List of proteins identified from the methanol fraction.

Description	Name	AccessID	Unique Peptide Sequence	MW(kDa)	Subcellular Location
Deoxyribonuc	DNS2A_HU	O00115	ALINSPEGAVGR	40.069	Lysosome.
Membrane-as	PGRC1_HU	O00264	FYGPEGPYGVFAGR KFYGPEGPYGVFAGR	21.772	Microsome r
Agrin precurs	AGRIN_HU	O00468	VLGAPVPAFEGR	222.861	Secreted, ex
Polyglutamine	PQBP1_HU	O60828	PLPVALQTR	30.511	Nucleus. Not
Core histone	H2AY_HUM	O75367	AGVIFPVGR SIAFPSIGSGR	39.764	Nucleus. Not
PC4 and SFR	PSIP1_HUM	O75475	DFKPGDLIFAK	60.181	Nucleus. Not
Cytosolic pho	PA24B_HU	O95712	VLQAHR	115.417	Cytoplasm, c
Superoxide di	SODC_HUM	P00441	LACGVIGIAQ	16.154	Cytoplasm.
Prothrombin p	THRB_HUM	P00734	LAVTTHGLPCLAWASAQAK RQECSIPVCGQDQVTVAMTPR	71.475	Secreted, ex
Haptoglobin p	HPT_HUMA	P00738	QLVEIEK ILGGHLDAK VGYVSGWGR VTSIQDWVQK NANFKFTDHLK DIAPTLTLYVGKK VMPICLPSKDYAEVGR AVGDKLPECEAVCGKPK TEGDGVYTLNNEKQWINK SPVGVQPILNEHTFCAGMSK	45.861	Secreted.
Complement	CFAB_HUM	P00751	YGLVTYATYPK FLCTGGVSPYADPNTCR LLQEGQALEYVCPSGFYPYPVQTR	86.847	Secreted.
Antithrombin-	ANT3_HUM	P01008	ANRPFLVFIR EVPLNTIIFMGR+Oxidation(M)	53.025	Secreted, ex
Alpha-1-antitr	A1AT_HUM	P01009	SPLFMGK SVLGQLGITK LSITGTYDLK QINDYVEKGTQGK	46.878	Secreted.

Alpha-1-anticl	AACT_HUM	P01011	ITLLSALVETR LYGSEAFATDFQDSAAAK AVLDVFEEGTEASAATAVK	47.792	Secreted.
Kininogen-1 p	KNG1_HUM	P01042	KIYPTVNCQPLGMISLMK	72.996	Secreted, ex
Somatoliberin	SLIB_HUM/	P01286	YADAIFTNSYR	12.496	Secreted.
Ig lambda cha	LV403_HUM	P01717	SYELTQPPSVSVSPGQTAR	11.624	extracellular r
Ig heavy chair	HV311_HUI	P01772	QVQLVESGGGVVQPGR+Pyro-glu(N-term Q)	13.938	extracellular r
Ig heavy chair	HV316_HUI	P01777	EVQLVESGGGLVQPGGSLR	12.908	extracellular r
Ig heavy chair	HV318_HUI	P01779	EVQLLESGGGLVQPGGSLR	12.537	extracellular r
Ig gamma-1 c	IGHG1_HU	P01857	ALPAPIEK GPSVFPLAPSSK	36.596	Secreted.
Ig gamma-2 c	IGHG2_HU	P01859	GLPAPIEK GPSVFPLAPCSR TTPPMLDSDGSFFLYSK	36.489	Secreted.
Ig gamma-3 c	IGHG3_HU	P01860	ALPAPIEK SCDTPPPCPR	33.222	Secreted.
Ig mu chain C	MUC_HUM/	P01871	GFPSVLR	50.21	membrane fr
Ig alpha-1 cha	IGHA1_HUI	P01876	GFSPKDVLVR TFTCTAAYPESK QEPSQGTTTFAVTSILR	38.486	
Hemoglobin s	HBD_HUM/	P02042	VVAGVANALAHK VNVDAVGGEALGR LLVVYPWTQR VVAGVANALAHKYH VLGAFSDGLAHLDNLK	16.159	hemoglobin c
Spectrin alpha	SPTA1_HU	P02549	AAVGQEEIQLR	280.884	spectrin
Apolipoprotein	APOA1_HU	P02647	LLDNWDSVTSTFSK	30.759	Secreted.
Fibrinogen alp	FIBA_HUM/	P02671	GGSTSYGTGSETESPR	95.656	Secreted.
Fibrinogen be	FIBB_HUM/	P02675	EEAPSLRPAPPPISGGGYR	56.577	Secreted.
Fibrinogen ga	FIBG_HUM	P02679	DNCCILDER	52.106	Secreted.
Beta-2-glycop	APOH_HUM	P02749	VCPFAGILENGAVR	39.584	Secreted.

Alpha-1-acid g	A1AG1_HU	P02763	SDVVYTDWKK EQLGEFYEALDCLR	23.725	Secreted.
Alpha-2-HS-g	FETUA_HU	P02765	TVVQPSVGAAAGPVVPPCPGR	40.098	Secreted.
Transthyretin	TTHY_HUM	P02766	AADDTWEPFASGK YTIAALLSPYSYSTTAVVTNPKE	15.991	Secreted.
Serum album	ALBU_HUM	P02768	AACLLPK AEFAEVSK YLYEIAR FQNALLVR TYETTLEK QTALVELVK LVAASQAALGL AFKAWAVAR CCTESLVNR KLVAASQAALGL CASLQKFGER AAFTECCQAADK YICENQDSISSK RHPDYSVVLLLR TCVADESAENCDK VPQVSTPTLVEVSR LKECCEKPLLEK CCAAADPHECYAK KVPQVSTPTLVEVSR RPCFSALEVDETYVPK VFDEFKPLVEEPQNLIK	71.317	Secreted.
Serotransferri	TRFE_HUM	P02787	CLVEKGDVAFVK SVIPSDGPSVACVK MYLGYEYVTAIR CSTSSLLEACTFR FDEFFSEGCAPGSK KPVEEYANCHLAR CSTSSLLEACTFRRP NLNEKDYELLCLDGTR SAGWNIPIGLLYCDLPEPR SDNCEDTPEAGYFAVAVVKK KPVDEYKDCHLAQVPSHTVVAR	79.28	Secreted.
Hemopexin p	HEMO_HUI	P02790	VDGALCMEK GGYTLVSGYPK QGHNSVFLIK YYCFQGNQFLR LLQDEFPGIPSPLDAAVECHR EVGTPHGIILDSVDAAFICPGSSR	52.385	Secreted.

Ferritin light c	FRIL_HUMA	P02792	LGGPEAGLGEYLFER	20.064	ferritin compl
Plasma kallikr	KLKB1_HUI	P03952	VLTPDAFVCR	73.433	Secreted.
Vitronectin pr	VTNC_HUM	P04004	IYISGMAPRPSLAK DVWGIEGPIDAAFTR SIAQYWLGCPAPGHL	55.069	Secreted, ex
Histidine-rich	HRG_HUMA	P04196	DGYLFQLLR DSPVLIDFFEDTER SGFPQVSMFFTHTFPK	60.51	Secreted.
Ig kappa chai	KV307_HUI	P04206	EIVLTQSPGTLSLSPGER	11.937	extracellular r
Alpha-1B-glyc	A1BG_HUM	P04217	CLAPLEGAR LETPDFQLFK	54.809	Secreted.
Keratin, type I	K2C1_HUM	P04264	SLVNLGGSK IEISELNR TLLEGEESR YEELQITAGR TNAENEFVTIK SLDLDSIIAEVK SLNNQFASFIDK TNAENEFVTIKK FLEQQNQVLQTK SLNNQFASFIDKVR QISNLQQSISDAEQR AEAESLYQSKYEELQITAGR	66.149	intermediate
Glyceraldehyc	G3P_HUMA	P04406	GALQNIIPASTGAAK DGRGALQNIIPASTGAAK	36.201	Cytoplasm.
Ig kappa chai	KV309_HUI	P04433	LLIYDASNR	12.681	extracellular r
Heat shock pr	HSPB1_HU	P04792	VPFSLLR LFDQAFGLPR AQLGGPEAAKSDETAAK LATQSNEITIPVTFESR	22.826	Cytoplasm. N
Sodium/potas	AT1A1_HUI	P05023	MSINAEEVVVGDLVEVK+Oxidation(M)	114.135	Membrane; I
Secretogranir	SCG1_HUM	P05060	CIIEVLSNALSK	78.313	Secreted. Nc
Protein S100-	S10A8_HUI	P05109	LLETECPQYIR	10.885	
60S acidic rib	RLA1_HUM	P05386	AAGVNVEPFWPGLFAK	11.621	cytosolic larg

