	2	3	1	1,495,757	1,397,280	1,464,404	1,721,700	176,402	169,020	153,314	112,454	26.4	27.1	23.4	14.6	-1.1	0.7	-1.0	0.9	1.2	0.3	1.0	0.8	1.2	0.1	1.2	0.2
				SQAFIEMETR	2	100.0%	2																									
				YQLLQLVEPFGVISNHLILNK	3	100.0%	1																									
IPI00964890	CTBP1	Protein	99.9%	13.6	2	2	2	1	1,302,723	1,630,595	1,364,584	1,648,510	119,821	84,184	131,915	93,926	20.6	11.5	21.6	12.7	1.3	0.06	1.0	0.7	1.3	0.05	-1.2	0.1	1.0	0.9	1.2	0.1
				AFGFNVLFYDPYLSDGVER	2	100.0%	1																									
				GAALDVHESEPFSFSQGPLK	3	89.9%	1																									
IPI00964927	UGDH	UDP-glucose 6-dehydrogenase isoform 3	100.0%	45.1	11	12	14	1	21,820,299	23,295,522	21,990,176	25,417,752	1,277,508	610,387	1,717,635	705,902	13.1	5.9	17.5	6.2	1.1	0.3	1.0	0.9	1.2	0.04	-1.1	0.5	1.1	0.05	1.2	0.1
				DVLNLVYLCEALNLPEVAR	3	100.0%	1																									
				EQIVVDLSHPGVSEDDQVSR	3	99.9%	2																									
				IFDANTKPNLNLQVLSNPEFLAEGTAIK	3	96.2%	1																									
				IIDSLFNTVTDKK	2	98.9%	1																									
				ILTTNTWSSELSK	2	100.0%	1																									
				ISSINSISALCEATGADVEEVATAIGMDQR	3	100.0%	1																									
				LAANAFLAQR	2	100.0%	1																									
				MLKPAFIFDGR	3	100.0%	1																									
				VLDGLHNELQTIGFQIETIGK	2	100.0%	1																									
				VLDGLHNELQTIGFQIETIGK	3	100.0%	1																									
				VLDGLHNELQTIGFQIETIGKK	3	99.9%	1																									
				YWQQVIDMNDYQR	2	100.0%	2																									
IPI00964936	CAMK2D	Protein	100.0%	24.2	2	2	2	1	467,386	471,714	440,406	485,237	27,375	12,466	31,284	19,693	13.1	5.9	15.9	9.1	1.0	0.9	-1.1	0.5	1.0	0.6	-1.1	0.4	1.0	0.6	1.1	0.3
				ICDPGLTAFEPEALGNLVEGMDFHR	3	100.0%	1																									
				VTEQLIEAINNGDFEAYTK	3	99.9%	1																									
IPI00965024	ACSL1	Uncharacterized protein	99.1%	2.3	1	1	1	2	1,194,574	1,230,543	1,287,459	1,270,113	51,827	47,190	44,360	58,023	9.7	8.6	7.7	10.2	1.0	0.6	1.1	0.2	1.1	0.4	1.0	0.4	1.0	0.6	-1.0	0.8
IPI00965595	ACSL1	Acyl-CoA synthetase long-chain family member 1 isoform c	99.1%	9.6	1	1	1	2	1,194,574	1,230,543	1,287,459	1,270,113	51,827	47,190	44,360	58,023	9.7	8.6	7.7	10.2	1.0	0.6	1.1	0.2	1.1	0.4	1.0	0.4	1.0	0.6	-1.0	0.8
				IGFFQGDIR	2	99.1%	1																									
IPI00965185	AIMP1	Uncharacterized protein	100.0%	20.7	2	2	2	1	5,234,920	5,042,703	6,148,073	5,213,460	283,069	340,930	390,504	287,804	12.1	15.1	14.2	12.3	-1.0	0.7	1.2	0.09	-1.0	1	1.2	0.07	1.0	0.7	-1.2	0.09
				EIEELKQELIQAEIQNGVK	3	100.0%	1																									
				GAEADQIIEYLK	2	100.0%	1																									
IPI00965254	BTF3	Uncharacterized protein	100.0%	26.6	2	3	4	2	12,175,142	12,214,179	11,501,393	13,671,405	587,946	652,644	784,389	615,451	10.8	12.0	15.3	10.1	1.0	1	-1.1	0.5	1.1	0.1	-1.1	0.5	1.1	0.1	1.2	0.06
IPI00967045	BTF3	9 kDa protein	100.0%	34.1	2	3	4	2	12,175,142	12,214,179	11,501,393	13,671,405	587,946	652,644	784,389	615,451	10.8	12.0	15.3	10.1	1.0	1	-1.1	0.5	1.1	0.1	-1.1	0.5	1.1	0.1	1.2	0.06
				LAEALPK	2	85.4%	1																									
				QLTEMLPSILNQLGADSLTSLR	2	100.0%	2																									
				QLTEMLPSILNQLGADSLTSLR	3	100.0%	1																									
IPI00965306	CDV3	Uncharacterized protein	99.9%	34.8	1	1	1	1	388,270	419,796	366,274	424,047	43,464	26,686	32,639	27,343	25.0	14.2	19.9	14.4	1.1	0.6	-1.1	0.7	1.1	0.5	-1.1	0.2	1.0	0.9	1.2	0.2
				TAPVQAPPAPVIVTETPEPAMTSGVYRPPGAR	3	98.7%	1																									
IPI00965314	ABCE1	Uncharacterized protein	100.0%	13.8	4	4	4	1	7,181,738	8,165,502	7,260,125	8,063,630	509,276	414,590	433,219	413,564	15.9	11.4	13.3	11.5	1.1	0.2	1.0	0.9	1.1	0.2	-1.1	0.2	-1.0	0.9	1.1	0.2
				ADIFMFDEPSSYLDVK	2	100.0%	1																									
				CPFGALSIVNLPSNLEK	2	99.0%	1																									
				IAIVNHDK	2	95.7%	1																									
				VAETANEEEVKKMCMYK	3	82.5%	1																									
IPI00965316	DBN1	Uncharacterized protein	93.4%	5.1	1	1	1	2	933,550	964,138	883,452	1,068,782	166,119	58,964	103,961	49,907	39.8	13.7	26.3	10.4	1.0	0.9	-1.1	0.8	1.1	0.5	-1.1	0.5	1.1	0.2	1.2	0.1
IPI01012874	DBN1	40 kDa protein	93.4%	5.3	1	1	1	2	933,550	964,138	883,452	1,068,782	166,119	58,964	103,961	49,907	39.8	13.7	26.3	10.4	1.0	0.9	-1.1	0.8	1.1	0.5	-1.1	0.5	1.1	0.2	1.2	0.1
				SESEVEEAAAIIAQRPDNPR	3	93.4%	1																									
IPI00965327	SDHA	Uncharacterized protein	100.0%	13.6	5	5	6	1	6,197,316	5,266,352	6,532,218	6,631,786	453,220	125,647	313,002	325,190	16.4	5.3	10.7	11.0	-1.2	0.1	1.1	0.6	1.1	0.5	1.2	0.006	1.3	0.01	1.0	0.8
				GEGGILINSQGER	2	100.0%	1																									
				HTLSYVDVGTGK	2	100.0%	1																									
				LGANSLLDLVVFGR	2	100.0%	2																									
				NTVVATGGYGR	2	100.0%	1																									
				VSDSISAQYPVVDHEFDAVVVGAGGAGLR	3	93.8%	1																									
IPI00965336	HSD17B4	cDNA FLJ36730 fis, clone UTERU2012610, highly similar to Peroxisomal multifuncti	100.0%	5.7	2	2	3	2	1,164,847	1,211,014	1,427,873	1,199,886	52,670	122,357	195,715	59,300	10.1	22.6	30.7	11.1	1.0	0.7	1.2	0.3	1.0	0.7	1.2	0.4	-1.0	0.9	-1.2	0.3
IPI00966832	HSD17B4	Uncharacterized protein	100.0%	5.7	2	2	3	2	1,164,847	1,211,014	1,427,873	1,199,886	52,670	122,357	195,715	59,300	10.1	22.6	30.7	11.1	1.0	0.7	1.2	0.3	1.0	0.7	1.2	0.4	-1.0	0.9	-1.2	0.3
				LGLLGLANSLAIEGR	2	100.0%	2																									
				SMMGGGLAEIPGLSINFAK	2	100.0%	1																									
IPI00965403	ADD1	Uncharacterized protein	100.0%	7.0	1	1	1	1	2,811,318	3,107,967	2,680,850	2,826,017	234,633	192,544	87,693	116,439	18.7	13.9	7.3	9.2	1.1	0.4	-1.0	0.6	1.0	1	-1.2	0.08	-1.1	0.2	1.1	0.3
				INLQGDIVDR	2	99.9%	1																									
IPI00965405	CTBP1	Uncharacterized protein	100.0%	5.4	1	1	1	1	577,335	594,382	561,393	641,080	48,355	32,969	39,721	39,342	18.7	12.4	15.8	13.7	1.0	0.8	-1.0	0.8	1.1	0.3	-1.1	0.5	1.1	0.4	1.1	0.2
				PLVALLDGR	2	99.9%	1																									
IPI00965445	FIP1L1	95 kDa protein	99.9%	5.2	3	3	3	1	15,699,607	16,760,825	14,154,730	17,184,922	1,589,085	1,311,953	1,034,114	917,126	22.6	17.5	16.3	11.9	1.1	0.6	-1.1	0.4	1.1	0.4	-1.2	0.2	1.0	0.8	1.2	0.06
				KKSMLDSEVK	3	84.8%	1																									
				KPGADLSDYFNYGFNEDTWK	3	99.7%	1																									
				MGLEVIPVTSTTNK	2	93.9%	1																									
IPI00965459	GNB2L1	30 kDa protein	100.0%	28.9	5	6	7	2	5,611,285	6,213,231	5,948,864	6,926,456	649,095	318,490	454,781	216,091	25.9	11.5	17.1	7.0	1.1	0.4	1.1	0.7	1.2	0.1	-1.0	0.6	1.1	0.1	1.2	0.09
IPI00967792	GNB2L1	Uncharacterized protein	100.0%	29.4	5	6	7	2	5,611,285	6,213,231	5,948,864	6,926,456	649,095	318,490	454,781	216,091	25.9	11.5	17.1	7.0	1.1	0.4	1.1	0.7	1.2	0.1	-1.0	0.6	1.1	0.1	1.2	0.09
				DGQAMLWDLNEGK	2	100.0%	2																									
				FSPNSSNPIIVSCGWDK	2	100.0%	1																									
				GHNGWVTQIATTPQFPDMILSASR	3	100.0%	1																									
				IIVDELKQEVISTSSK	2	100.0%	1																									
				IIVDELKQEVISTSSK	3	99.9%	1																									
				VWQVTIGTR	2	100.0%	1																									
IPI00965474	NLN	NLN protein	99.4%	1.8	1	1	1	2	1,633,126	1,588,898	1,643,700	2,091,634	150,386	127,855	256,365	257,336	20.6	18.0	34.9	27.5	-1.0	0.8	1.0	1	1.3	0.2	1.0	0.9	1.3	0.1	1.3	0.3
IPI01015957	NLN	70 kDa protein	99.4%	1.8	1	1	1	2	1,633,126	1,588,898	1,643,700	2,091,634	150,386	127,855	256,365	257,336	20.6	18.0	34.9	27.5	-1.0	0.8	1.0	1	1.3	0.2	1.0	0.9	1.3	0.1	1.3	0.3
				VTAFLDDLSQK	2	99.4%	1																									
IPI00965486	CAST	Uncharacterized protein	95.0%	20.9	1	1	1	1	274,198	311,287	311,522	267,670	18,396	33,050	32,109	19,271	15.0	23.7	23.1	16.1	1.1	0.4	1.1	0.3	-1.0	0.8	1.0	1	-1.2	0.3	-1.2	0.3
				SESELIDELSEDFDRSECK	3	95.0%	1																									
IPI00965501	CANX	cDNA FLJ54242, highly similar to Calnexin	100.0%	16.5	5	5	5	1	9,907,040	10,434,353	11,049,373	12,443,242	1,046,580	794,997	1,025,860	421,849	23.6	17.0	20.8	7.6	1.1	0.7	1.1	0.5	1.3	0.05	1.1	0.6	1.2	0.06	1.1	0.2
				CESAPGCGVWQRPVIDNPNYK	3	97.6%	1																									
				IPDPEAVKPDDWDEDAPAK	3	90.6%	1																									
				IVDDWANDGWGLK	2	98.1%	1																									
				KIPNPDFFEDLEPFR	3	100.0%	1																									
				TPELNLDQFHDK	3	100.0%	1																									
IPI00965502	CLTB	Uncharacterized protein	100.0%	8.0	1	1	2	1	2,320,857	2,249,087	2,185,973	2,553,010	197,882	167,358	175,383	52,181	19.1	16.6	17.9	4.6	-1.0	0.8	-1.1	0.6	1.1	0.3	-1.0	0.8	1.1	0.1	1.2	0.1
				VAQLCDFNPK	2	99.9%	2																									
IPI00965597	DBN1	Uncharacterized protein	99.5%	11.0	2	2	2	1	1,728,732	1,728,195	1,846,888	2,029,498	220,475	94,209	154,388	89,927	28.5	12.2	18.7	9.9	-1.0	1	1.1	0.7	1.2	0.2	1.1	0.5	1.2	0.05	1.1	0.3
				SESEVEEAAAIIAQRPDNPR	3	93.4%	1																									
				YVLINWVGEDVPDAR	2	99.5%	1																									
IPI00965828	11-Sep	Protein	100.0%	18.1	2	2	2	1	2,111,793	2,327,665	2,053,377	2,434,989	236,251	129,483	215,348	61,691	25.0	12.4	23.5	5.7	1.1	0.4	-1.0	0.9	1.2	0.2	-1.1	0.3	1.0	0.5	1.2	0.2
				AAAQLLQSQAQQSGAQQTK	3	100.0%	1																									
				RNEFLGELQK	3	95.2%	1																									
IPI00965916	ADD1	Protein	100.0%	13.3	4	4	6	1	2,829,848	3,097,426	2,532,080	3,077,050	240,540	172,817	253,190	200,107	19.0	12.5	22.4	14.5	1.1	0.4	-1.1	0.4	1.1	0.5	-1.2	0.1	-1.0	0.9	1.2	0.1
				SLVQGELVTASK	2	99.7%	2																									
				TAGPQSQVLCGVVMDR	2	99.9%	1																									
				TLASAGGPDNLVLLNPEK	2	100.0%	1																									
				WQIGEQEFEALMR	2	100.0%	2																									
IPI00965952	HNRNPD	Uncharacterized protein	100.0%	38.5	9	12	18	1	7,311,603	7,531,129	7,174,203	8,233,650	706,480	218,307	499,257	319,614	21.6	6.5	15.6	8.7	1.0	0.8	-1.0	0.9	1.1	0.3	-1.0	0.5	1.1	0.1	1.1	0.1
				ESESVDKVMDQK	2	99.9%	2																									
				EYFGGFGEVESIELPMDNK	2	100.0%	1																									
				EYFGGFGEVESIELPMDNK	3	100.0%	1																									
				FGEVVDCTLK	2	95.0%	2																									
				FGEVVDCTLKLDPITGR	3	99.9%	1																									
				GFGFVLFK	2	100.0%	2																									
				IFVGGLSPDTPEEK	2	100.0%	2																									
				IREYFGGFGEVESIELPMDNK	2	99.9%	1																									
				IREYFGGFGEVESIELPMDNK	3	100.0%	1																									
				MFIGGLSWDTTK	2	100.0%	2																									
				MFIGGLSWDTTKK	2	100.0%	2																									
				MFIGGLSWDTTKK	3	100.0%	1																									
IPI00966041	GNB2L1	Uncharacterized protein	100.0%	20.1	3	3	4	3	2,174,182	2,354,788	2,143,854	2,516,859	292,852	119,212	215,324	159,927	30.1	11.3	22.5	14.2	1.1	0.6	-1.0	0.9	1.2	0.3	-1.1	0.4	1.1	0.4	1.2	0.2
IPI00967322	GNB2L1	Uncharacterized protein	100.0%	13.0	3	3	4	3	2,174,182	2,354,788	2,143,854	2,516,859	292,852	119,212	215,324	159,927	30.1	11.3	22.5	14.2	1.1	0.6	-1.0	0.9	1.2	0.3	-1.1	0.4	1.1	0.4	1.2	0.2
IPI00967577	GNB2L1	Uncharacterized protein	100.0%	16.5	3	3	4	3	2,174,182	2,354,788	2,143,854	2,516,859	292,852	119,212	215,324	159,927	30.1	11.3	22.5	14.2	1.1	0.6	-1.0	0.9	1.2	0.3	-1.1	0.4	1.1	0.4	1.2	0.2
				DGQAMLWDLNEGK	2	100.0%	2																									
				FSPNSSNPIIVSCGWDK	2	100.0%	1																									
				LWNTLGVCK	2	96.6%	1																									

IPI00966084	COPS4	Uncharacterized protein	100.0%	21.5	4	5	5	1	4,708,702	5,193,946	5,401,537	5,873,219	410,414	366,320	375,630	189,690	19.5	15.8	15.6	7.2	1.1	0.4	1.1	0.2	1.2	0.03	1.0	0.7	1.1	0.1	1.1	0.3
				ATTADGSSILDR	2	96.6%	1																									
				IASQMITEGR	2	99.0%	1																									
				LYNNITFEELGALLEIPAAK	2	100.0%	1																									
				LYNNITFEELGALLEIPAAK	3	99.3%	1																									
				MNGFIDQIDGIVHFETR	3	99.9%	1																									
IPI00966101	ISOC1	Uncharacterized protein	100.0%	5.8	1	1	1	2	904,474	806,734	753,270	796,620	141,661	26,570	68,149	41,470	35.0	7.4	20.2	11.6	-1.1	0.5	-1.2	0.4	-1.1	0.5	-1.1	0.5	-1.0	0.8	1.1	0.6
IPI00966776	ISOC1	Uncharacterized protein	100.0%	5.9	1	1	1	2	904,474	806,734	753,270	796,620	141,661	26,570	68,149	41,470	35.0	7.4	20.2	11.6	-1.1	0.5	-1.2	0.4	-1.1	0.5	-1.1	0.5	-1.0	0.8	1.1	0.6
				YFGDIISVGQR	2	99.9%	1																									
IPI00966111	GNB2L1	Uncharacterized protein	100.0%	21.8	4	5	6	1	4,705,385	5,020,555	4,868,282	5,562,298	484,269	194,464	374,355	141,082	23.0	8.7	17.2	5.7	1.1	0.6	1.0	0.8	1.2	0.2	-1.0	0.7	1.1	0.05	1.1	0.1
				DGQAMLWDLNEGK	2	100.0%	2																									
				FSPNSSNPIIVSCGWDK	2	100.0%	1																									
				GHNGWVTQIATTPQFPDMILSASR	3	100.0%	1																									
				IIVDELKQEVISTSSK	2	100.0%	1																									
				IIVDELKQEVISTSSK	3	99.9%	1																									
IPI00966135	HINT1	Uncharacterized protein	100.0%	32.3	2	2	2	4	1,698,058	1,671,678	1,486,984	1,752,932	115,196	158,780	174,730	153,379	15.2	21.2	26.3	19.6	-1.0	0.9	-1.1	0.3	1.0	0.8	-1.1	0.5	1.0	0.7	1.2	0.3
IPI00967474	HINT1	Uncharacterized protein	100.0%	20.4	2	2	2	4	1,698,058	1,671,678	1,486,984	1,752,932	115,196	158,780	174,730	153,379	15.2	21.2	26.3	19.6	-1.0	0.9	-1.1	0.3	1.0	0.8	-1.1	0.5	1.0	0.7	1.2	0.3
IPI00967744	HINT1	Uncharacterized protein	100.0%	26.9	2	2	2	4	1,698,058	1,671,678	1,486,984	1,752,932	115,196	158,780	174,730	153,379	15.2	21.2	26.3	19.6	-1.0	0.9	-1.1	0.3	1.0	0.8	-1.1	0.5	1.0	0.7	1.2	0.3
IPI00968242	HINT1	Uncharacterized protein	100.0%	26.9	2	2	2	4	1,698,058	1,671,678	1,486,984	1,752,932	115,196	158,780	174,730	153,379	15.2	21.2	26.3	19.6	-1.0	0.9	-1.1	0.3	1.0	0.8	-1.1	0.5	1.0	0.7	1.2	0.3
				AQVARPGGDTIFGK	2	100.0%	1																									
				IIFEDDR	2	97.9%	1																									
IPI00966206	PDCD6	Protein	100.0%	28.9	3	3	4	1	5,811,460	5,857,610	5,547,320	6,291,707	419,425	282,409	419,209	387,066	16.1	10.8	16.9	13.8	1.0	0.9	-1.0	0.7	1.1	0.4	-1.1	0.6	1.1	0.4	1.1	0.2
				AGVNFSEFTGVWK	2	100.0%	2																									
				TYDRDNSGMIDKNELK	3	99.9%	1																									
				YITDWQNVFR	2	99.8%	1																									
IPI00966230	PAIP1	Uncharacterized protein	96.0%	4.5	1	1	1	1	1,536,040	1,625,533	1,646,222	1,599,707	159,463	115,179	131,203	57,952	23.2	15.8	17.8	8.1	1.1	0.7	1.1	0.6	1.0	0.7	1.0	0.9	-1.0	0.8	-1.0	0.8
				ADILQVGLR	2	96.0%	1																									
IPI00966482	COPS4	cDNA FLJ36919 fis, clone BRACE2003987, highly similar to COP9 signalosome cor	100.0%	16.5	4	4	4	1	8,925,360	9,666,665	9,446,335	11,204,341	1,082,599	643,203	708,245	389,581	27.1	14.9	16.8	7.8	1.1	0.6	1.1	0.7	1.3	0.1	-1.0	0.8	1.2	0.08	1.2	0.06
				AIQLSGAEQLEALK	2	99.9%	1																									
				ATTADGSSILDR	2	96.6%	1																									
				LYNNITFEELGALLEIPAAK	2	100.0%	1																									
				VISFEEQVASIR	2	98.2%	1																									
IPI00966516	RPS3A;SNORD73A	Uncharacterized protein	100.0%	23.5	3	3	3	2	3,253,305	3,594,515	3,390,002	3,891,371	135,106	167,364	205,387	253,450	9.3	10.4	13.6	14.6	1.1	0.2	1.0	0.6	1.2	0.06	-1.1	0.5	1.1	0.4	1.1	0.2
IPI00967641	RPS3A;SNORD73A	24 kDa protein	100.0%	16.4	3	3	3	2	3,253,305	3,594,515	3,390,002	3,891,371	135,106	167,364	205,387	253,450	9.3	10.4	13.6	14.6	1.1	0.2	1.0	0.6	1.2	0.06	-1.1	0.5	1.1	0.4	1.1	0.2
				ACQSIYPLHDVFVR	2	99.9%	1																									
				LMELHGEGSSSGK	2	99.6%	1																									
				MMEIMTR	2	88.7%	1																									
IPI00966528	HSD17B4	Uncharacterized protein	100.0%	2.5	1	1	1	1	340,626	368,637	367,376	397,081	54,948	46,671	30,342	30,530	36.1	28.3	18.5	17.2	1.1	0.7	1.1	0.7	1.2	0.4	-1.0	1	1.1	0.6	1.1	0.5
				VLQQFADNDVSR	2	100.0%	1																									
IPI00966648	SEC31A	Protein	99.9%	5.0	1	1	1	2	454,661	514,058	460,172	476,087	52,692	24,522	38,127	20,657	25.9	10.7	18.5	9.7	1.1	0.3	1.0	0.9	1.0	0.7	-1.1	0.3	-1.1	0.3	1.0	0.7
IPI00966669	SEC31A	Protein	99.9%	2.4	1	1	1	2	454,661	514,058	460,172	476,087	52,692	24,522	38,127	20,657	25.9	10.7	18.5	9.7	1.1	0.3	1.0	0.9	1.0	0.7	-1.1	0.3	-1.1	0.3	1.0	0.7
				TTFEDLIQR	2	98.3%	1																									
IPI00966657	SNHG4;MATR3	Uncharacterized protein	100.0%	30.7	9	9	13	1	6,949,708	6,781,074	7,011,246	7,629,885	458,523	220,338	540,297	374,003	14.8	7.3	17.2	11.0	-1.0	0.7	1.0	0.9	1.1	0.3	1.0	0.7	1.1	0.09	1.1	0.4
				DLDELSRYPEDKITPENLPQILLQLK	3	98.0%	1																									
				DLSAAGIGLLAAATQSLSMPASLGR	2	100.0%	2																									
				GDADQASNILASFGLSAR	2	100.0%	2																									
				GNLGAGNGNLQGPR	2	99.9%	1																									
				ITPENLPQILLQLK	2	100.0%	2																									
				SFQQSSLSR	2	100.0%	1																									
				SQESGYYDR	2	99.9%	1																									
				TEEGPTLSYGR	2	99.9%	2																									
				YQLLQLVEPFGVISNHLILNK	3	100.0%	1																									
IPI00966724	WDR1	Uncharacterized protein	100.0%	7.8	2	2	2	1	3,647,043	3,470,340	3,771,988	4,304,983	232,037	197,337	290,070	337,110	14.2	12.7	17.2	17.5	-1.1	0.6	1.0	0.7	1.2	0.1	1.1	0.4	1.2	0.07	1.1	0.3
				VFASLPQVER	2	89.8%	1																									
				YEYQPFAGK	2	99.7%	1																									
IPI00966770	COPS4	Uncharacterized protein	100.0%	19.1	6	7	7	1	11,629,483	12,470,644	12,207,692	14,328,561	1,252,033	784,126	784,557	307,731	24.1	14.1	14.4	4.8	1.1	0.6	1.0	0.7	1.2	0.1	-1.0	0.8	1.1	0.08	1.2	0.05
				AIQLSGAEQLEALK	2	99.9%	1																									
				ATTADGSSILDR	2	96.6%	1																									
				AVIEHNLLSASK	2	91.5%	1																									
				IASQMITEGR	2	99.0%	1																									
				LYNNITFEELGALLEIPAAK	2	100.0%	1																									
				LYNNITFEELGALLEIPAAK	3	99.3%	1																									
				VISFEEQVASIR	2	98.2%	1																									
IPI00966946	NSUN2	Uncharacterized protein	99.0%	7.9	1	1	1	1	2,384,653	2,108,020	2,903,460	2,859,950	199,643	350,071	109,551	263,438	18.7	37.1	8.4	20.6	-1.1	0.5	1.2	0.05	1.2	0.2	1.4	0.08	1.4	0.1	-1.0	0.9
				FHQFLVSETESGNISR	3	99.0%	1																									
IPI00967027	COPS4	Uncharacterized protein	100.0%	19.4	6	7	7	1	10,172,964	10,945,838	10,521,222	12,263,530	1,082,646	612,045	655,836	402,883	23.8	12.5	13.9	7.4	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.6	1.1	0.1	1.2	0.05
				AIQLSGAEQLEALK	2	99.9%	1																									
				AVIEHNLLSASK	2	91.5%	1																									
				IASQMITEGR	2	99.0%	1																									
				LYNNITFEELGALLEIPAAK	2	100.0%	1																									
				LYNNITFEELGALLEIPAAK	3	99.3%	1																									
				MNGFIDQIDGIVHFETR	3	99.9%	1																									
				VISFEEQVASIR	2	98.2%	1																									
IPI00967040	DBN1	Uncharacterized protein	99.5%	28.2	2	2	2	1	1,460,562	1,485,039	1,605,084	1,761,897	148,032	154,676	125,918	94,772	22.7	23.3	17.5	12.0	1.0	0.9	1.1	0.5	1.2	0.1	1.1	0.6	1.2	0.2	1.1	0.3
				LAASGEGGLQELSGHFENQK	3	95.7%	1																									
				YVLINWVGEDVPDAR	2	99.5%	1																									
IPI00967118	ABCE1	Uncharacterized protein	100.0%	11.9	2	2	2	1	4,464,523	5,111,427	4,426,820	5,157,640	373,494	317,006	308,046	265,756	18.7	13.9	15.6	11.5	1.1	0.2	-1.0	0.9	1.2	0.2	-1.2	0.2	1.0	0.9	1.2	0.1
				CPFGALSIVNLPSNLEK	2	99.0%	1																									
				IAIVNHDK	2	95.7%	1																									
IPI00967160	SNX2	Uncharacterized protein	98.8%	3.8	1	1	1	1	588,473	568,191	575,303	532,409	29,449	31,973	22,785	50,339	11.2	12.6	8.9	21.1	-1.0	0.7	-1.0	0.7	-1.1	0.4	1.0	0.9	-1.1	0.6	-1.1	0.5
				FSDFLGLHSK	3	98.8%	1																									
IPI00967345	GNB2L1	Protein	100.0%	62.3	5	5	6	1	5,722,296	6,439,854	5,677,025	7,191,373	835,618	379,574	598,758	163,916	32.7	13.2	23.6	5.1	1.1	0.5	-1.0	1	1.3	0.2	-1.1	0.3	1.1	0.1	1.3	0.06
				DGQAMLWDLNEGK	2	100.0%	2																									
				FSPNSSNPIIVSCGWDK	2	100.0%	1																									
				HLYTLDGGDIINALCFSPNR	3	99.9%	1																									
				TNHIGHTGYLNTVTVSPDGSLCASGGK	3	100.0%	1																									
				VWQVTIGTR	2	100.0%	1																									
IPI00967440	HARS	Uncharacterized protein	100.0%	20.0	1	1	1	1	507,203	577,816	382,753	522,948	109,422	54,531	45,266	81,133	48.2	21.1	26.4	34.7	1.1	0.6	-1.3	0.3	1.0	0.9	-1.5	0.02	-1.1	0.6	1.4	0.2
				ASAELIEEEVAK	2	100.0%	1																									
IPI00967443	11-Sep	10 kDa protein	100.0%	23.2	1	1	1	1	1,138,467	1,190,427	1,103,005	1,314,333	199,493	152,111	158,997	64,536	39.2	28.6	32.2	11.0	1.0	0.8	-1.0	0.9	1.2	0.4	-1.1	0.7	1.1	0.5	1.2	0.3
				AAAQLLQSQAQQSGAQQTK	3	100.0%	1																									
IPI00967451	CANX	Uncharacterized protein	100.0%	20.3	1	1	2	2	566,782	550,292	566,579	637,127	52,912	27,229	55,941	28,289	20.9	11.1	22.1	9.9	-1.0	0.8	-1.0	1	1.1	0.3	1.0	0.8	1.2	0.06	1.1	0.3
IPI00967720	CANX	Uncharacterized protein	100.0%	16.7	1	1	2	2	566,782	550,292	566,579	637,127	52,912	27,229	55,941	28,289	20.9	11.1	22.1	9.9	-1.0	0.8	-1.0	1	1.1	0.3	1.0	0.8	1.2	0.06	1.1	0.3
				APVPTGEVYFADSFDR	2	100.0%	2																									
IPI00967467	TPM3	33 kDa protein	100.0%	13.7	3	3	3	1	5,656,548	5,657,483	5,860,602	6,768,273	615,408	386,383	570,281	175,956	24.3	15.3	21.8	5.8	1.0	1	1.0	0.8	1.2	0.1	1.0	0.8	1.2	0.03	1.2	0.2
				ALKDEEKMELQEIQLK	3	100.0%	1																									
				KLVIIEGDLER	3	99.9%	1																									
				MLDQTLLDLNEM	2	100.0%	1																									
IPI00967473	DEK	Uncharacterized protein	98.2%	9.8	1	1	1	1	1,352,012	1,560,256	1,519,596	1,732,868	151,562	104,699	144,446	61,045	25.1	15.0	21.3	7.9	1.2	0.3	1.1	0.4	1.3	0.05	-1.0	0.8	1.1	0.2	1.1	0.2
				NVGQFSGFPFEK	2	99.0%	1																									
IPI00967506	ACSF2	cDNA FLJ50687, weakly similar to Long-chain-fatty-acid--CoA ligase	100.0%	2.4	1	1	1	1	864,984	783,842	722,666	815,460	51,975	36,135	52,767	36,165	13.4	10.3	16.3	9.9	-1.1	0.2	-1.2	0.09	-1.1	0.5	-1.1	0.4	1.0	0.6	1.1	0.2
				IMNMEAGTLAK	2	99.9%	1																									
IPI00967562	HNRNPD	Uncharacterized protein	100.0%	57.1	7	8	14	1	5,528,054	5,811,090	5,312,523	6,291,177	535,739	125,672	338,413	258,983	21.7	4.8	14.2	9.2	1.1	0.6	-1.0	0.7	1.1	0.2	-1.1	0.2	1.1	0.1	1.2	0.05
				ESESVDKVMDQK	2	99.9%	2																									
				FGEVVDCTLK	2	95.0%	2																									
				FGEVVDCTLKLDPITGR	3	99.9%	1																									
				GFGFVLFK	2	100.0%	2																									
				IFVGGLSPDTPEEK	2	100.0%	2																									
				MFIGGLSWDTTK	2	100.0%	2																									
				MFIGGLSWDTTKK	2	100.0%	2																									
				MFIGGLSWDTTKK	3	100.0%	1																									
IPI00967589	CAMK2D	22 kDa protein	100.0%	24.2	3	3	3	1	1,470,927	1,479,710	1,357,748	1,569,823	131,250	57,825	46,127	52,096	20.0	8.7	7.6	7.4	1.0	1	-1.1	0.5	1.1	0.5	-1.1	0.1	1.1	0.3	1.2	0.02
				AGAYDFPSPEWDTVTPEAK	2	100.0%	1																									
				STVASMMHR	2	87.2%	1																									
				VTEQLIEAINNGDFEAYTK	3	99.9%	1																									
IPI00967721	SNHG4;MATR3	Uncharacterized protein	100.0%	24.4	13	14	19	1	18,573,875	18,597,142	18,135,738	19,895,121	901,501	452,163	1,168,542	683,472	10.9	5.4	14.4	7.7	1.0	1	-1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.2	1.1	0.2
				DLDELSRYPEDKITPENLPQILLQLK	3	98.0%	1																									
				DLSAAGIGLLAAATQSLSMPASLGR	2	100.0%	2																									
				DSFDDRGPSLNPVLDYDHGSR	3	95.6%	1																									
				GDADQASNILASFGLSAR	2	100.0%	2																									
				GDADQASNILASFGLSAR	3	100.0%	1																									
				GNLGAGNGNLQGPR	2	99.9%	1																									
				ITPENLPQILLQLK	2	100.0%	2																									
				KDGSASAAAKK	2	91.3%	1																									
				SFQQSSLSR	2	100.0%	1																									
				SQAFIEMETR	2	100.0%	2																									
				TEEGPTLSYGR	2	99.9%	2																									
				VIHLSNLPHSGYSDSAVLK	3	100.0%	1																									
				VVHIMDFQR	3	99.9%	1																									
				YQLLQLVEPFGVISNHLILNK	3	100.0%	1																									
IPI00967902	C6orf108	26 kDa protein	100.0%	11.1	2	2	3	1	5,625,615	5,507,775	6,192,145	6,558,140	412,733	268,131	872,284	677,172	16.4	10.9	31.5	23.1	-1.0	0.8	1.1	0.6	1.2	0.3	1.1	0.5	1.2	0.2	1.1	0.7
				EGNGPGLGLR	2	93.0%	1																									
				FQVWDYEEGEVEALLDR	2	100.0%	2																									
IPI00968146	RPS3A;SNORD73A	Uncharacterized protein	100.0%	20.6	3	3	3	1	6,728,054	7,249,429	6,559,639	7,871,760	512,456	388,279	332,825	240,176	17.0	12.0	11.4	6.8	1.1	0.4	-1.0	0.8	1.2	0.08	-1.1	0.2	1.1	0.2	1.2	0.01
				ACQSIYPLHDVFVR	2	99.9%	1																									
				LITEDVQGK	2	96.4%	1																									
				VFEVSLADLQNDEVAFR	2	100.0%	1																									
IPI00968235	PPA2	Uncharacterized protein	100.0%	24.6	3	3	3	1	986,226	1,101,218	1,020,438	1,269,977	118,901	91,806	91,481	32,551	27.0	18.6	20.1	5.7	1.1	0.5	1.0	0.8	1.3	0.07	-1.1	0.6	1.2	0.1	1.2	0.05
				FKPGYLEATLNWFR	3	99.9%	1																									
				ILGILALIDEGETDWK	2	100.0%	1																									
				VPDGKPENQFAFNGEFK	3	95.7%	1																									
IPI00968273	DEK	Uncharacterized protein	98.2%	14.6	2	2	2	1	18,353,862	18,325,256	16,286,546	19,779,718	1,646,714	1,146,494	1,883,132	1,352,289	20.1	14.0	25.9	15.3	-1.0	1	-1.1	0.4	1.1	0.5	-1.1	0.4	1.1	0.4	1.2	0.2
				LTMQVSSLQR	2	92.7%	1																									
				NVGQFSGFPFEK	2	99.0%	1																									
IPI00968274	FAM114A1	Putative uncharacterized protein DKFZp686F20250	100.0%	9.8	2	2	2	1	4,134,390	4,179,380	3,852,025	4,296,480	264,781	229,136	235,664	139,320	14.3	12.3	13.7	7.3	1.0	0.9	-1.1	0.4	1.0	0.6	-1.1	0.3	1.0	0.7	1.1	0.1
				SVLTGGLDALEFIGK	2	99.8%	1																									
				VAELILHGQEEEKPAQDQAK	3	98.5%	1																									

