

Table. S1 Identification of proteins in each region of adult rat brain.

Rat brains were divided into six regions, and extracted, separated by SDS-PAGE. The samples were subjected to nano-LC-Q-TOF-MS/MS, and analyzed by Mascot search. Mascot scores were subtracted cut off scores, and the localizations and biological functions were serched by NCBI Entrez Gene

			Mascot score- cut off score=	>100	>10	>1	>0.1	>0	0			
gi(ID)	protein	Protein Mass	Tax.	Thal.	Hipp.	Frot.	Pari.	Occi.	Amyg.	Localizations	Biological functions	Representative Sequences
gil21450321	Na+/K+ -ATPase alpha 3 subunit	115894.1	M	585.9	609.4	405.8	600.2	414.1	228.5			DVAGDASESALLK
gil109504787	PREDICTED: similar to tubulin, beta 2	49776.0	R	224.6	394.1	304.5	473.6	476.1	403.8			TAVCDIPPR
gil62653035	PREDICTED: similar to Tubulin alpha-2 chain (Alpha-tubulin 2)	50247.7	R	14.9	404.5	149.4	435.0	472.5	358.7			YMACCLLYR
gil32189394	ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit precursor	56524.6	H	152.1	339.2	239.3	448.6	263.9	297.8	mitochondrion, intracellular cytoskeleton, protein complex	ATP synthesis coupled proton transport	VALVYQGMNEPPGAR
gil21361322	tubulin, beta 4	49553.9	H	162.4	205.5	169.5	305.9	414.8	254.3		microtubule-based movement	EVDEQMLSVQSK
gil9506497	clathrin, heavy polypeptide (Hc)	191476.6	R	252.7	58.0	82.3	347.5	173.6	42.6	cytoplasm, membrane coat, mitochondrion	intracellular protein transport	VANVELYYK
gil112382250	spectrin, beta, non-erythrocytic 1 isoform 1	274460.7	H	319.7	10.2	12.1	192.2	29.5		cytoskeleton, membrane	barbed-end actin filament capping	LQALDTGWNELHK
gil40254595	dihydropyrimidinase-like 2	62238.6	M	264.6	298.5	244.2	213.8	185.3	150.1	axon, cell soma, dendrite, mitochondrion	tricarboxylic acid cycle vesicle-mediated transport	SAAEVIAQAR
gil42476181	malate dehydrogenase, mitochondrial	35660.8	R	78.9	192.2	121.5	267.2	163.6	202.7	mitochondrion		IQEAGTEVVVK
gil4507297	syntaxin binding protein 1 isoform a	68692.2	H	222.8	174.8	200.4	260.7	163.0	126.0			DNALLAQLIQDK
gil40538742	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1.	59716.6	O	43.4	260.6	107.0	229.3	216.2	173.8	extracellular region, mitochondrion, intracellular	proton transport	LELAQYR
gil40538860	aconitase 2, mitochondrial	85380.0	R	250.6	70.5	91.3	35.8	20.6	90.3	mitochondrion	tricarboxylic acid cycle	ADIANLAEFEK
gil82801651	PREDICTED: similar to heat shock protein 8	70926.3	M	234.8	176.5	113.4	141.0	232.6	195.5	membrane		VCNPIITK
gil41349499	proteolipid protein 1 isoform 1	30057.1	H	207.0	175.8	140.4	226.8	187.5	81.9		GLLECCAR	
gil82954513	PREDICTED: similar to heat shock protein 8	78981.6	M	224.1	153.7	165.1	187.0	147.2	134.9			MKEIAEAYLGK
gil19705431	albumin	68674.0	R	219.8	25.1	26.0	57.8	55.3	10.4	cytoplasm, extracellular region,	body fluid osmoregulation	DNYGELADCCAK
gil63029937	heat shock protein 90kDa alpha (cytosolic), class A member 1 isoform 1	98051.5	H	215.3	74.2	139.0	89.2	28.6	114.0	cytoplasm	protein folding	ELHINLIPNK
gil13489067	N-ethylmaleimide sensitive fusion protein	82600.0	R	148.1	209.5	81.4	167.1	40.9	173.0			NIDSNPYDSDK
gil31560731	ATPase, H+ transporting, V1 subunit A, isoform 1	68282.6	M	207.3	92.8	67.1	59.4	92.8	89.0	mitochondrion, intracellular	ATP synthesis coupled proton transport, ion transport	EHMGEILYK
gil57977323	cyclic nucleotide phosphodiesterase 1	47238.6	R	207.0	152.5	46.4	202.0	147.5	62.5	membrane	microtubule cytoskeleton organization and biogenesis	HFISGDEPK
gil9507159	synapsin 1	73942.6	R	206.1	119.7	109.4	155.7	161.7	76.9	synapse	neurotransmitter secretion	QGPPQKPPGPAGPIR
gil26023949	enolase 2, gamma	47110.9	R	41.9	155.6	9.5	83.3	202.0	26.4			IEEELGEEAR
gil62657131	PREDICTED: glial fibrillary acidic protein	49926.6	R	88.2	184.0		118.2		2.6			ESASYQEALAR
gil28916677	calcium/calmodulin-dependent protein kinase II alpha isoform 2	54080.6	M	3.7	53.4	39.9	181.7	108.9	43.7	intracellular	protein amino acid phosphorylation, regulation of neurotransmitter secretion	ESSESTNTTIEDTDK
gil94410786	PREDICTED: similar to Aspartate aminotransferase, mitochondrial precursor (Transaminase A) (Glutamate oxaloacetate transaminase 2)	53390.1	O	6.7	22.3	114.7	168.1	57.6	73.4			MNLGVGAYR
gil82884353	PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	285169.7	O	164.9	11.7	82.2	120.7	47.3	32.7			SLQQLAEER
gil31981925	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	29170.4	O	160.3	135.4	91.3	111.5	100.3	161.0		protein targeting	HLIPAANTGESK