Integrin beta-1	ITB1_HUMA	P05556	GICECGVCK TVMPYISTTPAK	91.714	Cell membra
Alpha-enolase	ENOA_HUM	P06733	NFRNPLAK	47.481	Cytoplasm. C
Nucleophosm	NPM_HUMA	P06748	FINYVK LLSISGKR FINYVKNCFR MTDQEAIQDLWQWR MTDQEAIQDLWQWRK MSVQPTVSLGGFEITPPVVLR	32.726	Nucleus, nuc
Histone H1.0	H10_HUMA	P07305	QSIQKYIK LVTTGVLKQTK SHYKVGENADSQIK YSDMIVAAIQAEKNR	20.85	Nucleus.
Annexin A2 (A	ANXA2_HU	P07355	GVDEVTIVNILTNR	38.808	Secreted, ex
Tubulin beta c	TBB5_HUM	P07437	YLTVAAVFR LAVNMVPFPR AILVDLEPGTMDSVR LHFFMPGFAPLTSR	50.095	cytoskeleton
Decorin precu	PGS2_HUM	P07585	NQLKELPEK VSPGAFTPLVK ELHLDNNKLTR VDAASLKGLNNLAK DFEPSLGPVCPFR VVQCSDLGLDKVPK DLPPDTTLLDLQNNK	40.064	Secreted, ex
Cathepsin L p	CATL_HUM	P07711	NHCGIASAASYPTV	37.996	Lysosome.
Profilin-1 (Pro	PROF1_HU	P07737	TFVNITPAEVGVLVGKDR	15.216	
Cathepsin B p	CATB_HUM	P07858	LPASFDAR	38.766	Lysosome. M
Heat shock pr	HS90A_HU	P07900	GVVDSEDLPLNISR NPDDITNEEYGEFYK	85.006	Cytoplasm. M
Heterogeneou	HNRPC_HU	P07910	MYSYPAR VPPPPPIAR MIAGQVLDINLAAEPK MYSYPARVPPPPPIAR	33.707	Nucleus. Not
Heat shock pr	HS90B_HU	P08238	GVVDSEDLPLNISR	83.554	Cytoplasm. M
Extracellular s	SODE_HUM	P08294	VTGVVLFR	26.291	Secreted, ex

Complement	CFAH_HUM	P08603	CTSTGWIPAPR SIDVACHPGYALPK	143.654	Secreted.
Vimentin.	VIME_HUM	P08670	SLYASSPGGVYATR	53.676	cytoplasm;int
Alpha-2-antipl	A2AP_HUM	P08697	LCQDLGPGAFR	54.873	Secreted.
Keratin, type I	K1C19_HUI	P08727	LASYLDK FGPGVAFR LASYLDKVR	44.065	costamere;in
Glutathione S	GSTP1_HU	P09211	FQDGDLTLYQSNTILR ALPGQLKPFETLLSQNQGGK	23.569	cytoplasm
Galectin-1 (La	LEG1_HUM	P09382	DGGAWGTEQR	15.048	cytoplasm
High mobility	HMGB1_HU	P09429	GEHPGLSIGDVAK IKGEHPGLSIGDVAK RPPSAFFLFCSEYRPK	25.049	Nucleus.
Retinol-bindin	RET1_HUM	P09455	PVDFTGYWK	16.011	Cytoplasm.
Clathrin light	CLCA_HUM	P09496	SVLISLKQAPLVH	27.174	Cytoplasmic
Heterogeneou	ROA1_HUM	P09651	SESPKEPEQLR SSGPYGGGGQYFAKPR NQGGYGGSSSSSSYGSGR	38.936	Nucleus. Cyt
Cytochrome c	COX6C_HU	P09669	AGIFQSVK	8.776	Mitochondric
Ubiquitin carb	UCHL1_HU	P09936	FSAVALCK	25.151	Cytoplasm.
Histone H2A.:	H2AZ_HUM	P0C0S5	HLQLAIR AGLQFPVGR GDEELDSLIK AGLQFPVGRIHR ATIAGGGVIPHIHK	13.545	Nucleus.
Histone H1.4	H14_HUMA	P10412	KPAAAAGAK AVAASKER KATGAATPK SGVSLAALK LGLKSLVSK SGVSLAALKK KAASGEAKPK ALAAAGYDVEK GTGASGSFKLNK ASGPPVSELITK	21.852	Nucleus.

			KALAAAGYDVEK SLVSKGTLVQTK KASGPPVSELITK SETAPAAPAAPAPAEK GTLVQTKGTGASGSFK ALAAAGYDVEKNNSR ASGPPVSELITKAVAASK		
Cytochrome c	COX5B_HU	P10606	KGLDPYNVLAPK CGAHYKLVPQQLAH	13.915	Mitochondric
Clusterin prec	CLUS_HUM	P10909	EILSVDCSTNNPSQAK LFDSDPITVTVPVEVSR	53.031	Secreted.
Lysosome-as	LAMP2_HU	P13473	IPLNDLFR	45.503	Cell membra
Versican core	CSPG2_HU	P13611	AQCGGGLLGVR LGEPNYGAEIR LATVGELQAAWR	374.585	Secreted, ex
Keratin, type I	K1C10_HUI	P13645	LASYLDK VLDELTLTK LASYLDKVR VTMQNLNDR DAEAWFNEK LENEIQTYR SLLEGEGSSGGGGR ALEESNYELEGK GSLGGGFSSGGFSGGSFSR	59.711	intermediate
Keratin, type I	K2C5_HUM	P13647	ISISTSGGSFR	62.568	intermediate
Macrophage r	MIF_HUMA	P14174	LLCGLLAER PMFIVNTNVPR MPMFIVNTNVPR SYSKLLCGLLAER	12.639	extracellular r
Glucosidase 2	GLU2B_HU	P14314	SLEDQVEMLR	60.357	intracellular
Endoplasmin	ENPL_HUM	P14625	SGYLLPDTK SILFVPTSAPR GVVDSDDLPLNVSR	92.696	Endoplasmic
Myosin light p	MYL6B_HU	P14649	ALGQNPTNAEVLK	22.864	muscle myos
Cytochrome c	CX6B1_HU	P14854	NCWQNYLDFHR	10.414	Mitochondric
N-acetylgluco	GNS_HUM/	P15586	AFQNVFAPR	62.84	Lysosome.

Histone H1.5	H15_HUMA	P16401	AVAASKER LGLKSLVSK KAASGEAKPK NGLSLAALKK ALAAGGYDVEK GTGASGSFKLNK ATGPPVSELITK SLVSKGTLVQTK GTLVQTKGTGASGSFK ALAAGGYDVEKNNSR	22.566	Nucleus.
Stathmin (Phc	STMN1_HU	P16949	ASGQAFELILSPR	17.292	Cytoplasm.
60S ribosoma	RL35A_HUI	P18077	VMLYPSRI	12.587	
SON protein (	SON_HUM/	P18583	SLPNEEIVQK	264.079	Nucleus spe
Phosphoglyce	PGAM1_HU	P18669	YADLTEDQLPSCESLKDTIAR	28.9	cytosol
Nucleolin (Pro	NUCL_HUM	P19338	ALVATPGK TGISDVFAK NDLAVVDVR AIRLELQGPR SISLYYTGEK VFGNEIKLEKPK TGISDVFAKNDLAVVDVR VTQDELKEVFEDAAEIR	76.625	Nucleus, nuc
Inter-alpha-try	ITIH2_HUM	P19823	FYNQVSTPLLR	106.826	Secreted.
Inter-alpha-try	ITIH1_HUM	P19827	LDAQASFLPK	101.782	Secreted.
Mimecan prec	MIME_HUM	P20774	RLPIGSYF LTAKDFADIPNLR	34.243	Secreted, ex
Biglycan prec	PGS1_HUM	P21810	GVFSGLR LGLGHNQIR VVQCSDLGLK IQAIELEDLLR ELHLDNNKLAR VVQCSDLGLKSVPK NHLVEIPPNLPSSLVELR EISPDTTLLDLQNNDISELR	42.027	Secreted, ex
Catechol O-m	COMT_HUM	P21964	MARLLSPGAR	30.474	Isoform Solu
Heterogeneou	ROA2_HUM	P22626	GGNFGFGDSR TLETVPLER SGRGGNFGFGDSR	37.464	Nucleus. Not

			GGGGNFGPGPGSNFR ALSRQEMQEVQSSR NMGGPYGGGNYGPGGSGGSGGYGGR GGGGNFGPGPGSNFRGGSDGYGSGR GGNFGFGDSRGGGGNFGPGPGSNFR		
Elongation fac	EF1B_HUM	P24534	SIQADGLVWGSSK	24.919	eukaryotic tra
60S ribosoma	RL13_HUM	P26373	LILFPR SKLILFPR	24.304	cytosolic ribo
High mobility	HMGB2_HU	P26583	RPPSAFFLFCSEHRPK	24.19	Nucleus.
FK506-bindin	FKBP2_HU	P26885	LVIPSELGYGER	15.81	Endoplasmic
Calreticulin pr	CALR_HUM	P27797	QIDNPDYK IKDPDASKPEDWDER	48.283	Endoplasmic
Leiomodin-1 (	LMOD1_HU	P29536	TKTPEK	63.869	Cytoplasm. C
60S ribosoma	RL12_HUM	P30050	IGPLGLSPK CTGGEVGATSALAPK	17.979	
Protein disulfi	PDIA3_HUM	P30101	TADGIVSHLKK LAPEYEAAATR GFPTIYFSPANK	57.146	Endoplasmic
Histone H2B 1	H2B1B_HU	P33778	HAVSEGTK LLLPGELAK ESYSIYVYK QVHPDTGISSK+Pyro-glu(N-term Q) KESYSIYVYK STITSREIQTAVR VLKQVHPDTGISSK AMGIMNSFVNDIFER+Oxidation(M) LLLPGELAKHAVSEGTK	13.942	Nucleus.
Keratin, type I	K1C9_HUM	P35527	LASYLDK SGGGGGGGLGSGGSIR FSSSSGYGGGSSR GGSGGSYGGGGSGGGYGGGGSGSR	62.32	
RNA-binding	FUS_HUMA	P35637	GEATVSFDDPPSAK CPNPTCENMNFSWR AAIDWFDGKEFSGNPIK APKPDGPGGGPGGSHMGGNYGDDR	53.622	Nucleus.
Protein DEK.	DEK_HUMA	P35659	SICEVLDLER NVGQFSGFPFEK	42.933	Nucleus (Pot