IPI00969375	HADHB	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-C	100.0%	5.4	2	2	2	1	2,948,783	2,699,773	2,943,509	2,891,913	189,029	169,214	183,869	91,588	14.3	14.0	14.0	7.1	-1.1	0.4	-1.0	1	-1.0	0.8	1.1	0.4	1.1	0.3	-1.0	0.8
				LEQDEYALR	2	99.1%	1																									
				TPFLLSGTSYK	2	99.8%	1																									
IPI00969616	-	Desmoplakin Ia	100.0%	20.1	34	35	43	1	126,421,902	130,126,453	123,401,210	144,284,064	9,133,593	3,841,462	9,570,922	4,851,268	16.2	6.6	17.3	7.5	1.0	0.7	-1.0	0.8	1.1	0.1	-1.1	0.5	1.1	0.05	1.2	0.09
				AELIVQPELK	2	99.9%	1																									
				AFIGFEGVK	2	99.6%	1																									
				AITGFDDPFSGK	2	100.0%	2																									
				ALLQAILQTEDMLK	2	100.0%	1																									
				FGDSNTVMR	2	98.0%	1																									
				FLDQNLQKYQAECSQFKAK	3	87.6%	1																									
				FLEFQYLTGGLVDPEVHGR	3	100.0%	2																									
				GGGGYTCQSGSGWDEFTK	2	100.0%	1																									
				GIVDSITGQR	2	100.0%	1																									
				GLPSPYNMSSAPGSR	2	96.6%	1																									
				GYFNEELSEILSDPSDDTK	2	100.0%	2																									
				IEVLEEELR	2	96.8%	1																									
				IGLVRPGTALELLEAQAATGFIVDPVSNLR	3	100.0%	1																									
				IKDFLQGSSCIAGIYNETTK	3	99.9%	1																									
				IQSQFTDAQK	2	99.7%	1																									
				LGIYEAMK	2	99.9%	1																									
				LISPESTVMLLEAQAATGGIIDPHR	3	95.9%	1																									
				LLEAQIASGGVVDPVNSVFLPK	2	100.0%	2																									
				LLEAQIASGGVVDPVNSVFLPK	3	100.0%	1																									
				LLEAQIATGGIIDPK	2	100.0%	2																									
				LLQLQEQMR	2	99.8%	1																									
				LNDSILQATEQR	2	100.0%	1																									
				LSLQDAVSQGVIDQDMATR	2	100.0%	1																									
				LTVDSAIAR	2	99.9%	2																									
				QLQNIIQATSR	2	100.0%	1																									
				RQDSLESMK	2	99.8%	2																									
				SAIYQLEEEYENLLK	2	100.0%	1																									
				SGSLSLTQFADMISLK	2	100.0%	2																									
				SMVEDITGLR	2	98.3%	1																									
				SRELDECFAQANDQMEILDSLIR	3	100.0%	1																									
				TIADLELHYQEFIR	2	99.9%	1																									
				TMIQSPSGVILQEAADVHAR	3	100.0%	1																									
				TVSVSEAIKK	2	91.9%	1																									
				VLLQEEGTR	2	99.5%	1																									
				YGDGIQLTR	2	99.9%	1																									
IPI00971062	-	HNF1 alpha B splice variant 6	99.4%	15.3	1	1	1	3	47,728	42,718	44,821	49,576	7,512	5,069	2,862	4,827	35.2	26.5	14.3	21.8	-1.1	0.6	-1.1	0.7	1.0	0.8	1.0	0.7	1.2	0.4	1.1	0.4
IPI00972937	HNF1A	HNF1 alpha A splice variant 4	99.4%	16.0	1	1	1	3	47,728	42,718	44,821	49,576	7,512	5,069	2,862	4,827	35.2	26.5	14.3	21.8	-1.1	0.6	-1.1	0.7	1.0	0.8	1.0	0.7	1.2	0.4	1.1	0.4
IPI01013500	HNF1A	4 kDa protein	99.4%	46.3	1	1	1	3	47,728	42,718	44,821	49,576	7,512	5,069	2,862	4,827	35.2	26.5	14.3	21.8	-1.1	0.6	-1.1	0.7	1.0	0.8	1.0	0.7	1.2	0.4	1.1	0.4
				LSQLQTELLAALLESGLSK	2	99.4%	1																									
IPI00972980	CAPG	Uncharacterized protein	100.0%	11.5	3	3	4	1	3,454,110	3,783,930	3,439,520	4,148,435	412,606	278,612	380,925	289,917	26.7	16.5	24.8	15.6	1.1	0.5	-1.0	1	1.2	0.2	-1.1	0.5	1.1	0.4	1.2	0.2
				DLALAIR	2	95.0%	1																									
				EGNPEEDLTADK	2	99.9%	1																									
				EGNPEEDLTADKANAQAAALYK	3	99.9%	2																									
IPI00973068	MAT2B	Uncharacterized protein	100.0%	30.3	3	3	3	1	3,476,509	3,741,600	3,722,569	4,107,045	356,771	226,718	300,479	194,221	23.0	13.6	18.1	10.6	1.1	0.5	1.1	0.6	1.2	0.2	-1.0	1	1.1	0.3	1.1	0.3
				AVLENNLGAAVLR	2	100.0%	1																									
				IPILYGEVEKLEESAVTVMFDK	3	100.0%	1																									
				RPDVVENQPDAASQLNVDASGNLAK	3	99.9%	1																									
IPI00973560	STK39	Small intestine SPAK-like kinase	99.1%	2.9	1	1	1	1	325,960	254,069	248,630	378,111	49,931	38,525	31,505	41,740	34.3	33.9	28.3	24.7	-1.3	0.3	-1.3	0.2	1.2	0.4	-1.0	0.9	1.5	0.06	1.5	0.04
				NGVLEEAIIATILK	2	99.1%	1																									
IPI00973775	EIF3H	Uncharacterized protein	99.6%	7.0	1	1	2	2	483,633	466,625	525,663	503,093	45,933	61,555	56,309	33,696	21.2	29.5	24.0	15.0	-1.0	0.8	1.1	0.6	1.0	0.7	1.1	0.5	1.1	0.6	-1.0	0.7
IPI01011241	EIF3H	Uncharacterized protein	99.6%	7.2	1	1	2	2	483,633	466,625	525,663	503,093	45,933	61,555	56,309	33,696	21.2	29.5	24.0	15.0	-1.0	0.8	1.1	0.6	1.0	0.7	1.1	0.5	1.1	0.6	-1.0	0.7
				ANITFEYMFEEVPIVIK	2	99.6%	2																									
IPI00973785	TBCA	Uncharacterized protein	100.0%	12.7	1	1	1	1	1,734,705	1,696,305	1,659,233	2,003,568	120,684	62,532	108,334	74,279	15.6	8.2	14.6	8.3	-1.0	0.8	-1.0	0.7	1.2	0.09	-1.0	0.8	1.2	0.01	1.2	0.03
				LVLDSVKLEA	2	96.8%	1																									
IPI00973816	PSMD13	40 kDa protein	100.0%	12.9	3	3	3	3	2,316,250	2,296,838	2,486,175	2,649,755	198,689	107,281	190,066	79,286	19.2	10.4	17.1	6.7	-1.0	0.9	1.1	0.6	1.1	0.2	1.1	0.4	1.2	0.03	1.1	0.4
IPI00982005	PSMD13	Uncharacterized protein	100.0%	17.1	3	3	3	3	2,316,250	2,296,838	2,486,175	2,649,755	198,689	107,281	190,066	79,286	19.2	10.4	17.1	6.7	-1.0	0.9	1.1	0.6	1.1	0.2	1.1	0.4	1.2	0.03	1.1	0.4
IPI00982572	PSMD13	Protein	100.0%	20.4	3	3	3	3	2,316,250	2,296,838	2,486,175	2,649,755	198,689	107,281	190,066	79,286	19.2	10.4	17.1	6.7	-1.0	0.9	1.1	0.6	1.1	0.2	1.1	0.4	1.2	0.03	1.1	0.4
				ETIEDVEEMLNNLPGVTSVHSR	3	99.9%	1																									
				LNIGDLQVTK	2	93.1%	1																									
				YYQTIGNHASYYK	2	99.8%	1																									
IPI00973884	SKP1	Uncharacterized protein	100.0%	64.8	3	3	3	1	2,990,328	3,161,936	3,143,356	3,319,345	231,780	165,248	204,045	78,625	17.3	11.7	14.5	5.3	1.1	0.6	1.1	0.6	1.1	0.2	-1.0	0.9	1.0	0.4	1.1	0.5
				ELDQWIEQLNECK	2	100.0%	1																									
				LQSSDGEIFEVDVEIAK	2	100.0%	1																									
				TMLEDLGMDDEGDDDPVPLPNVNAAILKK	3	100.0%	1																									
IPI00973933	ERLIN2	Uncharacterized protein	100.0%	16.2	2	2	2	1	2,028,867	1,825,698	1,651,503	1,875,992	174,615	45,580	73,120	90,268	19.2	5.6	9.9	10.8	-1.1	0.3	-1.2	0.08	-1.1	0.5	-1.1	0.08	1.0	0.6	1.1	0.09
				LALQQDLTSMAPGLVIQAVR	3	99.9%	1																									
				VAQVAEITYGQK	2	99.7%	1																									
IPI00974072	-	Truncated glutaminase 2	93.3%	6.1	1	1	1	1	730,517	625,293	718,913	636,311	74,694	78,746	49,625	100,827	22.9	28.2	15.4	35.4	-1.2	0.4	-1.0	0.9	-1.1	0.5	1.1	0.3	1.0	0.9	-1.1	0.5
				MAGNEYMGFSNATAFLR	2	90.6%	1																									
IPI00974077	IKBKB	Uncharacterized protein	97.8%	31.2	2	2	2	1	9,963,450	8,876,090	9,336,590	10,575,670	657,802	440,856	566,763	289,596	14.8	11.1	13.6	6.1	-1.1	0.2	-1.1	0.5	1.1	0.4	1.1	0.5	1.2	0.01	1.1	0.09
				ERLGTGGFGNVIRWHNQDAALR	3	83.5%	1																									
				RLVCTLEVLHYR	3	86.6%	1																									
IPI00974078	PAFAH1B2	18 kDa protein	100.0%	11.4	1	1	1	1	783,381	975,995	712,704	782,909	96,943	117,562	147,782	112,149	27.7	26.9	46.4	32.0	1.2	0.2	-1.1	0.7	-1.0	1	-1.4	0.2	-1.2	0.3	1.1	0.7
				ICKPLHELIMQLLEETPEEK	3	99.8%	1																									
IPI00974080	EIF3E	Uncharacterized protein	100.0%	12.8	2	2	2	1	2,110,124	2,163,383	2,229,563	2,590,283	212,550	87,265	197,196	105,484	22.5	9.0	19.8	9.1	1.0	0.8	1.1	0.7	1.2	0.08	1.0	0.8	1.2	0.01	1.2	0.1
				LASEILMQNWDAAMEDLTR	2	100.0%	1																									
				YLTTAVITNK	2	95.7%	1																									
IPI00974151	EIF3E	Uncharacterized protein	100.0%	24.0	1	1	1	2	392,378	380,070	422,508	529,264	58,146	55,585	58,978	23,812	33.1	32.7	31.2	10.1	-1.0	0.9	1.1	0.7	1.3	0.06	1.1	0.6	1.4	0.04	1.3	0.1
IPI00977424	EIF3E	Protein	100.0%	24.3	1	1	1	2	392,378	380,070	422,508	529,264	58,146	55,585	58,978	23,812	33.1	32.7	31.2	10.1	-1.0	0.9	1.1	0.7	1.3	0.06	1.1	0.6	1.4	0.04	1.3	0.1
				LDLLSDTNMVDFAMDVYK	2	100.0%	1																									
IPI00980495	CDKL3	cDNA FLJ50492, highly similar to Cyclin-dependent kinase-like 3	100.0%	3.2	1	1	1	5	390,660	369,474	379,139	427,499	42,355	25,349	33,504	31,315	24.2	15.3	19.8	16.4	-1.1	0.7	-1.0	0.8	1.1	0.5	1.0	0.8	1.2	0.2	1.1	0.3
IPI00976419	PPP2CA	Serine/threonine-protein phosphatase	100.0%	11.9	1	1	1	5	390,660	369,474	379,139	427,499	42,355	25,349	33,504	31,315	24.2	15.3	19.8	16.4	-1.1	0.7	-1.0	0.8	1.1	0.5	1.0	0.8	1.2	0.2	1.1	0.3
IPI00984991	PPP2CA	Serine/threonine-protein phosphatase	100.0%	10.3	1	1	1	5	390,660	369,474	379,139	427,499	42,355	25,349	33,504	31,315	24.2	15.3	19.8	16.4	-1.1	0.7	-1.0	0.8	1.1	0.5	1.0	0.8	1.2	0.2	1.1	0.3
IPI00974178	PPP2CB	Serine/threonine-protein phosphatase	100.0%	8.2	1	1	1	5	390,660	369,474	379,139	427,499	42,355	25,349	33,504	31,315	24.2	15.3	19.8	16.4	-1.1	0.7	-1.0	0.8	1.1	0.5	1.0	0.8	1.2	0.2	1.1	0.3
IPI00985356	PPP2CB	Serine/threonine-protein phosphatase	100.0%	12.0	1	1	1	5	390,660	369,474	379,139	427,499	42,355	25,349	33,504	31,315	24.2	15.3	19.8	16.4	-1.1	0.7	-1.0	0.8	1.1	0.5	1.0	0.8	1.2	0.2	1.1	0.3
				SPDTNYLFMGDYVDR	2	100.0%	1																									
IPI00974396	TCEA1	Uncharacterized protein	100.0%	14.4	1	1	1	2	1,822,513	1,976,523	1,914,887	2,142,767	203,272	143,279	144,428	69,548	24.9	16.2	16.9	7.3	1.1	0.6	1.1	0.7	1.2	0.2	-1.0	0.8	1.1	0.3	1.1	0.2
IPI00975678	TCEA1	Uncharacterized protein	100.0%	11.7	1	1	1	2	1,822,513	1,976,523	1,914,887	2,142,767	203,272	143,279	144,428	69,548	24.9	16.2	16.9	7.3	1.1	0.6	1.1	0.7	1.2	0.2	-1.0	0.8	1.1	0.3	1.1	0.2
				NIPMTLELLQSTR	2	99.2%	1																									
IPI00974421	SREK1	Uncharacterized protein	99.4%	9.9	1	1	2	1	1,126,107	881,787	1,329,133	1,329,793	72,831	204,248	123,071	143,360	14.5	51.8	20.7	24.1	-1.3	0.3	1.2	0.2	1.2	0.2	1.5	0.1	1.5	0.1	1.0	1
				TLFSFLGEIEELR	2	99.4%	2																									
IPI00974484	RPS3	28 kDa protein	100.0%	34.8	7	7	9	1	9,580,427	10,607,130	9,765,388	10,790,688	1,118,591	649,952	918,577	573,480	26.1	13.7	21.0	11.9	1.1	0.5	1.0	0.9	1.1	0.4	-1.1	0.5	1.0	0.8	1.1	0.4
				AELNEFLTR	2	97.8%	1																									
				ELAEDGYSGVEVR	2	100.0%	2																									
				FVDGLMIHSGDPVNYYVDTAVR	3	100.0%	1																									
				GCEVVVSGK	2	99.8%	1																									
				GGKPEPPAMPQPVPTA	2	100.0%	2																									
				GLCAIAQAESLR	2	100.0%	1																									
				KFVADGIFK	2	96.7%	1																									
IPI00974544	YWHAE	isoform SV of 14-3-3 protein epsilon	100.0%	54.1	10	13	21	1	55,180,000	57,182,698	55,189,760	64,174,965	4,398,374	2,428,352	4,692,798	1,630,556	17.8	9.5	19.0	5.7	1.0	0.7	1.0	1	1.2	0.1	-1.0	0.7	1.1	0.04	1.2	0.1
				AAFDDAIAELDTLSEESYK	2	100.0%	2																									
				AAFDDAIAELDTLSEESYK	3	100.0%	2																									
				AASDIAMTELPPTHPIR	2	100.0%	1																									
				AASDIAMTELPPTHPIR	3	100.0%	3																									
				DNLTLWTSDMQGDGEEQNKEALQDVEDENQ	3	100.0%	1																									
				EAAENSLVAYK	2	100.0%	1																									
				HLIPAANTGESK	2	100.0%	2																									
				LICCDILDVLDK	2	100.0%	1																									
				LICCDILDVLDKHLIPAANTGESK	3	100.0%	1																									
				VAGMDVELTVEER	2	100.0%	2																									
				YLAEFATGNDR	2	100.0%	2																									
				YLAEFATGNDRK	2	100.0%	2																									
				YLAEFATGNDRK	3	99.9%	1																									
IPI00974560	G3BP1	Uncharacterized protein	100.0%	16.9	2	2	3	1	2,995,640	2,992,285	3,137,280	3,227,670	153,731	213,332	119,288	213,529	11.5	15.9	8.5	14.8	-1.0	1	1.0	0.5	1.1	0.4	1.0	0.6	1.1	0.5	1.0	0.7
				FMQTFVLAPEGSVANK	2	100.0%	1																									
				FYVHNDIFR	3	100.0%	2																									
IPI00974578	RBM4	Uncharacterized protein	100.0%	20.0	3	3	3	1	3,789,857	3,821,549	3,428,426	4,157,596	241,542	241,799	222,676	453,937	14.3	14.2	14.5	24.4	1.0	0.9	-1.1	0.3	1.1	0.5	-1.1	0.3	1.1	0.5	1.2	0.2
				ATAPVPTVGEGYGYGHESELSQASAAAR	3	99.9%	1																									
				GLDNTEFQGK	2	99.9%	1																									
				NYGFVHIEDK	2	99.2%	1																									
IPI00975486	RPS14	Uncharacterized protein	100.0%	7.5	1	2	2	2	2,060,780	2,296,550	2,191,010	2,763,673	261,279	245,186	253,279	100,300	28.4	23.9	25.9	8.1	1.1	0.5	1.1	0.7	1.3	0.05	-1.0	0.8	1.2	0.1	1.3	0.07
IPI00984977	RPS14	Protein	100.0%	8.3	1	2	2	2	2,060,780	2,296,550	2,191,010	2,763,673	261,279	245,186	253,279	100,300	28.4	23.9	25.9	8.1	1.1	0.5	1.1	0.7	1.3	0.05	-1.0	0.8	1.2	0.1	1.3	0.07
				ELGITALHIK	2	99.0%	1																									
				ELGITALHIK	3	99.8%	1																									
IPI00975549	CLINT1	clathrin interactor 1 isoform 1	100.0%	17.3	7	9	11	1	25,449,919	26,026,173	25,065,429	29,035,713	1,985,219	1,034,630	1,702,898	807,690	17.4	8.9	15.2	6.2	1.0	0.8	-1.0	0.9	1.1	0.1	-1.0	0.6	1.1	0.05	1.2	0.07
				ATFMYEQFPELMNMLWSR	2	100.0%	1																									
				ATFMYEQFPELMNMLWSR	3	100.0%	1																									
				ATNVVMNYSEIESK	2	100.0%	2																									
				HIHITQATETTTTR	2	96.6%	1																									
				HIHITQATETTTTR	3	100.0%	1																									
				IGSTIDDTISK	2	100.0%	1																									
				SQPLQNVSTVLQKPNPLYNQNTDMVQK	3	100.0%	1																									
				TIDLGAAAHYTGDK	2	99.9%	1																									
				YVGVSSDSVGGFR	2	100.0%	2																									
IPI00975639	DNM3	Uncharacterized protein	100.0%	7.6	2	2	2	1	327,887	329,598	333,141	415,501	14,884	19,392	51,531	32,355	10.2	13.2	34.6	17.4	1.0	0.9	1.0	0.9	1.3	0.04	1.0	1	1.3	0.05	1.2	0.2
				ALLQMVQQFAVDFEK	2	99.9%	1																									
				VYSPHVLNLTLIDLPGITK	3	100.0%	1																									
IPI00975674	SF3B2	Uncharacterized protein	100.0%	14.8	1	1	2	3	1,980,263	2,167,838	1,805,615	2,547,600	329,840	201,876	200,826	180,936	37.2	20.8	24.9	15.9	1.1	0.6	-1.1	0.7	1.3	0.2	-1.2	0.2	1.2	0.2	1.4	0.03
IPI00976190	SF3B2	Uncharacterized protein	100.0%	4.4	1	1	2	3	1,980,263	2,167,838	1,805,615	2,547,600	329,840	201,876	200,826	180,936	37.2	20.8	24.9	15.9	1.1	0.6	-1.1	0.7	1.3	0.2	-1.2	0.2	1.2	0.2	1.4	0.03
IPI00980249	SF3B2	Protein	100.0%	8.8	1	1	2	3	1,980,263	2,167,838	1,805,615	2,547,600	329,840	201,876	200,826	180,936	37.2	20.8	24.9	15.9	1.1	0.6	-1.1	0.7	1.3	0.2	-1.2	0.2	1.2	0.2	1.4	0.03
				VGEPVALSEEER	2	100.0%	2																									
IPI00975755	RPS3	15 kDa protein	100.0%	35.6	4	4	6	4	3,311,341	3,502,027	3,217,263	3,798,761	255,459	147,375	281,651	121,397	17.3	9.4	19.6	7.2	1.1	0.5	-1.0	0.8	1.1	0.1	-1.1	0.4	1.1	0.2	1.2	0.09
IPI00977127	RPS3	Protein	100.0%	39.0	4	4	6	4	3,311,341	3,502,027	3,217,263	3,798,761	255,459	147,375	281,651	121,397	17.3	9.4	19.6	7.2	1.1	0.5	-1.0	0.8	1.1	0.1	-1.1	0.4	1.1	0.2	1.2	0.09

IPI00978911	RPS3	Uncharacterized protein	100.0%	29.3	4	4	6	4	3,311,341	3,502,027	3,217,263	3,798,761	255,459	147,375	281,651	121,397	17.3	9.4	19.6	7.2	1.1	0.5	-1.0	0.8	1.1	0.1	-1.1	0.4	1.1	0.2	1.2	0.09
IPI00979604	RPS3	13 kDa protein	100.0%	41.0	4	4	6	4	3,311,341	3,502,027	3,217,263	3,798,761	255,459	147,375	281,651	121,397	17.3	9.4	19.6	7.2	1.1	0.5	-1.0	0.8	1.1	0.1	-1.1	0.4	1.1	0.2	1.2	0.09
				AELNEFLTR	2	97.8%	1																									
				ELAEDGYSGVEVR	2	100.0%	2																									
				FGFPEGSVELYAEK	2	100.0%	2																									
				GLCAIAQAESLR	2	100.0%	1																									
IPI00975821	RAB1B	Uncharacterized protein	100.0%	44.4	5	6	9	1	9,134,316	9,578,773	9,650,226	10,862,065	807,535	439,953	523,065	326,659	19.8	10.3	12.1	6.7	1.0	0.6	1.1	0.6	1.2	0.08	1.0	0.9	1.1	0.05	1.1	0.08
				EFADSLGIPFLETSAK	2	100.0%	2																									
				FADDTYTESYISTIGVDFK	2	100.0%	2																									
				FADDTYTESYISTIGVDFK	3	100.0%	1																									
				MGPGAASGGERPNLK	2	100.0%	1																									
				NATNVEQAFMTMAAEIK	2	100.0%	2																									
				QWLQEIDR	2	95.3%	1																									
IPI00975879	NSFL1C	30 kDa protein	100.0%	10.2	3	3	3	1	3,059,925	3,074,668	3,089,894	3,478,295	265,718	65,981	219,214	141,076	19.4	4.8	15.9	9.1	1.0	1	1.0	0.9	1.1	0.2	1.0	0.9	1.1	0.03	1.1	0.2
				LGAAPEEESAYVAGEK	2	99.9%	1																									
				LGAAPEEESAYVAGEKR	3	100.0%	1																									
				SPNELVDDLFK	2	99.7%	1																									
IPI00975917	RNH1	30 kDa protein	100.0%	28.8	6	7	8	1	13,467,217	13,959,569	13,553,613	15,204,190	1,229,374	483,316	941,118	461,874	20.4	7.7	15.5	6.8	1.0	0.7	1.0	1	1.1	0.2	-1.0	0.7	1.1	0.1	1.1	0.2
				ELCQGLGQPGSVLR	2	100.0%	1																									
				ELSLAGNELGDEGAR	2	100.0%	2																									
				ESLKELSLAGNELGDEGAR	3	99.9%	1																									
				FLLELQISNNR	2	100.0%	1																									
				LGDVGMAELCPGLLHPSSR	3	100.0%	1																									
				LLCETLLEPGCQLESLWVK	2	99.6%	1																									
				LLCETLLEPGCQLESLWVK	3	97.4%	1																									
IPI00975979	LARP1	Protein	98.2%	6.6	1	1	1	1	9,525,650	9,160,975	8,774,425	10,289,200	578,943	422,856	504,617	261,619	13.6	10.3	12.9	5.7	-1.0	0.6	-1.1	0.4	1.1	0.3	-1.0	0.6	1.1	0.05	1.2	0.03
				FQQVPTDALANK	2	98.2%	1																									
IPI00976007	FAM49B	Uncharacterized protein	100.0%	16.5	1	1	2	8	604,324	704,157	657,608	729,737	116,920	74,633	99,416	53,882	43.3	23.7	33.8	16.5	1.2	0.5	1.1	0.7	1.2	0.4	-1.1	0.7	1.0	0.8	1.1	0.5
IPI00977851	FAM49B	Uncharacterized protein	100.0%	20.6	1	1	2	8	604,324	704,157	657,608	729,737	116,920	74,633	99,416	53,882	43.3	23.7	33.8	16.5	1.2	0.5	1.1	0.7	1.2	0.4	-1.1	0.7	1.0	0.8	1.1	0.5
IPI00979101	FAM49B	Uncharacterized protein	100.0%	13.3	1	1	2	8	604,324	704,157	657,608	729,737	116,920	74,633	99,416	53,882	43.3	23.7	33.8	16.5	1.2	0.5	1.1	0.7	1.2	0.4	-1.1	0.7	1.0	0.8	1.1	0.5
IPI00979619	FAM49B	Uncharacterized protein	100.0%	8.4	1	1	2	8	604,324	704,157	657,608	729,737	116,920	74,633	99,416	53,882	43.3	23.7	33.8	16.5	1.2	0.5	1.1	0.7	1.2	0.4	-1.1	0.7	1.0	0.8	1.1	0.5
IPI00979649	FAM49B	Uncharacterized protein	100.0%	20.0	1	1	2	8	604,324	704,157	657,608	729,737	116,920	74,633	99,416	53,882	43.3	23.7	33.8	16.5	1.2	0.5	1.1	0.7	1.2	0.4	-1.1	0.7	1.0	0.8	1.1	0.5
IPI00980306	FAM49B	Uncharacterized protein	100.0%	14.0	1	1	2	8	604,324	704,157	657,608	729,737	116,920	74,633	99,416	53,882	43.3	23.7	33.8	16.5	1.2	0.5	1.1	0.7	1.2	0.4	-1.1	0.7	1.0	0.8	1.1	0.5
IPI00982499	FAM49B	Uncharacterized protein	100.0%	19.1	1	1	2	8	604,324	704,157	657,608	729,737	116,920	74,633	99,416	53,882	43.3	23.7	33.8	16.5	1.2	0.5	1.1	0.7	1.2	0.4	-1.1	0.7	1.0	0.8	1.1	0.5
IPI01011690	FAM49B	Uncharacterized protein	100.0%	13.0	1	1	2	8	604,324	704,157	657,608	729,737	116,920	74,633	99,416	53,882	43.3	23.7	33.8	16.5	1.2	0.5	1.1	0.7	1.2	0.4	-1.1	0.7	1.0	0.8	1.1	0.5
				DAEGILEDLQSYR	2	100.0%	2																									
IPI00976020	EIF4G2	50 kDa protein	91.1%	3.2	1	1	1	2	341,741	512,258	520,115	519,950	33,963	27,888	48,352	20,306	22.2	12.2	20.8	8.7	1.5	0.005	1.5	0.02	1.5	0.002	1.0	0.9	1.0	0.8	-1.0	1
IPI00979000	EIF4G2	32 kDa protein	91.1%	5.0	1	1	1	2	341,741	512,258	520,115	519,950	33,963	27,888	48,352	20,306	22.2	12.2	20.8	8.7	1.5	0.005	1.5	0.02	1.5	0.002	1.0	0.9	1.0	0.8	-1.0	1
				DMGEDLECLCQIMR	2	91.1%	1																									
IPI00976042	PKP3	Uncharacterized protein	100.0%	10.3	1	1	1	1	707,557	750,150	818,620	900,283	72,924	73,626	148,587	37,088	23.1	22.0	40.6	9.2	1.1	0.7	1.2	0.5	1.3	0.05	1.1	0.7	1.2	0.1	1.1	0.6
				GVGGAVPGAVLEPVAR	2	100.0%	1																									
IPI00976209	PIH1D2	cDNA FLJ60158	93.2%	7.3	1	1	1	1	1,412,115	1,590,210	1,341,414	1,656,440	140,172	40,217	65,432	99,372	22.2	5.7	10.9	13.4	1.1	0.3	-1.1	0.7	1.2	0.2	-1.2	0.01	1.0	0.6	1.2	0.03
				VELPGINSVSLCDLSVSEVS	2	93.2%	1																									
IPI00976338	DECR1	Uncharacterized protein	99.9%	22.0	3	3	3	3	1,454,625	1,848,187	1,615,149	2,035,147	215,447	135,844	74,809	114,050	33.1	16.4	10.4	12.5	1.3	0.2	1.1	0.5	1.4	0.04	-1.1	0.2	1.1	0.3	1.3	0.02
IPI00978507	DECR1	Uncharacterized protein	99.9%	24.9	3	3	3	3	1,454,625	1,848,187	1,615,149	2,035,147	215,447	135,844	74,809	114,050	33.1	16.4	10.4	12.5	1.3	0.2	1.1	0.5	1.4	0.04	-1.1	0.2	1.1	0.3	1.3	0.02
IPI00979062	DECR1	Uncharacterized protein	99.9%	29.8	3	3	3	3	1,454,625	1,848,187	1,615,149	2,035,147	215,447	135,844	74,809	114,050	33.1	16.4	10.4	12.5	1.3	0.2	1.1	0.5	1.4	0.04	-1.1	0.2	1.1	0.3	1.3	0.02
				ATAEQISSQTGNK	2	99.8%	1																									
				TITDIVLNGTAFVTLEIGK	2	94.7%	1																									
				VAFITGGGTGLGK	2	99.1%	1																									
IPI00976365	LMO7	Protein	100.0%	9.9	2	2	3	1	428,915	478,488	459,775	513,526	36,406	36,146	52,305	34,371	19.0	16.9	25.4	15.0	1.1	0.4	1.1	0.6	1.2	0.1	-1.0	0.8	1.1	0.5	1.1	0.4
				EPSLATWEATWSEGSK	2	100.0%	1																									
				WIDATSGIYNSEK	2	100.0%	2																									
IPI00976405	NUP214	cDNA, FLJ79316, highly similar to Nuclear pore complex protein Nup214	99.1%	2.4	1	1	1	3	224,339	254,892	243,577	237,160	40,208	41,756	37,219	20,699	40.1	36.6	34.2	19.5	1.1	0.6	1.1	0.7	1.1	0.8	-1.0	0.8	-1.1	0.7	-1.0	0.9
IPI00983618	NUP214	Similar to Nucleoporin 214kDa	99.1%	9.1	1	1	1	3	224,339	254,892	243,577	237,160	40,208	41,756	37,219	20,699	40.1	36.6	34.2	19.5	1.1	0.6	1.1	0.7	1.1	0.8	-1.0	0.8	-1.1	0.7	-1.0	0.9
IPI00983837	NUP214	Uncharacterized protein	99.1%	4.4	1	1	1	3	224,339	254,892	243,577	237,160	40,208	41,756	37,219	20,699	40.1	36.6	34.2	19.5	1.1	0.6	1.1	0.7	1.1	0.8	-1.0	0.8	-1.1	0.7	-1.0	0.9
				LGELLFPSSLAGETLGSFSGLR	2	99.1%	1																									
IPI00976521	FDFT1	Uncharacterized protein	100.0%	12.9	4	4	4	2	2,274,816	2,369,596	2,346,644	2,621,695	118,464	49,644	86,947	123,207	11.6	4.7	8.3	10.5	1.0	0.5	1.0	0.6	1.2	0.08	-1.0	0.8	1.1	0.09	1.1	0.1
IPI00983445	FDFT1	cDNA, FLJ79081, highly similar to Squalene synthetase	100.0%	11.2	4	4	4	2	2,274,816	2,369,596	2,346,644	2,621,695	118,464	49,644	86,947	123,207	11.6	4.7	8.3	10.5	1.0	0.5	1.0	0.6	1.2	0.08	-1.0	0.8	1.1	0.09	1.1	0.1
				DYLEDQQGGR	2	100.0%	1																									
				LFSASEFEDPLVGEDTER	2	100.0%	1																									
				MGIGMAEFLDK	2	100.0%	1																									
				SFAAVIQALDGEMR	2	100.0%	1																									
IPI00976532	SERPINH1	Uncharacterized protein	100.0%	42.0	3	4	7	6	2,332,483	2,462,579	2,537,435	2,723,654	164,083	61,475	119,489	89,210	15.7	5.6	10.5	7.3	1.1	0.5	1.1	0.3	1.2	0.07	1.0	0.6	1.1	0.04	1.1	0.2
IPI00978011	SERPINH1	Uncharacterized protein	100.0%	25.3	3	4	7	6	2,332,483	2,462,579	2,537,435	2,723,654	164,083	61,475	119,489	89,210	15.7	5.6	10.5	7.3	1.1	0.5	1.1	0.3	1.2	0.07	1.0	0.6	1.1	0.04	1.1	0.2
IPI00978907	SERPINH1	Uncharacterized protein	100.0%	38.7	3	4	7	6	2,332,483	2,462,579	2,537,435	2,723,654	164,083	61,475	119,489	89,210	15.7	5.6	10.5	7.3	1.1	0.5	1.1	0.3	1.2	0.07	1.0	0.6	1.1	0.04	1.1	0.2
IPI00981668	SERPINH1	Uncharacterized protein	100.0%	25.5	3	4	7	6	2,332,483	2,462,579	2,537,435	2,723,654	164,083	61,475	119,489	89,210	15.7	5.6	10.5	7.3	1.1	0.5	1.1	0.3	1.2	0.07	1.0	0.6	1.1	0.04	1.1	0.2
IPI00981937	SERPINH1	Uncharacterized protein	100.0%	37.7	3	4	7	6	2,332,483	2,462,579	2,537,435	2,723,654	164,083	61,475	119,489	89,210	15.7	5.6	10.5	7.3	1.1	0.5	1.1	0.3	1.2	0.07	1.0	0.6	1.1	0.04	1.1	0.2
IPI00984900	SERPINH1	Uncharacterized protein	100.0%	31.0	3	4	7	6	2,332,483	2,462,579	2,537,435	2,723,654	164,083	61,475	119,489	89,210	15.7	5.6	10.5	7.3	1.1	0.5	1.1	0.3	1.2	0.07	1.0	0.6	1.1	0.04	1.1	0.2
				AVLSAEQLRDEEVHAGLGELLR	3	100.0%	1																									
				DQAVENILVSPVVVASSLGLVSLGGK	2	100.0%	2																									
				DQAVENILVSPVVVASSLGLVSLGGK	3	100.0%	2																									
				LYGPSSVSFADDFVR	2	100.0%	2																									
IPI00976543	PAFAH1B2	platelet-activating factor acetylhydrolase IB subunit beta isoform c	100.0%	35.5	4	6	6	3	6,359,465	6,449,910	6,644,305	7,560,337	278,442	137,402	383,673	266,029	9.8	4.8	12.9	7.9	1.0	0.8	1.0	0.6	1.2	0.01	1.0	0.7	1.2	0.006	1.1	0.09
IPI00980480	PAFAH1B2	platelet-activating factor acetylhydrolase IB subunit beta isoform b	100.0%	27.2	4	6	6	3	6,359,465	6,449,910	6,644,305	7,560,337	278,442	137,402	383,673	266,029	9.8	4.8	12.9	7.9	1.0	0.8	1.0	0.6	1.2	0.01	1.0	0.7	1.2	0.006	1.1	0.09
IPI00982701	PAFAH1B2	platelet-activating factor acetylhydrolase IB subunit beta isoform d	100.0%	41.7	4	6	6	3	6,359,465	6,449,910	6,644,305	7,560,337	278,442	137,402	383,673	266,029	9.8	4.8	12.9	7.9	1.0	0.8	1.0	0.6	1.2	0.01	1.0	0.7	1.2	0.006	1.1	0.09
				DKEPDVLFVGDSMVQLMQQYEIWR	3	100.0%	1																									
				ELFSPLHALNFGIGGDTTR	2	100.0%	1																									
				ELFSPLHALNFGIGGDTTR	3	99.9%	1																									
				LKNGELENIKPK	2	99.7%	1																									
				LKNGELENIKPK	3	99.9%	1																									
				NGELENIKPK	2	99.0%	1																									
IPI00976545	NDRG1	11 kDa protein	100.0%	49.5	3	3	6	2	2,077,654	2,109,549	1,923,645	2,393,011	188,122	102,872	135,006	109,698	20.3	10.9	15.7	10.3	1.0	0.9	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.03
IPI01015403	NDRG1	cDNA FLJ53648, highly similar to Protein NDRG1	100.0%	38.3	3	3	6	2	2,077,654	2,109,549	1,923,645	2,393,011	188,122	102,872	135,006	109,698	20.3	10.9	15.7	10.3	1.0	0.9	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.03
				MADCGGLPQISQPAK	2	100.0%	2																									
				SHTSEGAHLDITPNSGAAGNSAGPK	3	100.0%	2																									
				TASGSSVTSLDGTR	2	100.0%	2																									
IPI00976571	EIF4G2	Uncharacterized protein	99.5%	17.2	2	2	2	1	1,568,884	1,589,677	1,629,382	1,835,443	94,490	93,766	118,140	129,035	13.5	13.2	16.2	15.7	1.0	0.9	1.0	0.7	1.2	0.1	1.0	0.8	1.2	0.2	1.1	0.3
				HFLPEMLSK	2	92.6%	1																									
				QEGIATSDNFMQAFLNVLDQCPK	3	99.5%	1																									
IPI00976589	EEF1D	Uncharacterized protein	100.0%	27.3	4	4	7	1	1,806,046	1,833,886	1,641,111	1,995,689	76,054	52,810	84,430	51,132	9.4	6.4	11.5	5.7	1.0	0.8	-1.1	0.2	1.1	0.07	-1.1	0.09	1.1	0.06	1.2	0.007
				ATAPQTQHVSPMR	3	92.1%	1																									
				FYEQMNGPVAGASR	2	100.0%	2																									
				GVVQELQQAISK	2	100.0%	2																									
				IASLEVENQSLR	2	100.0%	2																									
IPI00976594	MARS	cDNA FLJ55046, highly similar to Methionyl-tRNA synthetase	100.0%	5.4	2	2	3	2	2,272,733	2,277,134	2,354,712	2,519,178	150,474	182,530	100,946	131,439	14.8	17.9	9.6	11.7	1.0	1	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.3	1.1	0.4
IPI01015558	MARS	cDNA FLJ16674 fis, clone THYMU3008136, highly similar to Methionyl-tRNA synthe	100.0%	4.2	2	2	3	2	2,272,733	2,277,134	2,354,712	2,519,178	150,474	182,530	100,946	131,439	14.8	17.9	9.6	11.7	1.0	1	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.3	1.1	0.4
				GFVLQDTVEQLR	2	95.7%	1																									
				ITQDIFQQLLK	2	99.9%	2																									
IPI00976656	WASF2	wiskott-Aldrich syndrome protein family member 2 isoform 2	100.0%	7.8	2	2	2	1	1,576,098	2,021,761	1,607,790	2,043,618	118,521	207,188	181,940	159,597	16.8	22.9	25.3	17.5	1.3	0.1	1.0	0.9	1.3	0.05	-1.3	0.2	1.0	0.9	1.3	0.1
				FYTDPSYFFDLWK	2	100.0%	1																									
				MGQEFVESK	2	95.2%	1																									
IPI00976658	EPS8L2	Uncharacterized protein	100.0%	14.5	1	1	1	3	954,823	1,099,345	739,032	1,083,108	71,420	102,049	155,320	106,108	16.7	20.8	47.0	21.9	1.2	0.3	-1.3	0.2	1.1	0.3	-1.5	0.09	-1.0	0.9	1.5	0.1
IPI00977007	EPS8L2	Uncharacterized protein	100.0%	15.2	1	1	1	3	954,823	1,099,345	739,032	1,083,108	71,420	102,049	155,320	106,108	16.7	20.8	47.0	21.9	1.2	0.3	-1.3	0.2	1.1	0.3	-1.5	0.09	-1.0	0.9	1.5	0.1
IPI00984049	EPS8L2	Uncharacterized protein	100.0%	12.6	1	1	1	3	954,823	1,099,345	739,032	1,083,108	71,420	102,049	155,320	106,108	16.7	20.8	47.0	21.9	1.2	0.3	-1.3	0.2	1.1	0.3	-1.5	0.09	-1.0	0.9	1.5	0.1
				SEAITSVDDAIR	2	99.7%	1																									
IPI00976686	LOC100290337	DNA damage-binding protein 1-like isoform 5	100.0%	13.7	11	11	11	1	82,600,179	89,221,715	86,139,256	101,503,432	9,823,961	5,440,979	7,013,850	4,016,209	26.6	13.6	18.2	8.9	1.1	0.6	1.0	0.8	1.2	0.1	-1.0	0.7	1.1	0.1	1.2	0.09
				DLLFILTAK	2	99.6%	1																									
				EMLGGEIIPR	2	97.9%	1																									
				GAVYSMVEFNGK	2	96.1%	1																									
				IEVQDTSGGTTALRPSASTQALSSSVSSSK	3	100.0%	1																									
				LPSFELLHK	3	96.8%	1																									
				LVFSNVNLK	2	99.8%	1																									
				QSGESIDIITR	2	98.1%	1																									
				SVLLLAYKPMEGNFEEIAR	3	100.0%	1																									
				VTLGTQPTVLR	2	92.6%	1																									
				YLLGDMEGR	2	98.5%	1																									
				YNACILEYK	2	99.4%	1																									
IPI00976783	MYO18A	cDNA FLJ59676, highly similar to Myosin-18A	99.5%	5.6	1	1	1	2	230,952	216,069	216,223	218,466	29,691	7,413	23,288	8,717	28.8	7.7	24.1	8.9	-1.1	0.6	-1.1	0.7	-1.1	0.7	1.0	1	1.0	0.8	1.0	0.9
IPI00983025	MYO18A	Protein	99.5%	7.1	1	1	1	2	230,952	216,069	216,223	218,466	29,691	7,413	23,288	8,717	28.8	7.7	24.1	8.9	-1.1	0.6	-1.1	0.7	-1.1	0.7	1.0	1	1.0	0.8	1.0	0.9
				LQALQSQVEFLEQSMVDK	2	99.5%	1																									
IPI00976817	PUF60	Uncharacterized protein	100.0%	14.2	2	2	3	2	831,408	830,817	846,957	921,323	75,946	37,736	28,928	33,194	20.4	10.2	7.6	8.1	-1.0	1	1.0	0.9	1.1	0.3	1.0	0.7	1.1	0.1	1.1	0.1
IPI00983055	PUF60	Uncharacterized protein	100.0%	13.3	2	2	3	2	831,408	830,817	846,957	921,323	75,946	37,736	28,928	33,194	20.4	10.2	7.6	8.1	-1.0	1	1.0	0.9	1.1	0.3	1.0	0.7	1.1	0.1	1.1	0.1
				LGLPPLTPEQQEALQK	2	100.0%	2																									
				QTIAHQQQQLTNLQMAAQR	3	99.9%	1																									
IPI00976891	RCN1	Uncharacterized protein	100.0%	20.7	1	1	1	1	1,633,917	1,728,710	1,616,300	1,919,797	178,854	82,890	95,578	107,902	24.5	10.7	13.2	12.6	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.4	1.1	0.2	1.2	0.07
				AADLNGDLTATR	2	100.0%	1																									
IPI00976909	SF3B2	Uncharacterized protein	100.0%	9.0	2	2	3	2	2,569,445	2,763,974	2,598,043	3,229,690	310,595	174,126	201,001	161,907	27.0	14.1	17.3	11.2	1.1	0.6	1.0	0.9	1.3	0.1	-1.1	0.6	1.2	0.09	1.2	0.04
IPI00977486	SF3B2	42 kDa protein	100.0%	8.3	2	2	3	2	2,569,445	2,763,974	2,598,043	3,229,690	310,595	174,126	201,001	161,907	27.0	14.1	17.3	11.2	1.1	0.6	1.0	0.9	1.3	0.1	-1.1	0.6	1.2	0.09	1.2	0.04
				SSLGQSASETEEDTVSVSKK	3	99.8%	1																									
				VGEPVALSEEER	2	100.0%	2																									
IPI00976911	LOC100506072	mucin-19-like	99.6%	0.4	2	2	2	3	2,687,103	2,675,543	2,826,590	2,786,583	154,031	91,298	170,726	118,336	12.8	7.6	13.5	9.5	-1.0	1	1.1	0.6	1.0	0.6	1.1	0.5	1.0	0.5	-1.0	0.9
IPI00984245	LOC100506072	mucin-19-like	99.6%	0.4	2	2	2	3	2,687,103	2,675,543	2,826,590	2,786,583	154,031	91,298	170,726	118,336	12.8	7.6	13.5	9.5	-1.0	1	1.1	0.6	1.0	0.6	1.1	0.5	1.0	0.5	-1.0	0.9
IPI00984382	LOC100506072	mucin-19-like	99.6%	0.5	2	2	2	3	2,687,103	2,675,543	2,826,590	2,786,583	154,031	91,298	170,726	118,336	12.8	7.6	13.5	9.5	-1.0	1	1.1	0.6	1.0	0.6	1.1	0.5	1.0	0.5	-1.0	0.9
				TEATTFLGVSGTTNIGR	2	90.6%	1																									
				VCGLCGNNNGDLK	2	84.3%	1																									
IPI00976913	LMO7	Protein	100.0%	15.9	2	2	3	1	1,102,988	1,187,779	976,741	1,580,340	267,435	166,413	178,226	115,557	54.2	31.3	40.8	16.4	1.1	0.8	-1.1	0.7	1.4	0.1	-1.2	0.4	1.3	0.09	1.6	0.02
				FSYNDSKEWEEAMAK	3	98.4%	1																									
				WIDATSGIYNSEK	2	100.0%	2																									
IPI00976939	HARS	cDNA FLJ42841 fis, clone BRCOC2003213, highly similar to Histidyl-tRNA syntheta:	100.0%	20.0	7	7	7	1	5,951,580	6,188,755	5,939,143	6,895,567	462,244	232,763	418,808	168,328	17.4	8.4	15.8	5.5	1.0	0.7	-1.0	1	1.2	0.1	-1.0	0.6	1.1	0.04	1.2	0.07
				HGAEVIDTPVFELK	2	96.7%	1																									
				IFSIVEQR	2	90.1%	1																									
				IGDYVQQHGGVSLVEQLLQDPK	3	99.9%	1																									
				LLFEYLTLFGIDDK	2	89.3%	1																									
				QALEGLGDLK	2	96.4%	1																									
				YDGLVGMFDPK	2	98.9%	1																									
				YDLTVPFAR	2	86.3%	1																									
IPI00976960	NPEPPS	Uncharacterized protein	100.0%	5.5	1	1	1	1	908,337	914,494	936,406	882,577	82,275	17,766	49,291	44,599	20.3	4.3	11.8	11.3	1.0	0.9	1.0	0.8	-1.0	0.8	1.0	0.7	-1.0	0.5	-1.1	0.4