gil6754206	hexokinase 1	105506.5	M	159.7	38.9	9.3	17.5	70.0	2.8	cytoplasm, membrane, mitochondrion	glycolysis	LVPDS DVR
gil6755963	voltage-dependent anion channel 1	30736.6	M	4.5	159.3	48.5	17.1	20.5	38.0	membrane, mitochondrion	learning, synaptic transmission, transport	YQVDPDACFSAK
gil25742751	collapsin response mediator protein 1	62156.6	R	156.1	118.6	63.8	109.3	109.9	54.0	cell soma, dendrite	nervous system development	SIPHITSDR
gil6978543	ATPase, Na+/K+ transporting, alpha 1 polypeptide	112981.9	R	31.9		48.0	154.6	121.7	14.6	membrane	ATP hydrolysis coupled proton transport	LNIPVNQVNPR
gil30409956	ATPase, Na+/K+ transporting, alpha 2 polypeptide	112145.5	M	153.5	13.1	0.0	70.8	0.2	0.0	membrane	negative regulation of heart contraction, neurotransmitter uptake	DMTSEQLDEILR
gil61557085	spectrin beta 2	273416.2	R	149.7	34.6	45.4	40.4			nucleus, membrane	common-partner SMAD protein phosphorylation	ELEAESYHDIK
gil31542401	creatine kinase, brain	42685.3	R	27.8	145.2	124.3	130.3	65.0	85.5	cytoplasm, mitochondrion, membrane	brain development, phosphocreatine metabolism	LEQQQPIDDLMPAQK
gil17921989	tubulin, alpha 4a	49892.4	H		44.4	36.5	137.9	59.4	6.5	cytoskeleton, protein complex	microtubule-based movement	DVNAAIAAIK
gil9506811	internexin, alpha	56081.6	R	136.9	78.9	50.7	110.1	42.1		cytoskeleton	cytoskeleton organization, nervous system development	FANLNEQAAR
gil59853099	dynamin 1 isoform 1	97347.0	H	135.9	106.4	81.0	42.9	33.5	54.1	membrane, cytoskeleton	receptor mediated endocytosis	NLVDSYMAIVNK
gil15100179	malate dehydrogenase 1, NAD (soluble)	36460.1	R	74.0	39.3	105.2	134.0	69.0	108.5	cytoplasm		EVGVYEALK
gil82894806	PREDICTED: similar to creatine kinase, brain	44105.0	M		91.5	37.5	130.2	8.8	26.9			LLIEMEQR
gil51890229	heat shock 90kDa protein 1, beta	83264.2	R	117.6	37.5	76.6			23.5	cytoplasm, mitochondrion	protein folding	SIYYITGESK
gil51771467	PREDICTED: similar to L-lactate dehydrogenase B chain (LDH-B) (LDH heart subunit) (LDH-H) isoform 1	36674.2	O	116.1	45.6	48.4	103.9	4.0	20.1			LKDDEVAQLR
gil82893986	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	59781.4	M	7.0	11.2	56.9	115.4	62.0	16.7			GAAQNIIPASTGAAK
gil62664205	PREDICTED: similar to grp75	73698.8	R	114.7	3.3	9.4		15.5	15.6			EQQIVIQSSGGLSK
gil62657474	PREDICTED: similar to Actin, cytoplasmic 2 (Gamma-actin)	62115.1	R	102.4	69.2	12.9	102.6	114.2	76.2			EITALAPSTMK
gil31982483	calcium/calmodulin-dependent protein kinase II, beta	60456.7	M		113.7	23.9	59.0	37.8	47.2	intracellular	calcium ion transport, G1/S transition of mitotic cell cycle	GSLPAALEPQTTVIHNP
gil110347600	tubulin, beta-like	49931.0	R		86.2	48.4	113.2	70.5	111.6			VDGIK