Keratin, type I	K22E_HUM	P35908	IEISELNR YLDGLTAER FLEQQNQVLQTK	66.111	intermediate
Transgelin-2 (	TAGL2_HU	P37802	GASQAGMTGYGMPR	22.548	nuclear mem
Heterogeneou	HNRPG_HU	P38159	GFAFVTFESPADAK DVYLSPRDDGYSTK	42.306	Nucleus. Not
40S ribosoma	RS19_HUM	P39019	ALAAFLKK VLQALEGLK HKELAPYDENWFYTR	16.051	cytosolic sma
Collagen alph	COIA1_HUI	P39060	LQDLYSIVR GADFQCFQQAR ELLREETGAALKPR	179.361	collagen
Acidic leucine	AN32A_HU	P39687	IHLELR TPSDVKELVLDNSR	28.682	Nucleus. Cyt
60S ribosoma	RL13A_HUI	P40429	MVVPAALK	23.619	large ribosom
Lamina-assoc	LAP2B_HUI	P42167	PEFLEDPSVLTK HASPILPITEFSDIPR GPPDFSSDEEREPTPVLGSGAAAAGR	50.696	Nucleus inne
40S ribosoma	RS27_HUM	P42677	LTEGCSFR LVQSPNSYFMDVK	9.797	cytosolic sma
60S ribosoma	RL35_HUM	P42766	YKPLDLRPK KYKPLDLRPK	14.543	cytosolic larg
Matrin-3.	MATR3_HU	P43243	SFQQSSLSR	95.078	Nucleus mat
Ran-specific (	RANG_HUM	P43487	FASENDLPEWKER	23.467	cytoplasm;nu
60S ribosoma	RL27A_HUI	P46776	TGAAPIIDVVR	16.665	cytosolic larg
60S ribosoma	RL29_HUM	P47914	GVDPKFLR AEAIKALVKPK AQAAAPASVPAQAPK AQAAAPASVPAQAPKR	17.798	cytosolic larg
ATP synthase	ATPO_HUM	P48047	VAASVLNPYVK	23.377	Mitochondric
Nuclear autoa	NASP_HUM	P49321	KPTDGASSSNCVTDISHLVR	85.471	Cytoplasm (E
Histidine triad	HINT1_HUM	P49773	CAADLGLNKGYR	13.907	Cytoplasm. N

		AQVARPGGDTIFGK			
Cysteine-rich	CRIP1_HUI	P50238	CNKEVYFAER	8.926	cytoplasm
Serpin H1 pre	SERPH_HU	P50454	LYGPSSVSFADDFVR	46.525	Endoplasmic
B-cell recepto	BAP31_HUI	P51572	QAESASEAAKK	28.031	Endoplasmic
Hepatoma-de	HDGF_HUM	P51858	CGDLVFAK GFSEGLWEIENNPTVK	26.886	Cytoplasm.
Lumican prec	LUM_HUM/	P51884	YLYLR ILGPLSYSK FNALQYLR ILGPLSYSKIK SLEDLQLTHNKITK SLEYLDLSFNQIAR LDGNRISETSLPPDMYECLR	38.747	Secreted, ex
Prolargin prec	PRELP_HU	P51888	WINLDNNR SFPNLAFIR	44.181	Secreted, ex
NADH dehydr	NDUA8_HU	P51970	FYFWTK	20.548	Mitochondric
Heterogeneou	ROA3_HUM	P51991	SSGSPYGGGYGSGGGSGGYGSR	39.799	Nucleus (By
Adenylate kin	KAD2_HUM	P54819	APSVPAAEPEYPKGIR	26.689	Mitochondric
Neutrophil de	DEF3_HUM	P59666	IPACIAGER YGTCIYQGR IPACIAGERR YGTCIYQGRLWAFCC	10.58	Secreted.
Triosephosph	TPIS_HUM/	P60174	FFVGGNWK IAVAAQNCYK QSLGELIGTLNAAK VVLAYEPVWAIGTGK VPADTEVVCAPPTAYIDFAR	26.938	
Signal recogn	SRP54_HU	P61011	AWTPTK	55.953	Nucleus spe
40S ribosoma	RS3A_HUM	P61247	APAMFNIR ACQSIYPLHDVFVR	30.154	cytosolic sma
60S ribosoma	RL27_HUM	P61353	YSVDIPLDK	15.788	ribosome
Lysozyme C p	LYSC_HUM	P61626	LGMDGYR STDYGIFQINSR	16.982	extracellular s

40S ribosoma	RS14_HUM	P62263	TPGPGAQSALR	16.434	cytosolic sma
40S ribosoma	RS18_HUM	P62269	IPDWFLNR	17.708	Cytoplasm.
40S ribosoma	RS29_HUM	P62273	YGLNMCR GHQQLYWSHPR	6.9	cytosolic sma
40S ribosoma	RS13_HUM	P62277	LILIESR GLSQSALPYRR KGLTPSQIGVILR	17.212	cytosolic sma
Small nuclear	RUXE_HUM	P62304	VMVQPINLIFR	10.854	Nucleus.
60S ribosoma	RL23A_HUI	P62750	VNTLIRPDGEK LAPDYDALDVANK LAPDYDALDVANKIGII	17.684	cytosolic larg
Histone H4.	H4_HUMAN	P62805	VFLENVIR QGRTLYGFGG ISGLIYEETR TVTAMDVVYALK DNIQGITKPAIR TVTAMDVVYALKR DNIQGITKPAIRR ISGLIYEETRGVLK VLRDNIQGITKPAIR	11.36	Nucleus.
60S ribosoma	RL23_HUM	P62829	ISLGLPVGAVINCADNTGAK	14.97	ribosome
40S ribosoma	RS25_HUM	P62851	LITPAVVSER LITPAVVSERLK EVPNYKLITPAVVSER	13.791	cytosolic sma
40S ribosoma	RS30_HUM	P62861	FVNVVPTFGK FVNVVPTFGKK	6.644	cytosolic sma
60S ribosoma	RL8_HUMA	P62917	AVVGVVAGGGRIDKPILK	28.235	Cytoplasm.
Peptidyl-proly	PPIA_HUM	P62937	KITIADCGQLE VSFELFADKVPK IIPGFMCQGGDFTR SIYGEKFEDENFILK	18.229	Cytoplasm.
FK506-bindin	FKB1A_HU	P62942	GVQVETISPGDGR GVQVETISPGDGRTFPK	12.0	Cytoplasm.
Ubiquitin.	UBIQ_HUM	P62988	MQIFVK ESTLHLVLR MQIFVKTLTGK	8.56	Cytoplasm. N

			LIFAGKQLEDGR IQDKEGIPPDQQR TITLEVEPSDTIENVK TLTGKTITLEVEPSDTIENVK		
Actin, cytopla	ACTG_HUM	P63261	AGFAGDDAPR EITALAPSTMK SYELPDGQVITIGNER VAPEEHPVLLTEAPLNPK	42.108	Cytoplasm, c
Nuclease sen	YBOX1_HU	P67809	AADPPAENSSAPEAEQGGAE RPQYSNPPVQGEVMEGADNQGAGEQGRPVR SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK	35.903	Cytoplasm. N
Tubulin alpha	TBAK_HUM	P68363	AVFVDLEPTVIDEVR VGINYQPPTVVPGGDLAK	50.804	
Hemoglobin s	HBB_HUMA	P68871	SAVTALWGK VVAGVANALAHK LLVVYPWTQR VNVDEVGGEALGR EFTPPVQAAYQK VVAGVANALAHKYH VLGAFSDGLAHLDNLK VHLTPEEKSAVTALWGK FFESFGDLSTPDAVMGNPK FFESFGDLSTPDAVMGNPKVK	16.102	hemoglobin c
Hemoglobin s	HBA_HUMA	P69905	MFLSFPTTK FLASVSTVLTSK VGAHAGEYGAEALER TYFPHFDLSHGSAQVK AAWGKVGAHAGEYGAEALER TYFPHFDLSHGSAQVKGHGK VADALTNAVAHVDDMPNALSALSDLHAHK+Oxidation(M)	15.305	hemoglobin c
Nuclear prote	HCC1_HUM	P82979	FGLNVSSISR	23.713	Nucleus.
60S ribosoma	RL24_HUM	P83731	QINWTVLYR	17.882	cytosolic larg
60S ribosoma	RL19_HUM	P84098	VWLDPNETNEIANANSR	23.565	cytosolic larg
Splicing facto	SFRS3_HU	P84103	AFGYYGPLR	19.546	Nucleus.
Putative RNA	RBM3_HUM	P98179	YYDSRPGGYGYGYGR	17.16	
Cytochrome c	CYC_HUMA	P99999	TGPNLHGLFGR TGPNLHGLFGRK	11.855	Mitochondric

Heterogeneou	HNRPU_HU	Q00839	APQCLGKFIEIAAR QMADTGKLNTLLQR SSGPTSLFAVTVAPPGAR	91.198	Nucleus. Cel
Splicing facto	U2AF1_HU	Q01081	GGFCNFMHLKPISR	28.368	Nucleus.
Splicing facto	SFRS2_HU	Q01130	VGDVYIPR	25.461	Nucleus.
60S ribosoma	RL6_HUMA	Q02878	YYPTEDVPR AIPQLQGYLR	32.765	cytosolic larg
Keratin, type I	K1C17_HU	Q04695	LASYLDK LASYLDKVR	48.361	intermediate
Elongation fac	EF1A2_HU	Q05639	IGGIGTVPVGR	50.78	Nucleus (By
Fibromodulin	FMOD_HUM	Q06828	YLPFVPSR	43.562	Secreted, ex
Peroxiredoxin	PRDX1_HU	Q06830	IGHPAPNFK	22.324	Cytoplasm. N
60S ribosoma	RL18_HUM	Q07020	GCGTVLLSGPR ILTFDQLALDSPK	21.735	Cytoplasm.
Splicing facto	SFRS1_HU	Q07955	IYVGNLPPDIR	27.842	Cytoplasm. N
Galectin-3-bir	LG3BP_HU	Q08380	TLQALEFHTVPFQLLAR	66.202	Secreted. Se
TAR DNA-bin	TADBP_HU	Q13148	FGGNPGGFGNQGGFGNSR	45.053	Nucleus.
Heterogeneou	ROA0_HUM	Q13151	AVPKEDIYSGGGGGGSR	30.993	Nucleus (By
Splicing facto	SFRS6_HU	Q13247	LIVENLSSR	39.677	Nucleus.
Golgin subfan	GOGA4_HU	Q13439	RIAELR	261.892	Cytoplasm. (
CD166 antige	CD166_HU	Q13740	ALFLETEQLK	65.745	Membrane; S
Cold-inducible	CIRBP_HU	Q14011	SGGYGGSRDYYSSR	18.637	Nucleus, nuc
Heterogeneou	HNRPD_HU	Q14103	IFVGGLSPDTPEEK IFVGGLSPDTPEEKIR FGEVVDCTLKLDPITGR	38.581	Nucleus. Not
Scaffold attac	SAFB2_HU	Q14151	SEPVKEESSELEQPFAQDTSSVGPDR	107.921	Cytoplasm. N
Translation in	EI2BA_HUM	Q14232	KIMIER	33.976	eukaryotic tra
LIM and SH3	LASP1_HU	Q14847	QSFTMVADTPENLR	30.097	Cytoplasm, c