				ATFDISLVVPK	2	100.0%	1																									
IPI00976984	ARFGAP2	cDNA, FLJ78891, highly similar to Homo sapiens zinc finger protein 289, ID1 regulat	100.0%	13.1	2	2	2	1	1,701,305	1,457,691	1,607,516	1,462,362	46,738	40,867	62,739	98,336	6.1	6.3	8.7	15.0	-1.2	0.004	-1.1	0.3	-1.2	0.06	1.1	0.08	1.0	1	-1.1	0.2
				MAVLANGVMNSLQDR	2	99.9%	1																									
				SQLDLFDDVGTFASGPPK	2	100.0%	1																									
IPI00977070	SON	Conserved hypothetical protein	99.8%	1.0	1	1	1	1	306,350	352,059	327,872	316,521	31,531	36,305	36,366	17,156	23.0	23.1	24.8	12.1	1.1	0.4	1.1	0.7	1.0	0.8	-1.1	0.7	-1.1	0.4	-1.0	0.8
				AGIEGPLLASDVGR	2	99.6%	1																									
IPI00977111	C11orf54	Uncharacterized protein	100.0%	20.5	2	2	2	1	1,345,874	1,298,356	1,351,714	1,378,002	253,587	80,040	99,919	64,494	42.1	13.8	16.5	10.5	-1.0	0.9	1.0	1	1.0	0.9	1.0	0.7	1.1	0.5	1.0	0.8
				HYGNKPIGMGGTFIIQK	3	99.9%	1																									
				SHIMPAEFSSCPLNSDEEVNK	3	100.0%	1																									
IPI00977156	EIF3E	Uncharacterized protein	100.0%	26.7	2	2	2	1	4,272,945	4,205,151	4,352,529	4,807,340	224,996	274,761	233,175	149,746	11.8	14.6	12.0	7.0	-1.0	0.9	1.0	0.8	1.1	0.08	1.0	0.7	1.1	0.09	1.1	0.1
				MFEDPETTR	2	93.2%	1																									
				QLQAETEPIVK	2	100.0%	1																									
IPI00977237	EEF1D	Uncharacterized protein	100.0%	35.9	1	1	2	1	139,048	128,933	132,601	154,897	9,313	6,371	9,260	9,961	15.0	11.1	15.6	14.4	-1.1	0.4	-1.0	0.6	1.1	0.3	1.0	0.8	1.2	0.06	1.2	0.1
				FYEQMNGPVAGASR	2	100.0%	2																									
IPI00977285	EEF1D	Uncharacterized protein	100.0%	42.7	6	6	9	4	3,492,227	3,530,784	3,307,783	3,853,622	235,354	122,157	172,436	135,115	15.1	7.7	11.7	7.8	1.0	0.9	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00978462	EEF1D	Uncharacterized protein	100.0%	51.2	6	6	9	4	3,492,227	3,530,784	3,307,783	3,853,622	235,354	122,157	172,436	135,115	15.1	7.7	11.7	7.8	1.0	0.9	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00981462	EEF1D	Uncharacterized protein	100.0%	50.6	6	6	9	4	3,492,227	3,530,784	3,307,783	3,853,622	235,354	122,157	172,436	135,115	15.1	7.7	11.7	7.8	1.0	0.9	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
IPI00984173	EEF1D	Uncharacterized protein	100.0%	41.7	6	6	9	4	3,492,227	3,530,784	3,307,783	3,853,622	235,354	122,157	172,436	135,115	15.1	7.7	11.7	7.8	1.0	0.9	-1.1	0.5	1.1	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
				ATAPQTQHVSPMR	3	92.1%	1																									
				FYEQMNGPVAGASR	2	100.0%	2																									
				GVVQELQQAISK	2	100.0%	2																									
				IASLEVENQSLR	2	100.0%	2																									
				QENGASVILR	2	99.9%	1																									
				SLAGSSGPGASSGTSGDHGELVVR	3	99.9%	1																									
IPI00977329	ANP32E	Uncharacterized protein	100.0%	21.9	2	2	3	1	3,184,184	3,680,763	3,209,121	3,569,515	277,421	129,295	314,848	242,830	19.5	7.9	21.9	15.2	1.2	0.1	1.0	1	1.1	0.3	-1.1	0.2	-1.0	0.7	1.1	0.4
				CPNLTYLNLSGNK	2	99.9%	1																									
				DLSTVEALQNLK	2	99.9%	2																									
IPI00977375	PUF60	Protein	100.0%	14.0	3	3	4	1	1,492,612	1,456,480	1,469,357	1,729,699	76,187	65,538	97,564	56,929	11.4	10.1	14.9	7.4	-1.0	0.7	-1.0	0.9	1.2	0.04	1.0	0.9	1.2	0.01	1.2	0.05
				AQSSQDAVSSMNLFDLGGQYLR	2	100.0%	1																									
				GYGFIEYEK	2	99.7%	1																									
				LGLPPLTPEQQEALQK	2	100.0%	2																									
IPI00977506	PHB	Uncharacterized protein	100.0%	55.7	10	13	17	1	26,838,896	27,366,665	28,102,600	30,827,595	1,999,139	799,256	1,738,005	852,465	16.7	6.5	13.8	6.2	1.0	0.8	1.0	0.6	1.1	0.1	1.0	0.7	1.1	0.02	1.1	0.2
				AAELIANSLATAGDGLIELR	2	99.9%	1																									
				AAELIANSLATAGDGLIELR	3	100.0%	1																									
				AAIISAEGDSK	2	100.0%	2																									
				AATFGLILDDVSLTHLTFGK	2	99.7%	1																									
				AATFGLILDDVSLTHLTFGK	3	99.9%	1																									
				DLQNVNITLR	2	100.0%	2																									
				FDAGELITQR	2	100.0%	2																									
				FGLALAVAGGVVNSALYNVDAGHR	3	99.9%	1																									
				IFTSIGEDYDER	2	100.0%	2																									
				ILFRPVASQLPR	2	98.5%	1																									
				ILFRPVASQLPR	3	100.0%	1																									
				VFESIGK	2	96.6%	1																									
				VLPSITTEILK	2	99.5%	1																									
IPI00977541	-	Conserved hypothetical protein	100.0%	21.0	1	1	1	1	601,683	665,530	692,155	678,120	74,054	45,109	29,516	43,908	27.5	15.2	9.5	14.5	1.1	0.5	1.2	0.3	1.1	0.4	1.0	0.6	1.0	0.8	-1.0	0.8
				LQETEMMDPELDYTLMR	2	100.0%	1																									
IPI00977667	FDFT1	Uncharacterized protein	100.0%	25.7	2	2	3	1	1,176,645	1,242,484	1,177,274	1,153,084	58,194	98,800	53,165	19,280	11.1	17.8	10.1	3.7	1.1	0.6	1.0	1	-1.0	0.7	-1.1	0.6	-1.1	0.4	-1.0	0.7
				ALDTLEDDMTISVEK	2	98.1%	1																									
				QVLEDFPTISLEFR	2	100.0%	2																									
IPI00977701	C11orf54	Uncharacterized protein	100.0%	12.1	2	2	2	1	2,259,211	1,941,277	2,301,659	2,247,800	328,570	81,422	187,580	105,416	32.5	9.4	18.2	10.5	-1.2	0.4	1.0	0.9	-1.0	1	1.2	0.1	1.2	0.05	-1.0	0.8
				APLVCLPVFVSR	2	100.0%	1																									
				HYGNKPIGMGGTFIIQK	3	99.9%	1																									
IPI00977723	PAK1	Uncharacterized protein	100.0%	19.1	7	7	7	1	5,720,577	6,142,917	5,877,903	6,837,826	359,899	285,539	379,503	106,687	14.1	10.4	14.4	3.5	1.1	0.4	1.0	0.8	1.2	0.03	-1.0	0.6	1.1	0.07	1.2	0.06
				LLQTSNITK	2	90.3%	1																									
				LTDFGFCAQITPEQSK	2	100.0%	1																									
				MSDEEILEK	2	97.2%	1																									
				QMNLQQQPK	2	93.9%	1																									
				SAEDYNSSNALNVK	2	99.9%	1																									
				SDNILLGMDGSVK	2	99.8%	1																									
				STMVGTPYWMAPEVVTR	2	97.1%	1																									
IPI00977771	TXNRD1	Uncharacterized protein	100.0%	8.2	2	2	2	1	610,525	594,829	642,659	726,733	57,874	47,678	32,506	63,629	21.2	17.9	11.3	19.6	-1.0	0.8	1.1	0.6	1.2	0.2	1.1	0.4	1.2	0.1	1.1	0.3
				VVGFHVLGPNAGEVTQGFAAALK	3	100.0%	1																									
				WGLGGTCVNVGCIPK	2	94.9%	1																									
IPI00977865	SCP2	non-specific lipid-transfer protein isoform 8 proprotein	100.0%	19.7	9	9	11	1	8,968,856	8,784,782	9,175,901	10,413,621	894,950	305,615	649,467	467,665	22.3	7.8	15.8	10.0	-1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.6	1.2	0.02	1.1	0.2
				ADCTITMADSDFLALMTGK	2	100.0%	1																									
				AVEILAQEMMTDLPSSFEEK	3	87.9%	1																									
				EATWVVDVK	2	99.9%	2																									
				IGGIFAFK	2	100.0%	1																									
				KLEEEGEQFVK	2	100.0%	2																									
				KLEEEGEQFVKK	2	100.0%	1																									
				LQNLQLQPGNAK	2	100.0%	1																									
				LQNLQLQPGNAKL	2	99.5%	1																									
				MNPQSAFFQGK	2	99.4%	1																									
IPI00977878	CTTN	30 kDa protein	100.0%	12.8	2	2	3	2	998,477	987,030	970,050	1,052,532	42,954	26,035	66,072	34,415	9.6	5.9	15.2	7.3	-1.0	0.8	-1.0	0.7	1.1	0.4	-1.0	0.8	1.1	0.2	1.1	0.3
IPI00983145	CTTN	14 kDa protein	100.0%	26.6	2	2	3	2	998,477	987,030	970,050	1,052,532	42,954	26,035	66,072	34,415	9.6	5.9	15.2	7.3	-1.0	0.8	-1.0	0.7	1.1	0.4	-1.0	0.8	1.1	0.2	1.1	0.3
				GPVSGTEPEPVYSMEAADYR	2	100.0%	2																									
				LPSSPVYEDAASFK	2	100.0%	1																									
IPI00978082	RCN1	cDNA FLJ55835, highly similar to Reticulocalbin-1	100.0%	15.4	3	3	4	1	4,733,704	5,034,730	4,806,133	5,187,652	515,555	208,791	302,368	215,583	24.4	9.3	14.1	9.3	1.1	0.6	1.0	0.9	1.1	0.4	-1.0	0.6	1.0	0.6	1.1	0.3
				AADLNGDLTATR	2	100.0%	1																									
				HWILPQDYDHAQAEAR	3	100.0%	1																									
				IDNDGDGFVTTEELK	2	100.0%	2																									
IPI00978154	NAPRT1	Protein	100.0%	14.7	2	2	2	1	1,480,052	1,427,620	1,464,698	1,442,605	122,129	65,932	90,297	70,685	18.5	10.3	13.8	11.0	-1.0	0.7	-1.0	0.9	-1.0	0.8	1.0	0.7	1.0	0.9	-1.0	0.9
				ALDCSEVTVR	2	99.4%	1																									
				CPFGGAFALAAGLR	2	99.9%	1																									
IPI00978171	PSMC3	Uncharacterized protein	100.0%	30.4	5	5	6	2	10,245,421	10,321,513	11,829,881	11,547,704	1,165,584	612,600	805,320	259,763	25.4	13.3	15.2	5.0	1.0	1	1.2	0.3	1.1	0.3	1.1	0.2	1.1	0.1	-1.0	0.8
IPI00979951	PSMC3	Uncharacterized protein	100.0%	33.1	5	5	6	2	10,245,421	10,321,513	11,829,881	11,547,704	1,165,584	612,600	805,320	259,763	25.4	13.3	15.2	5.0	1.0	1	1.2	0.3	1.1	0.3	1.1	0.2	1.1	0.1	-1.0	0.8
				AMEVDERPTEQYSDIGGLDK	3	100.0%	1																									
				EKAPSIIFIDELDAIGTK	3	100.0%	1																									
				LAGPQLVQMFIGDGAK	2	100.0%	2																									
				MSTEEIIQR	2	100.0%	1																									
				QIQELVEAIVLPMNHK	3	99.8%	1																									
IPI00978180	RPS10-NUDT3	RPS10-NUDT3 protein	100.0%	19.2	4	4	4	1	13,638,433	14,782,636	13,438,438	16,915,183	1,928,166	1,132,353	1,668,189	1,210,761	31.6	17.1	27.8	16.0	1.1	0.6	-1.0	0.9	1.2	0.2	-1.1	0.5	1.1	0.2	1.3	0.1
				HFYWYLTNEGIQYLR	3	100.0%	1																									
				IAIYELLFK	2	100.0%	1																									
				KAEAGAGSATEFQFVLLVSSSR	2	84.9%	1																									
				LVGIFENQER	2	86.4%	1																									
IPI00978187	NDUFV1	isoform 2 of NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	96.6%	2.9	1	1	1	1	11,144,660	11,686,950	10,836,540	11,723,970	594,515	768,900	538,818	488,210	11.9	14.7	11.1	9.3	1.0	0.6	-1.0	0.7	1.1	0.5	-1.1	0.4	1.0	1	1.1	0.3
				LLGWSLPARTAPK	3	96.6%	1																									
IPI00978298	RPS3	Uncharacterized protein	100.0%	16.5	3	3	5	1	2,558,552	2,547,974	2,467,209	2,792,130	280,301	175,690	199,477	151,221	24.5	15.4	18.1	12.1	-1.0	1	-1.0	0.8	1.1	0.5	-1.0	0.8	1.1	0.3	1.1	0.2
				ELAEDGYSGVEVR	2	100.0%	2																									
				GGKPEPPAMPQPVPTA	2	100.0%	2																									
				KFVADGIFK	2	96.7%	1																									
IPI00978433	LMO7	Uncharacterized protein	100.0%	7.3	1	1	2	3	195,362	194,320	188,267	235,678	40,923	28,780	38,022	34,412	46.8	33.1	45.2	32.7	-1.0	1	-1.0	0.9	1.2	0.5	-1.0	0.9	1.2	0.4	1.3	0.4
IPI00981656	LMO7	Uncharacterized protein	100.0%	8.4	1	1	2	3	195,362	194,320	188,267	235,678	40,923	28,780	38,022	34,412	46.8	33.1	45.2	32.7	-1.0	1	-1.0	0.9	1.2	0.5	-1.0	0.9	1.2	0.4	1.3	0.4
IPI00982301	LMO7	Uncharacterized protein	100.0%	11.6	1	1	2	3	195,362	194,320	188,267	235,678	40,923	28,780	38,022	34,412	46.8	33.1	45.2	32.7	-1.0	1	-1.0	0.9	1.2	0.5	-1.0	0.9	1.2	0.4	1.3	0.4
				SMSDVSAEDVQNLR	2	100.0%	2																									
IPI00978457	NAP1L4	Uncharacterized protein	100.0%	34.6	2	2	2	2	1,987,035	1,865,109	2,251,196	2,142,528	113,398	112,006	112,002	149,034	12.8	13.4	11.1	15.6	-1.1	0.5	1.1	0.1	1.1	0.4	1.2	0.04	1.1	0.2	-1.1	0.6
IPI00983980	NAP1L4	Uncharacterized protein	100.0%	17.8	2	2	2	2	1,987,035	1,865,109	2,251,196	2,142,528	113,398	112,006	112,002	149,034	12.8	13.4	11.1	15.6	-1.1	0.5	1.1	0.1	1.1	0.4	1.2	0.04	1.1	0.2	-1.1	0.6
				LDNVPHTPSSYIETLPK	3	100.0%	1																									
				LTDQVMQNPR	2	100.0%	1																									
IPI00978476	DDX39B;SNORD84	Protein	100.0%	24.8	2	2	3	1	514,659	448,943	520,363	603,152	54,604	43,745	56,217	14,459	23.7	21.8	24.2	5.4	-1.1	0.4	1.0	0.9	1.2	0.2	1.2	0.3	1.3	0.02	1.2	0.2
				CIALAQLLVEQNFPAIAIHR	3	100.0%	2																									
				FMQDPMEIFVDDETK	2	99.8%	1																									
IPI00978541	CLNS1A	Uncharacterized protein	99.6%	14.0	1	1	1	1	493,373	643,475	830,998	623,207	45,182	111,512	110,582	61,338	20.5	38.8	29.8	22.0	1.3	0.2	1.7	0.02	1.3	0.1	1.3	0.3	-1.0	0.9	-1.3	0.1
				LSWLDGSGLGFSLEYPTISLHALSR	3	99.6%	1																									
IPI00978626	RCN1	Uncharacterized protein	100.0%	38.3	3	4	6	2	5,242,104	6,011,172	5,652,599	6,465,855	371,370	269,507	491,553	234,900	15.8	10.0	19.4	8.1	1.1	0.1	1.1	0.5	1.2	0.02	-1.1	0.5	1.1	0.2	1.1	0.2
IPI00981770	RCN1	Uncharacterized protein	100.0%	38.8	3	4	6	2	5,242,104	6,011,172	5,652,599	6,465,855	371,370	269,507	491,553	234,900	15.8	10.0	19.4	8.1	1.1	0.1	1.1	0.5	1.2	0.02	-1.1	0.5	1.1	0.2	1.1	0.2
				IDNDGDGFVTTEELK	2	100.0%	2																									
				TFDQLTPDESKER	2	100.0%	2																									
				TFDQLTPDESKER	3	95.9%	1																									
				VVRPDSELGERPPEDNQSFQYDHEAFLGK	3	95.8%	1																									
IPI00978637	CTNNB1	Conserved hypothetical protein	96.8%	21.3	1	1	1	1	2,000,220	2,177,470	2,061,490	2,014,750	238,173	205,206	134,676	46,050	26.6	21.1	14.6	5.1	1.1	0.6	1.0	0.8	1.0	1	-1.1	0.6	-1.1	0.5	-1.0	0.8
				HMQLLFCSECLRTSHK	3	96.8%	1																									
IPI00978725	APEX1	Conserved hypothetical protein	100.0%	11.0	2	2	2	1	2,725,762	2,893,863	3,441,990	3,062,520	185,484	182,835	333,390	130,660	15.2	14.1	21.7	9.5	1.1	0.5	1.3	0.1	1.1	0.2	1.2	0.2	1.1	0.5	-1.1	0.3
				GLDWVKEEAPDILCLQETK	3	99.4%	1																									
				QGFGELLQAVPLADSFR	2	100.0%	1																									
IPI00978735	PSMC3	Uncharacterized protein	100.0%	29.9	6	6	7	1	29,335,311	29,290,895	27,441,309	32,004,277	2,201,755	1,216,956	1,970,707	1,340,902	16.8	9.3	16.1	9.4	-1.0	1	-1.1	0.5	1.1	0.3	-1.1	0.4	1.1	0.2	1.2	0.09
				AMELVEAIVLPMNHK	2	97.0%	1																									
				DSYLILETLPTEYDSR	2	100.0%	1																									
				FENLGIQPPK	2	91.7%	1																									
				GVLMYGPPGTGK	2	100.0%	1																									
				LAGPQLVQMFIGDGAK	2	100.0%	2																									
				TMLELLNQLDGFQPNTQVK	3	100.0%	1																									
IPI00978761	YAP1	yorkie homolog isoform 4	100.0%	8.0	2	2	2	2	1,685,669	1,622,105	1,583,022	1,559,718	202,638	80,316	59,465	20,852	26.9	11.1	8.4	3.0	-1.0	0.8	-1.1	0.6	-1.1	0.6	-1.0	0.7	-1.0	0.5	-1.0	0.7
IPI01009567	YAP1	cDNA, FLJ79015, highly similar to 65 kDa Yes-associated protein	100.0%	6.2	2	2	2	2	1,685,669	1,622,105	1,583,022	1,559,718	202,638	80,316	59,465	20,852	26.9	11.1	8.4	3.0	-1.0	0.8	-1.1	0.6	-1.1	0.6	-1.0	0.7	-1.0	0.5	-1.0	0.7
				LDKESFLTWL	2	99.1%	1																									
				YFLNHIDQTTTWQDPR	3	99.4%	1																									
IPI00978767	CSRP1	cysteine and glycine-rich protein 1 isoform 3	100.0%	14.4	1	1	1	2	702,212	677,822	614,790	701,376	142,005	49,510	32,333	15,391	45.2	16.3	11.8	4.9	-1.0	0.9	-1.1	0.6	-1.0	1	-1.1	0.3	1.0	0.7	1.1	0.04
IPI01009912	CSRP1	Cysteine and glycine-rich protein 1 variant (Fragment)	100.0%	13.8	1	1	1	2	702,212	677,822	614,790	701,376	142,005	49,510	32,333	15,391	45.2	16.3	11.8	4.9	-1.0	0.9	-1.1	0.6	-1.0	1	-1.1	0.3	1.0	0.7	1.1	0.04
				GYGYGQGAGTLSTDKGESLGIK	3	99.9%	1																									
IPI00978796	CFL1	17 kDa protein	100.0%	40.3	5	5	9	1	16,083,676	16,790,003	15,963,005	19,251,007	1,193,602	728,960	1,384,806	685,984	16.6	9.7	19.4	8.0	1.0	0.6	-1.0	0.9	1.2	0.05	-1.1	0.6	1.1	0.04	1.2	0.07
				EILVGDVGQTVDDPYATFVK	2	100.0%	2																									
				LGGSAVISLEGKPL	2	100.0%	2																									
				MIYASSK	1	100.0%	1																									
				NIILEEGKEILVGDVGQTVDDPYATFVK	2	100.0%	2																									
				YALYDATYETK	2	100.0%	2																									

IPI00978805	TPD52	Uncharacterized protein	100.0%	53.3	1	1	1	1	237,123	267,408	228,208	280,364	30,093	17,378	18,732	11,957	28.4	14.5	18.4	9.5	1.1	0.4	-1.0	0.8	1.2	0.2	-1.2	0.2	1.0	0.6	1.2	0.05
				VGGTKPAGGDFGEVLNSAANASATTTEPLPEK	3	100.0%	1																									
IPI00978816	CHORDC1	Uncharacterized protein	100.0%	25.8	2	2	2	2	1,894,236	1,900,850	1,942,708	2,048,480	181,005	30,699	205,943	122,503	21.4	3.6	23.7	13.4	1.0	1	1.0	0.9	1.1	0.5	1.0	0.9	1.1	0.3	1.1	0.7
IPI00981208	CHORDC1	Uncharacterized protein	100.0%	26.7	2	2	2	2	1,894,236	1,900,850	1,942,708	2,048,480	181,005	30,699	205,943	122,503	21.4	3.6	23.7	13.4	1.0	1	1.0	0.9	1.1	0.5	1.0	0.9	1.1	0.3	1.1	0.7
				FQEHIIQAPKPVEAIK	3	95.0%	1																									
				TTDFSDFLSIVGCTK	2	100.0%	1																									
IPI00978855	EEF1D	Uncharacterized protein	100.0%	38.1	2	2	3	2	1,361,723	1,333,727	1,335,607	1,480,579	104,829	56,723	74,846	85,810	17.2	9.5	12.5	13.0	-1.0	0.8	-1.0	0.8	1.1	0.4	1.0	1	1.1	0.2	1.1	0.2
IPI00984413	EEF1D	Uncharacterized protein	100.0%	17.1	2	2	3	2	1,361,723	1,333,727	1,335,607	1,480,579	104,829	56,723	74,846	85,810	17.2	9.5	12.5	13.0	-1.0	0.8	-1.0	0.8	1.1	0.4	1.0	1	1.1	0.2	1.1	0.2
				FYEQMNGPVAGASR	2	100.0%	2																									
				QENGASVILR	2	99.9%	1																									
IPI00978891	IARS	cDNA FLJ55373, highly similar to Isoleucyl-tRNA synthetase, cytoplasmic	100.0%	9.5	5	5	6	1	8,311,871	8,351,841	7,975,987	9,651,031	938,514	568,660	850,354	413,198	25.3	15.2	23.8	9.6	1.0	1	-1.0	0.8	1.2	0.2	-1.0	0.7	1.2	0.1	1.2	0.1
				GSELEITLTR	2	99.8%	1																									
				LFLNETQTQEITEDIPVK	2	90.9%	1																									
				LQKEEEIEFLYNENTVR	3	89.2%	1																									
				QLSSEELEQFQK	2	99.7%	2																									
				TESAVSQMQSVIELGR	2	100.0%	1																									
IPI00978951	LMO7	Protein	100.0%	12.1	3	3	5	1	1,662,327	1,731,258	1,524,136	2,147,574	262,028	199,576	178,447	103,641	35.3	25.8	26.2	10.8	1.0	0.8	-1.1	0.7	1.3	0.1	-1.1	0.5	1.2	0.1	1.4	0.02
				FSYNDSKEWEEAMAK	3	98.4%	1																									
				ISINQTPGK	2	99.3%	2																									
				WIDATSGIYNSEK	2	100.0%	2																									
IPI00978953	TPT1	Uncharacterized protein	100.0%	20.4	3	4	6	2	5,007,403	5,276,436	4,748,264	5,845,939	465,244	289,212	321,221	316,417	20.8	12.3	15.1	12.1	1.1	0.6	-1.1	0.7	1.2	0.2	-1.1	0.3	1.1	0.2	1.2	0.04
IPI01015706	TPT1	18 kDa protein	100.0%	20.6	3	4	6	2	5,007,403	5,276,436	4,748,264	5,845,939	465,244	289,212	321,221	316,417	20.8	12.3	15.1	12.1	1.1	0.6	-1.1	0.7	1.2	0.2	-1.1	0.3	1.1	0.2	1.2	0.04
				EIADGLCLEVEGK	2	100.0%	2																									
				HILANFK	2	94.9%	1																									
				VKPFMTGAAEQIK	2	99.9%	2																									
				VKPFMTGAAEQIK	3	99.7%	1																									
IPI00978971	RPL13	60S ribosomal protein L13	99.9%	7.9	1	1	1	1	4,408,460	4,531,060	4,283,815	4,506,280	280,127	286,788	356,514	182,602	14.2	14.2	18.6	9.1	1.0	0.8	-1.0	0.8	1.0	0.8	-1.1	0.6	-1.0	0.9	1.1	0.6
				LATQLTGPVMPVR	2	98.4%	1																									
IPI00979002	EEF1D	Protein	100.0%	34.3	5	5	8	3	2,929,117	2,946,747	2,801,653	3,256,796	205,359	88,478	179,609	136,538	15.7	6.7	14.3	9.4	1.0	0.9	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.09	1.2	0.08
IPI00979705	EEF1D	Uncharacterized protein	100.0%	52.6	5	5	8	3	2,929,117	2,946,747	2,801,653	3,256,796	205,359	88,478	179,609	136,538	15.7	6.7	14.3	9.4	1.0	0.9	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.09	1.2	0.08
IPI00981244	EEF1D	Uncharacterized protein	100.0%	55.4	5	5	8	3	2,929,117	2,946,747	2,801,653	3,256,796	205,359	88,478	179,609	136,538	15.7	6.7	14.3	9.4	1.0	0.9	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.09	1.2	0.08
				FYEQMNGPVAGASR	2	100.0%	2																									
				GVVQELQQAISK	2	100.0%	2																									
				IASLEVENQSLR	2	100.0%	2																									
				QENGASVILR	2	99.9%	1																									
				SLAGSSGPGASSGTSGDHGELVVR	3	99.9%	1																									
IPI00979052	CTNND1	Protein	100.0%	19.5	2	2	2	1	229,410	296,476	263,452	324,693	22,590	26,824	15,049	16,116	22.0	20.2	12.8	11.1	1.3	0.09	1.1	0.2	1.4	0.009	-1.1	0.3	1.1	0.4	1.2	0.02
				SDFQVNLNNASR	2	99.9%	1																									
				SLDNNYSTPNER	2	99.7%	1																									
IPI00979179	LOC100508996	hypothetical protein LOC100508996	96.1%	4.2	1	1	1	1	3,568,750	4,173,400	3,828,790	4,941,870	415,229	416,676	391,768	312,750	26.0	22.3	22.9	14.2	1.2	0.3	1.1	0.7	1.4	0.03	-1.1	0.6	1.2	0.2	1.3	0.06
				NEQAHPASATSTTPR	2	96.1%	1																									
IPI00979268	TXNRD1	Uncharacterized protein	100.0%	17.1	2	2	2	5	491,509	533,829	574,786	652,428	52,872	43,528	25,874	42,546	24.1	18.2	10.1	14.6	1.1	0.6	1.2	0.2	1.3	0.05	1.1	0.4	1.2	0.09	1.1	0.2
IPI00979993	TXNRD1	11 kDa protein	100.0%	28.9	2	2	2	5	491,509	533,829	574,786	652,428	52,872	43,528	25,874	42,546	24.1	18.2	10.1	14.6	1.1	0.6	1.2	0.2	1.3	0.05	1.1	0.4	1.2	0.09	1.1	0.2
IPI00982356	TXNRD1	Uncharacterized protein	100.0%	41.7	2	2	2	5	491,509	533,829	574,786	652,428	52,872	43,528	25,874	42,546	24.1	18.2	10.1	14.6	1.1	0.6	1.2	0.2	1.3	0.05	1.1	0.4	1.2	0.09	1.1	0.2
IPI00984681	TXNRD1	Uncharacterized protein	100.0%	21.6	2	2	2	5	491,509	533,829	574,786	652,428	52,872	43,528	25,874	42,546	24.1	18.2	10.1	14.6	1.1	0.6	1.2	0.2	1.3	0.05	1.1	0.4	1.2	0.09	1.1	0.2
IPI00985249	TXNRD1	Uncharacterized protein	100.0%	42.9	2	2	2	5	491,509	533,829	574,786	652,428	52,872	43,528	25,874	42,546	24.1	18.2	10.1	14.6	1.1	0.6	1.2	0.2	1.3	0.05	1.1	0.4	1.2	0.09	1.1	0.2
				VMVLDFVTPTPLGTR	2	100.0%	1																									
				WGLGGTCVNVGCIPK	2	94.9%	1																									
IPI00979518	CFL1	Uncharacterized protein	100.0%	56.9	9	10	15	1	43,980,451	46,185,427	47,002,110	51,125,694	4,205,574	3,114,379	4,037,449	1,223,916	21.4	15.1	19.2	5.4	1.1	0.7	1.1	0.6	1.2	0.2	1.0	0.9	1.1	0.2	1.1	0.4
				EDLVFIFWAPESAPLK	2	99.9%	1																									
				EILVGDVGQTVDDPYATFVK	2	100.0%	2																									
				HELQANCYEEVKDR	3	100.0%	2																									
				KEDLVFIFWAPESAPLK	3	100.0%	2																									
				MIYASSK	1	100.0%	1																									
				MLPDKDCR	2	97.7%	1																									
				NIILEEGKEILVGDVGQTVDDPYATFVK	2	100.0%	2																									
				NIILEEGKEILVGDVGQTVDDPYATFVK	3	100.0%	1																									
				VFNDMK	2	99.2%	1																									
				YALYDATYETK	2	100.0%	2																									
IPI00979595	RPS2	Uncharacterized protein	100.0%	9.8	2	2	3	2	5,346,195	5,839,760	5,081,905	5,547,893	993,409	843,082	277,908	490,688	41.6	32.3	12.2	19.8	1.1	0.7	-1.1	0.8	1.0	0.9	-1.1	0.4	-1.1	0.8	1.1	0.4
IPI00981233	RPS2	Similar to 40S ribosomal protein S2	100.0%	12.0	2	2	3	2	5,346,195	5,839,760	5,081,905	5,547,893	993,409	843,082	277,908	490,688	41.6	32.3	12.2	19.8	1.1	0.7	-1.1	0.8	1.0	0.9	-1.1	0.4	-1.1	0.8	1.1	0.4
				SPYQEFTDHLVK	3	100.0%	1																									
				TYSYLTPDLWK	2	100.0%	2																									
IPI00979664	ATP6V1B2	Protein	100.0%	23.6	3	4	4	1	2,131,344	2,414,779	2,204,839	2,404,819	191,803	137,244	125,133	153,884	20.1	12.7	12.7	14.3	1.1	0.3	1.0	0.8	1.1	0.3	-1.1	0.3	-1.0	1	1.1	0.3
				AVVQVFEGTSGIDAK	2	99.4%	1																									
				IYPEEMIQTGISAIDGMNSIAR	2	98.1%	1																									
				IYPEEMIQTGISAIDGMNSIAR	3	99.9%	1																									
				TPVSEDMLGR	2	98.5%	1																									
IPI00979738	KIAA1967	Protein	100.0%	6.0	1	1	1	4	544,393	579,073	543,018	649,385	92,182	34,528	34,836	40,531	37.9	13.3	14.4	14.0	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.5	1.1	0.2	1.2	0.08
IPI00979880	KIAA1967	Protein	100.0%	7.4	1	1	1	4	544,393	579,073	543,018	649,385	92,182	34,528	34,836	40,531	37.9	13.3	14.4	14.0	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.5	1.1	0.2	1.2	0.08
IPI00980303	KIAA1967	Uncharacterized protein	100.0%	7.3	1	1	1	4	544,393	579,073	543,018	649,385	92,182	34,528	34,836	40,531	37.9	13.3	14.4	14.0	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.5	1.1	0.2	1.2	0.08
IPI00982682	KIAA1967	Uncharacterized protein	100.0%	6.8	1	1	1	4	544,393	579,073	543,018	649,385	92,182	34,528	34,836	40,531	37.9	13.3	14.4	14.0	1.1	0.7	-1.0	1	1.2	0.3	-1.1	0.5	1.1	0.2	1.2	0.08
				VQTLSNQPLLK	2	99.7%	1																									
IPI00979762	NUP214	Putative uncharacterized protein DKFZp686J0330	99.1%	2.4	2	2	2	1	1,171,882	1,131,877	1,135,953	1,258,767	87,548	70,231	54,870	52,685	16.7	13.9	10.8	9.4	-1.0	0.7	-1.0	0.7	1.1	0.4	1.0	1	1.1	0.2	1.1	0.1
				LGELLFPSSLAGETLGSFSGLR	2	99.1%	1																									
				TTLLEGFAGVEEAR	3	91.8%	1																									
IPI00979820	CORO1B	Conserved hypothetical protein	100.0%	11.2	1	1	2	1	2,692,045	2,501,795	3,274,275	3,819,215	186,998	51,623	522,767	749,700	15.5	4.6	35.7	43.9	-1.1	0.4	1.2	0.3	1.4	0.2	1.3	0.2	1.5	0.2	1.2	0.6
				AGEAGKLEEVMQELR	2	100.0%	2																									
IPI00979837	IQGAP1	Conserved hypothetical protein	100.0%	19.0	1	1	2	1	2,225,445	2,266,170	2,200,215	2,261,540	110,762	66,142	113,920	101,933	11.1	6.5	11.6	10.1	1.0	0.8	-1.0	0.9	1.0	0.8	-1.0	0.6	-1.0	1	1.0	0.7
				LEGVLAEVAQHYQDTLIR	3	100.0%	2																									
IPI00979867	LOC100510073	u2 small nuclear ribonucleoprotein A'-like, partial	99.9%	6.5	1	1	1	1	4,240,050	4,478,320	3,520,780	4,370,830	638,905	265,180	163,179	432,828	33.7	13.2	10.4	22.1	1.1	0.7	-1.2	0.3	1.0	0.9	-1.3	0.02	-1.0	0.8	1.2	0.1
				TFNPGAGLPTDK	2	99.6%	1																									
IPI00979872	EIF3F	11 kDa protein	100.0%	11.0	1	1	1	1	4,295,758	6,050,436	4,779,478	5,307,856	940,142	1,425,841	968,542	1,024,226	48.9	52.7	45.3	43.2	1.4	0.3	1.1	0.7	1.2	0.5	-1.3	0.5	-1.1	0.7	1.1	0.7
				FLMSLVNQVPK	2	100.0%	1																									
IPI00980081	YAP1	cDNA FLJ51192, highly similar to 65 kDa Yes-associated protein	100.0%	4.2	1	1	1	1	228,429	240,005	275,587	219,748	32,896	38,847	41,865	23,609	32.2	36.2	34.0	24.0	1.1	0.8	1.2	0.4	-1.0	0.8	1.1	0.6	-1.1	0.7	-1.3	0.3
				LDKESFLTWL	2	99.1%	1																									
IPI00980095	SERPINH1	Uncharacterized protein	100.0%	30.2	1	2	4	1	295,613	299,905	302,962	339,945	30,444	23,398	21,902	16,143	23.0	17.5	16.2	10.6	1.0	0.9	1.0	0.8	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.2
				DQAVENILVSPVVVASSLGLVSLGGK	2	100.0%	2																									
				DQAVENILVSPVVVASSLGLVSLGGK	3	100.0%	2																									
IPI00980105	EEF1D	Uncharacterized protein	100.0%	35.9	3	3	6	1	1,242,936	1,249,849	1,134,981	1,398,864	50,263	14,530	80,624	57,661	9.0	2.6	15.9	9.2	1.0	0.9	-1.1	0.3	1.1	0.08	-1.1	0.2	1.1	0.06	1.2	0.03
				FYEQMNGPVAGASR	2	100.0%	2																									
				GVVQELQQAISK	2	100.0%	2																									
				IASLEVENQSLR	2	100.0%	2																									
IPI00980111	-	Conserved hypothetical protein	96.8%	11.5	1	1	1	2	83,726	85,589	108,949	114,051	9,136	5,944	12,870	6,590	24.4	15.5	26.4	12.9	1.0	0.9	1.3	0.1	1.4	0.03	1.3	0.1	1.3	0.01	1.0	0.7
IPI01013521	DDB1	33 kDa protein	96.8%	3.0	1	1	1	2	83,726	85,589	108,949	114,051	9,136	5,944	12,870	6,590	24.4	15.5	26.4	12.9	1.0	0.9	1.3	0.1	1.4	0.03	1.3	0.1	1.3	0.01	1.0	0.7
				LPSFELLHK	3	96.8%	1																									
IPI00980391	CTNNA1	cDNA FLJ54047, highly similar to Alpha-1 catenin	100.0%	32.3	19	19	22	1	30,770,866	32,304,918	30,625,021	35,240,639	3,309,082	1,030,462	2,650,926	1,088,683	24.1	7.1	19.4	6.9	1.0	0.7	-1.0	1	1.1	0.3	-1.1	0.6	1.1	0.09	1.2	0.1
				AAAGEFADDPCSSVK	2	92.7%	1																									
				AEVQNLGGELVVSGVDSAMSLIQAAK	3	100.0%	2																									
				AIMAQLPQEQK	2	98.7%	1																									
				ALLSAVTR	2	85.8%	1																									
				AVMDHVSDSFLETNVPLLVLIEAAK	3	99.9%	1																									
				IAEQVASFQEEK	2	100.0%	1																									
				KAVMDHVSDSFLETNVPLLVLIEAAKNGNEK	3	96.7%	1																									
				LESIISGAALMADSSCTR	2	100.0%	1																									
				LLEPLVTQVTTLVNTNSK	2	89.9%	1																									
				LLSNTVMPR	2	85.6%	1																									
				MSASQLEALCPQVINAALALAAKPQSK	3	99.5%	1																									
				NAGNEQDLGIQYK	2	100.0%	2																									
				NLMNAVVQTVK	2	100.0%	1																									
				QIIVDPLSFSEER	2	100.0%	2																									
				SDALNSAIDK	2	97.4%	1																									
				SKLDAEVSKWDDSGNDIIVLAK	3	85.5%	1																									
				SQGMASLNLPAVSWK	2	100.0%	1																									
				VLTDAVDDITSIDDFLAVSENHILEDVNK	3	100.0%	1																									
				WDDSGNDIIVLAK	2	100.0%	1																									
IPI00980469	LOC100508006	aldo-keto reductase family 1 member C2-like isoform 2	100.0%	24.6	5	5	6	1	3,696,516	3,674,248	3,489,744	4,127,547	408,020	135,345	258,795	126,288	24.7	8.2	16.6	6.8	-1.0	1	-1.1	0.7	1.1	0.4	-1.1	0.5	1.1	0.04	1.2	0.06
				HIDSAHLYNNEEQVGLAIR	3	100.0%	1																									
				LAIEAGFR	2	97.8%	1																									
				LNDGHFMPVLGFGTYAPAEVPK	3	100.0%	1																									
				QNVQVFEFQLTSEEMK	2	98.0%	1																									
				TPALIALR	2	99.8%	2																									
IPI00980475	PICALM	Uncharacterized protein	100.0%	11.4	4	4	5	1	4,184,611	4,806,331	4,480,317	5,052,413	276,112	136,828	296,983	133,920	14.8	6.4	14.8	5.9	1.1	0.08	1.1	0.5	1.2	0.02	-1.1	0.3	1.1	0.2	1.1	0.1
				GDIPDLSQAPSSLLDALEQHLASLEGK	3	97.3%	1																									
				LFAAYNEGIINLLEK	2	99.3%	2																									
				NDVNWSQPGEK	2	99.5%	1																									
				QAALEEEQAR	2	97.0%	1																									
IPI00980481	00506946;LOC1005	peptidyl-prolyl cis-trans isomerase A-like	100.0%	13.4	3	4	5	1	49,794,225	51,975,660	52,390,585	61,462,615	5,474,074	2,994,522	3,118,254	1,944,326	24.6	12.9	13.3	7.1	1.0	0.7	1.1	0.7	1.2	0.1	1.0	0.9	1.2	0.03	1.2	0.04
				EGMDIVEAMER	2	100.0%	1																									
				VKEGMDIVEAMER	2	99.6%	1																									
				VKEGMDIVEAMER	3	100.0%	1																									
				VSFELFADK	2	100.0%	2																									
IPI00980509	NAP1L4	23 kDa protein	100.0%	8.8	1	2	3	1	573,826	576,869	546,881	713,277	53,167	22,179	40,064	29,250	20.7	8.6	16.4	9.2	1.0	1	-1.0	0.7	1.2	0.05	-1.1	0.5	1.2	0.006	1.3	0.01
				NVDMLSELVQEYDEPILK	2	100.0%	2																									
				NVDMLSELVQEYDEPILK	3	99.6%	1																									
IPI00980661	PSMC3	Uncharacterized protein	100.0%	11.4	1	1	1	1	639,190	678,546	669,048	780,250	94,616	31,677	98,574	43,947	33.1	10.4	33.0	12.6	1.1	0.7	1.0	0.8	1.2	0.2	-1.0	0.9	1.1	0.1	1.2	0.3
				AMEVDERPTEQYSDIGGLDK	3	100.0%	1																									
IPI00980706	PABPC1	Uncharacterized protein	100.0%	22.7	1	1	2	1	155,749	152,174	147,307	172,728	9,435	7,093	14,501	14,814	13.5	10.4	22.0	19.2	-1.0	0.8	-1.1	0.6	1.1	0.4	-1.0	0.8	1.1	0.2	1.2	0.3
				SLGYAYVNFQQPADAER	2	100.0%	2																									
IPI00980818	EIF4G2	27 kDa protein	99.5%	9.8	1	1	1	1	70,444	92,894	81,148	100,996	3,318	5,058	6,700	11,372	10.5	12.2	18.5	25.2	1.3	0.006	1.2	0.2	1.4	0.05	-1.1	0.2	1.1	0.5	1.2	0.2
				QEGIATSDNFMQAFLNVLDQCPK	3	99.5%	1																									
IPI00980919	PPP1CA	Uncharacterized protein	100.0%	13.8	3	3	6	1	2,385,877	2,382,487	2,448,004	2,734,120	175,315	41,728	154,218	146,168	16.4	3.9	14.1	12.0	-1.0	1	1.0	0.8	1.1	0.2	1.0	0.7	1.1	0.07	1.1	0.2
				EIFLSQPILLELEAPLK	2	100.0%	2																									
				HDLDLICR	2	99.9%	2																									
				NVQLTENEIR	2	100.0%	2																									
IPI00980968	SEPHS1	selenide, water dikinase 1 isoform 2	99.9%	4.6	1	1	1	1	2,723,197	2,781,280	2,975,023	2,885,057	161,679	34,204	219,406	284,255	13.3	2.8	16.5	22.0	1.0	0.7	1.1	0.4	1.1	0.6	1.1	0.4	1.0	0.7	-1.0	0.8
				NEVSFVIHNLPVLAK	2	99.7%	1																									