Platelet-activa	PA1B3_HUI	Q15102	VVVLGLLPR	25.832	Cytoplasm.
Prostaglandin	TEBP_HUM	Q15185	TDRSILCCLR	18.971	Cytoplasm.
RNA-binding	RNPS1_HU	Q15287	MIDMPVER	34.188	Nucleus spe
Protein ADRM	ADRM1_HU	Q16186	SQSAAVTPSSTTSSTR	42.412	Cytoplasm. N
Splicing facto	SFRS7_HU	Q16629	AFSYYGPLR VYVGNLGTGAGKGELER	27.578	Nucleus.
N-acetyltransf	ESCO2_HU	Q56NI9	HIKPVSR	69.233	Nucleus (Pro
Polymerase I	PTRF_HUM	Q6NZI2	SFTPDHVVYAR	43.45	Cell membra
Histone H3.2	H32_HUMA	Q71DI3	KLPFQR STELLIR EIAQDFK STELLIRK YRPGTVALR YQKSTELLIR EIAQDFKTDLR VTIMPKDIQLAR YRPGTVALREIR	15.436	Nucleus.
Zinc finger pro	ZN546_HUI	Q86UE3	LQGELTR	101.506	Nucleus (Pro
Histone H2B 1	H2B3B_HU	Q8N257	HAVSEGTK LLLPGELAK ESYSIYVYK QVHPDTGISSK+Pyro-glu(N-term Q) KESYSIYVYK VLKQVHPDTGISSK AMGIMNSFVNDIFER+Oxidation(M) LLLPGELAKHAVSEGTK	13.9	Nucleus.
Olfactory rece	O52E4_HUI	Q8NGH9	GLAGLACAPIK	35.969	Cell membra
Anterior gradi	AGR3_HUM	Q8TD06	IMFVDPSLTVR	19.273	Secreted (Pr
Probable D-ty	DTD1_HUM	Q8TEA8	SASSGAEGDVSSEREP	23.58	Cytoplasm (P
Caskin-2.	CSKI2_HUM	Q8WXE0	RLAELR	127.204	Cytoplasm (P
Histone H1x.	H1X_HUMA	Q92522	AAKPSVPKVPK YSQLVVETIR ALVQNDTLLQVK NQPGKYSQLVVETIR	22.474	Nucleus.

Hamartin (Tul	TSC1_HUM	Q92574	KTEELLK	129.767	Cytoplasm. N
TATA-binding	RBP56_HU	Q92804	GEATVSFDDPPSAK SGGGYGGDRSSGGGYSGDR	62.021	Nucleus (Pot
Gamma-gluta	GGH_HUM	Q92820	KPIIGILMQK	36.34	Secreted, ex
Histone H2A 1	H2A1C_HU	Q93077	TRIIPR HLQLAIR AGLQFPVGR SSRAGLQFPVGR NDEELNKLLGR AGLQFPVGRVHR VTIAQGGVLPNIQAVLLPK	14.097	Nucleus.
Histone H2B 1	H2B1H_HU	Q93079	HAVSEGTK LLLPGELAK ESYSVYVYK QVHPDTGISSK+Pyro-glu(N-term Q) KESYSVYVYK STITSREIQTAVR ESYSVYVYKVLK VLKQVHPDTGISSK AMGIMNSFVNDIFER+Oxidation(M) LLLPGELAKHAVSEGTK	13.884	Nucleus.
Phosphoglucc	PGM2_HUM	Q96G03	LFENLR	68.754	Cytoplasm (E
Histone H2A 1	H2A1H_HU	Q96KK5	TRIIPR HLQLAIR AGLQFPVGR NDEELNKLLGK SSRAGLQFPVGR AGLQFPVGRVHR VTIAQGGVLPNIQAVLLPK	13.898	Nucleus.
Histone H2A 1	H2A1A_HU	Q96QV6	TRIIPR HLQLAIR AGLQFPVGR SSRAGLQFPVGR AGLQFPVGRIHR	14.225	Nucleus.
Protein DJ-1 (	PARK7_HU	Q99497	ALVILAK APLVLKD VTVAGLAGKDPVQCSR	20.05	Nucleus. Cyt
Acidic leucine	AN32E_HU	Q9BTT0	INLELR	30.902	Cytoplasm (E
Tubulin beta-2	TBB2B_HU	Q9BVA1	LAVNMVPFPR	50.377	

			AILVDLEPGTMDSVR LHFFMPGFAPLTSR		
Periaxin.	PRAX_HUM	Q9BXM0	LPTLGAR	155.248	Nucleus (By
Asporin precu	ASPN_HUM	Q9BXN1	VVHCSDLGLTSVPTNIPFDTR	43.673	Secreted, ex
Membrane fri	MFRP_HUM	Q9BY79	RLLCGLLVPR	64.167	Membrane; S
SRA stem-loc	SLIRP_HUM	Q9GZT3	SINQPVAFVR	12.398	Mitochondric
H/ACA ribonu	NOLA3_HU	Q9NPE3	VLMTQQPRPVL	7.758	Nucleus, nuc
Bromodomair	BRWD1_HU	Q9NSI6	RLSALVWEVR	265.493	Cytoplasm. N
Uncharacteriz	CI039_HUM	Q9NXG0	QRLNVAVK	125.633	
RNA-binding	RALY_HUM	Q9UKM9	VTVPLVR	32.501	Nucleus (Pro
60S ribosoma	RL26L_HUM	Q9UNX3	MKFNPFVTSDR	17.246	
Serine/arginin	SRRM2_HU	Q9UQ35	VPLSAYER TAAALAPASLTSAR TPQAPASANLVGPR MAPALSGANLTSPR IPAASAAAMNLASAR MSQVPAPVPLMSLR	300.179	Nucleus spe
60S ribosoma	RL36_HUM	Q9Y3U8	ALRYPMAVGLNK	12.303	cytosolic larg
150 kDa oxyg	OXRP_HUM	Q9Y4L1	YFQHLLGK DAVVYPILVEFTR	111.494	
Mitochondrial	TIM13_HUM	Q9Y5L4	VQIAVANAQELLQR	10.721	Mitochondric
FH1/FH2 dom	FHOD1_HU	Q9Y613	LQLWAFK	127.328	Cytoplasm. N
Brefeldin A-in	BIG2_HUM	Q9Y6D5	EAWTSLLLLLLTK+Pyro-glu(N-term E)	204.418	cytosol;Golgi

Go Function	Go Process	Score	Mascot score for identity	Observed	Mr(calc)	Mr(error)	Peptide Gravy	Protein Gravy
deoxyribonuc	DNA metabc	44	24	592.33	1182.64	0.01	0.12	-0.26
protein bindin		44	25	758.87	1515.71	0.01	-0.27	-0.56
		23	25	548.94	1643.81	0.00	-0.51	
laminin bindin	acetylcholine	27	24	606.84	1211.67	0.00	0.55	-0.25
DNA binding;t	regulation of	48	17	497.81	993.60	0.01	0.19	-1.51
DNA binding	dosage com	41	26	458.27	914.53	0.00	1.18	-0.25
		31	26	546.30	1090.58	0.01	0.39	
		25	25	417.56	1249.67	-0.01	-0.10	-1.42
calcium ion bi	arachidonic a	23	20	362.23	722.42	0.02	-0.23	-0.31
chaperone bir	activation of	37	26	501.28	1000.54	0.01	1.88	-0.34
receptor bindi	caspase acti	31	23	665.69	1994.04	-0.01	0.60	-0.54
		33	23	811.38	2431.14	-0.02	-0.31	
	cellular iron i	27	27	429.75	857.49	0.00	-0.27	-0.42
		63	23	462.27	922.52	0.00	0.28	
		59	25	490.75	979.49	0.00	-0.03	
		46	26	602.33	1202.63	0.01	-0.39	
		45	25	667.85	1333.68	0.01	-1.00	
		47	20	473.61	1417.82	0.00	0.16	
		70	25	612.31	1833.91	0.00	0.11	
		49	25	465.23	1856.91	-0.02	-0.32	
		25	24	528.01	2108.02	0.01	-1.34	
		84	24	724.69	2171.05	0.00	0.09	
complement b	complement	40	25	638.33	1274.65	0.00	-0.13	-0.50
		42	22	957.93	1913.84	0.00	-0.08	
		33	22	939.12	2814.37	-0.03	-0.25	
protein bindin		45	22	411.58	1231.72	-0.01	0.58	-0.28
		54	25	703.39	1404.74	0.01	0.30	
protein bindin		47	27	390.21	778.40	0.00	0.26	-0.18
		46	22	508.31	1014.61	0.00	0.66	
		33	24	555.81	1109.60	0.01	0.08	
		26	26	493.92	1478.74	-0.01	-1.49	

chymotrypsin inflammatory	28	21	608.37	1214.72	-0.01	1.06	-0.07
	66	24	946.44	1890.86	0.01	-0.19	
	49	24	954.49	1906.95	0.01	0.41	
heparin bindir diuresis;elev	37	23	698.37	2092.09	0.00	0.33	-0.76
growth hormc G-protein sig	43	25	660.82	1319.61	0.01	-0.43	-0.43
antigen bindir immune resp	30	25	1002.51	2003.00	0.01	-0.64	-0.39
antigen bindir immune resp	48	24	796.93	1591.83	0.02	-0.05	-0.28
antigen bindir immune resp	61	22	941.51	1881.00	0.02	0.02	0.09
antigen bindir immune resp	29	21	948.52	1895.01	0.02	-0.01	0.09
antigen bindir immune resp	24	21	419.76	837.50	0.00	0.16	-0.43
	24	25	593.83	1185.64	0.01	0.09	
antigen bindir immune resp	26	21	412.75	823.48	0.01	-0.11	-0.41
	28	25	644.33	1286.64	0.01	0.32	
	30	24	953.46	1904.89	0.01	-0.26	
antigen bindir immune resp	24	21	419.76	837.50	0.00	0.16	-0.65
	51	20	593.75	1185.49	0.00	-1.09	
antigen bindir immune resp	30	26	388.23	774.44	0.00	0.50	-0.32
antigen bindir immune resp	40	25	373.21	1116.63	-0.01	0.03	-0.21
	51	22	688.32	1374.61	0.00	-0.36	
	38	24	918.49	1834.94	0.02	-0.25	
	25	22	383.89	1148.67	-0.01	1.05	-0.05
	54	25	628.84	1255.65	0.00	0.29	
	45	21	637.87	1273.72	0.01	0.35	
	98	23	725.41	1448.79	0.01	0.58	
	88	24	557.30	1668.88	0.00	0.41	
actin filament actin filamen	24	25	607.32	1212.65	-0.02	-0.25	-0.76
high-density li cholesterol n	23	25	806.90	1611.78	0.01	-0.32	-0.72
protein bindin	56	21	786.85	1571.67	0.01	-1.33	-0.82
	33	24	651.00	1950.00	-0.03	-0.85	-0.76
	35	17	597.75	1193.48	0.01	-0.58	-0.59
	30	24	751.91	1501.77	0.03	0.84	-0.27

protein bindin	acute-phase	27	25	620.82	1239.61	0.01	-1.01	-0.54
		65	23	871.90	1741.80	-0.01	-0.37	
kinase inhibit	acute-phase	53	22	1008.55	2015.06	0.03	0.49	-0.20
	transport	24	21	697.81	1393.61	-0.02	-0.82	-0.03
		48	23	1245.14	2488.27	0.00	0.12	
antioxidant ac	cellular resp	23	27	386.73	771.43	0.01	1.17	-0.35
		42	26	440.73	879.43	0.00	-0.14	
		37	25	464.25	926.49	0.01	-0.07	
		28	24	480.78	959.56	-0.01	0.61	
		39	25	492.75	983.48	0.01	-1.31	
		35	24	500.80	999.60	-0.01	0.69	
		29	23	507.31	1012.59	0.00	1.65	
		52	24	510.30	1018.57	0.00	0.54	
		49	22	569.76	1137.49	0.01	0.00	
		25	21	571.35	1140.69	0.00	1.18	
		27	25	399.20	1194.58	0.00	-0.57	
		40	18	686.29	1370.56	0.01	-0.01	
		52	23	722.33	1442.63	0.01	-0.84	
		50	22	489.95	1466.84	-0.01	0.03	
		101	13	749.80	1497.57	0.00	-0.78	
		38	23	756.43	1510.84	0.01	0.21	
		38	25	773.91	1545.79	0.01	-0.62	
		53	13	776.81	1551.59	0.01	-0.18	
		69	19	820.47	1638.93	0.00	-0.07	
		34	24	637.65	1909.92	0.01	-0.35	
		50	23	682.36	2044.09	-0.02	-0.35	
		24	25	455.58	1363.72	0.01	0.69	-0.34
		27	25	708.37	1414.71	0.01	0.57	
		27	25	739.87	1477.73	0.00	0.27	
		42	23	766.35	1530.68	0.01	0.42	
		44	18	789.34	1576.65	0.01	-0.41	
		92	25	529.59	1585.77	-0.01	-0.84	
		52	24	595.62	1783.83	-0.01	-0.05	
		46	23	651.65	1951.93	-0.01	-0.88	
		26	24	1086.05	2170.09	0.00	0.06	
		24	22	734.01	2199.02	-0.02	-0.34	
		26	23	638.07	2548.29	-0.02	-0.55	
binding;heme	cellular iron i	27	24	511.74	1021.46	0.00	0.32	-0.43
		26	25	571.29	1140.58	-0.02	-0.25	
		31	26	571.82	1141.62	0.00	0.00	
		58	23	748.34	1494.67	0.00	-0.55	
		37	23	788.72	2363.16	-0.01	-0.10	
		49	23	833.40	2497.23	-0.06	0.37	

identical prote	cellular iron i	29	25	804.41	1606.80	0.00	-0.23	-0.52
plasma kallikr	proteolysis	25	26	589.31	1176.60	0.01	0.90	-0.26
protein bindin	cell adhesior	55	23	501.95	1502.83	-0.01	0.24	-0.72
		71	25	823.91	1645.81	0.00	0.04	
		55	25	835.41	1668.81	-0.01	0.30	
		40	25	562.80	1123.60	-0.01	0.11	-0.96
		27	23	841.90	1681.78	0.00	-0.50	
		27	24	619.96	1856.89	-0.02	0.01	
antigen bindir	immune resp	51	23	942.52	1883.00	0.02	-0.15	-0.39
		59	25	493.76	985.50	0.00	0.41	-0.22
		34	25	619.33	1236.64	0.01	-0.35	
protein bindin	complement	47	26	437.76	873.49	0.00	0.22	-0.63
		43	27	487.27	972.52	0.00	-0.38	
		31	26	517.27	1032.51	0.01	-1.03	
		56	26	590.30	1178.59	0.00	-0.73	
		25	26	633.33	1264.63	0.01	-0.55	
		62	25	651.86	1301.71	-0.01	0.55	
		29	26	692.36	1382.68	0.01	-0.32	
		52	25	465.25	1392.72	0.00	-0.82	
		72	24	738.41	1474.78	0.02	-0.92	
		23	24	546.96	1637.85	0.00	-0.29	
		24	25	858.94	1715.84	0.01	-1.12	
		47	23	762.71	2285.12	0.00	-0.86	
glyceraldehyd	glycolysis	35	23	706.40	1410.78	0.00	0.35	-0.11
		23	23	870.48	1738.93	0.01	-0.18	
antigen bindir	immune resp	29	25	532.80	1063.57	0.01	0.03	-0.11
protein bindin	anti-apoptos	49	22	416.26	830.50	0.01	1.10	-0.57
		56	25	582.32	1162.61	0.01	0.15	
		98	25	822.42	1642.82	0.01	-0.76	
		75	24	953.50	1904.98	-0.01	-0.13	
protein bindin	cellular hydr	29	25	923.97	1845.94	-0.02	0.35	0.01
hormone acti		51	26	673.87	1345.73	-0.01	1.05	-1.55
calcium ion bi	inflammatory	25	26	711.36	1420.70	0.00	-0.36	-0.40
protein bindin	translation	27	25	851.95	1701.89	-0.01	0.46	0.11

identical prote	cell migratio	34	20	541.73	1081.44	0.02	0.89	-0.41
		27	25	654.85	1307.68	0.00	0.09	
phosphopyru	negative reg	26	26	480.27	958.53	0.00	-1.08	-0.22
NF-kappaB b	activation of	24	24	392.23	782.43	0.00	0.47	-0.97
		34	19	437.28	872.54	0.01	0.21	
		53	26	454.23	1359.68	-0.02	0.01	
		70	24	910.42	1818.84	-0.01	-1.14	
		56	24	649.98	1946.93	-0.02	-1.33	
		54	20	1114.11	2226.21	0.00	0.64	
		23	21	504.30	1006.58	0.00	-0.99	-1.07
		67	16	594.37	1186.73	0.00	0.20	
		46	26	525.93	1574.77	0.00	-1.27	
		28	25	854.94	1707.86	0.01	-0.27	
phospholipas	skeletal dev	26	24	771.92	1541.84	-0.01	0.36	-0.52
MHC class I p	cell motility;r	27	21	520.31	1038.59	0.02	1.34	-0.35
		67	25	572.32	1142.63	0.00	0.75	
		38	25	808.42	1614.83	0.00	0.38	
		42	25	540.94	1619.83	-0.03	0.49	
	organ morph	39	23	549.81	1097.61	0.01	-1.76	-0.25
		25	23	558.33	1114.64	0.01	0.71	
		60	24	451.58	1351.72	-0.01	-1.35	
		58	23	471.94	1412.80	-0.01	0.11	
		37	25	760.87	1519.71	0.01	-0.11	
		84	25	779.43	1556.82	0.01	0.11	
		28	24	848.95	1695.87	0.01	-0.95	
cathepsin L a		47	24	724.34	1446.66	0.02	0.31	-0.57
		30	21	639.03	1914.06	0.00	0.39	-0.12
cathepsin B a	proteolysis;r	45	27	438.73	875.45	0.00	-0.02	-0.39
ATP binding;r	mitochondria	53	25	757.41	1512.78	0.02	-0.11	-0.75
		26	17	917.38	1832.77	-0.03	-1.76	
identical prote	nuclear mRN	28	23	444.21	886.40	0.00	-0.83	-0.98
		47	23	472.30	942.57	0.01	-0.22	
		42	22	841.97	1681.91	0.02	0.51	
		27	23	604.66	1810.96	0.01	-0.49	
nitric-oxide sy	positive regu	53	25	757.41	1512.78	0.02	-0.11	-0.68
superoxide di		24	20	445.78	889.54	0.00	1.70	-0.37