IPI00981058	PHF1	Uncharacterized protein	95.6%	6.0	1	1	1	1	3,438,440	3,720,130	4,241,350	4,137,220	758,507	605,245	458,943	398,825	49.3	36.4	24.2	21.6	1.1	0.8	1.2	0.4	1.2	0.4	1.1	0.5	1.1	0.6	-1.0	0.9
				APGAEGAGSSAEGTAGLSVSTIPQP	2	95.6%	1																									
IPI00981068	SERPINH1	Uncharacterized protein	100.0%	22.8	4	6	9	2	4,526,925	4,821,784	4,685,872	5,153,499	398,144	175,326	184,615	172,300	19.7	8.1	8.8	7.5	1.1	0.5	1.0	0.7	1.1	0.2	-1.0	0.6	1.1	0.2	1.1	0.1
IPI00985439	SERPINH1	Uncharacterized protein	100.0%	25.1	4	6	9	2	4,526,925	4,821,784	4,685,872	5,153,499	398,144	175,326	184,615	172,300	19.7	8.1	8.8	7.5	1.1	0.5	1.0	0.7	1.1	0.2	-1.0	0.6	1.1	0.2	1.1	0.1
				AVLSAEQLRDEEVHAGLGELLR	3	100.0%	1																									
				DQAVENILVSPVVVASSLGLVSLGGK	2	100.0%	2																									
				DQAVENILVSPVVVASSLGLVSLGGK	3	100.0%	2																									
				LQIVEMPLAHK	2	99.9%	1																									
				LQIVEMPLAHK	3	99.1%	1																									
				LYGPSSVSFADDFVR	2	100.0%	2																									
IPI00981077	-	25 kDa protein	100.0%	6.8	1	1	1	1	475,998	482,944	532,048	490,782	42,603	48,002	53,154	54,486	20.0	22.2	22.3	24.8	1.0	0.9	1.1	0.4	1.0	0.8	1.1	0.5	1.0	0.9	-1.1	0.6
				LWDNELQYVDQLLK	2	96.7%	1																									
IPI00981169	CCT2	T-complex protein 1 subunit beta isoform 2	100.0%	46.9	18	22	29	1	44,535,940	44,282,878	44,096,178	49,688,952	3,268,212	1,313,897	2,601,668	1,180,249	16.4	6.6	13.2	5.3	-1.0	0.9	-1.0	0.9	1.1	0.2	-1.0	1	1.1	0.02	1.1	0.09
				AAHSEGNTTAGLDMR	2	100.0%	1																									
				AAHSEGNTTAGLDMR	3	95.2%	1																									
				DASLMVTNDGATILK	2	100.0%	2																									
				EGTIGDMAILGITESFQVK	2	100.0%	1																									
				FRQDLMNIAGTTLSSK	3	99.9%	1																									
				GATQQILDEAER	2	100.0%	2																									
				GSGNLEAIHIIK	2	87.3%	1																									
				ILIANTGMDTDK	2	90.4%	1																									
				KLGGSLADSYLDEGFLLDKK	3	100.0%	1																									
				LAVEAVLR	2	89.1%	1																									
				LGGSLADSYLDEGFLLDK	2	100.0%	1																									
				LGGSLADSYLDEGFLLDKK	2	100.0%	1																									
				LGGSLADSYLDEGFLLDKK	3	100.0%	2																									
				LIEEVMIGEDK	2	100.0%	1																									
				LKGSGNLEAIHIIK	3	98.0%	1																									
				MLPTIIADNAGYDSADLVAQLR	2	100.0%	2																									
				MLPTIIADNAGYDSADLVAQLR	3	100.0%	2																									
				QDLMNIAGTTLSSK	2	100.0%	1																									
				QLIYNYPEQLFGAAGVMAIEHADFAGVER	3	99.6%	1																									
				SLHDALCVLAQTVK	2	97.5%	1																									
				VQDDEVGDGTTSVTVLAAELLR	2	100.0%	2																									
				VQDDEVGDGTTSVTVLAAELLR	3	100.0%	2																									
IPI00981271	CTNNA1	cDNA FLJ54052, highly similar to Alpha-1 catenin	100.0%	35.1	19	19	22	1	30,089,021	31,596,903	30,045,076	34,702,334	3,341,412	1,094,948	2,648,599	1,065,927	24.8	7.8	19.7	6.9	1.1	0.7	-1.0	1	1.2	0.2	-1.1	0.6	1.1	0.08	1.2	0.1
				AAAGEFADDPCSSVK	2	92.7%	1																									
				AEVQNLGGELVVSGVDSAMSLIQAAK	3	100.0%	2																									
				AIMAQLPQEQK	2	98.7%	1																									
				ALLSAVTR	2	85.8%	1																									
				AVMDHVSDSFLETNVPLLVLIEAAK	3	99.9%	1																									
				IAEQVASFQEEK	2	100.0%	1																									
				KAVMDHVSDSFLETNVPLLVLIEAAKNGNEK	3	96.7%	1																									
				LESIISGAALMADSSCTR	2	100.0%	1																									
				LLILADMADVYK	2	100.0%	1																									
				LLSNTVMPR	2	85.6%	1																									
				MSASQLEALCPQVINAALALAAKPQSK	3	99.5%	1																									
				NAGNEQDLGIQYK	2	100.0%	2																									
				NLMNAVVQTVK	2	100.0%	1																									
				QIIVDPLSFSEER	2	100.0%	2																									
				SDALNSAIDK	2	97.4%	1																									
				SKLDAEVSKWDDSGNDIIVLAK	3	85.5%	1																									
				SQGMASLNLPAVSWK	2	100.0%	1																									
				VLTDAVDDITSIDDFLAVSENHILEDVNK	3	100.0%	1																									
				WDDSGNDIIVLAK	2	100.0%	1																									
IPI00981294	LYPLA1	Uncharacterized protein	100.0%	15.6	1	1	2	1	525,944	519,314	534,854	572,864	45,546	24,693	28,795	37,069	19.4	10.6	12.0	14.5	-1.0	0.9	1.0	0.9	1.1	0.4	1.0	0.7	1.1	0.3	1.1	0.4
				LAGVTALSCWLPLR	2	100.0%	2																									
IPI00981307	C10orf58	Conserved hypothetical protein	100.0%	11.4	1	1	1	1	1,347,708	1,449,930	1,514,195	1,550,038	65,812	72,995	93,043	173,825	10.9	11.3	13.7	25.1	1.1	0.3	1.1	0.2	1.2	0.3	1.0	0.6	1.1	0.6	1.0	0.9
				AALEYLEDIDLK	2	99.1%	1																									
IPI00981344	UBE2V2	Protein	99.9%	14.7	1	1	1	2	393,035	387,311	377,061	421,187	36,019	26,999	12,064	21,943	20.5	15.6	7.2	11.7	-1.0	0.9	-1.0	0.7	1.1	0.5	-1.0	0.7	1.1	0.4	1.1	0.1
IPI01015099	UBE2V2	12 kDa protein	99.9%	15.2	1	1	1	2	393,035	387,311	377,061	421,187	36,019	26,999	12,064	21,943	20.5	15.6	7.2	11.7	-1.0	0.9	-1.0	0.7	1.1	0.5	-1.0	0.7	1.1	0.4	1.1	0.1
				INMNGINNSSGMVDAR	2	100.0%	1																									
IPI00981366	PABPC1	Protein	100.0%	26.9	4	4	6	1	1,921,321	1,916,667	1,843,682	2,127,616	162,630	93,217	100,077	115,415	18.9	10.9	12.1	12.1	-1.0	1	-1.0	0.7	1.1	0.3	-1.0	0.6	1.1	0.2	1.2	0.1
				AKEFTNVYIK	3	99.9%	1																									
				ALDTMNFDVIK	2	100.0%	2																									
				MNGMLLNDR	2	95.6%	1																									
				SLGYAYVNFQQPADAER	2	100.0%	2																									
IPI00981682	PROSC	14 kDa protein	100.0%	13.3	1	1	1	1	339,465	349,072	371,877	347,827	48,019	71,060	58,653	35,864	31.6	45.5	35.3	23.1	1.0	0.9	1.1	0.7	1.0	0.9	1.1	0.8	-1.0	1	-1.1	0.7
				LMAVPNLFMLETVDSVK	2	100.0%	1																									
IPI00981781	LOC100132581	speedy protein E3-like	91.5%	8.7	1	1	1	1	2,653,271	3,342,823	3,971,800	3,606,050	808,693	898,870	606,919	659,697	68.2	60.1	34.2	40.9	1.3	0.6	1.5	0.2	1.4	0.4	1.2	0.6	1.1	0.8	-1.1	0.7
				TETRFGEMGQILGKIMMSHQPQPQEER	3	91.6%	1																									
IPI00981865	LOC100509382	putative tubulin beta-4q chain-like	95.8%	7.3	1	1	1	1	2,240,150	2,311,040	2,207,450	2,641,620	217,624	143,475	126,141	99,878	21.7	13.9	12.8	8.5	1.0	0.8	-1.0	0.9	1.2	0.1	-1.0	0.6	1.1	0.1	1.2	0.03
				ACRVAGEDVGSGGSGAPALRPLGSLPGTVEPGGWR	3	95.8%	1																									
IPI00981910	LOC100508006	aldo-keto reductase family 1 member C2-like isoform 1	100.0%	27.9	6	6	7	1	4,440,919	4,407,598	4,347,314	4,995,510	509,039	139,442	333,072	177,319	25.6	7.1	17.1	7.9	-1.0	1	-1.0	0.9	1.1	0.4	-1.0	0.9	1.1	0.03	1.1	0.1
				HIDSAHLYNNEEQVGLAIR	3	100.0%	1																									
				ILFDTVDLCATWEAMEK	2	99.4%	1																									
				LAIEAGFR	2	97.8%	1																									
				LNDGHFMPVLGFGTYAPAEVPK	3	100.0%	1																									
				QNVQVFEFQLTSEEMK	2	98.0%	1																									
				TPALIALR	2	99.8%	2																									
IPI00981914	EPS8L2	EPS8L2 protein	100.0%	10.1	6	6	6	1	10,400,070	11,266,065	10,982,515	12,755,476	1,275,037	779,810	460,308	814,746	27.4	15.5	9.4	14.3	1.1	0.6	1.1	0.7	1.2	0.2	-1.0	0.8	1.1	0.2	1.2	0.09
				EPQVPLYVPK	3	97.8%	1																									
				IWTQEMLLQVNDQSLR	3	95.5%	1																									
				SEAITSVDDAIR	2	99.7%	1																									
				SQPVSQPLTYESGPDEVR	2	99.6%	1																									
				SQTVLNQLR	2	86.6%	1																									
				VYSQLTMQK	2	97.3%	1																									
IPI00982009	AP2A2	cDNA FLJ57955, highly similar to Adapter-relatedprotein complex 2 alpha- 2 subunit	100.0%	6.8	2	2	2	1	1,886,873	1,768,682	2,035,215	2,167,422	79,567	110,552	134,291	78,842	9.4	14.0	14.8	8.1	-1.1	0.4	1.1	0.4	1.1	0.04	1.2	0.2	1.2	0.02	1.1	0.4
				IIGFGSALLEEVDPNPANFVGAGIIHTK	3	100.0%	1																									
				VGGYILGEFGNLIAGDPR	2	100.0%	1																									
IPI00982043	KIAA1967	Uncharacterized protein	100.0%	20.6	3	3	3	1	4,417,490	4,180,313	4,281,357	4,636,247	270,201	211,081	314,565	167,344	13.7	11.3	16.4	8.1	-1.1	0.5	-1.0	0.8	1.0	0.5	1.0	0.8	1.1	0.1	1.1	0.3
				FAEFQYLQPGPPR	2	99.3%	1																									
				KEEEAVLVGGEWSPSLDGLDPQADPQVLVR	3	100.0%	1																									
				VLLLSSPGLEELYR	2	98.5%	1																									
IPI00982064	-	Conserved hypothetical protein	99.4%	10.0	1	1	1	1	1,180,320	1,229,693	1,181,337	1,295,943	135,981	134,122	141,282	164,671	25.8	24.4	26.7	28.4	1.0	0.8	1.0	1	1.1	0.6	-1.0	0.8	1.1	0.8	1.1	0.6
				MAAADSVQQR	2	99.8%	1																									
IPI00982087	HYOU1	cDNA FLJ59408, highly similar to 150 kDa oxygen-regulated protein	100.0%	12.4	5	7	9	1	10,677,359	10,864,365	10,820,188	12,224,045	1,092,372	575,974	579,333	339,029	22.9	11.9	12.0	6.2	1.0	0.9	1.0	0.9	1.1	0.2	-1.0	1	1.1	0.08	1.1	0.07
				LCQGLFFR	2	98.5%	1																									
				LIPEMDQIFTEVEMTTLEK	2	100.0%	2																									
				LIPEMDQIFTEVEMTTLEK	3	100.0%	1																									
				LPATEKPVLLSK	3	99.6%	1																									
				LSAASTWLEDEGVGATTVMLK	2	100.0%	2																									
				LSAASTWLEDEGVGATTVMLK	3	100.0%	1																									
				VESVFETLVEDSAEEESTLTK	2	100.0%	1																									
IPI00982182	CCS	Uncharacterized protein	99.9%	19.1	1	1	1	1	880,543	995,207	880,053	1,078,350	54,831	100,053	103,301	10,744	13.9	22.5	26.3	2.2	1.1	0.3	-1.0	1	1.2	0.02	-1.1	0.4	1.1	0.5	1.2	0.1
				SLIIDEGEDDLGR	2	100.0%	1																									
IPI00982314	NPEPPS	cDNA FLJ38558 fis, clone HCHON2003327, highly similar to Puromycin-sensitive ar	100.0%	6.2	2	2	2	1	1,070,493	1,164,266	1,147,067	1,313,030	130,724	55,016	110,511	53,772	27.3	10.6	21.5	9.2	1.1	0.5	1.1	0.7	1.2	0.1	-1.0	0.9	1.1	0.09	1.1	0.2
				DYFNVPYPLPK	2	100.0%	1																									
				NAATEDLWESLENASGKPIAAVMNTWTK	3	99.9%	1																									
IPI00982388	NDUFS3	Uncharacterized protein	99.4%	19.2	1	1	1	2	1,912,946	1,865,392	2,031,256	2,176,822	205,920	130,083	133,825	80,964	24.1	15.6	14.7	8.3	-1.0	0.9	1.1	0.6	1.1	0.3	1.1	0.4	1.2	0.08	1.1	0.4
IPI00983082	NDUFS3	14 kDa protein	99.4%	12.4	1	1	1	2	1,912,946	1,865,392	2,031,256	2,176,822	205,920	130,083	133,825	80,964	24.1	15.6	14.7	8.3	-1.0	0.9	1.1	0.6	1.1	0.3	1.1	0.4	1.2	0.08	1.1	0.4
				QLSAFGEYVAEILPK	2	99.4%	1																									
IPI00982468	NDRG1	cDNA FLJ33828 fis, clone CTONG2003599, highly similar to Protein NDRG1	100.0%	33.2	5	5	9	2	2,922,352	2,963,715	3,043,535	3,558,593	299,094	104,121	291,480	140,089	22.9	7.9	21.4	8.8	1.0	0.9	1.0	0.8	1.2	0.09	1.0	0.8	1.2	0.009	1.2	0.1
IPI01011666	NDRG1	cDNA FLJ55222, highly similar to Protein NDRG1	100.0%	31.7	5	5	9	2	2,922,352	2,963,715	3,043,535	3,558,593	299,094	104,121	291,480	140,089	22.9	7.9	21.4	8.8	1.0	0.9	1.0	0.8	1.2	0.09	1.0	0.8	1.2	0.009	1.2	0.1
				FALNNPEMVEGLVLINVNPCAEGWMDWAASK	3	96.9%	1																									
				ISGWTQALPDMVVSHLFGK	3	100.0%	2																									
				MADCGGLPQISQPAK	2	100.0%	2																									
				SHTSEGAHLDITPNSGAAGNSAGPK	3	100.0%	2																									
				TASGSSVTSLDGTR	2	100.0%	2																									
IPI00982472	TALDO1	cDNA FLJ57988, highly similar to Transaldolase	100.0%	6.9	2	2	3	1	9,367,550	9,547,500	9,038,455	10,910,045	705,926	453,900	612,258	408,637	16.9	10.6	15.2	8.4	1.0	0.8	-1.0	0.7	1.2	0.1	-1.1	0.5	1.1	0.06	1.2	0.03
				LLGELLQDNAK	2	100.0%	2																									
				SYEPLEDPGVK	2	100.0%	1																									
IPI00982482	IARS	Uncharacterized protein	100.0%	12.5	12	12	13	1	27,370,063	27,958,460	27,740,000	32,006,191	2,511,868	1,552,607	2,243,148	854,288	20.5	12.4	18.1	6.0	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.9	1.1	0.05	1.2	0.1
				EFEDAFPADFIAEGIDQTR	2	100.0%	1																									
				FGWDCHGLPVEYEIDK	3	89.0%	1																									
				FVDILTNWYVR	2	100.0%	1																									
				GSELEITLTR	2	99.8%	1																									
				LQKEEEIEFLYNENTVR	3	89.2%	1																									
				NNDLCYWVPELVR	2	85.9%	1																									
				NVIVNGLVLASDGQK	2	98.8%	1																									
				QLSSEELEQFQK	2	99.7%	2																									
				TESAVSQMQSVIELGR	2	100.0%	1																									
				VENMVDQLLR	2	96.6%	1																									
				WIDFDNDYK	2	89.2%	1																									
				YGADALR	2	91.4%	1																									
IPI00982539	DAK	Dha kinase/FMN cyclase splice variant	100.0%	24.3	8	10	12	1	17,771,908	18,001,855	17,595,572	19,799,227	1,105,871	775,786	1,184,586	619,628	13.9	9.6	15.1	7.0	1.0	0.9	-1.0	0.9	1.1	0.1	-1.0	0.8	1.1	0.1	1.1	0.1
				AAGDGDCGTTHSR	3	95.7%	1																									
				EGPPPASPAQLLSK	2	99.9%	1																									
				SPGADLLQVLTK	2	100.0%	2																									
				TMLDSLWAAGQELQAWK	2	100.0%	2																									
				TSLPAWSAAMDAGLEAMQK	2	100.0%	1																									
				TSLPAWSAAMDAGLEAMQK	3	100.0%	1																									
				VAGALAEAGVGLEEIAK	2	100.0%	1																									
				VAPAEPQEAPDSTAAGGSASK	2	99.3%	1																									
				VCSTLLGLEEHLNALDR	2	100.0%	1																									
				VCSTLLGLEEHLNALDR	3	100.0%	1																									
IPI00982578	DSTN	15 kDa protein	100.0%	32.6	4	4	5	1	5,019,552	5,180,157	4,800,882	5,730,004	414,636	176,389	322,045	193,804	18.5	7.6	15.0	7.6	1.0	0.7	-1.0	0.7	1.1	0.2	-1.1	0.3	1.1	0.07	1.2	0.04

				HFVGMLPEK	2	99.9%	1																									
				KEELMFFLWAPELAPLK	3	99.3%	1																									
				MIYASSK	1	100.0%	1																									
				YALYDASFETK	2	100.0%	2																									
IPI01013328	LOC100293977;LOC	Uncharacterized protein	93.5%	6.6	1	1	1	2	2,167,035	2,749,280	2,414,890	2,636,885	70,022	202,173	150,422	205,735	7.2	16.4	13.9	17.5	1.3	0.04	1.1	0.2	1.2	0.08	-1.1	0.2	-1.0	0.7	1.1	0.4
IPI00982589	LOC100293977;LOC	Uncharacterized protein	93.5%	6.6	1	1	1	2	2,167,035	2,749,280	2,414,890	2,636,885	70,022	202,173	150,422	205,735	7.2	16.4	13.9	17.5	1.3	0.04	1.1	0.2	1.2	0.08	-1.1	0.2	-1.0	0.7	1.1	0.4
				RGTVTGPSR	2	93.5%	1																									
IPI00982634	SSH3	Uncharacterized protein	100.0%	12.6	2	2	2	1	2,453,643	2,657,485	2,562,903	2,803,228	204,253	212,972	281,050	128,959	18.6	17.9	24.5	10.3	1.1	0.5	1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.6	1.1	0.5
				QLQIYQGILTASR	2	99.4%	1																									
				VLDVSDLESVTSK	2	99.9%	1																									
IPI00982734	FKBP4	Conserved hypothetical protein	100.0%	23.0	3	3	3	1	8,230,833	8,899,180	8,125,643	10,076,397	1,214,853	865,172	1,007,662	530,235	33.0	21.7	27.7	11.8	1.1	0.7	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.3	1.2	0.1
				LYANMFER	2	99.6%	1																									
				TQLAVCQQR	2	99.9%	1																									
				VLQLYPNNK	2	99.8%	1																									
IPI00983023	LOC100290936	phosphoglycerate mutase 1-like	100.0%	22.9	3	3	5	1	12,883,310	13,868,756	12,374,720	16,202,065	1,776,468	957,191	1,383,481	737,349	30.8	15.4	25.0	10.2	1.1	0.6	-1.0	0.8	1.3	0.1	-1.1	0.4	1.2	0.09	1.3	0.04
				FSGWYDADLSPAGHEEAK	2	100.0%	1																									
				HGESAWNLENR	2	100.0%	2																									
				HYGGLTGLNK	2	99.9%	2																									
IPI00983098	LYPLA1	Uncharacterized protein	100.0%	12.7	2	2	3	1	1,564,727	1,526,222	1,656,697	1,794,066	104,528	59,524	162,408	187,971	14.9	8.7	21.9	23.4	-1.0	0.8	1.1	0.6	1.1	0.3	1.1	0.5	1.2	0.2	1.1	0.6
				LAGVTALSCWLPLR	2	100.0%	2																									
				TLVNPANVTFK	2	99.4%	1																									
IPI00983167	PPP2CB	Protein	100.0%	50.0	2	2	2	1	3,299,933	3,693,090	3,660,947	3,884,553	216,927	153,871	301,058	79,724	14.7	9.3	18.4	4.6	1.1	0.2	1.1	0.4	1.2	0.05	-1.0	0.9	1.1	0.3	1.1	0.5
				CGNQAAIMELDDTLK	2	99.9%	1																									
				YSFLQFDPAPR	2	100.0%	1																									
IPI00983315	NUP214	Protein	99.5%	9.1	1	1	1	1	306,760	300,625	326,742	321,797	17,143	17,414	35,705	5,988	12.5	13.0	24.4	4.2	-1.0	0.8	1.1	0.6	1.0	0.4	1.1	0.5	1.1	0.3	-1.0	0.9
				QSDQINWESWLLEDSSR	2	99.5%	1																									
IPI00983370	PAK1	Protein	100.0%	15.6	2	2	2	1	1,108,866	1,000,490	1,137,032	979,731	89,858	52,418	52,112	138,671	18.1	11.7	10.3	31.7	-1.1	0.3	1.0	0.8	-1.1	0.5	1.1	0.1	-1.0	0.9	-1.2	0.3
				SAEDYNSSNALNVK	2	99.9%	1																									
				SVIEPLPVTPTR	2	99.9%	1																									
IPI00983378	GANAB	Uncharacterized protein	100.0%	21.0	12	13	16	1	31,391,497	31,558,242	33,328,321	36,694,258	2,488,502	1,408,388	2,180,628	1,473,758	17.7	10.0	14.6	9.0	1.0	1	1.1	0.6	1.2	0.1	1.1	0.5	1.2	0.04	1.1	0.2
				DENSVELTMAEGPYK	2	100.0%	1																									
				FGAVWTGDNTAEWDHLK	3	100.0%	1																									
				FSFSGNTLVSSSADPEGHFETPIWIER	3	100.0%	2																									
				GLLEFEHQR	2	99.3%	1																									
				LSFQHDPETSVLVLR	3	100.0%	1																									
				LVAIVDPHIK	2	99.9%	1																									
				LVAIVDPHIK	3	99.7%	1																									
				MMDYLQGSGETPQTDVR	2	100.0%	2																									
				NPEPELLVR	2	98.3%	1																									
				QYASLTGTQALPPLFSLGYHQSR	3	100.0%	1																									
				VVIIGAGKPAAVVLQTK	2	100.0%	1																									
				WYQMGAYQPFFR	2	100.0%	2																									
				YFTWDPSR	2	98.7%	1																									
IPI00983506	ERGIC1	Protein	100.0%	14.4	1	1	1	1	2,451,690	2,701,297	2,689,747	1,975,027	253,147	249,880	269,335	147,745	23.1	20.7	22.4	16.7	1.1	0.5	1.1	0.5	-1.2	0.1	-1.0	1	-1.4	0.04	-1.4	0.05
				LSFGDTLQVQNIHGAFNALGGADR	3	99.9%	1																									
IPI00983557	RPS3	Protein	100.0%	17.0	2	2	4	1	1,066,392	1,136,504	1,021,674	1,213,940	78,127	54,164	74,051	55,298	16.4	10.7	16.2	10.2	1.1	0.5	-1.0	0.7	1.1	0.2	-1.1	0.2	1.1	0.3	1.2	0.07
				ELAEDGYSGVEVR	2	100.0%	2																									
				GGKPEPPAMPQPVPTA	2	100.0%	2																									
IPI00983604	TXNRD1	Uncharacterized protein	100.0%	28.3	1	1	1	1	241,229	290,539	325,783	348,105	38,677	36,885	17,530	37,588	35.9	28.4	12.0	24.1	1.2	0.4	1.4	0.08	1.4	0.08	1.1	0.4	1.2	0.3	1.1	0.6
				VMVLDFVTPTPLGTR	2	100.0%	1																									
IPI00983632	PSMA5	proteasome subunit alpha type-5 isoform 2	100.0%	10.4	1	1	1	1	793,420	960,792	724,022	1,103,355	109,492	132,210	115,316	82,733	30.9	30.8	35.6	16.8	1.2	0.4	-1.1	0.7	1.4	0.05	-1.3	0.2	1.1	0.4	1.5	0.03
				AIGSASEGAQSSLQEVYHK	2	100.0%	1																									
IPI00983735	PROSC	Uncharacterized protein	100.0%	19.7	2	2	3	1	1,287,363	1,351,742	1,345,748	1,249,700	122,239	141,851	144,050	82,213	21.2	23.5	23.9	14.7	1.1	0.7	1.0	0.8	-1.0	0.8	-1.0	1	-1.1	0.6	-1.1	0.6
				LMAVPNLFMLETVDSVK	2	100.0%	1																									
				TFGENYVQELLEK	2	100.0%	2																									
IPI00983774	PPP2CB	14 kDa protein	100.0%	24.2	2	2	2	1	2,623,071	2,602,547	3,006,764	2,905,403	230,183	137,278	167,693	132,410	19.6	11.8	12.5	10.2	-1.0	0.9	1.1	0.2	1.1	0.3	1.2	0.1	1.1	0.2	-1.0	0.6
				AHQLVMEGYNWCHDR	3	99.9%	1																									
				CGNQAAIMELDDTLK	2	99.9%	1																									
IPI00983900	RPS7	Ribosomal protein S7 variant (Fragment)	100.0%	29.5	2	2	2	1	3,497,453	3,204,697	3,739,273	4,135,253	428,521	198,649	323,489	209,075	27.4	13.9	19.3	11.3	-1.1	0.6	1.1	0.7	1.2	0.2	1.2	0.2	1.3	0.01	1.1	0.3
				TLTAVHDAILEDLVFPSEIVGK	3	99.8%	1																									
				TLTAVHDAILEDLVFPSEIVGKR	3	100.0%	1																									
IPI00984011	NUDT5	Protein	100.0%	11.0	1	1	2	1	443,868	492,677	471,652	545,690	5,820	23,881	35,575	31,968	2.9	10.8	16.9	13.1	1.1	0.1	1.1	0.5	1.2	0.03	-1.0	0.6	1.1	0.2	1.2	0.2
				EQTADGVAVIPVLQR	2	100.0%	2																									
IPI00984022	UBA2	cDNA FLJ42740 fis, clone BRAWH2016655, highly similar to Ubiquitin-like 1-activati	100.0%	2.2	1	1	1	1	3,957,170	3,313,365	4,357,985	4,067,520	216,046	151,653	398,223	190,938	12.2	10.2	20.4	10.5	-1.2	0.04	1.1	0.4	1.0	0.7	1.3	0.06	1.2	0.01	-1.1	0.5
				QFILVMNALDNR	2	99.8%	1																									
IPI00984035	EIF3E	Uncharacterized protein	100.0%	16.5	4	4	4	1	5,882,234	5,970,929	6,241,434	6,885,228	350,728	283,597	379,493	286,140	13.3	10.6	13.6	9.3	1.0	0.8	1.1	0.5	1.2	0.06	1.0	0.6	1.2	0.05	1.1	0.2
				LASEILMQNWDAAMEDLTR	2	100.0%	1																									
				LGHVVMGNNAVSPYQQVIEK	3	99.7%	1																									
				MFEDPETTR	2	93.2%	1																									
				YLTTAVITNK	2	95.7%	1																									
IPI00984197	SF1	cDNA FLJ54056, highly similar to Splicing factor 1	100.0%	6.6	2	2	2	1	1,165,255	1,124,414	1,124,991	1,286,854	84,523	48,897	85,152	51,834	16.2	9.7	16.9	9.0	-1.0	0.7	-1.0	0.7	1.1	0.3	1.0	1	1.1	0.05	1.1	0.1
				VMIPQDEYPEINFVGLLIGPR	3	100.0%	1																									
				WNQDTMEQK	2	99.9%	1																									
IPI00984217	CTNNA1	Catenin (Cadherin-associated protein), alpha 1, 102kDa, isoform CRA_c	100.0%	20.2	5	5	6	1	3,988,140	3,650,983	4,142,443	4,481,034	383,070	303,229	390,491	231,039	21.5	18.6	21.1	11.5	-1.1	0.5	1.0	0.8	1.1	0.3	1.1	0.3	1.2	0.06	1.1	0.5
				AEVQNLGGELVVSGVDSAMSLIQAAK	3	100.0%	2																									
				AVMDHVSDSFLETNVPLLVLIEAAK	3	99.9%	1																									
				SQGMASLNLPAVSWK	2	100.0%	1																									
				VLTDAVDDITSIDDFLAVSENHILEDVNK	3	100.0%	1																									
				WDDSGNDIIVLAK	2	100.0%	1																									
IPI00984262	FKBP9	cDNA FLJ53831, highly similar to FK506-binding protein 9	92.5%	2.7	1	1	1	1	682,987	821,107	552,254	803,713	102,416	64,574	91,229	119,729	33.5	17.6	36.9	33.3	1.2	0.3	-1.2	0.4	1.2	0.5	-1.5	0.04	-1.0	0.9	1.5	0.1
				YHYVGTFPDGQK	2	92.5%	1																									
IPI00984327	LOC100505836	hypothetical protein LOC100505836 isoform 2	93.9%	16.5	1	1	1	1	3,504,202	4,400,062	4,183,280	4,103,560	1,209,428	1,364,804	678,962	918,916	77.2	69.4	36.3	50.1	1.3	0.6	1.2	0.6	1.2	0.7	-1.1	0.9	-1.1	0.9	-1.0	0.9
				NDNGSCLEDCISYYILLNLR	3	93.9%	1																									
IPI00984346	-	Conserved hypothetical protein	100.0%	16.2	2	2	3	1	669,162	697,038	588,886	694,626	45,637	37,383	42,961	20,314	15.3	12.0	16.3	6.5	1.0	0.6	-1.1	0.2	1.0	0.6	-1.2	0.09	-1.0	1	1.2	0.06
				NYQQNYQNSESGEKNEGSESAPEGQAQQR	3	100.0%	1																									
				SVGDGETVEFDVVEGEK	2	100.0%	2																									
IPI00984351	FAM49B	cDNA FLJ10364 fis, clone NT2RM2001319	93.4%	10.7	1	1	1	1	625,950	708,707	664,273	789,783	32,689	43,189	31,912	57,182	11.7	13.6	10.7	16.2	1.1	0.2	1.1	0.4	1.3	0.04	-1.1	0.4	1.1	0.3	1.2	0.09
				INNVPAEGENEVNNELANR	3	93.4%	1																									
IPI00984387	DPYSL2	cDNA FLJ53166, highly similar to Dihydropyrimidinase-related protein 2	100.0%	37.5	12	13	19	1	15,107,966	15,913,641	15,833,527	17,437,810	1,328,623	605,060	1,352,197	482,460	19.7	8.5	19.1	6.2	1.1	0.6	1.0	0.7	1.2	0.2	-1.0	1	1.1	0.08	1.1	0.3
				AITIANQTNCPLYITK	2	100.0%	1																									
				DIGAIAQVHAENGDIIAEEQQR	3	100.0%	2																									
				DNFTLIPEGTNGTEER	2	88.3%	1																									
				FQLTDCQIYEVLSVIR	2	96.3%	1																									
				FQLTDCQIYEVLSVIR	3	97.5%	1																									
				FQMPDQGMTSADDFFQGTK	2	100.0%	2																									
				GIQEEMEALVK	2	100.0%	2																									
				GLYDGPVCEVSVTPK	2	100.0%	2																									
				ILDLGITGPEGHVLSRPEEVEAEAVNR	3	100.0%	1																									
				MDENQFVAVTSTNAAK	2	98.9%	1																									
				NLHQSGFSLSGAQIDDNIPR	3	100.0%	1																									
				QIGENLIVPGGVK	2	99.9%	2																									
				SSAEVIAQAR	2	99.4%	2																									
IPI00984405	DDX5	Putative uncharacterized protein (Fragment)	100.0%	8.3	3	3	4	1	6,203,759	6,570,963	6,320,141	7,199,750	367,686	356,187	370,642	304,976	13.3	12.1	13.1	9.5	1.1	0.5	1.0	0.8	1.2	0.07	-1.0	0.6	1.1	0.2	1.1	0.1
				APILIATDVASR	2	100.0%	2																									
				ELAQQVQQVAAEYCR	2	99.8%	1																									
				NFYQEHPDLAR	2	99.8%	1																									
IPI00827972	PARF	Putative GTP-binding protein Parf	100.0%	7.0	2	2	3	1	960,290	1,007,055	955,098	1,253,767	58,405	117,341	36,394	107,462	13.6	26.1	8.5	19.2	1.0	0.7	-1.0	0.9	1.3	0.04	-1.1	0.7	1.2	0.2	1.3	0.05
				FFNIPFLQLQR	2	100.0%	2																									
				PFVEEYIPTQEIQVTSIHWSYK	3	99.8%	1																									
IPI00984546	-	cDNA FLJ53223, highly similar to Adapter-relatedprotein complex 2 beta-1 subunit	100.0%	17.1	11	11	13	1	7,073,207	7,835,270	7,652,488	8,172,174	703,863	324,673	606,691	115,990	22.3	9.3	17.7	3.2	1.1	0.4	1.1	0.6	1.2	0.2	-1.0	0.8	1.0	0.4	1.1	0.4
				AAMIWIVGEYAER	2	100.0%	2																									
				APEVSQYIYQVYDSILK	2	92.8%	1																									
				CVSTLLDLIQTK	2	100.0%	1																									
				LAPPLVTLLSGEPEVQYVALR	2	99.9%	1																									
				LASQANIAQVLAELK	2	100.0%	2																									
				LASQANIAQVLAELKEYATEVDVDFVR	3	100.0%	1																									
				LHDINAQMVEDQGFLDSLR	3	100.0%	1																									
				LTNGIWILAELR	2	100.0%	1																									
				MEPLNNLQVAVK	2	99.8%	1																									
				SQPDMAIMAVNSFVK	2	99.7%	1																									
				YNDPIYVK	2	99.7%	1																									
IPI00984548	PUF60	Uncharacterized protein	100.0%	12.3	2	2	3	1	952,035	973,197	760,577	933,049	74,011	41,842	71,509	86,426	17.4	9.6	21.0	20.7	1.0	0.8	-1.3	0.1	-1.0	0.9	-1.3	0.03	-1.0	0.7	1.2	0.2
				LGLPPLTPEQQEALQK	2	100.0%	2																									
				SIDMSWDSVTMK	2	97.5%	1																									
IPI00984608	RPS18	10 kDa protein	100.0%	24.4	2	2	3	1	5,165,615	5,388,575	4,854,478	6,330,765	556,135	436,038	352,594	359,718	24.1	18.1	16.2	12.7	1.0	0.8	-1.1	0.6	1.2	0.1	-1.1	0.4	1.2	0.1	1.3	0.02
				IPDWFLNR	2	99.9%	2																									
				YSQVLANGLDNK	2	99.9%	1																									
IPI00984618	ELF3	Conserved hypothetical protein	100.0%	16.3	1	1	1	1	703,225	746,140	572,820	740,153	68,067	62,566	52,874	38,996	21.6	18.8	20.6	11.8	1.1	0.7	-1.2	0.2	1.1	0.7	-1.3	0.07	-1.0	0.9	1.3	0.03
				VKIEPGVDPDDTYNETPYEK	3	99.8%	1																									
IPI00984629	PKP3	Uncharacterized protein	100.0%	15.7	2	2	2	1	9,776,407	10,685,250	9,714,470	11,112,183	488,714	461,221	547,314	277,925	11.2	9.7	12.6	5.6	1.1	0.2	-1.0	0.9	1.1	0.04	-1.1	0.2	1.0	0.5	1.1	0.05
				GVGGAVPGAVLEPVAR	2	100.0%	1																									
				LSSGFDDIDLPSAVK	2	99.9%	1																									
IPI00984655	ACOX1	peroxisomal acyl-coenzyme A oxidase 1 isoform c	100.0%	2.3	1	1	1	2	475,678	526,740	579,595	530,935	47,833	42,706	42,877	30,283	22.5	18.1	16.5	12.8	1.1	0.4	1.2	0.1	1.1	0.4	1.1	0.4	1.0	0.9	-1.1	0.4
IPI01015174	ACOX1	cDNA FLJ54384, highly similar to Acyl-coenzyme A oxidase 1, peroxisomal	100.0%	2.4	1	1	1	2	475,678	526,740	579,595	530,935	47,833	42,706	42,877	30,283	22.5	18.1	16.5	12.8	1.1	0.4	1.2	0.1	1.1	0.4	1.1	0.4	1.0	0.9	-1.1	0.4
				YDGNVYENLFEWAK	2	100.0%	1																									
IPI00984835	UBQLN1	16 kDa protein	100.0%	6.4	1	1	1	1	866,864	824,921	758,215	902,068	106,339	52,721	32,270	30,274	27.4	14.3	9.5	7.5	-1.1	0.7	-1.1	0.4	1.0	0.8	-1.1	0.3	1.1	0.2	1.2	0.01
				NPAMMQEMMR	2	100.0%	1																									
IPI00984869	LOC100508805	hypothetical protein LOC100508805	91.6%	1.5	1	1	1	1	7,995,200	6,854,770	7,350,740	7,564,360	327,111	399,318	935,232	389,952	9.2	13.0	28.5	11.5	-1.2	0.06	-1.1	0.5	-1.1	0.4	1.1	0.6	1.1	0.2	1.0	0.8
				EGENAEQKR	2	91.6%	1																									
IPI00984887	RPS3	Uncharacterized protein	100.0%	38.6	5	5	8	1	4,529,380	4,598,696	4,392,831	5,074,918	455,004	216,614	394,437	197,296	22.5	10.5	20.1	8.7	1.0	0.9	-1.0	0.8	1.1	0.3	-1.0	0.7	1.1	0.1	1.2	0.2
				AELNEFLTR	2	97.8%	1																									
				ELAEDGYSGVEVR	2	100.0%	2																									
				FGFPEGSVELYAEK	2	100.0%	2																									
				GGKPEPPAMPQPVPTA	2	100.0%	2																									
				KFVADGIFK	2	96.7%	1																									
IPI00984905	-	Truncated aryl hydrocarbon receptor interacting protein	100.0%	14.3	2	2	2	2	2,625,454	2,542,762	2,534,395	2,796,837	146,874	81,362	143,649	172,592	12.5	7.2	12.7	13.8	-1.0	0.6	-1.0	0.7	1.1	0.5	-1.0	1	1.1	0.2	1.1	0.3
IPI00985244	AIP	Uncharacterized protein	100.0%	9.6	2	2	2	2	2,625,454	2,542,762	2,534,395	2,796,837	146,874	81,362	143,649	172,592	12.5	7.2	12.7	13.8	-1.0	0.6	-1.0	0.7	1.1	0.5	-1.0	1	1.1	0.2	1.1	0.3

				EGEIAQFLCDIK	2	100.0%	1																									
				HVVLYPLVAK	2	99.5%	1																									
IPI00984945	EHD1	EF-Hand type domain containing protein	100.0%	14.8	3	3	3	1	10,867,967	10,373,489	10,581,940	12,090,010	637,945	585,563	583,331	489,327	13.1	12.6	12.3	9.1	-1.0	0.6	-1.0	0.7	1.1	0.2	1.0	0.8	1.2	0.05	1.1	0.08
				LADVDKDGLLDDEEFALANHLIK	3	100.0%	1																									
				MQELLQTQDFSK	2	100.0%	1																									
				QEESLMPSQVVK	2	99.9%	1																									
IPI00984968	LOC100510275	ubiquilin-4-like	97.6%	4.8	1	1	1	1	1,078,997	926,220	1,203,866	1,393,059	115,157	175,355	143,574	66,981	23.9	42.3	26.7	10.8	-1.2	0.5	1.1	0.5	1.3	0.05	1.3	0.3	1.5	0.05	1.2	0.3
				QLMSNPEMLLQIMENPLVQDMMSNPDLMR	3	97.6%	1																									
IPI00985102	ST14	Uncharacterized protein	99.9%	3.6	2	2	2	1	2,349,220	2,324,675	2,250,925	2,738,020	209,483	201,154	263,642	161,391	19.9	19.4	26.2	13.2	-1.0	0.9	-1.0	0.8	1.2	0.2	-1.0	0.8	1.2	0.1	1.2	0.2
				IFQAGVVSWGDGCAQR	2	98.9%	1																									
				SQFVVTSNSNK	2	99.7%	1																									
IPI00985156	PUF60	Uncharacterized protein	100.0%	20.4	4	4	5	1	2,024,088	1,987,086	1,987,721	2,306,364	132,263	76,776	100,059	61,319	14.6	8.6	11.3	5.9	-1.0	0.8	-1.0	0.8	1.1	0.09	1.0	1	1.2	0.01	1.2	0.03
				AQSSQDAVSSMNLFDLGGQYLR	2	100.0%	1																									
				GYGFIEYEK	2	99.7%	1																									
				LGLPPLTPEQQEALQK	2	100.0%	2																									
				QTIAHQQQQLTNLQMAAQR	3	99.9%	1																									
IPI00985176	GDA	cDNA, FLJ78887, highly similar to Guanine deaminase	100.0%	25.8	4	5	5	1	2,519,675	2,574,825	2,632,703	2,903,884	261,980	196,498	206,313	118,723	23.3	17.1	17.5	9.1	1.0	0.9	1.0	0.7	1.2	0.2	1.0	0.8	1.1	0.2	1.1	0.3
				ASDSPIDLFYGDFFGDISEAVIQK	2	100.0%	1																									
				ASDSPIDLFYGDFFGDISEAVIQK	3	100.0%	1																									
				AVMVSNILLINK	2	97.5%	1																									
				LATLGGSQALGLDGEIGNFEVGKEFDAILINPK	3	100.0%	1																									
				TLKNGTTTACYFATIHTDSSLLLADITDK	3	96.7%	1																									
IPI00985284	LARP1	23 kDa protein	99.3%	9.7	1	1	1	1	1,258,710	1,258,605	1,105,943	1,341,833	59,516	117,531	47,020	41,519	10.6	20.9	9.5	6.9	-1.0	1	-1.1	0.08	1.1	0.3	-1.1	0.3	1.1	0.5	1.2	0.006
				FSHLTSLPQQLPSQQLMSK	3	99.0%	1																									
IPI00985293	SEC24C	112 kDa protein	100.0%	1.7	1	1	1	1	199,856	188,899	239,810	238,017	14,278	14,179	24,092	29,447	16.0	16.8	22.5	27.7	-1.1	0.6	1.2	0.2	1.2	0.3	1.3	0.1	1.3	0.2	-1.0	1
				AVITSLLDQIPEMFADTR	2	100.0%	1																									
IPI00985362	LOC100508008	putative solute carrier family 22 member ENSG00000182157-like	100.0%	14.3	3	3	4	1	13,916,090	12,666,299	15,655,640	14,392,460	688,002	1,065,691	859,488	643,796	11.1	18.8	12.3	10.0	-1.1	0.4	1.1	0.2	1.0	0.6	1.2	0.06	1.1	0.2	-1.1	0.3
				GAGLGLVLGAGFLGQAAGLLDTLHGR	2	99.1%	1																									
				GAGLGLVLGAGFLGQEAGCPQHTLSHR	2	99.9%	2																									
				LLHGGTLAGALLALYLAR	3	92.0%	1																									
IPI00985413	LOC100510476	e3 SUMO-protein ligase RanBP2-like	100.0%	2.7	2	2	2	1	5,069,193	5,308,803	4,919,590	4,878,420	267,644	179,503	406,185	269,791	11.8	7.6	18.5	12.4	1.0	0.5	-1.0	0.8	-1.0	0.6	-1.1	0.4	-1.1	0.2	-1.0	0.9
				ELLQSFDSALQSVK	2	99.1%	1																									
				EQLLDCEGEDGWNK	3	99.4%	1																									
IPI01008798	-	Disrupted in schizophrenia 1 isoform 53	99.8%	6.5	1	1	1	1	1,128,783	1,221,625	1,037,875	1,286,328	124,743	95,287	48,918	81,721	24.7	17.4	10.5	14.2	1.1	0.6	-1.1	0.5	1.1	0.3	-1.2	0.1	1.1	0.6	1.2	0.03
				SFQQELDAR	2	97.2%	1																									
IPI01008821	CTNND1	Uncharacterized protein	100.0%	11.1	1	1	1	1	28,876	28,758	24,683	31,990	3,951	4,830	1,082	1,731	30.6	37.6	9.8	12.1	-1.0	1	-1.2	0.4	1.1	0.5	-1.2	0.5	1.1	0.6	1.3	0.007
				QPELPEVIAMLGFR	2	99.9%	1																									
IPI01008863	DNM1	Dynamin 1 isoform 2 variant	100.0%	3.8	2	2	2	1	858,748	854,679	864,520	915,073	62,221	33,965	42,534	49,820	16.2	8.9	11.0	12.2	-1.0	1	1.0	0.9	1.1	0.5	1.0	0.9	1.1	0.3	1.1	0.5
				SSVLENFVGR	2	99.9%	1																									
				VPVGDQPPDIEFQIR	2	99.9%	1																									
IPI01008879	FDFT1	cDNA, FLJ79430, highly similar to Squalene synthetase	100.0%	11.1	3	3	3	1	1,797,231	1,813,534	1,851,459	2,053,176	117,128	44,915	74,403	112,961	14.6	5.5	9.0	12.3	1.0	0.9	1.0	0.7	1.1	0.2	1.0	0.7	1.1	0.08	1.1	0.2
				DYLEDQQGGR	2	100.0%	1																									
				LFSASEFEDPLVGEDTER	2	100.0%	1																									
				MGIGMAEFLDK	2	100.0%	1																									
IPI01008914	EIF4A1	eukaryotic initiation factor 4A-I isoform 2	100.0%	34.0	9	9	11	1	17,832,545	17,534,762	17,607,298	19,535,361	1,233,338	1,100,707	1,103,728	528,306	15.5	14.0	14.0	6.1	-1.0	0.9	-1.0	0.9	1.1	0.2	1.0	1	1.1	0.1	1.1	0.2
				DFTVSAMHGDMDQK	2	98.9%	1																									
				GFKDQIYDIFQK	2	99.9%	1																									
				GIYAYGFEKPSAIQQR	3	99.8%	1																									
				GYDVIAQAQSGTGK	2	100.0%	2																									
				KEELTLEGIR	2	89.7%	1																									
				LNSNTQVVLLSATMPSDVLEVTK	2	100.0%	1																									
				LNSNTQVVLLSATMPSDVLEVTKK	3	99.5%	1																									
				LQMEAPHIIVGTPGR	2	100.0%	1																									
				MFVLDEADEMLSR	2	100.0%	2																									
IPI01008933	CTNND1	Uncharacterized protein	100.0%	8.1	2	2	2	1	292,392	301,720	278,794	345,498	26,930	13,661	10,004	11,955	20.6	10.1	8.0	7.7	1.0	0.8	-1.0	0.7	1.2	0.1	-1.1	0.2	1.1	0.04	1.2	0.003
				QDVYGPQPQVR	2	100.0%	1																									
				VGGSSVDLHR	2	99.7%	1																									
IPI01008952	LMO7	LIM domain 7	100.0%	11.4	8	8	11	1	3,419,606	3,517,766	3,455,567	4,180,240	380,993	284,724	325,375	161,190	24.9	18.1	21.1	8.6	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.9	1.2	0.08	1.2	0.08
				EPSLATWEATWSEGSK	2	100.0%	1																									
				FSYNDSKEWEEAMAK	3	98.4%	1																									
				ISINQTPGK	2	99.3%	2																									
				KWEQQLQEEQEQKR	3	92.3%	1																									
				SMSDVSAEDVQNLR	2	100.0%	2																									
				TEEASSGFLPGDR	2	99.7%	1																									
				TPNNVVSTPAPSPDASQLASSLSSQK	3	100.0%	1																									
				WIDATSGIYNSEK	2	100.0%	2																									
IPI01009006	SRSF5	cDNA FLJ57437, highly similar to Splicing factor, arginine/serine-rich 5	100.0%	6.5	1	1	1	1	1,738,601	2,198,900	1,838,980	2,396,040	409,047	358,035	240,048	241,545	52.6	36.4	29.2	22.5	1.3	0.4	1.1	0.8	1.4	0.2	-1.2	0.4	1.1	0.7	1.3	0.1
				LIVENLSSR	2	99.9%	1																									
IPI01009017	CCT2	cDNA FLJ50585, highly similar to T-complex protein 1 subunit beta	100.0%	28.9	11	13	19	1	25,797,580	25,276,283	25,726,143	28,474,417	1,657,694	804,514	1,681,960	1,064,101	14.4	7.1	14.6	8.4	-1.0	0.8	-1.0	1	1.1	0.2	1.0	0.8	1.1	0.04	1.1	0.2
				AAHSEGNTTAGLDMR	2	100.0%	1																									
				DASLMVTNDGATILK	2	100.0%	2																									
				FRQDLMNIAGTTLSSK	3	99.9%	1																									
				GATQQILDEAER	2	100.0%	2																									
				KLGGSLADSYLDEGFLLDKK	3	100.0%	1																									
				LAVEAVLR	2	89.1%	1																									
				LGGSLADSYLDEGFLLDKK	2	100.0%	1																									
				LGGSLADSYLDEGFLLDKK	3	100.0%	2																									
				LKGSGNLEAIHIIK	3	98.0%	1																									
				LTSFIGAIAIGDLVK	2	100.0%	2																									
				MLPTIIADNAGYDSADLVAQLR	2	100.0%	2																									
				MLPTIIADNAGYDSADLVAQLR	3	100.0%	2																									
				QDLMNIAGTTLSSK	2	100.0%	1																									
IPI01009141	NUMA1	NUMA1 protein	100.0%	4.2	3	3	4	2	2,609,485	3,091,813	2,895,123	3,280,113	278,514	124,681	256,966	182,535	23.9	9.0	19.9	12.4	1.2	0.2	1.1	0.5	1.3	0.08	-1.1	0.5	1.1	0.4	1.1	0.3
IPI01010610	NUMA1	cDNA FLJ76708, highly similar to Homo sapiens nuclear mitotic apparatus protein 1	100.0%	4.2	3	3	4	2	2,609,485	3,091,813	2,895,123	3,280,113	278,514	124,681	256,966	182,535	23.9	9.0	19.9	12.4	1.2	0.2	1.1	0.5	1.3	0.08	-1.1	0.5	1.1	0.4	1.1	0.3
				HQVEQLSSSLK	2	98.5%	1																									
				LDFVCSFLQK	2	88.6%	1																									
				LEILQQQLQVANEAR	2	100.0%	2																									
IPI01009143	STARD10	14 kDa protein	100.0%	19.9	2	2	3	2	6,100,992	6,201,079	6,132,637	6,716,483	340,422	264,114	367,060	334,158	12.5	9.5	13.4	11.1	1.0	0.8	1.0	1	1.1	0.2	-1.0	0.9	1.1	0.3	1.1	0.3
IPI01013724	STARD10	10 kDa protein	100.0%	29.2	2	2	3	2	6,100,992	6,201,079	6,132,637	6,716,483	340,422	264,114	367,060	334,158	12.5	9.5	13.4	11.1	1.0	0.8	1.0	1	1.1	0.2	-1.0	0.9	1.1	0.3	1.1	0.3
				AGVSVWVQAVEMDR	2	95.9%	1																									
				ESVQVPDDQDFR	2	99.9%	2																									
IPI01009160	CALU	Calumenin isoform 9	100.0%	32.5	3	3	3	1	3,636,386	3,704,033	3,735,283	4,010,455	253,072	185,053	226,298	110,081	15.6	11.2	13.6	6.1	1.0	0.8	1.0	0.8	1.1	0.2	1.0	0.9	1.1	0.2	1.1	0.3
				EEIVDKYDLFVGSQATDFGEALVR	3	100.0%	1																									
				HLVYESDQNKDGK	3	100.0%	1																									
				TFDQLTPEESKER	3	99.6%	1																									
IPI01009186	PCBP2	cDNA FLJ58476, highly similar to Poly(rC)-binding protein 2	100.0%	33.9	8	9	13	1	6,852,683	7,217,401	6,648,454	8,038,219	747,743	280,438	434,940	342,064	24.4	8.7	14.6	9.5	1.1	0.7	-1.0	0.8	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.04
				AFAMIIDK	2	94.2%	1																									
				AITIAGIPQSIIECVK	2	100.0%	2																									
				ESTGAQVQVAGDMLPNSTER	2	100.0%	2																									
				ESTGAQVQVAGDMLPNSTER	3	99.9%	1																									
				EVGSIIGK	2	94.3%	1																									
				IITLAGPTNAIFK	2	99.8%	1																									
				INISEGNCPER	2	100.0%	2																									
				LVVPASQCGSLIGK	2	100.0%	1																									
				QICVVMLESPPK	2	99.0%	2																									
IPI01009196	STARD10	28 kDa protein	100.0%	25.7	4	4	5	3	2,744,763	3,370,201	3,092,070	4,003,590	193,157	151,842	278,150	290,999	15.7	10.1	20.1	16.3	1.2	0.03	1.1	0.3	1.5	0.007	-1.1	0.4	1.2	0.09	1.3	0.05
IPI01010352	STARD10	19 kDa protein	100.0%	37.3	4	4	5	3	2,744,763	3,370,201	3,092,070	4,003,590	193,157	151,842	278,150	290,999	15.7	10.1	20.1	16.3	1.2	0.03	1.1	0.3	1.5	0.007	-1.1	0.4	1.2	0.09	1.3	0.05
IPI01015084	STARD10	17 kDa protein	100.0%	42.0	4	4	5	3	2,744,763	3,370,201	3,092,070	4,003,590	193,157	151,842	278,150	290,999	15.7	10.1	20.1	16.3	1.2	0.03	1.1	0.3	1.5	0.007	-1.1	0.4	1.2	0.09	1.3	0.05
				AVSIQTGYLIQSTGPK	2	100.0%	2																									
				MECCDVPAETLYDVLHDIEYR	3	99.4%	1																									
				SCVITYLAQVDPK	2	99.5%	1																									
				WDSNVIETFDIAR	2	99.2%	1																									
IPI01009205	RAD23B	35 kDa protein	100.0%	15.7	4	5	6	1	8,080,462	7,908,627	7,727,205	8,814,655	621,273	250,335	327,102	180,317	17.2	7.1	9.5	4.6	-1.0	0.8	-1.0	0.6	1.1	0.3	-1.0	0.7	1.1	0.02	1.1	0.02
				ASFNNPDR	2	93.1%	1																									
				NENLAANFLLQQNFDED	2	91.7%	1																									
				NQPQFQQMR	2	99.9%	1																									
				QIIQQNPSLLPALLQQIGR	2	100.0%	2																									
				QIIQQNPSLLPALLQQIGR	3	100.0%	1																									
IPI01009289	RDX	cDNA FLJ58499, highly similar to Radixin	100.0%	8.5	3	3	3	1	5,540,627	5,560,303	5,395,910	6,175,610	446,086	256,650	502,794	176,764	18.0	10.3	20.8	6.4	1.0	1	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.08	1.1	0.2
				AFAAQEDLEK	2	99.2%	1																									
				NQEQLAAELAEFTAK	2	100.0%	1																									
				QLQALSSELAQAR	2	99.9%	1																									
IPI01009322	IARS	132 kDa protein	100.0%	13.6	12	12	13	1	25,655,650	25,984,242	25,794,723	29,722,680	2,246,008	1,435,925	2,051,031	922,259	19.6	12.4	17.8	6.9	1.0	0.9	1.0	1	1.2	0.1	-1.0	0.9	1.1	0.06	1.2	0.1
				EFEDAFPADFIAEGIDQTR	2	100.0%	1																									
				FVDILTNWYVR	2	100.0%	1																									
				GSELEITLTR	2	99.8%	1																									
				LFLNETQTQEITEDIPVK	2	90.9%	1																									
				LQKEEEIEFLYNENTVR	3	89.2%	1																									
				NNDLCYWVPELVR	2	85.9%	1																									
				NVIVNGLVLASDGQK	2	98.8%	1																									
				QLSSEELEQFQK	2	99.7%	2																									
				TESAVSQMQSVIELGR	2	100.0%	1																									
				VENMVDQLLR	2	96.6%	1																									
				WIDFDNDYK	2	89.2%	1																									
				YGADALR	2	91.4%	1																									
IPI01009326	CCT8	cDNA FLJ53379, highly similar to T-complex protein 1 subunit theta	100.0%	35.2	16	16	21	1	37,736,497	37,909,250	36,385,073	42,076,126	3,204,722	1,563,002	2,276,544	1,135,149	19.0	9.2	14.0	6.0	1.0	1	-1.0	0.7	1.1	0.3	-1.0	0.6	1.1	0.06	1.2	0.06
				AVDDGVNTFK	2	100.0%	1																									
				DMLEAGILDTYLGK	2	100.0%	2																									
				FAEAFEAIPR	2	100.0%	1																									
				GEENLMDAQVK	2	100.0%	2																									
				GSTDNLMDDIER	2	100.0%	2																									
				HFSGLEEAVYR	2	99.3%	1																									
				IAVYSCPFDGMITETK	2	97.7%	1																									
				IGLSVSEVIEGYEIACR	2	100.0%	1																									
				LATNAAVTVLR	2	100.0%	2																									
				LFVTNDAATILR	2	100.0%	1																									
				LVPGGGATEIELAK	2	88.3%	1																									

				MVINHLEK	2	85.5%	1																									
				NVGLDIEAEVPAVK	2	100.0%	2																									
				TAEELMNFSK	2	100.0%	1																									
				TVGATALPR	2	98.5%	1																									
				YNIMLVR	2	99.0%	1																									
IPI01009334	-	18 kDa protein	100.0%	9.7	1	1	1	2	1,464,172	1,572,214	1,518,816	1,661,928	130,775	71,887	116,312	67,315	20.0	10.2	17.1	9.1	1.1	0.5	1.0	0.8	1.1	0.2	-1.0	0.7	1.1	0.4	1.1	0.3
IPI01012250	-	13 kDa protein	100.0%	13.0	1	1	1	2	1,464,172	1,572,214	1,518,816	1,661,928	130,775	71,887	116,312	67,315	20.0	10.2	17.1	9.1	1.1	0.5	1.0	0.8	1.1	0.2	-1.0	0.7	1.1	0.4	1.1	0.3
				IEINFPAEYPFKPPK	3	100.0%	1																									
IPI01009339	PSPC1	27 kDa protein	100.0%	9.3	1	1	1	1	207,608	231,697	212,119	222,886	18,013	25,226	35,903	25,252	19.4	24.4	37.9	25.3	1.1	0.5	1.0	0.9	1.1	0.6	-1.1	0.7	-1.0	0.8	1.1	0.8
				NLSPVVSNELLEQAFSQFGPVEK	2	100.0%	1																									
IPI01009353	PGD	6-phosphogluconate dehydrogenase, decarboxylating	100.0%	17.5	5	6	8	1	8,648,019	9,043,201	9,198,225	9,910,266	487,551	489,626	587,693	250,082	12.6	12.1	14.3	5.6	1.0	0.6	1.1	0.5	1.1	0.05	1.0	0.8	1.1	0.2	1.1	0.3
				DAFDRNPELQDLLLDDFFK	3	99.2%	1																									
				GILFVGSGVSGGEEGAR	2	100.0%	2																									
				LVPLLDTGDIIIDGGNSEYR	2	100.0%	2																									
				LVPLLDTGDIIIDGGNSEYR	3	99.8%	1																									
				SFLEDIRK	2	98.6%	1																									
				YGPSLMPGGNK	2	99.4%	1																									
IPI01009538	DARS	Putative uncharacterized protein DKFZp781B11202	100.0%	20.2	7	7	7	1	15,361,837	17,194,738	15,397,053	17,864,119	1,363,984	647,277	1,147,993	576,316	19.9	8.4	16.7	7.2	1.1	0.3	1.0	1	1.2	0.1	-1.1	0.2	1.0	0.5	1.2	0.09
				ESIVDVEGVVR	2	99.9%	1																									
				FQTEIQTVNK	2	98.6%	1																									
				LEYCEALAMLR	2	100.0%	1																									
				LLGHLVK	2	95.9%	1																									
				LPLQLDDAVRPEAEGEEEGR	3	99.9%	1																									
				NNAYLAQSPQLYK	2	100.0%	1																									
				TSTSQAVFR	2	92.4%	1																									
IPI01009580	STK24	cDNA FLJ60706, highly similar to Serine/threonine-protein kinase 24	100.0%	12.3	4	4	5	1	3,175,457	2,986,752	3,174,505	3,596,924	456,209	157,485	218,928	189,619	32.1	11.8	15.4	11.8	-1.1	0.7	-1.0	1	1.1	0.4	1.1	0.5	1.2	0.04	1.1	0.2
				ADIWSLGITAIELAR	2	100.0%	2																									
				LADFGVAGQLTDTQIK	2	99.5%	1																									
				LADFGVAGQLTDTQIKR	3	99.9%	1																									
				TSYLTELIDR	2	99.8%	1																									
IPI01009673	STARD10	16 kDa protein	100.0%	29.6	3	3	4	1	2,646,075	3,265,148	2,986,336	3,876,259	181,452	149,036	264,669	285,734	15.3	10.2	19.8	16.5	1.2	0.03	1.1	0.3	1.5	0.007	-1.1	0.4	1.2	0.09	1.3	0.05
				AVSIQTGYLIQSTGPK	2	100.0%	2																									
				SCVITYLAQVDPK	2	99.5%	1																									
				WDSNVIETFDIAR	2	99.2%	1																									
IPI01009730	NOMO1;NOMO3	Putative uncharacterized protein DKFZp547A1913	100.0%	4.6	3	3	3	3	1,018,474	1,046,683	1,037,126	1,152,680	69,464	43,006	81,397	37,800	15.3	9.2	17.6	7.3	1.0	0.7	1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.1	1.1	0.2
IPI01012164	NOMO1;NOMO3	NOMO3 protein	100.0%	4.6	3	3	3	3	1,018,474	1,046,683	1,037,126	1,152,680	69,464	43,006	81,397	37,800	15.3	9.2	17.6	7.3	1.0	0.7	1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.1	1.1	0.2
IPI01013036	NOMO2	NOMO2 protein	100.0%	4.6	3	3	3	3	1,018,474	1,046,683	1,037,126	1,152,680	69,464	43,006	81,397	37,800	15.3	9.2	17.6	7.3	1.0	0.7	1.0	0.9	1.1	0.1	-1.0	0.9	1.1	0.1	1.1	0.2
				EGYVLTAVEGTIGDFK	2	99.9%	1																									
				FEPSSQMIEVQEGQNLK	2	99.2%	1																									
				VIEVGNNDIDDVNIIVFR	2	99.6%	1																									
IPI01009733	CTSB	cDNA FLJ40065 fis, clone TESOP2000400, highly similar to CATHEPSIN B	100.0%	23.2	4	4	6	2	5,232,050	5,313,938	5,429,128	5,746,668	445,639	126,934	284,548	58,406	19.1	5.3	11.7	2.3	1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.01	1.1	0.3
IPI01014579	CTSB	cDNA FLJ59133, highly similar to Cathepsin B	100.0%	26.1	4	4	6	2	5,232,050	5,313,938	5,429,128	5,746,668	445,639	126,934	284,548	58,406	19.1	5.3	11.7	2.3	1.0	0.9	1.0	0.7	1.1	0.3	1.0	0.7	1.1	0.01	1.1	0.3
				GQDHCGIESEVVAGIPR	2	100.0%	2																									
				ICEPGYSPTYK	2	99.4%	1																									
				NGPVEGAFSVYSDFLLYK	2	100.0%	1																									
				SGVYQHVTGEMMGGHAIR	3	100.0%	2																									
IPI01009760	NAP1L4	Uncharacterized protein	100.0%	35.9	4	5	6	1	2,093,190	2,144,083	2,023,539	2,564,008	189,643	136,196	139,591	71,999	20.3	14.2	15.4	6.3	1.0	0.8	-1.0	0.8	1.2	0.07	-1.1	0.6	1.2	0.03	1.3	0.009
				FYEEVHDLER	2	100.0%	1																									
				LDNVPHTPSSYIETLPK	3	100.0%	1																									
				NVDMLSELVQEYDEPILK	2	100.0%	2																									
				NVDMLSELVQEYDEPILK	3	99.6%	1																									
				YAALYQPLFDK	2	99.7%	1																									
IPI01009763	ANK3	cDNA FLJ35208 fis, clone PLACE6018938, highly similar to Mus musculus epithelia	100.0%	7.8	4	4	4	1	1,603,153	1,666,652	1,645,891	2,000,870	192,415	97,175	144,300	97,866	26.8	13.0	19.6	10.9	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.9	1.2	0.04	1.2	0.08
				IDIVTLLEGPIFDYGNISGTR	2	99.9%	1																									
				INRIDIVTLLEGPIFDYGNISGTR	3	89.8%	1																									
				LVEMGPAGAQFLGPVIVEIPHFGSMR	3	97.8%	1																									
				NATTDALTSVLTK	2	99.3%	1																									
IPI01009770	C1orf101	cDNA FLJ58653	99.9%	1.5	1	1	1	1	595,520	642,690	610,148	686,033	42,927	47,061	63,407	61,619	16.1	16.4	23.2	20.1	1.1	0.5	1.0	0.9	1.2	0.3	-1.1	0.7	1.1	0.6	1.1	0.4
				KIFLVIYNEDTK	2	99.8%	1																									
IPI01009789	HADHB	50 kDa protein	100.0%	6.3	2	2	2	1	4,405,990	4,011,138	4,123,283	4,495,195	467,499	132,184	274,441	99,914	23.7	7.4	14.9	5.0	-1.1	0.5	-1.1	0.6	1.0	0.9	1.0	0.7	1.1	0.02	1.1	0.3
				FNNWGGSLSLGHPFGATGCR	3	80.9%	1																									
				LEQDEYALR	2	99.1%	1																									
IPI01009792	SAR1A	cDNA FLJ58922, highly similar to GTP-binding protein SAR1a	100.0%	14.8	1	1	1	1	545,868	435,788	653,227	594,681	66,664	35,277	18,463	42,865	27.3	18.1	6.3	16.1	-1.3	0.2	1.2	0.2	1.1	0.6	1.5	0.0006	1.4	0.02	-1.1	0.2
				VELNALMTDETISNVPILILGNK	2	100.0%	1																									
IPI01009969	ITGAV	cDNA FLJ57822, highly similar to Integrin alpha-V	99.9%	5.4	1	1	1	1	177,809	162,575	173,196	186,305	22,673	11,157	20,738	11,773	28.5	15.4	26.8	14.1	-1.1	0.6	-1.0	0.9	1.0	0.7	1.1	0.7	1.1	0.2	1.1	0.6
				VLLGGPGSFYWQGQLISDQVAEIVSK	3	99.8%	1																									
IPI01009977	ME1	Malic enzyme	100.0%	7.9	2	2	3	2	295,452	272,715	362,074	337,987	38,414	11,243	50,795	19,448	29.1	9.2	31.4	12.9	-1.1	0.6	1.2	0.3	1.1	0.4	1.3	0.2	1.2	0.02	-1.1	0.7
IPI01016024	ME1	45 kDa protein	100.0%	9.6	2	2	3	2	295,452	272,715	362,074	337,987	38,414	11,243	50,795	19,448	29.1	9.2	31.4	12.9	-1.1	0.6	1.2	0.3	1.1	0.4	1.3	0.2	1.2	0.02	-1.1	0.7
				GSEYDDFLDEFMEAVSSK	2	100.0%	2																									
				QITDNIFLTTAEVIAQQVSDK	2	99.5%	1																									
IPI01010050	VDAC2	cDNA, FLJ78818, highly similar to Voltage-dependent anion-selective channel prote	100.0%	30.2	6	6	8	1	7,381,040	7,442,197	6,995,972	8,339,088	601,286	352,947	587,670	217,527	18.2	10.6	18.8	5.8	1.0	0.9	-1.1	0.7	1.1	0.2	-1.1	0.5	1.1	0.06	1.2	0.08
				LTFDTTFSPNTGK	2	98.8%	1																									
				LTLSALVDGK	2	100.0%	1																									
				NNFAVGYR	2	99.2%	1																									
				TGDFQLHTNVNDGTEFGGSIYQK	3	100.0%	2																									
				WCEYGLTFTEK	2	99.3%	1																									
				YQLDPTASISAK	2	100.0%	2																									
IPI01010062	CCAR1	76 kDa protein	97.8%	4.8	2	2	2	1	723,481	647,798	667,484	785,518	84,586	46,949	46,058	75,769	26.1	16.2	15.4	21.6	-1.1	0.5	-1.1	0.6	1.1	0.6	1.0	0.8	1.2	0.2	1.2	0.2
				FSLDCPSCDMMELR	2	97.8%	1																									
				IQTLPNQNQSQTQPLLK	2	97.3%	1																									
IPI01010147	SF3A1	cDNA FLJ55438, highly similar to Splicing factor 3 subunit 1	100.0%	15.7	7	7	7	1	11,284,576	11,173,821	11,419,332	12,744,580	661,122	422,854	569,885	248,783	13.1	8.5	11.2	4.4	-1.0	0.9	1.0	0.9	1.1	0.09	1.0	0.7	1.1	0.01	1.1	0.07
				ASKPLPPAPAPDEYLVSPITGEK	3	100.0%	1																									
				IHEATGMPAGK	2	81.0%	1																									
				TDIFGVEETAIGK	2	98.6%	1																									
				TQQAAQANITLQEQIEAIHK	3	99.9%	1																									
				VMQQQQQTTQQQLPQK	3	99.6%	1																									
				VQAQVIQETIVPK	2	100.0%	1																									
				VTWDGHSGSMAR	2	97.3%	1																									
IPI01010189	PDIA6	cDNA FLJ16143 fis, clone BRAMY2038516, highly similar to Protein disulfide-isome	100.0%	46.5	16	18	28	1	28,900,230	28,344,018	28,028,015	31,639,828	1,805,124	735,702	1,600,478	1,300,425	14.0	5.8	12.8	9.2	-1.0	0.8	-1.0	0.7	1.1	0.3	-1.0	0.9	1.1	0.06	1.1	0.1
				AATALKDVVK	2	98.5%	1																									
				ALDLFSDNAPPPELLEIINEDIAK	2	100.0%	2																									
				ALDLFSDNAPPPELLEIINEDIAK	3	100.0%	2																									
				ALDLFSDNAPPPELLEIINEDIAKR	3	100.0%	2																									
				DGELPVEDDIDLSDVELDDLGKDEL	2	100.0%	2																									
				EPWDGRDGELPVEDDIDLSDVELDDLGKDEL	3	100.0%	1																									
				GESPVDYDGGR	2	100.0%	2																									
				GSFSEQGINEFLR	2	100.0%	2																									
				GSTAPVGGGAFPTIVER	2	100.0%	1																									
				IFGSNK	1	90.8%	1																									
				LAAVDATVNQVLASR	2	100.0%	2																									
				MRIITAPASKVSR	2	88.7%	1																									
				NLEPEWAAAASEVK	2	100.0%	2																									
				NSYLEVLLK	2	99.9%	2																									
				TCEEHQLCVVAVLPHILDTGAAGR	3	100.0%	1																									
				TGEAIVDAALSALR	2	100.0%	2																									
				TGEAIVDAALSALR	3	100.0%	1																									
				VGAVDADKHHSLGGQYGVQGFPTIK	3	100.0%	1																									
IPI01010252	PHB2	24 kDa protein	100.0%	15.9	3	3	4	1	2,479,300	2,758,260	2,517,577	2,791,567	297,219	107,493	250,208	124,017	26.8	8.7	22.2	9.9	1.1	0.4	1.0	0.9	1.1	0.4	-1.1	0.4	1.0	0.8	1.1	0.4
				FNASQLITQR	2	99.9%	2																									
				IGGVQQDTILAEGLHFR	3	100.0%	1																									
				LGLDYEER	2	99.9%	1																									
IPI01010287	DDX1	cDNA FLJ51031, highly similar to ATP-dependent RNA helicase DDX1	100.0%	13.2	6	7	9	1	9,905,354	9,782,870	9,621,506	10,971,675	694,749	523,044	605,904	347,204	15.7	12.0	14.1	7.1	-1.0	0.9	-1.0	0.8	1.1	0.2	-1.0	0.8	1.1	0.09	1.1	0.09
				ELAEQTLNNIK	2	100.0%	2																									
				FGFGFGGTGK	2	99.6%	1																									
				FLVLDEADGLLSQGYSDFINR	2	100.0%	2																									
				FLVLDEADGLLSQGYSDFINR	3	100.0%	1																									
				NQALFPACVLK	2	99.9%	1																									
				TGAFSIPVIQIVYETLKDQQEGK	3	98.6%	1																									
				YIDNPK	2	91.3%	1																									
IPI01010313	GLUD1	cDNA FLJ37463 fis, clone BRAWH2011400, highly similar to Glutamate dehydroger	100.0%	21.6	8	9	9	2	8,589,233	9,226,297	8,954,388	10,168,113	796,592	275,362	742,511	245,428	20.7	6.7	18.5	5.4	1.1	0.5	1.0	0.7	1.2	0.1	-1.0	0.7	1.1	0.03	1.1	0.2
IPI01015023	GLUD1	cDNA FLJ55203, highly similar to Glutamate dehydrogenase 1, mitochondrial	100.0%	26.1	8	9	9	2	8,589,233	9,226,297	8,954,388	10,168,113	796,592	275,362	742,511	245,428	20.7	6.7	18.5	5.4	1.1	0.5	1.0	0.7	1.2	0.1	-1.0	0.7	1.1	0.03	1.1	0.2
				ALASLMTYK	2	99.8%	1																									
				DSNYHLLMSVQESLER	2	95.3%	1																									
				DSNYHLLMSVQESLER	3	99.9%	1																									
				GFIGPGIDVPAPDMSTGER	2	100.0%	1																									
				HGGTIPIVPTAEFQDR	2	100.0%	1																									
				IIAEGANGPTTPEADKIFLER	3	100.0%	1																									
				NLNHVSYGR	2	99.9%	1																									
				TAAYVNAIEK	2	99.7%	1																									
				YSTDVSVDEVK	2	100.0%	1																									
IPI01010326	CCAR1	9 kDa protein	97.3%	21.3	1	1	1	1	133,873	117,133	142,007	168,756	11,277	9,796	17,036	8,987	18.8	18.7	26.8	11.9	-1.1	0.3	1.1	0.7	1.3	0.04	1.2	0.2	1.4	0.005	1.2	0.2
				IQTLPNQNQSQTQPLLK	2	97.3%	1																									
IPI01010478	EEA1	92 kDa protein	99.5%	2.9	2	2	2	1	4,926,553	5,048,023	5,006,393	5,861,883	439,284	297,036	450,017	247,773	19.9	13.2	20.1	9.5	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.9	1.2	0.07	1.2	0.1
				AAQLATEIADIK	2	99.5%	1																									
				EQALQDLQQQR	2	99.2%	1																									
IPI01010485	PHEX	cDNA FLJ59234, highly similar to Phosphate-regulating neutral endopeptidase	99.3%	5.9	2	2	2	1	9,627,740	9,155,750	9,548,550	10,669,350	799,852	618,129	376,388	471,374	18.6	15.1	8.8	9.9	-1.1	0.7	-1.0	0.9	1.1	0.3	1.0	0.6	1.2	0.09	1.1	0.1
				LDQATLSLAVR	2	96.9%	1																									
				QGLEEPLLPGITFTNNQLFFLSYAHGQWCN	3	99.0%	1																									
IPI01010498	SCRN1	secernin-1 isoform c	100.0%	4.6	1	2	2	1	502,233	427,203	433,308	493,595	99,609	18,530	56,174	18,625	44.4	9.7	29.0	8.4	-1.2	0.5	-1.2	0.6	-1.0	0.9	1.0	0.9	1.2	0.04	1.1	0.4
				EPAAEIEALLGMDLVR	2	99.7%	1																									
				EPAAEIEALLGMDLVR	3	100.0%	1																									
IPI01010511	CTNNA1	65 kDa protein	100.0%	25.9	9	9	10	1	12,910,670	12,913,016	12,864,091	14,668,004	1,051,894	649,181	940,543	370,654	18.2	11.2	16.4	5.7	1.0	1	-1.0	1	1.1	0.2	-1.0	1	1.1	0.05	1.1	0.1
				AEVQNLGGELVVSGVDSAMSLIQAAK	3	100.0%	2																									
				AIMAQLPQEQK	2	98.7%	1																									
				AVMDHVSDSFLETNVPLLVLIEAAK	3	99.9%	1																									
				IAEQVASFQEEK	2	100.0%	1																									
				NLMNAVVQTVK	2	100.0%	1																									