	complement	64	25	623.31	1244.60	0.00	-0.22	-0.60
		33	24	509.92	1526.76	0.00	0.16	
protein bindin	cell motility	59	25	714.87	1427.70	0.01	-0.07	-0.82
protein bindin		51	26	617.31	1232.60	0.01	0.07	-0.12
protein bindin	sarcomere o	34	24	405.22	808.43	0.00	-0.01	-0.54
		45	26	425.73	849.45	0.00	0.59	
		56	23	532.81	1063.60	0.01	-0.04	
protein bindin	anti-apoptos	27	24	942.49	1882.94	0.01	-0.45	-0.12
		37	21	709.40	2125.15	0.01	-0.57	
protein bindin	positive regu	45	21	538.75	1075.47	0.01	-1.60	-0.15
DNA bending	anti-apoptos	23	25	640.34	1278.66	0.01	-0.26	-1.61
		83	23	507.62	1519.84	0.00	-0.19	
		60	24	668.00	2000.99	0.00	-0.48	
retinoid bindir	vitamin A me	24	25	556.78	1111.53	0.01	-0.59	-0.49
	intracellular	28	9	702.95	1403.85	0.02	0.95	-0.73
protein bindin	nuclear impo	41	25	433.89	1298.65	-0.01	-2.13	-0.90
		127	25	814.90	1627.77	0.01	-1.04	
		106	17	847.86	1693.69	0.01	-1.23	
	generation o	25	24	425.25	848.48	0.00	0.59	-0.27
cysteine-type	protein deub	27	25	448.24	894.46	0.00	1.53	-0.30
		45	19	425.77	849.52	0.00	0.39	-0.31
		61	26	472.77	943.52	0.00	0.24	
		43	26	559.79	1117.55	0.01	-0.70	
		24	23	450.92	1349.77	-0.02	-0.08	
		49	21	685.91	1369.78	0.01	0.54	
DNA binding;	nucleosome	64	22	392.74	783.46	0.01	-0.09	-0.78
		33	27	416.24	830.46	0.01	-0.39	
		43	26	422.75	843.48	0.00	-0.64	
		42	23	423.26	844.50	0.01	1.06	
		62	11	472.81	943.61	0.01	0.64	
		54	20	487.31	972.60	0.00	0.56	
		24	25	493.79	985.56	0.01	-1.26	
		64	26	554.29	1106.56	0.01	0.24	
		90	25	389.54	1165.61	-0.01	-0.53	
		77	24	599.84	1197.66	0.01	0.08	

	106	25	618.34	1234.66	0.01	-0.11	
	78	17	630.88	1259.74	0.01	0.11	
	87	22	663.89	1325.76	0.02	-0.22	
	44	25	739.88	1477.74	0.00	-0.39	
	82	24	513.61	1537.81	-0.01	-0.25	
	115	25	526.93	1577.78	0.00	-0.65	
	119	22	575.99	1724.97	-0.01	0.33	
cytochrome-c	respiratory g	27	24	657.88	1313.73	0.01	-0.51	-0.30
		27	25	541.27	1620.82	-0.02	-0.19	
	complement	52	24	881.92	1761.82	0.01	-0.58	-0.66
		55	24	937.49	1872.98	-0.02	0.39	
		26	25	494.29	986.55	0.00	0.22	-0.04
hyaluronic aci	cell adhesior	37	26	544.29	1086.56	0.01	0.59	-0.52
		25	26	609.81	1217.60	0.00	-0.78	
		69	25	657.87	1313.71	0.01	0.31	
protein bindin	epidermis de	34	24	405.22	808.43	0.00	-0.01	-0.63
		39	25	516.30	1030.59	-0.01	0.37	
		56	23	532.81	1063.60	0.01	-0.04	
		31	26	545.77	1089.52	0.00	-1.03	
		28	22	555.25	1108.48	0.00	-1.38	
		57	25	583.30	1164.58	0.00	-1.36	
		36	24	631.80	1261.59	0.00	-0.62	
		60	25	691.34	1380.64	0.02	-1.21	
		26	23	854.40	1706.76	0.02	-0.02	
protein bindin	epidermis de	25	25	556.29	1110.57	0.00	0.24	-0.43
cytokine activ	cell proliferat	35	26	522.80	1043.58	0.00	1.23	0.00
		76	24	644.36	1286.68	0.02	0.20	
		29	25	709.88	1417.72	0.03	0.34	
		37	25	503.94	1508.80	-0.01	0.33	
	protein kinas	23	26	610.31	1218.59	0.01	-0.56	-0.91
calcium ion bi	anti-apoptos	28	26	497.27	992.52	0.00	-0.51	-0.71
		23	23	594.35	1186.67	0.01	0.65	
		29	25	743.38	1484.75	0.00	-0.14	
motor activity	muscle filam	44	24	677.87	1353.73	0.01	-0.40	-0.51
cytochrome-c	electron tran	26	21	518.23	1551.67	0.00	-1.35	-0.99
N-acetylgluco	glycosamino	31	26	525.28	1048.55	0.00	0.03	-0.29

DNA binding	nucleosome	33	27	416.24	830.46	0.01	-0.39	-0.74
		62	11	472.81	943.61	0.01	0.64	
		24	25	493.79	985.56	0.01	-1.26	
		45	20	507.82	1013.62	0.00	0.25	
		47	26	547.28	1092.55	0.00	0.04	
		90	25	389.54	1165.61	-0.01	-0.53	
		41	24	606.84	1211.68	0.00	0.09	
		78	17	630.88	1259.74	0.01	0.11	
		82	24	513.61	1537.81	-0.01	-0.25	
		72	25	522.26	1563.76	-0.01	-0.79	
signal transdu	intracellular s	29	25	694.89	1387.75	0.01	0.26	-1.31
protein bindin		28	25	489.78	977.54	0.00	0.77	-0.58
DNA binding;l	anti-apoptos	26	25	578.82	1155.61	0.01	-0.78	-0.56
bisphosphogl	glycolysis	32	23	809.06	2424.15	0.00	-0.63	-0.50
protein C-tern	angiogenesis	27	22	378.74	755.45	0.00	0.62	-1.13
		49	25	469.25	936.49	0.00	0.44	
		24	26	500.77	999.53	0.00	0.36	
		37	19	384.90	1151.68	0.01	-0.41	
		30	26	580.79	1159.58	-0.01	-0.44	
		32	22	467.94	1400.80	-0.01	-0.74	
		51	23	640.35	1918.02	0.01	0.40	
		68	24	664.66	1990.98	-0.02	-0.62	
endopeptidas		25	24	669.37	1336.71	0.00	-0.12	-0.29
calcium ion bi	hyaluronan r	36	26	545.30	1088.59	-0.01	0.07	-0.28
		30	24	476.77	951.52	0.01	0.31	-0.27
		23	24	491.94	1472.80	0.00	-0.21	
extracellular r		36	25	368.21	734.41	0.00	0.67	-0.25
		53	24	504.29	1006.57	-0.01	-0.38	
		53	26	559.80	1117.58	0.01	0.64	
		48	23	656.88	1311.74	0.00	0.34	
		57	24	441.58	1321.71	-0.01	-1.13	
		31	24	510.62	1528.83	-0.01	0.31	
		31	21	676.37	2026.12	-0.02	0.00	
		74	23	1143.57	2285.14	-0.01	-0.64	
O-methyltrans		23	25	536.30	1070.60	-0.01	0.13	0.16
protein bindin	nuclear mRN	24	22	507.23	1012.44	0.01	-0.83	-0.93
		23	25	529.30	1056.58	0.01	-0.30	
		24	22	438.54	1312.59	0.00	-1.08	

	70	24	689.32	1376.62	0.01	-0.85	
	64	25	550.27	1647.80	-0.01	-1.23	
	190	18	1095.47	2188.90	0.02	-0.96	
	28	18	757.66	2269.98	-0.02	-1.02	
	37	21	791.35	2371.05	-0.01	-0.84	
protein bindin translational	26	26	674.35	1346.68	0.01	-0.05	-0.49
RNA binding;; translation	29	24	379.74	757.49	-0.01	1.47	-0.85
	29	18	487.31	972.61	0.00	0.51	
DNA bending base-excisio	49	24	494.75	1974.99	-0.02	-0.59	-1.70
FK506 bindin	35	25	666.87	1331.71	0.01	0.03	-0.20
calcium ion bi cellular calci	35	25	496.74	991.46	0.00	-2.04	-1.10
	50	24	900.93	1799.83	0.01	-2.13	
	28	27	352.20	702.39	-0.01	-2.38	-1.16
	48	20	441.28	880.54	0.00	0.38	-0.35
	49	26	709.86	1417.69	0.01	0.23	
cysteine-type protein impo	24	23	390.22	1167.66	-0.01	-0.19	-0.51
	34	26	596.30	1190.59	-0.02	-0.37	
	43	25	671.35	1340.68	0.00	-0.16	
DNA binding nucleosome	29	25	414.72	827.41	0.01	-0.81	-0.75
	50	17	477.31	952.60	0.01	0.84	
	37	26	576.29	1150.55	0.01	-0.47	
	36	26	576.29	1150.56	0.01	-0.32	
	37	25	640.33	1278.65	0.00	-0.81	
	55	24	487.94	1460.79	-0.01	-0.36	
	75	22	754.93	1507.84	0.01	-0.40	
	97	23	880.41	1758.81	-0.01	0.17	
	114	20	588.34	1762.00	-0.01	0.06	
protein bindin epidermis de	34	24	405.22	808.43	0.00	-0.01	-0.71
	108	25	616.81	1231.59	0.01	-0.16	
	55	21	618.27	1234.52	0.01	-0.72	
	114	17	896.37	1790.72	0.01	-0.74	
protein bindin	67	24	710.83	1419.65	0.00	-0.69	-1.32
	27	15	906.87	1811.72	0.01	-1.03	
	41	25	632.32	1893.93	0.01	-0.45	
	65	18	751.66	2251.97	0.00	-1.42	
histone bindir regulation of	75	26	617.32	1232.61	0.02	0.30	-1.29
	48	24	678.84	1355.65	0.00	-0.42	