				SDALNSAIDK	2	97.4%	1																									
				SQGMASLNLPAVSWK	2	100.0%	1																									
				VLTDAVDDITSIDDFLAVSENHILEDVNK	3	100.0%	1																									
				WDDSGNDIIVLAK	2	100.0%	1																									
IPI01010523	GNS	Protein	99.4%	4.3	1	1	1	2	654,557	569,776	746,823	715,484	34,268	58,403	21,409	38,292	11.7	22.9	6.4	12.0	-1.1	0.2	1.1	0.05	1.1	0.3	1.3	0.04	1.3	0.07	-1.0	0.5
IPI01015586	GNS	28 kDa protein	99.4%	5.2	1	1	1	2	654,557	569,776	746,823	715,484	34,268	58,403	21,409	38,292	11.7	22.9	6.4	12.0	-1.1	0.2	1.1	0.05	1.1	0.3	1.3	0.04	1.3	0.07	-1.0	0.5
				WQTLLSVDDLVEK	2	98.0%	1																									
IPI01010565	DLAT	cDNA FLJ51063, highly similar to Dihydrolipoyllysine-residue acetyltransferasecomp	100.0%	7.2	2	2	3	1	1,616,008	1,518,360	1,574,970	1,698,438	154,609	111,806	122,962	79,017	21.4	16.5	17.5	10.4	-1.1	0.6	-1.0	0.8	1.1	0.6	1.0	0.7	1.1	0.2	1.1	0.4
				GVETIANDVVSLATK	2	100.0%	2																									
				VVDGAVGAQWLAEFR	2	100.0%	1																									
IPI01010570	VPS35	Putative uncharacterized protein DKFZp686O2462	100.0%	13.6	6	6	6	1	15,340,175	15,951,240	15,856,531	17,659,425	1,169,257	759,190	1,359,419	602,558	17.0	10.6	19.2	7.6	1.0	0.7	1.0	0.8	1.2	0.1	-1.0	1	1.1	0.1	1.1	0.3
				IREDLPNLESSEETEQINK	3	90.7%	1																									
				LFDIFSQQVATVIQSR	2	100.0%	1																									
				LNLEHIATSSAVSK	2	96.7%	1																									
				QIVLTGILEQVVNCR	2	98.8%	1																									
				SEDPDQQYLILNTAR	2	99.9%	1																									
				VLETTVEIFNK	2	99.9%	1																									
IPI01010635	HDLBP	cDNA FLJ16432 fis, clone BRACE3010076, highly similar to Vigilin	100.0%	2.6	1	1	2	1	2,248,105	2,407,358	2,159,320	2,554,285	181,618	181,498	154,441	168,240	18.1	16.9	16.0	14.7	1.1	0.6	-1.0	0.7	1.1	0.3	-1.1	0.3	1.1	0.6	1.2	0.1
				EIAEEYGGVMVSFPR	2	100.0%	2																									
IPI01010637	VAT1	cDNA FLJ39753 fis, clone SMINT2018343, highly similar to Synaptic vesicle membr	100.0%	24.3	4	4	6	1	7,552,084	7,612,490	7,408,834	8,356,475	861,347	289,615	541,802	161,926	25.5	8.5	16.4	4.3	1.0	0.9	-1.0	0.9	1.1	0.4	-1.0	0.7	1.1	0.06	1.1	0.2
				GVDIVMDPLGGSDTAK	2	100.0%	2																									
				QGLYDRLPPLPVTPGMEGAGVVIAVGEGVSDR	3	99.3%	1																									
				VLLVPGPEKEN	2	100.0%	2																									
				VVTYGMANLLTGPK	2	99.9%	1																									
IPI01010649	IDH2	Isocitrate dehydrogenase	100.0%	16.5	6	7	8	1	19,202,734	19,724,452	19,913,935	23,769,943	1,935,602	1,131,528	1,927,831	680,691	22.5	12.8	21.7	6.4	1.0	0.8	1.0	0.8	1.2	0.08	1.0	0.9	1.2	0.02	1.2	0.1
				GKLDGNQDLIR	2	99.5%	1																									
				LIDDMVAQVLK	2	100.0%	2																									
				LNEHFLNTTDFLDTIK	2	99.5%	1																									
				LNEHFLNTTDFLDTIK	3	100.0%	1																									
				LNEHFLNTTDFLDTIKSNLDRALGR	3	84.9%	1																									
				TIEAEAAHGTVTR	2	100.0%	1																									
				YFDLGLPNR	2	91.7%	1																									
IPI01010654	BUB3	cDNA FLJ57899, highly similar to Mitotic checkpoint protein BUB3	100.0%	12.9	3	3	4	1	2,632,250	2,384,685	2,320,443	2,531,843	316,575	147,132	154,993	117,727	26.9	13.8	14.9	10.4	-1.1	0.5	-1.1	0.4	-1.0	0.8	-1.0	0.8	1.1	0.5	1.1	0.3
				NMGYVQQR	2	99.4%	1																									
				VAVEYLDPSPEVQK	2	100.0%	2																									
				VYTLSVSGDR	2	99.4%	1																									
IPI01010714	ATP6V1A	cDNA FLJ53889, highly similar to Vacuolar ATP synthase catalytic subunit A, ubiquit	100.0%	5.1	2	2	2	1	1,087,815	1,372,481	1,447,717	1,309,112	131,556	117,100	116,827	113,551	27.0	19.1	18.0	19.4	1.3	0.1	1.3	0.08	1.2	0.2	1.1	0.7	-1.0	0.7	-1.1	0.4
				IKSDYAQLLEDMQNAFR	3	100.0%	1																									
				SDYAQLLEDMQNAFR	2	100.0%	1																									
IPI01010755	DDX1	cDNA FLJ57326, highly similar to ATP-dependent RNA helicase DDX1	100.0%	20.4	9	11	13	1	17,336,612	16,601,123	16,124,994	18,188,040	1,279,168	754,550	1,139,445	625,493	16.5	10.2	15.8	7.7	-1.0	0.6	-1.1	0.5	1.0	0.6	-1.0	0.7	1.1	0.1	1.1	0.2
				DQLSVLENGVDIVVGTPGR	2	97.4%	1																									
				EAQTSFLHLGYLPNQLFR	2	97.9%	1																									
				ELAEQTLNNIK	2	100.0%	2																									
				ELLIIGGVAAR	2	98.7%	1																									
				FGFGFGGTGK	2	99.6%	1																									
				FLVLDEADGLLSQGYSDFINR	2	100.0%	2																									
				FLVLDEADGLLSQGYSDFINR	3	100.0%	1																									
				GHVDILAPTVQELAALEK	2	83.1%	1																									
				GHVDILAPTVQELAALEK	3	100.0%	1																									
				NQALFPACVLK	2	99.9%	1																									
				YIDNPK	2	91.3%	1																									
IPI01010759	SRP68	cDNA FLJ40643 fis, clone THYMU2017099, highly similar to SIGNAL RECOGNITIO	90.7%	3.5	1	1	1	1	754,353	702,900	685,785	714,562	59,771	31,800	93,445	72,884	17.7	10.1	30.5	22.8	-1.1	0.5	-1.1	0.6	-1.1	0.7	-1.0	0.9	1.0	0.9	1.0	0.8
				WSEALVLYDR	2	85.4%	1																									
IPI01010763	TTN	Uncharacterized protein	99.8%	0.3	7	7	7	1	6,181,607	5,984,180	7,065,319	7,062,741	567,838	267,360	547,761	219,964	20.5	10.0	17.3	7.0	-1.0	0.8	1.1	0.3	1.1	0.2	1.2	0.1	1.2	0.01	-1.0	1
				AEDLSATVTDVVEGQEYSFR	3	97.1%	1																									
				DSCSAQLGVQEPPRFIKK	2	88.8%	1																									
				ITQFLKAEASKEIAK	2	84.0%	1																									
				MPDDDGGDR	1	92.2%	1																									
				STVTIVDSKR	2	89.8%	1																									
				VLDTPGPPVNVTVK	2	90.2%	1																									
				VTGLSEGCEYFFR	3	94.3%	1																									
IPI01010797	CAPN2	cDNA, FLJ96158, highly similar to Homo sapiens calpain 2, (m/II) large subunit (CAF	100.0%	18.4	8	10	11	1	11,498,597	11,981,696	12,007,353	13,049,016	1,079,794	273,297	542,441	405,451	21.0	5.1	10.1	7.0	1.0	0.7	1.0	0.7	1.1	0.2	1.0	1	1.1	0.06	1.1	0.2
				FADDQLIIDFDNFVR	2	100.0%	1																									
				FADDQLIIDFDNFVR	3	95.2%	1																									
				GHAYSVTGAEEVESNGSLQK	3	82.0%	1																									
				LEICNLTPDTLTSDTYKK	3	99.9%	1																									
				LFAQLAGEDAEISAFELQTILR	2	100.0%	1																									
				LFAQLAGEDAEISAFELQTILR	3	100.0%	1																									
				NPWGEVEWTGR	2	100.0%	1																									
				NYPNTFWMNPQYLIK	2	100.0%	2																									
				RPTEICADPQFIIGGATR	3	86.0%	1																									
				YLNQDYEALR	2	99.8%	1																									
IPI01010829	CDH1	CDH1 protein	100.0%	7.4	3	3	5	1	3,503,188	3,639,346	3,599,113	3,967,498	221,552	163,150	241,061	166,709	14.1	10.0	15.0	9.4	1.0	0.6	1.0	0.8	1.1	0.1	-1.0	0.9	1.1	0.2	1.1	0.2
				DTANWLEINPDTGAISTR	2	100.0%	2																									
				GQVPENEANVVITTLK	2	100.0%	1																									
				NTGVISVVTTGLDR	2	100.0%	2																									
IPI01010895	HSPA4	HS24/P52	100.0%	20.5	7	7	13	1	15,388,345	16,360,790	16,120,340	17,505,325	687,394	212,256	1,055,859	537,324	10.0	2.9	14.7	6.9	1.1	0.2	1.0	0.6	1.1	0.04	-1.0	0.8	1.1	0.1	1.1	0.3
				AFSDPFVEAEK	2	100.0%	2																									
				AGGIETIANEYSDR	2	100.0%	2																									
				EDIYAVEIVGGATR	2	100.0%	2																									
				EFSITDVVPYPISLR	2	100.0%	2																									
				ELSTTLNADEAVTR	2	100.0%	2																									
				NFTTEQVTAMLLSK	2	100.0%	2																									
				SVMDATQIAGLNCLR	2	100.0%	1																									
IPI01011037	ENO2	35 kDa protein	100.0%	21.9	4	6	9	1	31,019,453	31,821,741	32,008,008	36,332,118	2,267,707	1,325,615	2,524,665	1,416,141	16.4	9.3	17.6	8.7	1.0	0.8	1.0	0.8	1.2	0.08	1.0	0.9	1.1	0.05	1.1	0.2
				AAVPSGASTGIYEALELR	2	100.0%	2																									
				AAVPSGASTGIYEALELR	3	100.0%	1																									
				IVIGMDVAASEFYR	2	100.0%	2																									
				SGETEDTFIADLVVGLCTGQIK	2	100.0%	2																									
				SGETEDTFIADLVVGLCTGQIK	3	100.0%	1																									
				VNQIGSVTEAIQACK	2	100.0%	1																									
IPI01011083	SEC23A	cDNA FLJ55960, highly similar to Protein transport protein Sec23A	100.0%	9.5	4	4	4	2	8,261,243	8,341,132	8,026,589	9,272,251	614,808	185,390	333,944	346,039	16.6	5.0	9.3	8.3	1.0	0.9	-1.0	0.7	1.1	0.2	-1.0	0.4	1.1	0.05	1.2	0.03
IPI01011543	SEC23A	cDNA FLJ45429 fis, clone BRHIP3039057, highly similar to Protein transport protein	100.0%	11.2	4	4	4	2	8,261,243	8,341,132	8,026,589	9,272,251	614,808	185,390	333,944	346,039	16.6	5.0	9.3	8.3	1.0	0.9	-1.0	0.7	1.1	0.2	-1.0	0.4	1.1	0.05	1.2	0.03
				HLLQAPVDDAQEILHSR	3	100.0%	1																									
				IMMFIGGPATQGPGMVVGDELK	2	99.5%	1																									
				ISGAIGPCVSLNSK	2	99.2%	1																									
				MGFGGTLEIK	2	99.6%	1																									
IPI01011178	PHB2	29 kDa protein	100.0%	7.7	2	2	3	1	7,015,308	6,928,442	7,492,167	7,186,467	429,819	343,441	317,985	204,477	13.7	11.1	9.5	6.4	-1.0	0.9	1.1	0.4	1.0	0.7	1.1	0.3	1.0	0.5	-1.0	0.4
				DLQMVNISLR	2	99.9%	1																									
				FNASQLITQR	2	99.9%	2																									
IPI01011191	PLS3	cDNA FLJ59681, highly similar to Plastin-3	100.0%	20.4	9	9	10	1	13,846,803	13,771,631	13,719,242	15,862,163	1,562,615	605,225	940,751	577,878	25.2	9.8	15.3	8.2	-1.0	1	-1.0	0.9	1.1	0.3	-1.0	1	1.2	0.04	1.2	0.09
				AESMLQQADK	2	98.7%	1																									
				ANDDIIVNWVNR	2	99.9%	1																									
				IDINMSGFNETDDLKR	2	99.9%	1																									
				ISFDEFVYIFQEVK	2	100.0%	1																									
				LNLAFVANLFNK	2	100.0%	1																									
				MEDLNSNGFICDYELHELFK	2	99.6%	1																									
				QFVTPADVVSGNPK	2	100.0%	2																									
				VYALPEDLVEVKPK	3	96.0%	1																									
				YTLNVLEDLGDGQK	2	100.0%	1																									
IPI01011200	C1RL	34 kDa protein	94.6%	5.4	1	1	1	1	12,539,530	14,318,500	12,621,300	15,386,100	1,440,286	443,745	1,644,442	867,730	25.7	6.9	29.1	12.6	1.1	0.3	1.0	1	1.2	0.1	-1.1	0.4	1.1	0.3	1.2	0.2
				FFSVCLSADGQSPPLPR	2	94.6%	1																									
IPI01011208	DDB1	19 kDa protein	95.5%	6.1	1	1	1	2	668,853	729,683	792,660	883,665	130,774	57,518	60,404	67,757	43.7	17.6	17.0	17.2	1.1	0.7	1.2	0.4	1.3	0.2	1.1	0.5	1.2	0.1	1.1	0.3
IPI01011629	DDB1	16 kDa protein	95.5%	7.2	1	1	1	2	668,853	729,683	792,660	883,665	130,774	57,518	60,404	67,757	43.7	17.6	17.0	17.2	1.1	0.7	1.2	0.4	1.3	0.2	1.1	0.5	1.2	0.1	1.1	0.3
				LEELHVIDVK	3	85.2%	1																									
IPI01011282	RAN;RANP1	23 kDa protein	100.0%	28.1	5	6	10	1	8,554,051	8,689,158	8,487,183	9,959,825	731,397	366,974	522,809	463,433	19.1	9.4	13.8	10.4	1.0	0.9	-1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.06	1.2	0.07
				FNVWDTAGQEK	2	100.0%	2																									
				HLTGEFEK	2	99.9%	2																									
				NLQYYDISAK	2	100.0%	2																									
				SNYNFEKPFLWLAR	2	99.8%	1																									
				SNYNFEKPFLWLAR	3	100.0%	1																									
				VCENIPIVLCGNK	2	100.0%	2																									
IPI01011326	PMM2	Phosphomannomutase 2 variant (Fragment)	100.0%	6.7	1	1	1	2	2,574,507	2,701,343	2,647,613	2,943,303	188,800	249,059	145,704	204,080	16.4	20.6	12.3	15.5	1.0	0.7	1.0	0.8	1.1	0.2	-1.0	0.9	1.1	0.5	1.1	0.3
IPI01014747	PMM2	cDNA FLJ52163, highly similar to Phosphomannomutase 2	100.0%	6.8	1	1	1	2	2,574,507	2,701,343	2,647,613	2,943,303	188,800	249,059	145,704	204,080	16.4	20.6	12.3	15.5	1.0	0.7	1.0	0.8	1.1	0.2	-1.0	0.9	1.1	0.5	1.1	0.3
				NGMLNVSPIGR	2	96.5%	1																									
IPI01011356	PGM1	cDNA FLJ51818, highly similar to Phosphoglucomutase-1	100.0%	38.3	14	14	16	1	58,953,489	62,145,687	61,518,973	72,443,224	7,467,448	4,903,940	6,558,826	4,177,630	28.3	17.6	23.8	12.9	1.1	0.7	1.0	0.8	1.2	0.2	-1.0	0.9	1.2	0.1	1.2	0.2
				ADNFEYSDPVDGSISR	2	100.0%	1																									
				AIGGIILTASHNPGGPNGDFGIK	3	100.0%	1																									
				FNISNGGPAPEAITDK	2	100.0%	1																									
				IAAANGIGR	2	99.8%	1																									
				IALYETPTGWK	2	100.0%	2																									
				IDAMHGVVGPYVK	3	94.5%	1																									
				INQDPQVMLAPLISIALK	3	99.5%	1																									
				LSGTGSAGATIR	2	100.0%	2																									
				LYIDSYEKDVAK	2	94.3%	1																									
				SGEHDFGAAFDGDGDRNMILGK	3	98.4%	1																									
				SIFDFSALK	2	91.5%	1																									
				TIEEYAVCPDLK	2	100.0%	1																									
				VDLGVLGK	2	99.6%	1																									
				VFQSSANYAENFIQSIISTVEPAQR	3	99.9%	1																									
IPI01011389	HUWE1	HECT, UBA and WWE domain containing 1	96.0%	1.1	1	1	1	1	585,616	566,556	613,678	593,824	61,715	79,953	42,552	19,342	23.6	31.6	15.5	7.3	-1.0	0.9	1.0	0.7	1.0	0.9	1.1	0.6	1.0	0.8	-1.0	0.7
				LLSLISIALPENK	2	96.0%	1																									
IPI01011438	AIP	Uncharacterized protein	100.0%	10.5	2	2	2	1	7,204,504	6,975,152	6,987,112	7,655,115	455,944	300,044	258,345	298,037	14.2	9.6	8.3	8.7	-1.0	0.7	-1.0	0.7	1.1	0.4	1.0	1	1.1	0.1	1.1	0.1
				EGEIAQFLCDIK	2	100.0%	1																									
				YYDAIACLK	2	99.9%	1																									
IPI01011496	TPD52	Similar to Tumor protein D52	100.0%	34.9	6	6	6	1	3,022,127	3,111,944	3,089,138	3,413,609	236,064	150,722	260,304	84,751	17.5	10.8	18.8	5.6	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.1	1.1	0.3
				ASAAFSSVGSVITK	2	100.0%	1																									

				ELAKVEEEIQTLSQVLAAK	3	100.0%	1																									
				GWQDVTATSAYK	2	99.9%	1																									
				LGINSLQELK	2	100.0%	1																									
				TDPVPEEGEDVAATISATETLSEEEQEELRR	3	100.0%	1																									
				TSETLSQAGQK	2	99.5%	1																									
IPI01011575	LRPPRC	cDNA FLJ60080, highly similar to 130 kDa leucine-rich protein (Fragment)	100.0%	10.8	9	9	9	1	24,213,294	25,779,212	25,464,634	27,917,119	1,792,157	1,178,949	1,679,256	1,021,600	16.6	10.2	14.8	8.2	1.1	0.5	1.1	0.6	1.2	0.1	-1.0	0.9	1.1	0.2	1.1	0.2
				AGDMENAENILTVMR	2	100.0%	1																									
				GDVENIEVVQK	2	96.5%	1																									
				IQEENVIPR	2	99.7%	1																									
				LIASYCNVGDIEGASK	2	96.7%	1																									
				LLMSEDYFTQAMEVK	2	100.0%	1																									
				MEEANIQPNR	2	96.6%	1																									
				MLNGLEDSIGLSK	2	99.8%	1																									
				SMNINLWSEITELLYK	2	100.0%	1																									
				SNTLPISLQSIR	2	87.0%	1																									
IPI01011576	PHB2	15 kDa protein	100.0%	12.2	1	1	1	3	486,496	610,334	541,365	579,670	68,681	50,666	76,076	52,725	31.6	18.6	31.4	20.3	1.3	0.2	1.1	0.6	1.2	0.3	-1.1	0.5	-1.1	0.7	1.1	0.7
IPI01011917	PHB2	9 kDa protein	100.0%	19.5	1	1	1	3	486,496	610,334	541,365	579,670	68,681	50,666	76,076	52,725	31.6	18.6	31.4	20.3	1.3	0.2	1.1	0.6	1.2	0.3	-1.1	0.5	-1.1	0.7	1.1	0.7
IPI01012506	PHB2	12 kDa protein	100.0%	15.2	1	1	1	3	486,496	610,334	541,365	579,670	68,681	50,666	76,076	52,725	31.6	18.6	31.4	20.3	1.3	0.2	1.1	0.6	1.2	0.3	-1.1	0.5	-1.1	0.7	1.1	0.7
				IGGVQQDTILAEGLHFR	3	100.0%	1																									
IPI01011639	RPN1	cDNA FLJ50809, highly similar to Dolichyl-diphosphooligosaccharide--protein glycos	100.0%	4.8	2	2	2	1	6,469,777	6,151,700	6,163,443	7,047,570	450,334	315,895	318,927	370,939	15.6	11.5	11.6	11.8	-1.1	0.6	-1.0	0.6	1.1	0.4	1.0	1	1.1	0.1	1.1	0.1
				QPDSGISSIR	2	92.5%	1																									
				SEDLLDYGPFR	2	97.6%	1																									
IPI01011662	CAPG	12 kDa protein	100.0%	12.6	1	1	2	1	2,741,773	2,822,370	2,747,578	3,029,675	267,206	141,032	171,649	115,882	21.8	11.2	14.0	8.6	1.0	0.8	1.0	1	1.1	0.4	-1.0	0.7	1.1	0.3	1.1	0.2
				QAALQVAEGFISR	2	100.0%	2																									
IPI01011685	G3BP1	31 kDa protein	100.0%	9.5	2	3	4	1	5,955,188	5,951,310	5,975,778	6,367,845	533,096	49,142	442,240	219,376	20.0	1.9	16.6	7.7	-1.0	1	1.0	1	1.1	0.5	1.0	1	1.1	0.1	1.1	0.4
				LPNFGFVVFDDSEPVQK	2	100.0%	2																									
				LPNFGFVVFDDSEPVQK	3	100.0%	1																									
				TFSWASVTSK	2	99.5%	1																									
IPI01011706	SOD1	Superoxide dismutase 1 (Fragment)	100.0%	38.9	1	1	2	1	7,338,450	7,676,500	6,857,600	8,277,350	637,017	208,160	483,140	491,542	19.4	6.1	15.8	13.3	1.0	0.6	-1.1	0.6	1.1	0.3	-1.1	0.2	1.1	0.3	1.2	0.07
				GDGPVQGIINFEQK	2	100.0%	2																									
IPI01011710	ERI3	Prion protein interacting protein	97.0%	4.8	1	1	1	1	611,967	630,363	689,577	828,188	56,572	51,958	94,179	21,794	20.7	18.4	30.5	5.9	1.0	0.8	1.1	0.5	1.4	0.02	1.1	0.6	1.3	0.008	1.2	0.2
				SIFVTCGDWDLK	2	97.0%	1																									
IPI01011716	SELENBP1	Selenium binding protein 1	100.0%	16.9	4	4	4	1	4,219,697	4,582,125	4,151,630	5,403,088	423,372	179,463	400,614	289,196	22.4	8.8	21.6	12.0	1.1	0.5	-1.0	0.9	1.3	0.05	-1.1	0.4	1.2	0.04	1.3	0.04
				GGFVLLDGETFEVK	2	99.9%	1																									
				HNVMISTEWAAPNVLR	2	99.8%	1																									
				IYVVDVGSEPR	2	99.7%	1																									
				NTGTEAPDYLATVDVDPK	2	100.0%	1																									
IPI01011912	PGK1	Phosphoglycerate kinase	100.0%	79.4	28	42	69	1	376,298,641	374,701,347	374,880,671	437,965,416	########	########	########	########	20.0	10.1	17.6	7.1	-1.0	1	-1.0	1	1.2	0.1	1.0	1	1.2	0.02	1.2	0.09
				AAVPSIK	1	98.8%	3																									
				ACANPAAGSVILLENLR	2	100.0%	3																									
				AGGFLMK	2	99.9%	2																									
				AHSSMVGVNLPQK	2	100.0%	2																									
				AHSSMVGVNLPQK	3	100.0%	1																									
				AKQIVWNGPVGVFEWEAFAR	3	100.0%	1																									
				ALESPERPFLAILGGAK	2	100.0%	2																									
				ALESPERPFLAILGGAK	3	100.0%	2																									
				ALMDEVVK	1	100.0%	1																									
				DVLFLK	1	99.5%	2																									
				DVLFLK	2	98.2%	2																									
				FCLDNGAK	1	100.0%	1																									
				FCLDNGAK	2	99.4%	1																									
				FHVEEEGK	1	100.0%	1																									
				FHVEEEGK	2	99.2%	1																									
				FHVEEEGKGK	2	99.9%	1																									
				GCITIIGGGDTATCCAK	2	100.0%	2																									
				ITLPVDFVTADKFDENAK	2	100.0%	2																									
				ITLPVDFVTADKFDENAK	3	99.8%	2																									
				KYAEAVTR	2	99.9%	1																									
				LGDVYVNDAFGTAHR	2	100.0%	2																									
				LGDVYVNDAFGTAHR	3	100.0%	2																									
				QIVWNGPVGVFEWEAFAR	2	100.0%	3																									
				QIVWNGPVGVFEWEAFAR	3	100.0%	1																									
				SVVLMSHLGRPDGVPMPDK	3	100.0%	2																									
				SVVLMSHLGRPDGVPMPDKYSLEPVAVELK	3	100.0%	1																									
				TGQATVASGIPAGWMGLDCGPESSK	2	100.0%	2																									
				TGQATVASGIPAGWMGLDCGPESSKK	2	100.0%	1																									
				TGQATVASGIPAGWMGLDCGPESSKK	3	100.0%	2																									
				VADKIQLINNMLDK	2	100.0%	2																									
				VADKIQLINNMLDK	3	100.0%	1																									
				VLNNMEIGTSLFDEEGAK	2	100.0%	1																									
				VLNNMEIGTSLFDEEGAK	3	100.0%	1																									
				VLPGVDALSNI	1	100.0%	1																									
				VLPGVDALSNI	2	100.0%	1																									
				VNEMIIGGGMAFTFLK	2	100.0%	2																									
				VSHVSTGGGASLELLEGK	2	100.0%	2																									
				VSHVSTGGGASLELLEGK	3	100.0%	1																									
				WNTEDKVSHVSTGGGASLELLEGK	2	100.0%	2																									
				WNTEDKVSHVSTGGGASLELLEGK	3	100.0%	2																									
				YAEAVTR	1	100.0%	2																									
				YSLEPVAVELK	2	100.0%	2																									
IPI01011918	STRAP	Protein	100.0%	13.7	1	1	1	1	468,225	428,638	397,916	484,650	48,988	35,831	22,654	15,008	23.4	18.7	12.7	6.9	-1.1	0.5	-1.2	0.2	1.0	0.8	-1.1	0.5	1.1	0.2	1.2	0.01
				YDYNSGEELESYK	2	100.0%	1																									
IPI01011936	GSR	14 kDa protein	100.0%	9.9	1	1	1	1	1,384,831	1,357,714	1,414,286	1,609,521	43,848	72,729	86,934	86,497	7.1	12.0	13.7	12.0	-1.0	0.8	1.0	0.8	1.2	0.05	1.0	0.6	1.2	0.06	1.1	0.2
				LGGTCVNVGCVPK	2	100.0%	1																									
IPI01011952	VCL	cDNA FLJ59659, highly similar to Vinculin	100.0%	8.9	7	7	9	1	16,767,405	17,419,296	17,493,679	19,631,725	1,392,119	780,638	1,433,960	660,919	18.6	10.0	18.3	7.5	1.0	0.7	1.0	0.7	1.2	0.1	1.0	1	1.1	0.06	1.1	0.2
				AVAGNISDPGLQK	2	100.0%	2																									
				MLGQMTDQVADLR	2	99.7%	1																									
				MSAEINEIIR	2	99.9%	1																									
				MTGLVDEAIDTK	2	100.0%	1																									
				NQWIDNVEK	2	90.5%	1																									
				VLQLTSWDEDAWASK	2	100.0%	1																									
				WIDNPTVDDR	2	98.7%	2																									
IPI01011965	ACO1	Iron regulatory protein 1	100.0%	15.1	8	8	9	1	16,389,412	16,586,202	17,674,897	19,921,183	1,401,561	466,266	1,629,667	621,069	19.1	6.3	20.6	7.0	1.0	0.9	1.1	0.6	1.2	0.05	1.1	0.6	1.2	0.003	1.1	0.3
				AVDAGLNVMPYIK	2	91.3%	1																									
				DFNDPSQDPDFTQVVELDLK	2	100.0%	1																									
				FVEFFGPGVAQLSIADR	2	100.0%	2																									
				NQDLEFER	2	93.0%	1																									
				QAPQTIHLPSGEILDVFDAAER	3	99.4%	1																									
				SPPFFENLTLDLQPPK	2	91.4%	1																									
				YLQAVGMFR	2	99.9%	1																									
				YQQAGLPLIVLAGK	2	100.0%	1																									
IPI01011970	PGD	51 kDa protein	100.0%	11.9	5	5	7	1	9,654,811	10,136,855	9,708,426	10,957,232	893,739	739,903	551,105	582,115	20.7	16.3	12.7	11.9	1.0	0.7	1.0	1	1.1	0.3	-1.0	0.7	1.1	0.4	1.1	0.2
				AGQAVDDFIEK	2	100.0%	2																									
				FQFDGDKK	2	97.1%	1																									
				GILFVGSGVSGGEEGAR	2	100.0%	2																									
				SFLEDIRK	2	98.6%	1																									
				YGPSLMPGGNK	2	99.4%	1																									
IPI01011988	CORO1C	cDNA, FLJ79403, highly similar to Coronin-1C	99.9%	12.2	2	2	2	1	1,804,108	1,811,980	1,795,705	2,485,958	278,251	135,206	75,672	89,797	34.5	16.7	9.4	8.1	1.0	1	-1.0	1	1.4	0.07	-1.0	0.9	1.4	0.003	1.4	0.0004
				AIFLADGNVFTTGFSR	2	93.7%	1																									
				KSDLFQDDLYPDTAGPEAALEAEEWFEGK	3	99.9%	1																									
IPI01011993	RRBP1	cDNA FLJ36146 fis, clone TESTI2025117, highly similar to Ribosome-binding protei	100.0%	39.2	23	23	28	1	27,252,396	29,681,302	28,145,660	32,622,032	2,685,891	1,529,705	2,212,507	1,176,368	22.0	11.5	17.6	8.1	1.1	0.5	1.0	0.8	1.2	0.1	-1.1	0.6	1.1	0.2	1.2	0.1
				AQEQQQQMAELHSK	3	100.0%	2																									
				EHTSHLEAELEK	2	99.9%	1																									
				EQEITAVQAR	2	100.0%	1																									
				HLEEIVEK	2	100.0%	2																									
				HPPAPAEPSSDLASK	2	100.0%	1																									
				KLTSDLGR	2	81.1%	1																									
				LKELESQVSGLEK	2	99.9%	1																									
				LKGELESSDQVR	3	99.9%	1																									
				LLATEQEDAAVAK	2	100.0%	2																									
				LQQENSILR	2	98.0%	1																									
				LQSSEAEVR	2	89.3%	1																									
				LTAEFEEAQTSACR	2	99.9%	1																									
				QLLLESQSQLDAAK	2	100.0%	2																									
				QSDELALVR	2	88.6%	1																									
				QVLQLQASHR	2	88.0%	1																									
				SHVEDGDIAGAPASSPEAPPAEQDPVQLK	3	100.0%	1																									
				SIEALLEAGQAR	2	99.9%	1																									
				SILAETEGMLR	2	100.0%	2																									
				SVEEEEQVWR	2	100.0%	1																									
				TAGPLESSETEEASQLKER	3	98.7%	1																									
				TLQEQLENGPNTQLAR	2	100.0%	1																									
				TQLEWTEAILEDEQTQR	3	100.0%	1																									
				VGAAEEELQK	2	98.3%	1																									
IPI01012065	PSMA1	27 kDa protein	100.0%	15.6	2	2	3	1	2,229,660	2,315,090	2,043,610	2,586,567	148,591	124,067	89,921	180,198	14.9	12.0	9.8	15.6	1.0	0.7	-1.1	0.3	1.2	0.2	-1.1	0.1	1.1	0.2	1.3	0.03
				DLEFTIYDDDDVSPFLEGLEERPQR	3	100.0%	1																									
				ETLPAEQDLTTK	2	100.0%	2																									
IPI01012138	PLOD1	cDNA FLJ52901, highly similar to Procollagen-lysine,2-oxoglutarate5-dioxygenase 1	95.7%	3.1	1	1	1	1	680,628	664,580	669,673	726,755	57,045	49,330	27,834	57,976	18.7	16.6	9.3	17.8	-1.0	0.8	-1.0	0.9	1.1	0.6	1.0	0.9	1.1	0.4	1.1	0.4
				FLLEYIAPMTEK	2	95.7%	1																									
IPI01012144	RAN;RANP1	Protein	100.0%	29.1	3	3	5	1	6,741,061	6,823,763	6,130,601	7,244,914	722,888	449,077	426,004	236,056	24.0	14.7	15.5	7.3	1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.3	1.1	0.4	1.2	0.05
				FNVWDTAGQEK	2	100.0%	2																									
				HLTGEFEK	2	99.9%	2																									
				LVLVGDGGTGK	2	96.9%	1																									
IPI01012157	LARS	Proliferation-inducing protein 44	100.0%	4.1	2	2	2	1	5,328,300	5,626,208	4,998,920	6,355,684	627,482	235,414	415,588	301,385	26.3	9.4	18.6	10.6	1.1	0.7	-1.1	0.7	1.2	0.2	-1.1	0.2	1.1	0.09	1.3	0.03
				FDDPLLGPR	2	99.9%	1																									
				ILDLQLEFDEK	2	99.7%	1																									
IPI01012172	TARS	cDNA FLJ38533 fis, clone HCHON2001108, highly similar to Threonyl-tRNA synthet	100.0%	21.8	12	12	15	1	21,086,730	21,622,511	20,723,201	24,679,288	1,728,691	1,003,473	1,223,347	456,203	18.3	10.4	13.2	4.1	1.0	0.8	-1.0	0.9	1.2	0.1	-1.0	0.6	1.1	0.02	1.2	0.03