protein bindin	keratinizatio	43	27	487.27	972.52	0.00	-0.38	-0.47
		37	26	519.27	1036.52	0.00	-0.50	
		72	24	738.41	1474.78	0.02	-0.92	
		57	23	692.32	1382.61	0.02	-0.47	-0.61
protein bindin		46	25	743.87	1485.71	0.02	0.26	-1.37
		35	24	808.39	1614.75	0.00	-1.27	
protein bindin	erythrocyte c	28	14	431.28	860.55	0.00	1.00	-0.61
		28	21	485.80	969.59	0.01	0.68	
		38	23	656.98	1967.92	0.01	-1.53	
	negative reg	35	24	553.82	1105.61	0.00	0.30	-0.47
		29	23	664.30	1326.58	0.01	-0.65	
		76	22	528.30	1581.88	-0.01	-0.79	
protein bindin	intracellular	30	19	390.74	779.47	0.00	0.15	-1.26
		52	25	524.94	1571.82	-0.01	-0.74	
structural con		34	24	414.76	827.49	0.00	1.52	-0.48
lamin binding		27	26	687.87	1373.71	0.01	-0.38	-0.76
		23	23	598.33	1791.95	0.00	0.01	
		23	23	857.41	2569.20	-0.01	-0.75	
RNA binding;	cell prolifera	48	23	485.23	968.44	0.00	-0.10	-0.51
		40	25	764.39	1526.74	0.02	-0.15	
mRNA bindin	translation	31	23	377.23	1128.67	-0.01	-1.41	-1.05
		25	19	419.92	1256.76	-0.01	-1.66	
protein bindin		25	25	520.26	1038.51	0.00	-0.90	-0.93
GDP-dissocia	signal transc	34	24	540.92	1619.76	-0.02	-1.60	-1.10
RNA binding;	translation	41	21	556.33	1110.64	0.01	0.94	-0.65
heparin bindir	embryo impl	37	25	466.27	930.53	0.01	-0.39	-1.09
		57	16	389.92	1166.74	-0.02	0.10	
		60	24	689.38	1376.74	0.01	0.02	
		52	23	511.95	1532.84	0.00	-0.26	
transporter ac		34	22	580.84	1159.66	0.01	0.81	-0.02
Hsp90 proteir	blastocyst de	34	24	715.35	2143.03	-0.01	-0.38	-0.83
protein kinase	signal transc	39	25	446.56	1336.66	-0.01	-0.32	-0.17

	30	25	708.89	1415.75	0.01	-0.27	
zinc ion bindir	cell prolifera	37	24	658.31	1314.60	0.00	-0.89	-0.81
collagen bindi	response to	51	25	830.43	1658.79	0.04	0.16	-0.22
receptor bindi	immune resp	38	26	560.29	1118.56	0.01	-1.15	-0.16
heparin bindir	cell prolifera	24	25	455.23	908.44	0.00	0.91	-1.34
		30	25	910.45	1818.88	0.02	-0.68	
collagen bindi	collagen fibri	34	25	364.21	726.41	0.00	0.10	-0.28
		25	24	489.29	976.56	0.00	0.37	
		66	24	512.79	1023.55	0.01	-0.08	
		49	20	406.92	1217.74	-0.01	0.35	
		38	21	820.46	1638.89	0.01	-0.81	
		45	25	834.93	1667.85	-0.01	-0.06	
		27	23	789.38	2365.10	0.02	-0.67	
extracellular r	skeletal deve	38	26	522.77	1043.51	0.02	-1.39	-0.36
		46	24	532.81	1063.58	0.01	0.59	
NADH dehydı	mitochondria	27	27	446.23	890.43	0.01	-0.20	-0.76
RNA binding		107	18	955.91	1909.78	0.01	-0.87	-0.99
adenylate kin		42	24	561.30	1680.88	0.00	-0.64	-0.28
		55	26	493.76	985.50	0.00	0.57	0.23
		59	24	559.26	1116.50	0.01	-0.57	
		46	26	571.82	1141.60	0.02	0.06	
		60	20	977.92	1953.83	0.00	0.49	
triose-phosph		25	24	477.75	953.48	0.01	0.09	-0.12
		51	26	569.29	1136.56	0.01	0.44	
		55	23	707.90	1413.78	0.01	0.20	
		32	23	801.95	1601.88	0.00	0.79	
		36	24	1096.55	2191.06	0.03	0.36	
RNA binding		28	27	352.20	702.37	0.01	-1.00	-0.24
protein bindin	induction of	38	26	460.24	918.47	0.00	0.40	-0.62
		24	25	568.95	1703.85	-0.01	0.39	
structural con	translation	39	26	525.28	1048.54	0.00	-0.23	-0.64
lysozyme acti	inflammatory	24	23	406.19	810.37	0.00	-0.63	-0.19
		25	25	700.84	1399.67	0.00	-0.60	

protein bindin	maturation o	62	25	527.79	1053.56	0.01	-0.55	-0.50
RNA binding;	translation	40	27	530.79	1059.55	0.01	-0.36	-0.71
protein bindin	translation	46	20	457.21	912.39	0.01	-0.21	-0.77
		65	25	704.85	1407.68	0.01	-1.74	
protein bindin	translation	41	22	422.27	842.52	0.00	1.11	-0.45
		49	25	416.57	1246.68	-0.01	-0.73	
		23	14	691.43	1380.85	0.00	0.38	
protein bindin	spliceosome	24	21	665.39	1328.76	0.01	1.16	-0.35
protein bindin	translation	32	24	621.35	1240.68	0.01	-0.83	-0.73
		75	26	702.86	1403.69	0.01	-0.28	
		32	24	900.99	1799.97	-0.01	0.56	
DNA binding;	establishme	45	23	495.29	988.57	0.00	1.00	-0.52
		29	25	528.27	1054.52	0.00	-0.50	
		27	25	590.82	1179.61	0.00	-0.19	
		54	24	655.86	1309.70	0.01	0.98	
		88	21	663.39	1324.75	0.01	-0.53	
		80	23	733.91	1465.80	0.01	0.56	
		75	20	494.63	1480.85	0.01	-0.83	
		52	21	789.45	1576.88	0.00	0.13	
		50	17	424.26	1693.00	-0.01	-0.19	
structural con	ribosomal pr	26	23	985.52	1969.03	-0.01	0.71	-0.19
RNA binding;	translation	46	22	542.83	1083.63	0.01	0.74	-0.86
		33	17	442.61	1324.81	-0.01	0.61	
		34	23	605.67	1813.99	-0.01	-0.14	
RNA binding;	translation	34	24	554.32	1106.61	0.01	0.81	-1.36
		30	22	412.57	1234.71	-0.01	0.38	
RNA binding;	translation	31	12	583.69	1748.07	-0.01	0.79	-0.53
unfolded prot	protein foldir	75	26	624.33	1246.62	0.01	0.15	-0.32
		52	24	460.59	1378.75	0.00	0.20	
		50	24	799.88	1597.74	0.01	0.29	
		35	24	916.47	1830.90	0.01	-0.63	
protein bindin	positive regu	68	25	657.84	1313.66	0.01	-0.49	-0.41
		55	25	596.64	1786.92	-0.02	-0.58	
protein bindin	axon guidan	27	24	383.23	764.43	0.01	1.00	-0.49
		51	23	356.54	1066.61	-0.01	0.32	
		57	20	633.37	1264.72	0.01	0.37	

	90	25	449.59	1345.74	0.00	-0.25	
	55	24	762.40	1522.77	0.01	-1.85	
	35	24	894.47	1786.92	0.01	-0.29	
	68	22	763.41	2287.22	-0.01	-0.31	
protein bindin	cell motility	55	24	488.73	975.44	0.01	-0.57	-0.20
		63	26	581.31	1160.61	0.00	0.24	
		28	25	895.94	1789.88	-0.01	-0.64	
		31	22	652.02	1953.06	-0.02	-0.27	
double-strand	regulation of	38	19	949.41	1896.80	0.01	-1.05	-1.48
		43	20	806.63	3222.52	-0.02	-1.36	
		27	21	1158.23	3471.66	0.01	-0.31	
		35	24	851.46	1700.90	0.00	0.59	-0.23
		25	23	913.00	1823.98	0.01	0.02	
hemoglobin b	nitric oxide tr	28	25	466.77	931.51	0.00	0.54	0.01
		25	22	383.89	1148.67	-0.01	1.05	
		45	21	637.87	1273.72	0.01	0.35	
		46	25	657.84	1313.66	0.00	-0.12	
		29	26	689.86	1377.69	0.01	-0.75	
		98	23	725.41	1448.79	0.01	0.58	
		88	24	557.30	1668.88	0.00	0.41	
		56	23	622.68	1865.00	0.00	-0.21	
		66	22	1029.97	2057.94	-0.01	-0.22	
		41	23	762.71	2285.10	0.02	-0.18	
protein bindin	oxygen trans	46	25	536.29	1070.55	0.01	0.40	0.05
		41	23	626.86	1251.71	-0.01	1.07	
		108	25	765.37	1528.73	0.01	-0.37	
		45	25	917.46	1832.88	0.01	-0.47	
		32	24	681.67	2042.00	0.00	-0.36	
		80	24	554.03	2212.08	-0.01	-0.77	
		36	22	753.88	3011.48	0.00	0.09	
nucleic acid b	regulation of	30	25	540.29	1078.58	0.00	0.45	-0.91
protein bindin	translation	53	25	596.83	1191.64	0.00	-0.21	-0.93
RNA binding;	translation	26	24	971.97	1941.92	0.00	-0.99	-1.11
protein bindin		44	25	522.27	1042.52	0.00	-0.12	-1.52
RNA binding	RNA proces	46	20	577.59	1729.75	-0.01	-1.56	-1.09
electron trans	caspase acti	34	25	390.21	1167.61	0.00	-0.39	-0.71
		48	24	432.91	1295.71	0.00	-0.68	