				CGPLIDLCR	2	91.2%	1																									
				FLGDIEVWDQAEK	2	100.0%	2																									
				FMADIDLDPGCTLNK	2	99.6%	1																									
				FMADIDLDPGCTLNKK	3	99.0%	1																									
				GAYIYNALIEFIR	2	100.0%	2																									
				IYGISFPDPK	2	99.9%	1																									
				LADFGVLHR	2	98.8%	1																									
				MIAILTENYGGK	2	99.7%	1																									
				NAQLAQYNFILVVGEK	2	99.3%	1																									
				NELSGALTGLTR	2	100.0%	2																									
				QVMVVPVGPTCDEYAQK	2	100.0%	1																									
				WPFWLSPR	2	100.0%	1																									
IPI01012260	DDX18	cDNA FLJ33908 fis, clone CTONG2008518, highly similar to DEAD/H (Asp-Glu-Ala-	97.2%	2.9	1	1	1	1	3,201,475	3,139,720	2,858,935	3,539,400	367,860	153,364	342,534	287,554	25.7	10.9	26.8	18.2	-1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.5	1.1	0.3	1.2	0.2
				VPLSEFDFSWSK	2	97.2%	1																									
IPI01012309	MPI	41 kDa protein	100.0%	20.9	5	5	5	1	5,212,351	5,375,619	5,370,797	5,975,985	608,221	219,655	418,897	189,653	26.1	9.1	17.4	7.1	1.0	0.8	1.0	0.8	1.1	0.3	-1.0	1	1.1	0.07	1.1	0.2
				FIDVPTLCEMLSYTPSSSK	2	100.0%	1																									
				SQEDPYLSIYDPPVPDFTIMK	2	100.0%	1																									
				TEVPGSVTEYK	2	80.4%	1																									
				TLSQWIAENQDSLGSK	2	100.0%	1																									
				VVVEQLNLLVK	2	99.8%	1																									
IPI01012312	EPS8	77 kDa protein	96.8%	6.4	2	2	2	1	2,392,200	2,947,363	2,114,220	2,903,427	356,812	179,631	342,986	228,634	33.4	13.6	36.3	17.6	1.2	0.2	-1.1	0.6	1.2	0.3	-1.4	0.06	-1.0	0.9	1.4	0.09
				DVQILNHILDDIEFFITK	2	83.2%	1																									
				NASGDSGFVPNNILDIVRPPESGLGR	3	80.8%	1																									
IPI01012346	S100A4	11 kDa protein	100.0%	20.0	2	2	3	1	3,907,850	3,809,670	3,837,205	4,571,575	509,142	200,412	309,984	136,309	29.1	11.8	18.1	6.7	-1.0	0.9	-1.0	0.9	1.2	0.3	1.0	0.9	1.2	0.01	1.2	0.06
				RTDEAAFQK	2	100.0%	2																									
				SELKELLTR	2	99.3%	1																									
IPI01012360	FKBP9	cDNA FLJ53833, highly similar to FK506-binding protein 9	98.8%	3.9	1	1	1	1	1,140,693	1,137,933	1,035,907	1,297,657	142,722	136,376	132,874	66,769	28.0	26.8	28.7	11.5	-1.0	1	-1.1	0.6	1.1	0.3	-1.1	0.6	1.1	0.3	1.3	0.1
				TYDTYVGIGWLIPGMDK	2	98.8%	1																									
IPI01012403	PCK2	cDNA, FLJ79105, highly similar to Phosphoenolpyruvate carboxykinase (GTP), mito	100.0%	3.2	1	1	1	1	1,915,437	1,739,520	1,744,640	1,644,103	257,614	130,419	98,612	70,209	30.1	16.8	12.6	9.6	-1.1	0.6	-1.1	0.6	-1.2	0.4	1.0	1	-1.1	0.5	-1.1	0.4
				LGTPVLQALGDGDFVK	2	99.1%	1																									
IPI01012417	NSUN2	59 kDa protein	100.0%	4.9	2	2	2	1	3,280,453	3,103,127	3,212,940	3,560,003	239,768	127,435	258,386	153,337	16.3	9.2	18.0	9.6	-1.1	0.5	-1.0	0.9	1.1	0.4	1.0	0.7	1.1	0.05	1.1	0.3
				DGQWFTDWDAVPHSR	3	100.0%	1																									
				ILLTQENPFFR	2	96.5%	1																									
IPI01012480	ACTR3	cDNA FLJ52521, highly similar to Actin-like protein 3	100.0%	14.5	4	4	6	1	2,456,194	2,744,996	2,722,400	3,012,517	164,306	157,007	115,992	115,885	15.0	12.8	9.5	8.6	1.1	0.2	1.1	0.2	1.2	0.02	-1.0	0.9	1.1	0.2	1.1	0.1
				DITYFIQQLLR	2	100.0%	2																									
				LSEELSGGR	2	99.2%	1																									
				NIVLSGGSTMFR	2	100.0%	1																									
				YSYVCPDLVK	2	100.0%	2																									
IPI01012526	GANAB	96 kDa protein	100.0%	25.7	15	16	19	1	35,004,937	35,282,075	37,413,364	40,966,781	2,837,511	1,432,393	2,503,616	1,506,189	18.1	9.1	15.0	8.2	1.0	0.9	1.1	0.5	1.2	0.1	1.1	0.5	1.2	0.03	1.1	0.3
				DENSVELTMAEGPYK	2	100.0%	1																									
				FGAVWTGDNTAEWDHLK	3	100.0%	1																									
				FRIDELEPR	3	93.3%	1																									
				FSFSGNTLVSSSADPEGHFETPIWIER	3	100.0%	2																									
				GLLEFEHQR	2	99.3%	1																									
				HHGPQTLYLPVTLSSIPVFQR	2	97.1%	1																									
				LSFQHDPETSVLVLR	3	100.0%	1																									
				LVAIVDPHIK	2	99.9%	1																									
				LVAIVDPHIK	3	99.7%	1																									
				MMDYLQGSGETPQTDVR	2	100.0%	2																									
				NPEPELLVR	2	98.3%	1																									
				QYASLTGTQALPPLFSLGYHQSR	3	100.0%	1																									
				VTEGGEPYR	2	98.6%	1																									
				VVIIGAGKPAAVVLQTK	2	100.0%	1																									
				WYQMGAYQPFFR	2	100.0%	2																									
				YFTWDPSR	2	98.7%	1																									
IPI01012564	MYO1C	cDNA FLJ52405, highly similar to Myosin Ic	100.0%	20.1	13	13	16	1	8,164,481	8,128,529	7,840,570	9,220,355	581,066	249,596	411,276	367,095	15.9	6.9	11.7	8.9	-1.0	1	-1.0	0.7	1.1	0.2	-1.0	0.6	1.1	0.04	1.2	0.04
				DQAVMISGESGAGK	2	100.0%	1																									
				DRVGVQDFVLLENFTSEAAFIENLR	3	99.7%	1																									
				FDEVLIR	2	99.4%	1																									
				GVSFYEVPPHLFAVADTVYR	3	100.0%	1																									
				KRPETVATQFK	2	99.5%	1																									
				KYEAFLQR	2	86.0%	1																									
				LLQSNPVLEAFGNAK	2	100.0%	2																									
				MSLLQLVEILQSK	2	100.0%	2																									
				NPIMSQCFDR	2	100.0%	1																									
				PQDGVAVLVR	2	99.7%	1																									
				TFTWLVGK	2	99.4%	1																									
				TLFATEDALEVR	2	95.4%	1																									
				YMDVQFDFK	2	99.3%	2																									
IPI01012597	ILF3	30 kDa protein	100.0%	4.9	1	1	2	2	463,880	489,288	430,901	494,533	23,034	16,563	38,024	23,717	11.1	7.6	19.7	10.7	1.1	0.4	-1.1	0.5	1.1	0.4	-1.1	0.2	1.0	0.9	1.1	0.2
IPI01012962	ILF3	cDNA FLJ58801, highly similar to Interleukin enhancer-binding factor 3	100.0%	2.8	1	1	2	2	463,880	489,288	430,901	494,533	23,034	16,563	38,024	23,717	11.1	7.6	19.7	10.7	1.1	0.4	-1.1	0.5	1.1	0.4	-1.1	0.2	1.0	0.9	1.1	0.2
				VLQDMGLPTGAEGR	2	100.0%	2																									
IPI01012656	NUMA1	Nuclear mitotic apparatus protein 1, isoform CRA_e	100.0%	7.3	5	5	7	1	7,245,474	7,932,217	7,739,799	9,364,893	755,963	363,688	499,376	471,621	23.3	10.3	14.4	11.3	1.1	0.4	1.1	0.6	1.3	0.04	-1.0	0.8	1.2	0.04	1.2	0.05
				DAQIAMMQQR	2	98.9%	1																									
				INQLSEENGDLSFK	2	100.0%	2																									
				LGHELQQAGLK	2	82.8%	1																									
				LQAQLNELQAQLSQK	2	100.0%	2																									
				SQAPLESSLDSLGDVFLDSGR	2	100.0%	1																									
IPI01012694	SAE1	cDNA FLJ58436, highly similar to Ubiquitin-like 1-activating enzyme E1A	100.0%	26.7	3	4	4	1	4,993,521	5,244,533	5,271,358	6,075,189	452,367	386,984	288,926	221,326	20.3	16.5	12.3	8.2	1.1	0.7	1.1	0.6	1.2	0.06	1.0	1	1.2	0.1	1.2	0.06
				AKLDSSETTMVK	2	99.8%	1																									
				EALEVDWSSEK	2	97.0%	1																									
				YCFSEMAPVCAVVGGILAQEIVK	2	100.0%	1																									
				YCFSEMAPVCAVVGGILAQEIVK	3	100.0%	1																									
IPI01012696	MSH2	cDNA FLJ50998, highly similar to DNA mismatch repair protein Msh2	98.4%	3.4	2	2	2	1	924,241	894,594	987,144	946,763	125,328	67,778	62,959	55,491	30.3	16.9	14.3	13.1	-1.0	0.8	1.1	0.7	1.0	0.9	1.1	0.3	1.1	0.6	-1.0	0.6
				GVSTFMAEMLETASILR	2	98.4%	1																									
				QVGVGYVDSIQR	2	85.1%	1																									
IPI01012741	GART	cDNA FLJ51866, highly similar to Trifunctional purine biosynthetic protein adenosine	99.8%	2.0	1	1	1	1	2,553,770	2,590,925	3,147,840	3,181,950	379,983	155,531	231,823	307,327	33.3	13.4	16.5	21.6	1.0	0.9	1.2	0.2	1.2	0.2	1.2	0.08	1.2	0.1	1.0	0.9
				LGVDLDAQTWR	2	94.7%	1																									
IPI01012797	STARD10	9 kDa protein	100.0%	40.2	2	2	3	1	4,361,888	4,295,665	4,151,410	4,576,930	268,337	173,339	264,635	140,171	13.8	9.0	14.3	6.9	-1.0	0.8	-1.1	0.6	1.0	0.5	-1.0	0.7	1.1	0.2	1.1	0.2
				ESVQVPDDQDFR	2	99.9%	2																									
				MECCDVPAETLYDVLHDIEYR	3	99.4%	1																									
IPI01012856	SNRNP200	Activating signal cointegrator 1 complex subunit 3-like 1	100.0%	3.8	2	2	2	1	2,158,012	1,907,610	2,342,784	1,958,385	276,781	232,892	107,256	130,925	28.7	27.3	10.2	15.0	-1.1	0.5	1.1	0.6	-1.1	0.5	1.2	0.1	1.0	0.9	-1.2	0.05
				LIGLSATLPNYEDVATFLR	2	99.5%	1																									
				YAQAGFEGFK	2	99.0%	1																									
IPI01012899	RPIA	Putative uncharacterized protein RPIA (Fragment)	100.0%	16.4	2	2	2	1	8,996,800	14,178,055	9,195,930	10,067,735	2,829,549	3,860,213	1,245,893	1,874,328	70.3	60.9	30.3	41.6	1.6	0.3	1.0	1	1.1	0.8	-1.5	0.3	-1.4	0.4	1.1	0.7
				GIPIEVIPMAYVPVSR	2	98.7%	1																									
				VYFGMQDGSVNMR	2	99.7%	1																									
IPI01012905	NDRG1	cDNA FLJ53637, highly similar to Protein NDRG1	100.0%	24.3	3	3	6	1	2,077,654	2,109,549	1,923,645	2,393,011	188,122	102,872	135,006	109,698	20.3	10.9	15.7	10.3	1.0	0.9	-1.1	0.5	1.2	0.2	-1.1	0.3	1.1	0.1	1.2	0.03
				MADCGGLPQISQPAK	2	100.0%	2																									
				SHTSEGAHLDITPNSGAAGNSAGPK	3	100.0%	2																									
				TASGSSVTSLDGTR	2	100.0%	2																									
IPI01012955	ACTR3	cDNA, FLJ79295, highly similar to Actin-like protein 3	100.0%	14.7	5	5	7	1	5,928,959	6,348,856	6,254,975	6,685,567	397,573	412,886	336,906	103,944	15.0	14.5	12.0	3.5	1.1	0.5	1.1	0.5	1.1	0.1	-1.0	0.9	1.1	0.5	1.1	0.3
				DITYFIQQLLR	2	100.0%	2																									
				HGIVEDWDLMER	2	100.0%	1																									
				LSEELSGGR	2	99.2%	1																									
				NIVLSGGSTMFR	2	100.0%	1																									
				YSYVCPDLVK	2	100.0%	2																									
IPI01012981	P4HB	cDNA FLJ59361, highly similar to Protein disulfide-isomerase	100.0%	57.7	24	34	51	1	147,707,687	148,142,392	150,951,400	171,186,245	########	5,107,796	9,876,105	4,756,950	17.1	7.7	14.6	6.2	1.0	1	1.0	0.8	1.2	0.09	1.0	0.8	1.2	0.01	1.1	0.1
				ALAPEYAK	1	97.3%	1																									
				ALAPEYAK	2	99.3%	1																									
				DHENIVIAK	2	100.0%	2																									
				HNQLPLVIEFTEQTAPK	2	100.0%	2																									
				HNQLPLVIEFTEQTAPK	3	100.0%	2																									
				IKPHLMSQELPEDWDKQPVK	3	100.0%	2																									
				ILEFFGLK	2	99.1%	1																									
				ILFIFIDSDHTDNQR	2	100.0%	2																									
				ILFIFIDSDHTDNQR	3	99.9%	2																									
				LGETYKDHENIVIAK	2	100.0%	1																									
				LGETYKDHENIVIAK	3	100.0%	2																									
				LITLEEEMTK	2	100.0%	2																									
				LKAEGSEIR	2	87.3%	1																									
				MDSTANEVEAVK	2	100.0%	1																									
				NFEDVAFDEK	2	99.8%	2																									
				NFEDVAFDEKK	2	99.9%	1																									
				NFEDVAFDEKK	3	100.0%	1																									
				NNFEGEVTK	2	99.8%	1																									
				NNFEGEVTKENLLDFIK	3	100.0%	2																									
				NVFVEFYAPWCGHCK	3	99.7%	1																									
				QFLQAAEAIDDIPFGITSNSDVFSK	2	100.0%	2																									
				QFLQAAEAIDDIPFGITSNSDVFSK	3	100.0%	1																									
				QLAPIWDK	2	99.7%	2																									
				TAAESFK	1	98.5%	2																									
				TGPAATTLPDGAAAESLVESSEVAVIGFFK	2	100.0%	2																									
				TGPAATTLPDGAAAESLVESSEVAVIGFFK	3	100.0%	1																									
				TVIDYNGER	2	100.0%	2																									
				VDATEESDLAQQYGVR	2	100.0%	1																									
				VDATEESDLAQQYGVR	3	100.0%	1																									
				VHSFPTLK	2	88.9%	1																									
				YKPESEELTAER	2	100.0%	2																									
				YKPESEELTAER	3	100.0%	1																									
				YQLDKDGVVLFK	2	100.0%	1																									
				YQLDKDGVVLFK	3	100.0%	2																									
IPI01012991	LUC7L2	isoform 1 of Putative RNA-binding protein Luc7-like 2	100.0%	22.2	7	7	9	1	12,797,433	11,045,048	10,256,570	11,589,834	1,142,693	537,655	684,707	867,443	20.0	10.9	14.9	16.7	-1.2	0.2	-1.2	0.09	-1.1	0.4	-1.1	0.4	1.0	0.6	1.1	0.3
				AMLDQLMGTSR	2	100.0%	2																									
				LAETQEEISAEVAAK	2	100.0%	1																									
				MDLGECLK	2	96.6%	1																									
				NSMPASSFQQQK	2	99.9%	1																									

				SHLLNCCPHDVLSGTR	3	96.2%	1																									
				VEQLGAEGNVEESQK	2	100.0%	2																									
				VHELNEEIGK	2	99.4%	1																									
IPI01013021	EIF3F	cDNA FLJ52478, highly similar to Eukaryotic translation initiation factor 3 subunit 5	100.0%	25.5	4	4	4	1	7,936,974	9,859,981	8,514,576	9,406,458	1,072,358	1,432,630	1,120,616	1,002,570	30.2	32.5	29.4	23.8	1.2	0.3	1.1	0.7	1.2	0.3	-1.2	0.5	-1.0	0.8	1.1	0.6
				AYVSTLMGVPGR	2	100.0%	1																									
				EAPNPIHLTVDTSLQNGR	3	100.0%	1																									
				FLMSLVNQVPK	2	100.0%	1																									
				TMGVMFTPLTVK	2	99.6%	1																									
IPI01013025	PKP2	Truncated plakophilin-2	99.8%	1.3	1	1	1	1	1,581,137	1,561,933	1,586,943	1,940,287	127,348	151,890	84,579	103,353	18.0	21.7	11.9	11.9	-1.0	0.9	1.0	1	1.2	0.06	1.0	0.9	1.2	0.07	1.2	0.03
				IQEQVQQTLAR	2	99.7%	1																									
IPI01013091	ACTR1A	35 kDa protein	100.0%	21.9	4	4	4	2	3,767,984	3,709,900	3,751,915	4,323,702	272,934	89,760	230,699	195,856	16.2	5.4	13.8	10.1	-1.0	0.8	-1.0	1	1.1	0.1	1.0	0.9	1.2	0.02	1.2	0.1
IPI01013552	ACTR1A	cDNA FLJ52800, highly similar to Alpha-centractin	100.0%	20.1	4	4	4	2	3,767,984	3,709,900	3,751,915	4,323,702	272,934	89,760	230,699	195,856	16.2	5.4	13.8	10.1	-1.0	0.8	-1.0	1	1.1	0.1	1.0	0.9	1.2	0.02	1.2	0.1
				AQYYLPDGSTIEIGPSR	2	100.0%	1																									
				LYSTWIGGSILASLDTFK	2	86.9%	1																									
				LYSTWIGGSILASLDTFKK	3	100.0%	1																									
				TTGVVLDSGDGVTHAVPIYEGFAMPHSIMR	3	100.0%	1																									
IPI01013108	ACADVL	isoform 1 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	100.0%	24.0	12	12	14	1	18,663,825	20,352,639	19,935,317	24,079,580	2,590,385	1,358,673	1,611,634	660,497	31.0	14.9	18.1	6.1	1.1	0.6	1.1	0.7	1.3	0.1	-1.0	0.8	1.2	0.04	1.2	0.04
				AGLGSGLSLSGLVHPELSR	3	100.0%	1																									
				ALEQFATVVEAK	2	100.0%	1																									
				ASNTAEVFFDGVR	2	100.0%	1																									
				EGMAALQSDPWQQELYR	2	99.9%	1																									
				FGMAAALAGTMR	2	100.0%	1																									
				GIVNEQFLLQR	2	99.9%	1																									
				IFEGTNDILR	2	99.4%	1																									
				IHNFGLIQEK	2	99.8%	1																									
				NPFGNAGLLLGEAGK	2	99.9%	2																									
				QLLRLGGGSSR	3	93.7%	1																									
				TPVTDPATGAVK	2	98.9%	2																									
				VPSENVLGEVGSGFK	2	100.0%	1																									
IPI01013158	ASL	cDNA, FLJ79233, highly similar to Argininosuccinate lyase	100.0%	22.1	4	4	4	1	3,837,719	4,321,171	3,551,924	5,102,581	624,147	363,245	444,072	354,384	36.4	18.8	28.0	15.5	1.1	0.5	-1.1	0.7	1.3	0.1	-1.2	0.2	1.2	0.2	1.4	0.03
				FVGAVDPIMEK	2	97.3%	1																									
				HLWEVDVQGSK	2	99.9%	1																									
				QTCSTLSGLLWELIR	2	99.9%	1																									
				SRNDQVVTDLR	2	87.9%	1																									
IPI01013183	COPE	Epsilon-COP	100.0%	24.4	4	4	5	1	12,013,540	12,603,592	14,268,982	14,350,311	1,190,518	747,176	1,479,860	490,473	22.2	13.3	23.2	7.6	1.0	0.7	1.2	0.3	1.2	0.1	1.1	0.3	1.1	0.09	1.0	1
				DSIVAELDREMSR	2	81.0%	1																									
				FGVVLDEIKPSSAPELQAVR	3	100.0%	1																									
				LQDAYYIFQEMADK	2	100.0%	2																									
				SVDVTNTTFLLMAASIYLHDQNPDAALR	3	99.2%	1																									
IPI01013215	DNAJA1	HDJ2 protein (Fragment)	96.6%	14.7	2	2	2	2	2,885,467	3,144,330	3,180,880	2,863,733	224,298	165,995	206,303	174,379	17.4	11.8	14.5	13.6	1.1	0.4	1.1	0.4	-1.0	0.9	1.0	0.9	-1.1	0.3	-1.1	0.3
IPI01015967	DNAJA1	29 kDa protein	96.6%	14.8	2	2	2	2	2,885,467	3,144,330	3,180,880	2,863,733	224,298	165,995	206,303	174,379	17.4	11.8	14.5	13.6	1.1	0.4	1.1	0.4	-1.0	0.9	1.0	0.9	-1.1	0.3	-1.1	0.3
				ITFHGEGDQEPGLEPGDIIIVLDQK	3	96.6%	1																									
				TIVITSHPGQIVK	2	91.4%	1																									
IPI01013219	PHB2	30 kDa protein	100.0%	20.6	4	4	5	1	3,464,426	3,828,219	3,863,595	4,092,483	308,957	143,993	438,339	161,205	19.9	8.4	25.4	8.8	1.1	0.3	1.1	0.5	1.2	0.1	1.0	0.9	1.1	0.3	1.1	0.6
				FNASQLITQR	2	99.9%	2																									
				IGGVQQDTILAEGLHFR	3	100.0%	1																									
				IVQAEGEAEAAK	2	100.0%	1																									
				VLSRPNAQELPSMYQR	3	95.0%	1																									
IPI01013273	CCT6A	cDNA, FLJ79129, highly similar to T-complex protein 1 subunit zeta	100.0%	42.6	16	18	22	1	51,170,549	53,033,972	52,540,073	57,577,065	3,213,815	1,898,037	3,510,316	1,479,528	14.0	8.0	14.9	5.8	1.0	0.6	1.0	0.8	1.1	0.1	-1.0	0.9	1.1	0.1	1.1	0.2
				AGMSSLKG	2	96.9%	2																									
				ALQFLEEVK	2	99.9%	1																									
				AQLGVQAFADALLIIPK	2	100.0%	2																									
				DGNVLLHEMQIQHPTASLIAK	3	100.0%	1																									
				EMDRETLIDVAR	2	91.2%	1																									
				GIDPFSLDALSK	2	95.1%	1																									
				HKSETDTSLIR	3	98.5%	1																									
				HTLTQIK	2	96.9%	1																									
				IITEGFEAAK	2	98.8%	1																									
				KQDEPIDLFMIEIMEMK	2	99.9%	1																									
				KQDEPIDLFMIEIMEMK	3	100.0%	1																									
				MLVSGAGDIK	2	87.7%	1																									
				NAIDDGCVVPGAGAVEVAMAEALIK	2	100.0%	1																									
				NAIDDGCVVPGAGAVEVAMAEALIK	3	100.0%	1																									
				QADLYISEGLHPR	2	97.8%	1																									
				QDEPIDLFMIEIMEMK	2	98.8%	1																									
				VATAQDDITGDGTTSNVLIIGELLK	2	100.0%	2																									
				VLAQNSGFDLQETLVK	2	100.0%	2																									
IPI01013292	PHB2	cDNA FLJ60175, highly similar to Prohibitin-2	100.0%	12.7	2	2	3	1	1,343,405	1,514,575	1,501,332	1,642,937	177,162	77,383	195,792	96,711	29.5	11.4	29.2	13.2	1.1	0.4	1.1	0.6	1.2	0.2	-1.0	1	1.1	0.3	1.1	0.5
				FNASQLITQR	2	99.9%	2																									
				IGGVQQDTILAEGLHFR	3	100.0%	1																									
IPI01013347	-	29 kDa protein	100.0%	10.2	2	2	2	1	466,226	410,386	495,570	500,584	38,927	26,017	32,555	37,437	18.7	14.2	14.7	16.7	-1.1	0.3	1.1	0.6	1.1	0.5	1.2	0.08	1.2	0.08	1.0	0.9
				EGYLQIGANTQAAQK	2	100.0%	1																									
				EVAFWTNLFAK	2	90.8%	1																									
IPI01013361	CALU	calumenin isoform e precursor	100.0%	12.1	2	2	2	1	7,414,797	9,010,083	8,442,433	8,922,410	1,765,924	1,535,383	1,449,462	633,201	53.3	38.1	38.4	15.9	1.2	0.5	1.1	0.7	1.2	0.5	-1.1	0.8	-1.0	1	1.1	0.8
				IDGDKDGFVTVDELKDWIK	3	100.0%	1																									
				WIYEDVER	2	99.9%	1																									
IPI01013413	ACTR3	cDNA FLJ51082, highly similar to Actin-like protein 3	100.0%	8.7	3	3	4	1	2,349,087	2,641,455	2,623,612	2,874,692	156,571	158,983	107,152	101,823	14.9	13.5	9.1	7.9	1.1	0.2	1.1	0.2	1.2	0.02	-1.0	0.9	1.1	0.3	1.1	0.1
				LSEELSGGR	2	99.2%	1																									
				NIVLSGGSTMFR	2	100.0%	1																									
				YSYVCPDLVK	2	100.0%	2																									
IPI01013481	GSS	cDNA FLJ50601, highly similar to Glutathione synthetase	100.0%	27.5	7	7	8	1	31,755,753	32,544,520	30,474,243	36,428,767	3,112,375	1,611,634	2,053,527	1,048,120	21.9	11.1	15.1	6.4	1.0	0.8	-1.0	0.7	1.1	0.2	-1.1	0.5	1.1	0.08	1.2	0.03
				AIEHADGGVAAGVAVLDNPYPV	2	100.0%	1																									
				AIENELLAR	2	99.9%	1																									
				ASYILMEK	2	99.3%	1																									
				CPDIATQLAGTK	2	90.1%	1																									
				EGGGNNLYGEEMVQALK	2	99.9%	1																									
				QIEINTISASFGGLASR	2	99.6%	1																									
				QYSLQNWEAR	2	98.1%	2																									
IPI01013515	PTGR1	Prostaglandin reductase 1	100.0%	18.6	2	3	3	1	3,154,223	3,295,703	3,798,120	3,357,670	222,404	241,244	137,979	102,112	15.8	16.4	8.1	6.8	1.0	0.7	1.2	0.04	1.1	0.4	1.2	0.1	1.0	0.8	-1.1	0.03
				GGETVMVNAAAGAVGSVVGQIAK	2	98.3%	1																									
				GGETVMVNAAAGAVGSVVGQIAK	3	100.0%	1																									
				LGFDVVFNYK	2	100.0%	1																									
IPI01013523	UCHL5	Ubiquitin carboxyl-terminal hydrolase L5	95.5%	3.1	1	1	1	1	498,477	446,438	440,707	451,483	57,899	23,807	46,176	27,557	26.0	11.9	23.4	13.7	-1.1	0.4	-1.1	0.5	-1.1	0.5	-1.0	0.9	1.0	0.9	1.0	0.8
				LYELDGLR	2	95.5%	1																									
IPI01013525	CORO1B	20 kDa protein	100.0%	15.3	3	3	4	1	5,843,168	6,334,088	5,513,868	6,443,068	550,738	393,946	490,684	474,577	21.1	13.9	19.9	16.5	1.1	0.5	-1.1	0.7	1.1	0.4	-1.1	0.2	1.0	0.9	1.2	0.2
				HVFGQPVK	2	98.2%	1																									
				NDQCYEDIR	2	93.7%	1																									
				VGIIAWHPTAR	3	100.0%	2																									
IPI01013542	HSD17B4	54 kDa protein	100.0%	14.6	5	5	6	1	10,400,509	11,701,192	10,892,996	12,564,437	869,033	503,312	933,541	377,331	18.7	9.6	19.2	6.7	1.1	0.2	1.0	0.7	1.2	0.05	-1.1	0.5	1.1	0.2	1.2	0.1
				AYALAFAER	2	87.2%	1																									
				GALVVVNDLGGDFK	2	100.0%	2																									
				IDVVVNNAGILR	2	100.0%	1																									
				LPPFSYAYTELEAIMYALGVGASIK	3	88.6%	1																									
				VVLVTGAGAGLGR	2	100.0%	1																									
IPI01013571	CCND1	29 kDa protein	98.8%	16.7	2	2	2	1	4,374,012	4,355,450	4,840,743	4,395,072	544,896	263,242	622,307	336,488	27.9	13.5	28.8	17.1	-1.0	1	1.1	0.6	1.0	1	1.1	0.5	1.0	0.9	-1.1	0.5
				AGPAAPGLPLRAGSLGDPGRLLALHLGAVWEDVPR	3	89.4%	1																									
				MPEAEENK	2	89.6%	1																									
IPI01013653	FKBP4	Protein	100.0%	31.0	3	3	3	1	8,230,833	8,899,180	8,125,643	10,076,397	1,214,853	865,172	1,007,662	530,235	33.0	21.7	27.7	11.8	1.1	0.7	-1.0	0.9	1.2	0.2	-1.1	0.6	1.1	0.3	1.2	0.1
				LYANMFER	2	99.6%	1																									
				TQLAVCQQR	2	99.9%	1																									
				VLQLYPNNK	2	99.8%	1																									
IPI01013673	TIAL1	TIAL1 protein	100.0%	20.6	4	4	5	1	5,105,070	5,051,235	4,683,520	5,478,341	453,210	185,652	287,128	227,057	19.9	8.2	13.7	9.3	-1.0	0.9	-1.1	0.5	1.1	0.5	-1.1	0.3	1.1	0.2	1.2	0.06
				FEDVVNQSSPK	2	100.0%	1																									
				GYGFVSFYNK	2	83.3%	1																									
				LDAENAIVHMGGQWLGGR	3	100.0%	1																									
				QTFSPFGQIMEIR	2	100.0%	2																									
IPI01013700	HSDL2	cDNA FLJ61200, highly similar to Homo sapiens hydroxysteroid dehydrogenase like	95.8%	6.4	1	1	1	1	2,131,955	2,547,030	3,066,565	2,404,240	150,413	477,128	642,094	191,001	15.8	41.9	46.8	17.8	1.2	0.4	1.4	0.2	1.1	0.3	1.2	0.5	-1.1	0.8	-1.3	0.4
				VAHILNISPPLNLNPVWFK	3	95.8%	1																									
IPI01013732	FKBP2	11 kDa protein	100.0%	13.7	1	1	1	1	2,789,775	2,833,480	2,827,995	3,217,585	209,529	98,293	203,064	167,586	16.8	7.8	16.1	11.7	1.0	0.9	1.0	0.9	1.2	0.1	-1.0	1	1.1	0.08	1.1	0.2
				GWDQGLLGMCEGEK	2	100.0%	1																									
IPI01013747	TNKS1BP1	cDNA FLJ45975 fis, clone PLACE7018479, highly similar to 182 kDa tankyrase 1-bi	100.0%	1.1	1	1	1	1	1,434,940	1,522,353	1,532,863	1,941,373	243,418	94,079	319,943	128,739	37.9	13.8	46.7	14.8	1.1	0.8	1.1	0.8	1.4	0.1	1.0	1	1.3	0.03	1.3	0.3
				SQEADVQDWEFR	2	99.9%	1																									
IPI01013815	SAFB	cDNA FLJ54736, highly similar to Scaffold attachment factor B	100.0%	3.8	2	2	3	1	1,663,165	1,584,847	1,794,868	1,982,733	204,191	118,018	157,479	71,935	27.5	16.7	19.6	8.1	-1.0	0.7	1.1	0.6	1.2	0.2	1.1	0.3	1.3	0.02	1.1	0.3
				NFWVSGLSSTTR	2	100.0%	2																									
				SWQGTADGGMMDR	2	92.6%	1																									
IPI01013843	VBP1	cDNA FLJ59776, highly similar to Prefoldin subunit 3	100.0%	20.3	3	3	3	1	13,025,153	13,048,154	13,984,206	14,322,945	945,721	910,540	651,548	776,043	16.2	15.6	10.4	12.1	1.0	1	1.1	0.4	1.1	0.3	1.1	0.4	1.1	0.3	1.0	0.7
				MAPQPMIHTQQGLR	2	97.3%	1																									
				NLDSLEEDLDFLR	2	99.6%	1																									
				NLDSLEEDLDFLRDQFTTTEVNMAR	3	100.0%	1																									
IPI01013860	ATP6V1B2	cDNA FLJ53854, highly similar to Vacuolar ATP synthase subunit B, brain isoform	99.8%	5.0	1	1	1	1	441,434	437,720	607,159	592,723	81,835	38,048	96,786	71,309	41.5	19.4	35.6	26.9	-1.0	1	1.4	0.2	1.3	0.2	1.4	0.2	1.4	0.09	-1.0	0.9
				TVFETLDIGWQLLR	2	99.8%	1																									
IPI01013899	SERPINB1	cDNA FLJ57130, highly similar to Leukocyte elastase inhibitor	100.0%	14.9	3	3	4	1	10,251,890	10,105,870	10,393,723	12,174,373	1,285,461	509,565	975,993	269,534	28.0	11.3	21.0	5.0	-1.0	0.9	1.0	0.9	1.2	0.2	1.0	0.8	1.2	0.007	1.2	0.1
				FKLEESYTLNSDLAR	3	100.0%	1																									
				IEEQLTLEK	2	98.9%	1																									
				LVLVNAIYFK	2	100.0%	2																									
IPI01013908	HSPA1A;HSPA1B	cDNA FLJ54392, highly similar to Heat shock 70 kDa protein 1	100.0%	3.7	2	2	3	1	8,196,133	8,492,450	7,985,870	8,965,710	519,317	299,631	477,293	313,228	14.2	7.9	13.4	7.8	1.0	0.6	-1.0	0.8	1.1	0.2	-1.1	0.4	1.1	0.3	1.1	0.1
				AFYPEEISSMVLTK	2	100.0%	2																									
				LLQDFFNGR	2	95.2%	1																									
IPI01013928	NPLOC4	cDNA FLJ57969, highly similar to Nuclear protein localization protein 4 homolog	100.0%	3.1	1	1	1	1	574,815	586,175	635,330	709,143	72,473	58,189	65,157	53,273	28.2	22.2	22.9	16.8	1.0	0.9	1.1	0.6	1.2	0.2	1.1	0.6	1.2	0.2	1.1	0.4
				VGWIFTDLVSEDTR	2	100.0%	1																									
IPI01013939	CTTN	src substrate cortactin isoform c	100.0%	21.8	10	10	13	1	11,859,097	11,750,405	12,031,769	13,762,364	778,613	550,758	835,438	584,768	14.7	10.5	15.5	9.5	-1.0	0.9	1.0	0.9	1.2	0.09	1.0	0.8	1.2	0.04	1.1	0.1
				ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK	3	100.0%	2																									
				DYSSGFGGK	1	90.9%	1																									
				GPVSGTEPEPVYSMEAADYR	2	100.0%	2																									
				LPSSPVYEDAASFK	2	100.0%	1																									
				LRENVFQEHQTLK	3	100.0%	1																									
				NASTFEDVTQVSSAYQK	2	100.0%	1																									

				SAVGFDYQGK	2	100.0%	2																									
				SAVGFEYQGK	2	100.0%	1																									
				VDQSAVGFEYQGK	2	99.0%	1																									
				YGVQADRVDK	2	99.3%	1																									
IPI01014050	MMS19	MMS19 nucleotide excision repair homolog	96.1%	2.2	1	1	1	1	2,769,772	2,579,966	2,731,142	3,409,000	226,992	114,775	351,848	125,473	18.3	10.0	28.8	8.2	-1.1	0.5	-1.0	0.9	1.2	0.04	1.1	0.7	1.3	0.001	1.2	0.1
				FLNLSSSPSMAVR	2	96.1%	1																									
IPI01014057	AKR1C3	cDNA FLJ57019, highly similar to Aldo-keto reductase family 1 member C3	100.0%	22.1	3	3	4	1	2,036,667	1,958,434	2,033,209	2,373,527	246,155	24,682	231,735	81,562	27.0	2.8	25.5	7.7	-1.0	0.8	-1.0	1	1.2	0.3	1.0	0.8	1.2	0.005	1.2	0.2
				TPALIALR	2	99.8%	2																									
				VIFDIVDLCTTWEAMEK	2	100.0%	1																									
				WVDPNSPVLLEDPVLCALAK	2	100.0%	1																									
IPI01014072	STARD10	16 kDa protein	100.0%	34.1	3	3	4	1	6,199,680	6,306,132	6,238,371	6,843,814	350,079	262,926	381,028	327,881	12.6	9.3	13.7	10.7	1.0	0.8	1.0	0.9	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.3
				AGVSVWVQAVEMDR	2	95.9%	1																									
				ESVQVPDDQDFR	2	99.9%	2																									
				MECCDVPAETLYDVLHDIEYR	3	99.4%	1																									
IPI01014113	VCL	cDNA FLJ45031 fis, clone BRAWH3018548, highly similar to Vinculin	100.0%	14.9	10	10	12	1	16,040,343	17,045,282	17,252,852	18,750,415	1,205,495	672,061	1,383,694	416,995	16.8	8.8	17.9	5.0	1.1	0.5	1.1	0.5	1.2	0.09	1.0	0.9	1.1	0.06	1.1	0.4
				AGEVINQPMMMAAR	2	99.0%	1																									
				AVAGNISDPGLQK	2	100.0%	2																									
				GILSGTSDLLLTFDEAEVRK	3	99.1%	1																									
				MSAEINEIIR	2	99.9%	1																									
				MTGLVDEAIDTK	2	100.0%	1																									
				NQWIDNVEK	2	90.5%	1																									
				TNISDEESEQATEMLVHNAQNLMQSVK	3	100.0%	1																									
				VAMANIQPQMLVAGATSIAR	2	100.0%	1																									
				VLQLTSWDEDAWASK	2	100.0%	1																									
				WIDNPTVDDR	2	98.7%	2																									
IPI01014133	RUVBL2	cDNA FLJ32936 fis, clone TESTI2007533, highly similar to RuvB-like 2	100.0%	27.8	9	9	10	1	21,433,786	22,098,076	21,269,761	25,171,996	2,444,912	731,597	1,459,074	837,884	25.5	7.4	15.3	7.4	1.0	0.8	-1.0	1	1.2	0.2	-1.0	0.6	1.1	0.02	1.2	0.05
				AAGVVLEMIR	2	99.3%	1																									
				ALESDMAPVLIMATNR	2	100.0%	1																									
				AVLIAGQPGTGK	2	100.0%	1																									
				DYDAMGSQTK	2	99.9%	1																									
				EYQDAFLFNELKGETMDTS	2	100.0%	1																									
				FVQCPDGELQK	2	99.9%	1																									
				GTSYQSPHGIPIDLLDR	3	100.0%	1																									
				IGLETSLR	2	95.8%	1																									
				TTEMETIYDLGTK	2	100.0%	2																									
IPI01014177	ST13	ST13 protein	100.0%	12.8	2	2	4	1	3,585,091	3,724,734	3,749,899	3,514,640	166,743	339,220	217,407	536,091	10.4	20.4	13.0	34.1	1.0	0.7	1.0	0.6	-1.0	0.9	1.0	1	-1.1	0.7	-1.1	0.7
				AIEINPDSAQPYK	2	100.0%	2																									
				VAAIEALNDGELQK	2	100.0%	2																									
IPI01014181	ADD1	12 kDa protein	100.0%	15.2	1	1	1	1	205,746	265,469	239,417	246,906	36,888	21,100	26,894	16,608	40.1	17.8	25.1	15.0	1.3	0.2	1.2	0.5	1.2	0.3	-1.1	0.5	-1.1	0.5	1.0	0.8
				TAGPQSQVLCGVVMDR	2	99.9%	1																									
IPI01014198	EIF3K	cDNA FLJ55131, highly similar to Eukaryotic translation initiation factor 3 subunit 12	100.0%	12.9	1	1	2	1	152,448	138,513	208,863	171,922	17,619	18,644	18,875	15,618	25.8	30.1	20.2	20.3	-1.1	0.6	1.4	0.06	1.1	0.4	1.5	0.03	1.2	0.2	-1.2	0.2
				WLLAEMLGDLSDSQLK	2	100.0%	2																									
IPI01014209	YWHAG	cDNA FLJ51843, highly similar to 14-3-3 protein gamma	100.0%	44.4	6	8	10	1	18,619,800	19,471,017	18,579,902	21,623,182	1,822,756	1,069,490	1,602,126	695,633	21.9	12.3	19.3	7.2	1.0	0.7	-1.0	1	1.2	0.2	-1.0	0.7	1.1	0.1	1.2	0.1
				DNLTLWTSDQQDDDGGEGNN	2	100.0%	2																									
				EHMQPTHPIR	3	99.1%	1																									
				LGLALNYSVFYYEIQNAPEQACHLAK	3	100.0%	1																									
				NVTELNEPLSNEER	2	100.0%	2																									
				TAFDDAIAELDTLNEDSYK	2	100.0%	1																									
				TAFDDAIAELDTLNEDSYK	3	100.0%	1																									
				YLAEVATGEKR	2	100.0%	1																									
				YLAEVATGEKR	3	100.0%	1																									
IPI01014215	OTUB1	32 kDa protein	100.0%	22.7	5	6	7	1	7,893,174	8,001,722	7,858,327	9,232,363	742,924	338,863	479,936	304,384	21.1	9.5	13.7	7.4	1.0	0.9	-1.0	1	1.2	0.1	-1.0	0.8	1.2	0.03	1.2	0.04
				AFGFSHLEALLDDSKELQR	3	100.0%	2																									
				EYAEDDNIYQQK	2	99.9%	1																									
				FFEHFIEGGR	2	96.7%	1																									
				FFEHFIEGGR	3	99.6%	1																									
				IQQEIAVQNPLVSER	2	100.0%	1																									
				LLTSGYLQR	2	99.9%	1																									
IPI01014338	YWHAQ	cDNA FLJ52118, highly similar to 14-3-3 protein theta	100.0%	15.2	5	5	7	1	9,234,790	9,955,990	9,246,875	11,148,900	1,093,351	474,149	1,010,391	368,506	26.5	10.7	24.4	7.4	1.1	0.6	1.0	1	1.2	0.2	-1.1	0.5	1.1	0.08	1.2	0.1
				KQTIDNSQGAYQEAFDISK	3	100.0%	1																									
				KQTIDNSQGAYQEAFDISKK	3	100.0%	1																									
				QTIDNSQGAYQEAFDISK	2	100.0%	1																									
				QTIDNSQGAYQEAFDISKK	3	100.0%	2																									
				SICTTVLELLDK	2	100.0%	2																									
IPI01014379	EIF3L	cDNA FLJ53220, highly similar to Eukaryotic translation initiation factor 3 subunit 6-i	100.0%	15.2	3	3	3	2	1,625,084	1,685,268	1,683,252	1,841,281	175,511	83,026	177,917	80,790	24.2	11.0	23.6	9.8	1.0	0.8	1.0	0.8	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.4
IPI01015554	EIF3L	cDNA FLJ36221 fis, clone THYMU2000950, highly similar to Eukaryotic translation i	100.0%	9.7	3	3	3	2	1,625,084	1,685,268	1,683,252	1,841,281	175,511	83,026	177,917	80,790	24.2	11.0	23.6	9.8	1.0	0.8	1.0	0.8	1.1	0.3	-1.0	1	1.1	0.2	1.1	0.4
				GDPQVYEELFSYSCPK	2	99.5%	1																									
				LAGFLDLTEQEFR	2	100.0%	1																									
				VFSDEVQQQAQLSTIR	3	98.9%	1																									
IPI01014443	DNM1L	cDNA FLJ59948, highly similar to Dynamin-1-like protein	100.0%	12.2	1	1	1	1	226,354	201,619	264,776	287,352	18,549	42,208	20,986	34,074	18.3	46.8	17.7	26.5	-1.1	0.6	1.2	0.2	1.3	0.2	1.3	0.2	1.4	0.2	1.1	0.6
				IFSPNVVNLTLVDLPGMTK	2	99.4%	1																									
IPI01014476	GOT1	Aspartate aminotransferase	100.0%	38.3	11	13	16	1	26,135,623	26,920,167	26,409,286	30,767,904	2,285,816	835,740	2,163,718	637,061	19.6	6.9	18.3	4.6	1.0	0.8	1.0	0.9	1.2	0.1	-1.0	0.8	1.1	0.006	1.2	0.1
				FLFPFFDSAYQGFASGNLER	2	100.0%	2																									
				FLFPFFDSAYQGFASGNLER	3	100.0%	1																									
				HIYLLPSGR	2	97.6%	1																									
				IANDNSLNHEYLPILGLAEFR	3	100.0%	1																									
				IGADFLAR	2	99.9%	1																									
				INVSGLTTK	2	83.5%	1																									
				ITWSNPPAQGAR	2	99.7%	1																									
				IVASTLSNPELFEEWTGNVK	2	100.0%	2																									
				IVASTLSNPELFEEWTGNVK	3	100.0%	1																									
				LALGDDSPALK	2	99.9%	1																									
				QVEYLVNEK	2	98.1%	1																									
				VGNLTVVGKEPESILQVLSQMEK	3	93.8%	1																									
				WYNGTNNK	2	99.8%	2																									
IPI01014503	HNRNPA2B1	Uncharacterized protein	100.0%	56.2	16	22	33	1	68,520,724	69,432,209	68,474,716	77,823,694	4,525,979	1,298,282	3,996,551	2,071,925	14.8	4.2	13.1	6.0	1.0	0.9	-1.0	1	1.1	0.1	-1.0	0.8	1.1	0.009	1.1	0.07
				DYFEEYGKIDTIEIITDR	3	100.0%	1																									
				GFGFVTFDDHDPVDK	2	100.0%	2																									
				GFGFVTFDDHDPVDK	3	100.0%	1																									
				GFGFVTFDDHDPVDKIVLQK	2	100.0%	1																									
				GFGFVTFDDHDPVDKIVLQK	3	100.0%	2																									
				GFGFVTFSSMAEVDAAMAAR	2	99.4%	1																									
				GGGGNFGPGPGSNFR	2	100.0%	2																									
				GGNFGFGDSR	1	95.5%	1																									
				GGNFGFGDSR	2	99.9%	2																									
				IDTIEIITDR	2	100.0%	1																									
				KLFIGGLSFETTEESLR	3	100.0%	1																									
				LFIGGLSFETTEESLR	2	100.0%	3																									
				LFIGGLSFETTEESLR	3	99.9%	1																									
				LTDCVVMRDPASK	2	100.0%	1																									
				LTDCVVMRDPASKR	3	95.8%	1																									
				NMGGPYGGGNYGPGGSGGSGGYGGR	2	100.0%	2																									
				NMGGPYGGGNYGPGGSGGSGGYGGR	3	99.9%	1																									
				NYYEQWGK	2	99.7%	2																									
				QEMQEVQSSR	2	100.0%	2																									
				TLETVPLER	2	99.7%	2																									
				YHTINGHNAEVR	2	100.0%	1																									
				YHTINGHNAEVR	3	100.0%	2																									
IPI01014601	NPEPPS	85 kDa protein	100.0%	15.5	8	8	8	1	8,416,343	9,484,687	8,891,301	9,969,864	988,339	345,177	1,034,402	145,430	26.3	8.1	26.0	3.3	1.1	0.4	1.1	0.7	1.2	0.2	-1.1	0.6	1.1	0.2	1.1	0.4
				DYFNVPYPLPK	2	100.0%	1																									
				HGDGTTLDIMLK	2	99.6%	1																									
				ILMDKPEMNVVLK	2	97.4%	1																									
				LGWDPKPGEGHLDALLR	3	98.7%	1																									
				NAATEDLWESLENASGKPIAAVMNTWTK	3	99.9%	1																									
				SPVYLTVLK	2	98.7%	1																									
				TQYSSAMLESLLPGIR	2	98.5%	1																									
				VALSNMNVIDR	2	99.9%	1																									
IPI01014604	CCT4	T-complex protein 1 subunit delta	100.0%	18.1	6	6	7	1	7,779,124	8,701,631	8,873,538	9,475,827	735,779	638,049	423,690	199,615	21.2	16.4	10.7	4.7	1.1	0.4	1.1	0.2	1.2	0.08	1.0	0.8	1.1	0.3	1.1	0.2
				DALSDLALHFLNK	2	100.0%	1																									
				GIEILTDMSRPVELSDRETLLNSATTSLNSK	3	94.9%	1																									
				IDDVVNTR	2	99.4%	2																									
				TDMDNQIVVSDYAQMDR	2	100.0%	1																									
				TGCNVLLIQK	2	99.8%	1																									
				VIDPATATSVDLR	2	100.0%	1																									
IPI01014611	AGPS	cDNA, FLJ79139, highly similar to Alkyldihydroxyacetonephosphate synthase, perox	90.7%	3.7	1	1	1	1	1,971,750	2,127,200	2,095,465	2,340,955	263,839	78,583	165,518	254,740	29.9	8.3	17.7	24.3	1.1	0.6	1.1	0.7	1.2	0.3	-1.0	0.9	1.1	0.5	1.1	0.4
				TIISLDTSQMNR	2	90.7%	1																									
IPI01014618	STARD10	29 kDa protein	100.0%	35.3	6	6	8	1	8,845,755	9,571,280	9,224,707	10,720,073	521,071	340,016	618,712	553,202	13.2	7.9	15.0	11.5	1.1	0.3	1.0	0.7	1.2	0.04	-1.0	0.6	1.1	0.1	1.2	0.1
				AGVSVWVQAVEMDR	2	95.9%	1																									
				AVSIQTGYLIQSTGPK	2	100.0%	2																									
				ESVQVPDDQDFR	2	99.9%	2																									
				MECCDVPAETLYDVLHDIEYR	3	99.4%	1																									
				SCVITYLAQVDPK	2	99.5%	1																									
				WDSNVIETFDIAR	2	99.2%	1																									
IPI01014620	ME1;NME1-NME2;NM	Uncharacterized protein	100.0%	39.6	4	5	8	1	8,785,466	9,013,826	8,941,308	10,389,454	1,121,721	337,288	831,713	295,123	28.6	8.4	20.8	6.4	1.0	0.9	1.0	0.9	1.2	0.2	-1.0	0.9	1.2	0.02	1.2	0.2
				DRPFFAGLVK	3	99.9%	1																									
				GDFCIQVGR	2	100.0%	2																									
				VMLGETNPADSKPGTIR	2	100.0%	2																									
				VMLGETNPADSKPGTIR	3	100.0%	1																									
				YMHSGPVVAMVWEGLNVVK	3	100.0%	2																									
IPI01014635	SLC3A2	Protein	100.0%	9.8	1	1	1	1	255,238	233,163	287,802	310,590	11,495	6,747	29,871	24,825	10.1	6.5	23.2	17.9	-1.1	0.1	1.1	0.4	1.2	0.08	1.2	0.1	1.3	0.03	1.1	0.6
				LLTSFLPAQLLR	2	100.0%	1																									
IPI01014705	ACTN3	cDNA FLJ58651, highly similar to Alpha-actinin-3	91.6%	1.2	1	1	1	1	4,347,950	4,242,890	3,872,130	3,858,550	397,987	352,852	251,066	335,694	20.5	18.6	14.5	19.5	-1.0	0.8	-1.1	0.3	-1.1	0.4	-1.1	0.4	-1.1	0.5	-1.0	1
				MGIGLCVPPAR	2	91.6%	1																									
IPI01014729	NAP1L4	Uncharacterized protein	100.0%	12.4	2	2	2	1	1,023,790	1,055,982	987,646	1,246,456	125,998	68,470	76,110	62,033	27.5	14.5	17.2	11.1	1.0	0.8	-1.0	0.8	1.2	0.2	-1.1	0.5	1.2	0.07	1.3	0.03
				FYEEVHDLER	2	100.0%	1																									
				YAALYQPLFDK	2	99.7%	1																									
IPI01014739	MAN1B1	63 kDa protein	99.9%	4.5	2	2	2	1	4,689,385	4,960,824	4,775,164	5,931,880	508,679	589,342	825,423	505,246	24.3	26.6	38.7	19.1	1.1	0.7	1.0	0.9	1.3	0.1	-1.0	0.9	1.2	0.2	1.2	0.3

				DVDVNLFESTIR	2	91.9%	1																									
				VDGAAMAACEGRR	3	99.1%	1																									
IPI01014783	LARS	cDNA FLJ58533, highly similar to Leucyl-tRNA synthetase, cytoplasmic	100.0%	9.4	8	8	8	1	12,818,941	14,041,301	12,159,210	14,639,460	1,261,564	567,965	815,824	483,994	22.0	9.0	15.0	7.4	1.1	0.4	-1.1	0.7	1.1	0.2	-1.2	0.09	1.0	0.4	1.2	0.03
				ELMGEEILGASLSAPLTSYK	2	99.9%	1																									
				EVWDYVFFK	2	97.5%	1																									
				FDDPLLGPR	2	99.9%	1																									
				GFYEGIMLVDGFK	2	100.0%	1																									
				GTGVVTSVPSDSPDDIAALR	2	99.6%	1																									
				ILDLQLEFDEK	2	99.7%	1																									
				SLGLSDEEIVK	2	99.4%	1																									
				VFASELNAGIIK	2	100.0%	1																									
IPI01014812	ACADM	cDNA FLJ52595, highly similar to Medium-chain specific acyl-CoA dehydrogenase,	99.9%	5.6	1	1	1	1	269,752	226,757	221,786	237,666	60,608	22,049	31,609	25,612	50.2	21.7	31.9	24.1	-1.2	0.5	-1.2	0.5	-1.1	0.6	-1.0	0.9	1.0	0.8	1.1	0.7
				IYQIYEGTSQIQR	2	99.8%	1																									
IPI01014848	SRP68	41 kDa protein	92.5%	6.5	1	1	1	1	2,079,192	2,153,487	2,173,748	2,054,285	214,105	151,933	254,168	286,276	23.0	15.8	26.2	31.2	1.0	0.8	1.0	0.8	-1.0	0.9	1.0	0.9	-1.0	0.8	-1.1	0.8
				IFLLGLADNEAAIVQAESEETKER	3	92.5%	1																									
IPI01014849	GSPT2	cDNA FLJ55563, highly similar to Homo sapiens G1 to S phase transition 2 (GSPT2	100.0%	5.3	3	3	3	1	3,934,200	3,830,332	3,759,592	4,372,344	294,272	161,710	208,108	237,226	16.7	9.4	12.4	12.1	-1.0	0.8	-1.0	0.6	1.1	0.3	-1.0	0.8	1.1	0.1	1.2	0.09
				GQQLVMMPNK	2	100.0%	1																									
				HFTILDAPGHK	3	99.2%	1																									
				HLIVLINK	2	95.5%	1																									
IPI01014861	HNRNPM	Heterogeneous nuclear ribonucleoprotein M isoform a variant (Fragment)	100.0%	7.6	4	4	7	1	8,793,020	8,969,547	8,022,423	10,046,127	600,594	381,519	582,291	495,477	15.3	9.5	16.2	11.0	1.0	0.8	-1.1	0.4	1.1	0.1	-1.1	0.2	1.1	0.1	1.3	0.03
				INEILSNALK	2	100.0%	2																									
				MGLVMDR	2	99.1%	1																									
				MGPAMGPALGAGIER	2	100.0%	2																									
				QGGGGGGGSVPGIER	2	100.0%	2																									
IPI01014863	ACAT2	Acetyl-CoA acetyltransferase, cytosolic	100.0%	25.7	5	6	8	1	23,237,500	22,817,089	22,851,870	26,081,100	1,952,555	1,276,429	1,905,629	813,842	18.8	12.5	18.7	7.0	-1.0	0.9	-1.0	0.9	1.1	0.2	1.0	1	1.1	0.06	1.1	0.2
				ATVAPEDVSEVIFGHVLAAGCGQNPVR	3	100.0%	1																									
				IVSWSQVGVEPSIMGIGPIPAIK	2	100.0%	2																									
				IVSWSQVGVEPSIMGIGPIPAIK	3	100.0%	1																									
				TIIGSFNGALAAVPVQDLGSTVIK	3	100.0%	2																									
				VAVLSQNR	2	99.7%	1																									
				VNIEGGAIALGHPLGASGCR	3	100.0%	1																									
IPI01014868	CCT7	T-complex protein 1 subunit eta isoform b	100.0%	11.8	3	3	4	1	4,487,169	4,322,150	4,106,950	4,655,344	346,751	194,604	440,000	241,602	17.3	10.1	24.0	11.6	-1.0	0.7	-1.1	0.5	1.0	0.7	-1.1	0.7	1.1	0.3	1.1	0.3
				GGAEQFMEETER	2	100.0%	1																									
				QLCDNAGFDATNILNK	2	100.0%	1																									
				TFSYAGFEMQPK	2	100.0%	2																									
IPI01014869	PSMD3	cDNA FLJ54148, highly similar to 26S proteasome non-ATPase regulatory subunit 3	95.3%	3.1	1	1	1	1	1,658,853	1,522,110	1,533,720	1,926,943	212,596	116,388	152,790	128,786	28.7	17.1	22.3	14.9	-1.1	0.6	-1.1	0.6	1.2	0.3	1.0	1	1.3	0.05	1.3	0.08
				FNQVLDQFGEK	2	95.3%	1																									
IPI01014950	TOLLIP	Uncharacterized protein	99.8%	10.2	2	2	2	1	4,761,053	4,608,840	4,817,930	4,751,090	341,417	346,700	120,617	71,835	16.0	16.8	5.6	3.4	-1.0	0.8	1.0	0.9	-1.0	1	1.0	0.6	1.0	0.7	-1.0	0.6
				LGYAVYETPTAHNGAK	3	81.1%	1																									
				LNITVVQAK	2	99.0%	1																									
IPI01014951	EIF3A	163 kDa protein	100.0%	10.2	11	11	13	1	31,625,563	35,192,663	30,827,891	38,427,466	3,457,182	1,408,926	3,058,510	1,553,228	24.4	9.0	22.2	9.0	1.1	0.4	-1.0	0.9	1.2	0.1	-1.1	0.2	1.1	0.2	1.2	0.06
				DLYNWLEVEFNPLK	2	100.0%	1																									
				EDAPIGPHLQSMPSEQIR	3	96.9%	1																									
				FNVLQYVVPEVK	2	100.0%	2																									
				ITTMQLER	2	99.2%	1																									
				LESLNIQR	2	93.3%	1																									
				LLDMDGIIVEK	2	99.3%	1																									
				LTSLVPFVDAFQLER	2	97.9%	1																									
				LVQLDSAISMELWQEAFK	2	100.0%	1																									
				NQLTAMSSVLAK	2	99.7%	2																									
				RVPPPALSR	2	98.9%	1																									
				TLSFGSDLNYATR	2	96.9%	1																									
IPI01014975	TLN1	Talin 1	100.0%	16.8	23	23	25	1	43,014,428	44,308,537	43,041,033	47,756,813	3,089,244	1,389,027	2,495,769	871,948	16.1	7.0	13.0	4.1	1.0	0.7	1.0	1	1.1	0.2	-1.0	0.7	1.1	0.07	1.1	0.1
				ALDGAFTEENR	2	99.7%	1																									
				ALSTDPAAPNLK	2	99.7%	1																									
				AQEACGPLEMDSALSVVQNLEKDLQEVK	3	98.4%	1																									
				AVSSAIAQLLGEVAQGNENYAGIAAR	3	100.0%	1																									
				DHFGLEGDEESTMLEDSVSPKK	3	99.4%	1																									
				EADESLNFEEQILEAAK	2	100.0%	1																									
				GVAALTSDPAVQAIVLDTASDVLDK	2	100.0%	1																									
				GVGAAATAVTQALNELLQHVK	3	100.0%	1																									
				ILAQATSDLVNAIK	2	100.0%	2																									
				LAQAAQSSVATITR	2	100.0%	1																									
				LHTDDELNWLDHGR	3	98.0%	1																									
				LNEAAAGLNQAATELVQASR	2	100.0%	1																									
				MVAAATNNLCEAANAAVQGHASQEK	3	100.0%	1																									
				NCGQMSEIEAK	2	89.1%	1																									
				NGNLPEFGDAISTASK	2	99.7%	1																									
				QAAASATQTIAAAQHAASTPK	3	100.0%	2																									
				QEDVIATANLSR	2	99.9%	1																									
				TLAESALQLLYTAK	2	98.8%	1																									
				VGAIPANALDDGQWSQGLISAAR	3	100.0%	1																									
				VGDDPAVWQLK	2	99.8%	1																									
				VMVTNVTSLLK	2	99.6%	1																									
				VSQMAQYFEPLTLAAVGAASK	2	99.9%	1																									
				VVAPTISSPVCQEQLVEAGR	3	99.2%	1																									
IPI01015014	HEBP1	7 kDa protein	99.4%	24.2	1	1	1	1	676,537	726,867	673,423	760,943	42,625	27,707	43,135	37,044	14.1	8.5	14.3	10.9	1.1	0.4	-1.0	1	1.1	0.2	-1.1	0.3	1.0	0.5	1.1	0.2
				IPNQFQSDPPAPSDK	2	99.4%	1																									
IPI01015016	UBC	7 kDa protein	100.0%	47.5	2	2	4	1	806,114	820,935	781,944	957,643	64,713	30,896	51,049	26,741	18.0	8.4	14.6	6.2	1.0	0.8	-1.0	0.8	1.2	0.06	-1.0	0.5	1.2	0.01	1.2	0.02
				IQDKEGIPPDQQR	2	99.9%	2																									
				TITLEVEPSDTIENVK	2	100.0%	2																									
IPI01015038	CCT4	T-complex protein 1 subunit delta	100.0%	28.6	11	13	14	1	16,090,961	18,396,470	18,006,171	19,290,217	1,166,097	1,032,807	1,565,995	434,807	16.2	12.6	19.5	5.0	1.1	0.2	1.1	0.4	1.2	0.05	-1.0	0.8	1.0	0.4	1.1	0.5
				DALSDLALHFLNK	2	100.0%	1																									
				DALSDLALHFLNK	3	88.5%	1																									
				GDVTITNDGATILK	2	95.2%	1																									
				IDDVVNTR	2	99.4%	2																									
				KLGGTIDDCELVEGLVLTQKVSNSGITR	3	98.0%	1																									
				LGGTIDDCELVEGLVLTQK	2	100.0%	1																									
				LGGTIDDCELVEGLVLTQK	3	99.3%	1																									
				MIQDGKGDVTITNDGATILK	3	100.0%	1																									
				QMQVLHPAAR	2	98.6%	1																									
				TDMDNQIVVSDYAQMDR	2	100.0%	1																									
				TGCNVLLIQK	2	99.8%	1																									
				VIDPATATSVDLR	2	100.0%	1																									
				VVSQYSSLLSPMSVNAVMK	2	100.0%	1																									
IPI01015040	EIF3J	Protein	99.9%	11.3	1	1	1	1	598,353	666,250	675,255	693,863	32,313	29,234	40,880	39,633	12.1	9.8	13.5	12.8	1.1	0.2	1.1	0.2	1.2	0.1	1.0	0.9	1.0	0.6	1.0	0.8
				ITNSLTVLCSEK	2	100.0%	1																									
IPI01015096	FAM129B	Niban-like protein 1	100.0%	12.1	3	3	3	1	1,808,946	1,979,642	1,748,629	2,192,605	144,072	108,298	242,791	84,032	17.8	12.2	31.1	8.6	1.1	0.4	-1.0	0.8	1.2	0.05	-1.1	0.4	1.1	0.2	1.3	0.1
				EQMDNAVYTFETLLHQELGK	3	99.8%	1																									
				EVTDMNLNVINEGGIDK	2	100.0%	1																									
				FQELIFEDFAR	2	100.0%	1																									
IPI01015144	PLS3	cDNA FLJ50527, highly similar to Plastin-3	96.0%	6.3	1	1	1	1	1,276,508	1,136,795	1,268,020	1,281,570	119,230	79,056	96,477	101,348	20.9	15.6	17.0	17.7	-1.1	0.4	-1.0	1	1.0	1	1.1	0.3	1.1	0.3	1.0	0.9
				VYALPEDLVEVKPK	3	96.0%	1																									
IPI01015196	CCT7	cDNA FLJ59454, highly similar to T-complex protein 1 subunit eta	100.0%	30.4	8	8	9	1	12,959,197	12,838,501	12,212,554	14,426,337	1,113,374	638,385	992,494	804,469	19.2	11.1	18.2	12.5	-1.0	0.9	-1.1	0.6	1.1	0.3	-1.1	0.6	1.1	0.2	1.2	0.1
				CAMTALSSK	2	99.3%	1																									
				GGAEQFMEETER	2	100.0%	1																									
				INALTAASEAACLIVSVDETIKNPR	3	100.0%	1																									
				QLCDNAGFDATNILNK	2	100.0%	1																									
				SLHDAIMIVR	2	96.7%	1																									
				TFSYAGFEMQPK	2	100.0%	2																									
				VHTVEDYQAIVDAEWNILYDKLEK	3	97.4%	1																									
				VQGGALEDSQLVAGVAFK	2	100.0%	1																									
IPI01015219	PSMC2	cDNA FLJ52353, highly similar to 26S protease regulatory subunit 7	100.0%	14.2	3	3	3	1	8,530,405	9,379,905	9,624,150	10,577,195	436,676	566,402	679,461	344,695	11.5	13.5	15.8	7.3	1.1	0.3	1.1	0.2	1.2	0.006	1.0	0.8	1.1	0.1	1.1	0.2
				ACLIFFDEIDAIGGAR	2	93.9%	1																									
				LCPNSTGAEIR	2	99.4%	1																									
				TMLELINQLDGFDPR	2	100.0%	1																									
IPI01015230	NPEPPS	cDNA FLJ53354, highly similar to Puromycin-sensitive aminopeptidase	100.0%	12.2	7	7	7	1	9,982,233	11,293,321	10,501,589	11,881,367	1,302,543	429,752	1,095,530	178,850	29.2	8.5	23.3	3.4	1.1	0.4	1.1	0.8	1.2	0.2	-1.1	0.5	1.1	0.2	1.1	0.3
				DYFNVPYPLPK	2	100.0%	1																									
				HGDGTTLDIMLK	2	99.6%	1																									
				LGWDPKPGEGHLDALLR	3	98.7%	1																									
				NAATEDLWESLENASGKPIAAVMNTWTK	3	99.9%	1																									
				SPVYLTVLK	2	98.7%	1																									
				TQYSSAMLESLLPGIR	2	98.5%	1																									
				YQGGFLISR	2	99.8%	1																									
IPI01015265	RPN1	cDNA FLJ51908, highly similar to Dolichyl-diphosphooligosaccharide--proteinglycos	100.0%	5.8	2	2	2	1	3,194,150	3,338,723	3,338,382	3,461,803	252,913	261,394	248,417	129,316	17.7	17.5	16.6	8.4	1.0	0.7	1.0	0.7	1.1	0.4	-1.0	1	1.0	0.7	1.0	0.7
				ALTSEIALLQSR	2	100.0%	1																									
				QPDSGISSIR	2	92.5%	1																									
IPI01015270	STARD10	30 kDa protein	100.0%	34.7	6	6	8	1	8,210,263	8,597,234	8,319,925	9,729,405	445,746	253,087	567,149	475,524	12.1	6.6	15.2	10.9	1.0	0.5	1.0	0.9	1.2	0.05	-1.0	0.7	1.1	0.07	1.2	0.09
				AVSIQTGYLIQSTGPK	2	100.0%	2																									
				ESVQVPDDQDFR	2	99.9%	2																									
				MECCDVPAETLYDVLHDIEYR	3	99.4%	1																									
				MGGAGGEGSDDDTSLT	3	93.9%	1																									
				SCVITYLAQVDPK	2	99.5%	1																									
				WDSNVIETFDIAR	2	99.2%	1																									
IPI01015316	PPP1CA	18 kDa protein	100.0%	16.0	2	2	4	1	828,935	815,427	908,467	945,742	56,129	43,440	61,913	21,260	15.1	11.9	15.2	5.0	-1.0	0.9	1.1	0.4	1.1	0.1	1.1	0.3	1.2	0.03	1.0	0.6
				EIFLSQPILLELEAPLK	2	100.0%	2																									
				NVQLTENEIR	2	100.0%	2																									
IPI01015329	BPNT1	cDNA FLJ52203, highly similar to 3'(2'),5'-bisphosphate nucleotidase 1	98.9%	6.3	1	1	1	1	591,586	601,820	658,540	655,834	22,208	44,668	33,497	99,286	8.4	16.6	11.4	33.9	1.0	0.8	1.1	0.1	1.1	0.6	1.1	0.3	1.1	0.6	-1.0	1
				LVTDCVAAMNPDAVLR	2	98.9%	1																									
IPI01015342	STRAP	cDNA, FLJ79540, highly similar to Serine-threonine kinase receptor-associatedprote	100.0%	30.1	4	4	5	1	7,584,591	7,844,464	7,187,173	8,503,230	600,082	240,306	531,169	181,598	17.7	6.9	16.5	4.8	1.0	0.7	-1.1	0.6	1.1	0.2	-1.1	0.3	1.1	0.06	1.2	0.07
				FSPDGELYASGSEDGTLR	2	100.0%	1																									
				SFEAPATINSASLHPEKEFLVAGGEDFK	3	100.0%	1																									
				TVDFTQDSNYLLTGGQDK	2	100.0%	2																									
				YDYNSGEELESYK	2	100.0%	1																									
IPI01015355	ACO2	83 kDa protein	100.0%	4.1	2	2	2	1	2,824,227	3,154,000	2,245,368	2,898,352	256,891	209,005	204,130	238,630	20.3	14.8	20.3	18.4	1.1	0.3	-1.3	0.1	1.0	0.8	-1.4	0.01	-1.1	0.4	1.3	0.07
				NAVTQEFGPVPDTAR	2	99.9%	1																									
				QGLLPLTFADPADYNK	2	99.9%	1																									

IPI01015379	ACADVL	39 kDa protein	100.0%	37.6	10	10	11	1	14,791,429	15,687,516	16,034,327	18,275,664	1,712,139	680,373	1,548,453	550,261	25.9	9.7	21.6	6.7	1.1	0.6	1.1	0.6	1.2	0.1	1.0	0.8	1.2	0.02	1.1	0.2
				AGLGSGLSLSGLVHPELSR	3	100.0%	1																									
				ALEQFATVVEAK	2	100.0%	1																									
				ASNTAEVFFDGVR	2	100.0%	1																									
				EGMAALQSDPWQQELYR	2	99.9%	1																									
				FGMAAALAGTMR	2	100.0%	1																									
				GIVNEQFLLQR	2	99.9%	1																									
				IFEGTNDILR	2	99.4%	1																									
				IHNFGLIQEK	2	99.8%	1																									
				NPFGNAGLLLGEAGK	2	99.9%	2																									
				VPSENVLGEVGSGFK	2	100.0%	1																									
IPI01015420	ARF3	23 kDa protein	100.0%	25.2	4	4	5	1	5,121,873	5,083,270	5,574,457	5,953,131	445,970	213,253	601,550	163,204	19.5	9.4	24.1	6.1	-1.0	0.9	1.1	0.6	1.2	0.1	1.1	0.5	1.2	0.01	1.1	0.6
				LGEIVTTIPTIGFNVETVEYK	2	100.0%	2																									
				MLAEDELR	2	88.1%	1																									
				MLAEDELRDAVLLVFANK	3	99.6%	1																									
				NISFTVWDVGGQDK	2	100.0%	1																									
IPI01015427	PSMC1	cDNA FLJ58247, highly similar to 26S protease regulatory subunit 4	100.0%	18.5	4	5	6	1	8,319,952	8,435,578	8,366,845	9,459,542	615,069	492,382	509,619	439,085	16.5	13.1	13.6	10.4	1.0	0.9	1.0	1	1.1	0.2	-1.0	0.9	1.1	0.2	1.1	0.1
				AVANQTSATFLR	2	100.0%	1																									
				TMLELLNQLDGFDSR	2	100.0%	2																									
				VAEEHAPSIVFIDEIDAIGTK	3	100.0%	1																									
				VHAVIGVLMDDTDPLVTVMK	2	96.8%	1																									
				VHAVIGVLMDDTDPLVTVMK	3	100.0%	1																									
IPI01015433	GLUD1	Glutamate dehydrogenase	100.0%	28.0	5	5	5	1	3,572,130	3,754,108	3,592,551	4,054,773	314,160	114,702	252,525	132,645	19.7	6.8	15.7	7.3	1.1	0.6	1.0	1	1.1	0.2	-1.0	0.6	1.1	0.1	1.1	0.1
				DSNYHLLMSVQESLER	2	95.3%	1																									
				HGGTIPIVPTAEFQDR	2	100.0%	1																									
				IIAEGANGPTTPEADKIFLER	3	100.0%	1																									
				NLNHVSYGR	2	99.9%	1																									
				TAAYVNAIEK	2	99.7%	1																									
IPI01015454	PPM1G	PPM1G protein	100.0%	7.4	3	3	3	1	24,142,277	24,632,883	23,428,463	28,459,507	1,772,528	1,693,306	1,566,675	2,179,947	16.4	15.4	15.0	17.1	1.0	0.8	-1.0	0.8	1.2	0.2	-1.1	0.6	1.2	0.2	1.2	0.1
				ALEDAFLAIDAK	2	99.5%	1																									
				NLPPEEQMISALPDIK	2	100.0%	1																									
				QLIVANAGDSR	2	99.7%	1																									
IPI01015519	STARD10	Protein	100.0%	24.0	2	2	3	1	1,170,521	1,605,511	1,343,748	2,010,684	235,193	152,326	170,374	212,561	44.9	21.2	28.4	23.6	1.4	0.2	1.1	0.6	1.7	0.03	-1.2	0.3	1.3	0.2	1.5	0.04
				AVSIQTGYLIQSTGPK	2	100.0%	2																									
				SCVITYLAQVDPK	2	99.5%	1																									
IPI01015522	ACTB	cDNA FLJ55253, highly similar to Actin, cytoplasmic 1	100.0%	49.6	11	13	19	1	276,407,360	280,601,730	265,516,550	318,724,260	########	########	########	########	18.1	10.5	18.2	8.1	1.0	0.9	-1.0	0.7	1.2	0.1	-1.1	0.6	1.1	0.06	1.2	0.06
				AGFAGDDAPR	1	98.5%	1																									
				CPEALFQPSFLGMESCGIHETTFNSIMK	3	100.0%	2																									
				DLYANTVLSGGTTMYPGIADR	2	100.0%	1																									
				DLYANTVLSGGTTMYPGIADR	3	100.0%	1																									
				EITALAPSTMK	1	100.0%	1																									
				EITALAPSTMK	2	99.9%	2																									
				KDLYANTVLSGGTTMYPGIADR	2	100.0%	1																									
				LCYVALDFEQEMATAASSSSLEK	2	100.0%	2																									
				QEYDESGPSIVHR	2	100.0%	2																									
				QEYDESGPSIVHRK	2	100.0%	2																									
				SYELPDGQVITIGNER	3	100.0%	1																									
				TTGIVMDSGDGVTHTVPIYEGYALPHAILR	3	100.0%	1																									
				VAPEEHPVLLTEAPLNPK	2	92.7%	2																									
IPI01015580	AP2B1	Putative uncharacterized protein	100.0%	11.1	5	5	6	1	1,202,550	1,210,020	1,280,847	1,360,646	114,350	68,563	99,530	61,449	21.3	12.7	17.4	10.1	1.0	1	1.1	0.6	1.1	0.3	1.1	0.6	1.1	0.1	1.1	0.5
				AAMIWIVGEYAER	2	100.0%	2																									
				CVSTLLDLIQTK	2	100.0%	1																									
				LASQANIAQVLAELKEYATEVDVDFVR	3	100.0%	1																									
				LTNGIWILAELR	2	100.0%	1																									
				MEPLNNLQVAVK	2	99.8%	1																									
IPI01015585	CSE1L	cDNA FLJ59343, highly similar to Exportin-2	100.0%	16.0	6	7	9	1	9,676,110	9,564,606	9,291,904	10,623,068	626,493	477,394	517,822	349,848	14.5	11.2	12.5	7.4	-1.0	0.9	-1.0	0.6	1.1	0.2	-1.0	0.7	1.1	0.1	1.1	0.07
				ALTLPGSSENEYIMK	2	99.9%	1																									
				EDFPQKWPDLLTEMVNR	3	96.9%	1																									
				FFEGPVTGIFSGYVNSMLQEYAK	2	100.0%	2																									
				FFEGPVTGIFSGYVNSMLQEYAK	3	100.0%	1																									
				LLQTDDEEEAGLLELLK	2	100.0%	1																									
				LVLDAFALPLTNLFK	2	100.0%	2																									
				VIVPNMEFR	2	99.6%	1																									
IPI01015604	SAFB2	cDNA FLJ57435, highly similar to Scaffold attachment factor B2	98.9%	5.5	1	1	1	1	2,481,085	2,475,730	1,999,970	2,604,855	176,345	142,882	272,889	138,878	15.9	12.9	30.5	11.9	-1.0	1	-1.2	0.2	1.0	0.6	-1.2	0.2	1.1	0.5	1.3	0.08
				NTLETSSLNFK	2	98.9%	1																									
IPI01015627	HADHB	cDNA FLJ59448, highly similar to Trifunctional enzyme subunit beta, mitochondrial	100.0%	4.1	2	2	2	1	2,139,635	2,131,983	2,143,800	2,074,018	148,155	192,726	206,182	92,950	15.5	20.2	21.5	10.0	-1.0	1	1.0	1	-1.0	0.7	1.0	1	-1.0	0.8	-1.0	0.8
				DFMYVSQDPK	2	99.9%	1																									
				LEQDEYALR	2	99.1%	1																									
IPI01015637	ME1	Malic enzyme (Fragment)	100.0%	9.0	1	1	1	1	90,509	96,927	116,779	123,622	10,962	14,308	19,380	13,700	27.1	33.0	37.1	24.8	1.1	0.7	1.3	0.3	1.4	0.1	1.2	0.4	1.3	0.2	1.1	0.8
				QITDNIFLTTAEVIAQQVSDK	2	99.5%	1																									
IPI01015694	MAP4	isoform 5 of Microtubule-associated protein 4	100.0%	13.3	7	8	9	1	3,240,165	3,420,468	3,225,781	3,553,882	190,344	75,745	189,371	183,019	13.1	5.0	13.1	11.5	1.1	0.4	-1.0	1	1.1	0.3	-1.1	0.4	1.0	0.5	1.1	0.2
				DFIATLEAEAFDDVVGETVGK	2	100.0%	2																									
				DFIATLEAEAFDDVVGETVGK	3	100.0%	1																									
				DMQPSMESDMALVK	2	99.5%	1																									
				EAQTLDSQIQETSI	2	95.4%	1																									
				SVPADLSRPK	2	86.6%	1																									
				TTTAAAVASTGPSSR	2	99.6%	1																									
				TTTLSGTAPAAGVVPSR	2	100.0%	1																									
				VGSLDNVGHLPAGGAVK	3	100.0%	1																									
IPI01015783	NUMA1	Putative uncharacterized protein	100.0%	4.9	3	3	4	1	1,731,335	1,776,614	1,711,532	2,000,326	69,937	63,686	139,305	85,660	9.0	8.0	18.2	9.6	1.0	0.6	-1.0	0.9	1.2	0.04	-1.0	0.7	1.1	0.07	1.2	0.1
				LQAQLNELQAQLSQK	2	100.0%	2																									
				SQAPLESSLDSLGDVFLDSGR	2	100.0%	1																									
				VEFATLQEALAHALTEK	3	100.0%	1																									
IPI01015801	GLUD1	cDNA FLJ16138 fis, clone BRALZ2017531, highly similar to Glutamate dehydrogena	100.0%	25.3	7	8	8	1	8,047,501	8,709,544	8,438,958	9,590,721	638,522	222,444	704,812	230,288	17.7	5.7	18.7	5.4	1.1	0.4	1.0	0.7	1.2	0.07	-1.0	0.7	1.1	0.02	1.1	0.2
				DSNYHLLMSVQESLER	2	95.3%	1																									
				DSNYHLLMSVQESLER	3	99.9%	1																									
				GFIGPGIDVPAPDMSTGER	2	100.0%	1																									
				HGGTIPIVPTAEFQDR	2	100.0%	1																									
				IIAEGANGPTTPEADKIFLER	3	100.0%	1																									
				NLNHVSYGR	2	99.9%	1																									
				TAAYVNAIEK	2	99.7%	1																									
				YNLGLDLR	2	100.0%	1																									
IPI01015813	TRMT112	14 kDa protein	100.0%	10.8	1	1	1	1	2,228,210	2,083,673	2,203,330	2,340,667	109,301	136,602	129,596	135,138	11.0	14.7	13.2	12.9	-1.1	0.4	-1.0	0.9	1.1	0.5	1.1	0.5	1.1	0.2	1.1	0.5
				ICPVEFNPNFVAR	2	100.0%	1																									
IPI01015887	DBNL	cDNA FLJ54066, highly similar to Drebrin-like protein	100.0%	20.6	5	5	6	1	3,749,717	3,958,843	3,709,123	4,213,564	374,140	194,357	343,936	208,252	22.3	11.0	20.7	11.1	1.1	0.6	-1.0	0.9	1.1	0.3	-1.1	0.5	1.1	0.4	1.1	0.2
				AEEDVEPECIMEK	2	96.0%	1																									
				AMSTTSISSPQPGK	2	100.0%	1																									
				FQDVGPQAPVGSVYQK	2	100.0%	1																									
				GYGPDGHFGMFPANYVELIE	2	100.0%	1																									
				TWEQQQEVVSR	2	100.0%	2																									
IPI01015911	CA9	Truncated carbonic anhydrase 9	100.0%	7.0	2	2	2	1	13,322,100	12,843,755	12,451,500	14,059,955	980,947	519,267	662,961	607,842	16.5	9.0	11.9	9.7	-1.0	0.7	-1.1	0.5	1.1	0.5	-1.0	0.7	1.1	0.2	1.1	0.1
				FPAEIHVVHLSTAFAR	3	100.0%	1																									
				YGGDPPWPR	2	100.0%	1																									
IPI01015917	CCT4	T-complex protein 1 subunit delta	100.0%	15.7	5	5	6	1	7,222,024	8,102,691	8,258,278	8,903,397	698,797	606,007	387,523	200,861	21.6	16.7	10.5	5.0	1.1	0.4	1.1	0.2	1.2	0.07	1.0	0.8	1.1	0.3	1.1	0.2
				DALSDLALHFLNK	2	100.0%	1																									
				IDDVVNTR	2	99.4%	2																									
				TDMDNQIVVSDYAQMDR	2	100.0%	1																									
				TGCNVLLIQK	2	99.8%	1																									
				VIDPATATSVDLR	2	100.0%	1																									
IPI01015924	SHMT1	Serine hydroxymethyltransferase	100.0%	7.5	2	2	3	1	1,970,012	1,816,276	1,721,289	2,030,820	306,931	86,401	86,451	145,364	34.8	10.6	11.2	16.0	-1.1	0.7	-1.1	0.5	1.0	0.9	-1.1	0.5	1.1	0.2	1.2	0.1
				ALSEALTELGYK	2	99.1%	1																									
				ISATSIFFESMPYK	2	100.0%	2																									
IPI01015928	USO1	106 kDa protein	100.0%	18.7	13	13	13	1	20,192,042	21,439,025	20,436,205	23,652,469	1,661,716	721,198	1,253,307	700,230	18.4	7.5	13.7	6.6	1.1	0.5	1.0	0.9	1.2	0.09	-1.0	0.5	1.1	0.06	1.2	0.06
				DNQHQGSYSEGAQMNGIQPEEIGR	3	99.9%	1																									
				DSEQVAELKQELATLK	3	100.0%	1																									
				EQDDLLVLLADQDQK	2	100.0%	1																									
				EQDLQLEELR	2	99.8%	1																									
				IVAFENAFER	2	100.0%	1																									
				LMDLLADSR	2	95.8%	1																									
				LSALLQETK	2	83.1%	1																									
				NDGVLLLQALTR	2	100.0%	1																									
				NQELLQSQLTEK	2	83.8%	1																									
				NQELLQSQLTEKDSMIENMK	3	99.8%	1																									
				QLGPQVQQIILVSPMGVSR	2	99.9%	1																									
				QSEDLGSQFTEIFIK	2	100.0%	1																									
				SSQTSGTNEQSSAIVSAR	2	100.0%	1																									
IPI01015950	STARD10	22 kDa protein	100.0%	39.8	5	5	7	1	7,930,066	8,270,924	8,153,762	9,030,913	339,148	318,491	512,575	425,622	9.6	8.6	14.1	10.5	1.0	0.5	1.0	0.7	1.1	0.08	-1.0	0.9	1.1	0.2	1.1	0.2
				AGVSVWVQAVEMDR	2	95.9%	1																									
				AVSIQTGYLIQSTGPK	2	100.0%	2																									
				ESVQVPDDQDFR	2	99.9%	2																									
				MECCDVPAETLYDVLHDIEYR	3	99.4%	1																									
				WDSNVIETFDIAR	2	99.2%	1																									
IPI01015955	ANK3	Ankyrin 3 isoform 1 variant (Fragment)	100.0%	3.8	2	2	2	1	7,772,316	7,850,696	8,640,851	8,468,439	260,374	158,126	302,177	518,435	7.5	4.5	7.8	13.7	1.0	0.8	1.1	0.06	1.1	0.3	1.1	0.05	1.1	0.3	-1.0	0.8
				FTLAHVPQR	2	85.6%	1																									
				LVEMGPAGAQFLGPVIVEIPHFGSMR	3	97.8%	1																									
IPI01015994	ATP6V1B2	cDNA FLJ51779, highly similar to Vacuolar ATP synthase subunit B, brain isoform	100.0%	14.8	3	3	3	1	1,229,662	1,315,812	1,582,832	1,557,118	156,688	130,501	202,559	138,444	28.5	22.2	28.6	19.9	1.1	0.7	1.3	0.2	1.3	0.2	1.2	0.3	1.2	0.2	-1.0	0.9
				AVVGEEALTSDDLLYLEFLQK	2	98.6%	1																									
				IYPEEMIQTGISAIDGMNSIAR	3	99.9%	1																									
				TVFETLDIGWQLLR	2	99.8%	1																									
IPI01015996	MYO18A	Uncharacterized protein	99.9%	3.5	3	3	3	1	2,239,578	2,228,608	2,105,599	2,497,463	463,993	140,156	167,137	181,455	46.3	14.1	17.8	16.3	-1.0	1	-1.1	0.8	1.1	0.6	-1.1	0.6	1.1	0.3	1.2	0.2
				ISELTSELTDER	2	97.7%	1																									
				QMEVMEMEVMEAR	2	99.4%	1																									
				RLESLASR	2	98.4%	1																									
IPI01016003	PITRM1	cDNA FLJ53321, highly similar to Homo sapiens pitrilysin metallopeptidase 1 (PITRM	99.0%	2.1	2	2	2	1	11,388,420	12,927,770	13,834,370	14,015,300	871,927	562,233	1,671,220	750,022	17.1	9.7	27.0	12.0	1.1	0.2	1.2	0.2	1.2	0.05	1.1	0.6	1.1	0.3	1.0	0.9
				LGCGLLDYR	2	91.1%	1																									
				TCTPQSVAMEQYK	3	88.8%	1																									