DNA binding;|	RNA proces	64	24	525.29	1572.84	0.00	0.44	-0.98
		39	25	530.28	1587.84	-0.01	-0.65	
		88	24	857.97	1713.90	0.01	0.36	
protein bindin	nuclear mRI	41	25	555.27	1662.81	-0.02	0.00	-1.06
transcription (	mRNA proce	39	26	459.76	917.50	0.00	0.20	-1.62
DNA binding;|	regulation of	50	24	570.28	1138.53	0.01	-1.53	-0.73
		35	24	579.84	1157.66	0.00	-0.09	
protein bindin	epidermis de	34	24	405.22	808.43	0.00	-0.01	-0.61
		56	23	532.81	1063.60	0.01	-0.04	
protein bindin		63	21	513.31	1024.60	0.00	0.82	-0.31
protein bindin	transforming	38	25	489.78	977.53	0.01	0.12	-0.45
	cell prolifera	31	24	490.77	979.52	0.00	-0.57	-0.26
RNA binding;|	translation	40	26	558.80	1115.58	0.01	0.50	-0.72
		23	23	730.91	1459.79	0.01	0.23	
protein bindin	mRNA splice	23	24	628.85	1255.69	0.00	0.05	-1.15
protein bindin	cellular defe	27	21	662.03	1983.09	-0.02	0.44	-0.13
microtubule b	mitosis;trans	33	22	863.89	1725.76	0.01	-0.87	-0.53
RNA binding	mRNA proce	29	24	536.26	1605.77	-0.01	-0.69	-0.59
protein bindin	mRNA splice	54	26	515.80	1029.58	-0.01	0.36	-1.55
	vesicle-medi	31	24	379.24	756.46	0.00	-0.40	-1.05
receptor bindi	cell adhesior	28	24	596.34	1190.65	0.00	0.09	-0.33
protein bindin	response to	65	20	504.56	1510.64	0.00	-1.51	-1.06
protein bindin	regulation of	44	25	744.89	1487.75	0.01	-0.33	-0.92
		26	24	586.65	1756.94	-0.01	-0.29	
		30	24	640.67	1918.98	0.00	0.18	
		35	21	950.10	2847.30	-0.02	-1.27	-1.29
protein bindin	cellular resp	25	25	395.23	788.46	-0.01	-0.17	0.07
ion transmem	cortical cytos	47	26	804.89	1607.76	0.01	-0.56	-1.02

protein bindin	lipid metabol	29	4	483.34	964.64	0.01	1.94	-0.35
prostaglandin	prostaglandi	28	25	431.88	1292.63	-0.01	0.31	-1.05
protein bindin	RNA splicing	31	26	495.75	989.47	0.01	-0.07	-1.57
proteasome a	proteasome	26	25	784.39	1566.75	0.01	-0.59	-0.31
protein bindin	mRNA proce	60	26	537.28	1072.53	0.01	-0.17	-1.40
		47	24	573.97	1718.90	0.00	-0.30	
		36	18	418.76	835.50	0.00	-0.76	-0.70
protein bindin	transcription	33	26	646.32	1290.64	0.00	-0.24	-0.74
protein bindin		38	24	394.75	787.47	0.01	-1.15	-0.60
		57	24	416.25	830.49	0.01	0.37	
		25	26	425.72	849.42	0.00	-0.76	
		34	20	480.30	958.58	0.01	-0.16	
		33	24	516.80	1031.59	0.00	-0.36	
		77	22	625.86	1249.70	0.00	-0.61	
		57	25	445.91	1334.68	0.02	-0.93	
		94	23	462.27	1383.79	-0.01	0.25	
		67	23	358.46	1429.82	-0.02	-0.56	
		25	27	408.74	815.45	0.01	-0.71	-0.82
		29	25	414.72	827.41	0.01	-0.81	-0.76
		50	17	477.31	952.60	0.01	0.84	
		37	26	576.29	1150.55	0.01	-0.47	
		36	26	576.29	1150.56	0.01	-0.32	
		37	25	640.33	1278.65	0.00	-0.81	
		75	22	754.93	1507.84	0.01	-0.40	
		97	23	880.41	1758.81	-0.01	0.17	
		114	20	588.34	1762.00	-0.01	0.06	
		28	23	535.82	1069.60	0.03	1.25	0.88
		40	24	639.36	1276.68	0.01	0.94	-0.28
		30	21	782.84	1563.66	0.01	-1.07	-0.74
		31	24	379.24	756.46	0.00	-0.52	-0.50
DNA binding	nucleosome	48	16	374.57	1120.70	-0.01	-0.48	-0.98
		31	24	604.34	1206.66	0.00	0.24	
		73	23	671.39	1340.77	0.00	0.25	
		30	24	577.98	1730.93	-0.01	-0.70	

chaperone bir	activation of	23	25	430.76	859.50	0.00	-1.13	-0.61
		67	24	710.83	1419.65	0.00	-0.69	-1.52
		29	16	583.58	1747.71	-0.01	-1.34	
gamma-gluta		27	17	570.86	1139.71	-0.01	0.59	-0.09
DNA binding	nucleosome	36	20	378.25	754.48	0.00	-0.38	-0.46
		45	19	425.77	849.52	0.00	0.39	
		61	26	472.77	943.52	0.00	0.24	
		41	25	637.85	1273.69	0.00	-0.33	
		47	26	434.23	1299.68	0.00	-1.35	
		42	22	446.26	1335.75	0.00	-0.11	
		56	15	644.39	1930.16	-0.02	0.92	
DNA binding	nucleosome	29	25	414.72	827.41	0.01	-0.81	-0.74
		50	17	477.31	952.60	0.01	0.84	
		48	25	569.28	1136.54	0.01	-0.50	
		36	26	576.29	1150.56	0.01	-0.32	
		65	26	633.33	1264.63	0.01	-0.84	
		55	24	487.94	1460.79	-0.01	-0.36	
		28	25	493.27	1476.79	-0.01	-0.03	
		75	22	754.93	1507.84	0.01	-0.40	
		97	23	880.41	1758.81	-0.01	0.17	
		114	20	588.34	1762.00	-0.01	0.06	
phosphoglucc		35	25	396.22	790.43	0.00	-0.18	-0.40
		36	20	378.25	754.48	0.00	-0.38	-0.43
		45	19	425.77	849.52	0.00	0.39	
		61	26	472.77	943.52	0.00	0.24	
		52	26	424.89	1271.67	-0.02	-1.30	
		41	25	637.85	1273.69	0.00	-0.33	
		42	22	446.26	1335.75	0.00	-0.11	
		56	15	644.39	1930.16	-0.02	0.92	
		36	20	378.25	754.48	0.00	-0.38	-0.48
		45	19	425.77	849.52	0.00	0.39	
		61	26	472.77	943.52	0.00	0.24	
		41	25	637.85	1273.69	0.00	-0.33	
		24	23	450.92	1349.77	-0.02	-0.08	
protein bindin	Ras protein	31	18	364.26	726.50	0.01	2.29	0.01
		25	22	378.24	754.46	0.00	0.66	
		30	24	553.30	1656.86	0.01	0.20	
phosphatase		50	24	379.23	756.45	0.00	0.10	-1.18
		67	25	572.32	1142.63	0.00	0.75	-0.41

		38	25	808.42	1614.83	0.00	0.38	
		42	25	540.94	1619.83	-0.03	0.49	
	axon enshea	26	23	364.22	726.44	-0.01	0.31	-0.23
		33	24	776.72	2327.16	-0.01	0.21	-0.34
	embryonic d	33	20	399.57	1195.72	-0.02	1.09	-0.05
		24	25	565.82	1129.62	0.00	0.36	-0.58
	pseudouridir	25	23	641.37	1280.73	-0.01	0.23	-0.85
		31	25	614.85	1227.71	-0.02	0.36	-0.81
		24	23	464.28	926.57	-0.02	-0.18	-0.93
RNA binding		33	16	392.26	782.50	0.01	1.37	-0.64
		27	25	671.34	1340.65	0.01	-0.62	-1.08
protein bindin		46	26	467.75	933.49	0.00	-0.24	-1.36
		32	24	650.87	1299.71	0.01	0.66	
		25	25	689.88	1377.74	0.00	-0.34	
		58	26	693.37	1384.71	0.00	0.07	
		23	24	707.89	1413.74	0.02	0.77	
		23	24	763.43	1524.82	0.02	0.51	
structural con	translation	55	24	444.92	1331.74	-0.01	0.17	-0.83
		28	25	503.29	1004.54	0.01	-0.24	-0.55
		34	24	761.42	1520.82	0.00	0.80	
protein bindin	protein targe	59	20	776.95	1551.87	0.01	0.28	-0.51
protein bindin		23	23	453.27	904.52	0.00	0.56	-0.30
guanyl-nuclec	exocytosis;ir	27	19	741.94	1481.89	-0.02	0.44	-0.26
								0.00