gil18250284	isocitrate dehydrogenase 3 (NAD+) alpha	39613.1	M		10.5		113.0	45.7	19.2	mitochondrion	tricarboxylic acid cycle	INVYYNEAAGNK
gil46485440	glucose phosphate isomerase	62787.1	R	47.7	47.1	35.8	72.7	111.9	60.3			APIQWEER
gil19705578	vacuolar H+ATPase B2	56514.9	M		15.6		110.6	79.0	37.9	cytoplasm, protein complex	ATP synthesis coupled proton transport	AVVQVFEGTSGIDAK
gil8393823	neurofilament 3, medium	95591.5	R	108.1			55.4			axon, cytoskeleton	intermediate filament	EIEAEIHALR
gil6978549	ATPase, Na+/K+ transporting, beta 1 polypeptide	35210.9	R	21.5	65.7	28.8	106.7	24.2	19.2	membrane	ion transport	YNPNVLPVQCTGK
gil62643850	PREDICTED: similar to Eno1 protein	47502.3	R	6.9	59.7	61.0	105.9	59.1	62.7			SCNCLLLK
gil6756041	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	27753.7	O	86.3	99.3	104.7	103.5	95.1	89.3	mitochondrion, nucleus	protein targeting	YLAEVAAGDDKK
gil82942194	PREDICTED: similar to tubulin, alpha 1	69491.0	M	45.0	90.1	46.1	103.6	87.1	84.3			DVNAAIATIK
gil39204499	neurofilament, light polypeptide	61471.1	M	101.5	8.6		101.4	36.4		cytoskeleton	intermediate filament	TLEIEACR
gil6981146	lactate dehydrogenase B	36589.1	R	99.4	19.1	36.8	56.1	44.6	46.4	cytoplasm		MVVD SAYEVIK
gil62078615	hypothetical protein LOC299052	39467.3	R	95.9	78.9	26.0	56.2	52.5	43.5			ALANSLACQ GK
gil6980970	glutamate oxaloacetate transaminase 1	46299.4	R	76.4	29.2	29.2	94.6	62.1	65.2	cytoplasm	aspartate catabolism	ITWSNPQAQGAR
gil6978487	aldolase A	39327.3	R	1.7	94.2	7.5	0.0	8.1	55.7		fructose metabolism, striated muscle contraction	ELADIAHR
gil6978489	aldolase C, fructose-biphosphate	39259.2	R		91.5	36.3	54.7		6.7	mitochondrion	fructose metabolism	ALQASALSAWR
gil55741544	ubiquinol-cytochrome c reductase core protein II	48366.2	R	59.2	18.8		39.7	91.5		membrane, mitochondrion	electron transport	AVAFQNPQTR
gil20302061	mitochondrial ATP synthase, O subunit	23382.8	R				90.7	18.0		mitochondrion, intracellular	ATP biosynthesis, hydrogen transport	LVRPPVQVY GIEGR
gil83030135	PREDICTED: similar to Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)	33436.1	M	21.3	26.7	39.1	90.5	39.9				IAVAAQNCYK

gil5032139	synaptotagmin I	47542.8	H	35.4	67.1	42.9	64.9	45.6	87.4	membrane, synapse	regulation of exocytosis, synaptic transmission	VPYSELGGK
gil56090293	pyruvate dehydrogenase (lipoamide) beta	38957.0	R				86.8	3.8	25.6	mitochondrion	glycolysis	EGIECEVINLR
gil19923985	RAB3C, member RAS oncogene family	25935.6	H	4.7	21.0		86.4		0.5	membrane	small GTPase mediated signal transduction	TITTAAYR
gil8393910	phosphatidylethanolamine binding protein	20788.4	R		36.1		86.2	47.7		cell surface	negative regulation of MAPKKK cascade, spermatid development	GNDISSGTVLSEYVGS GP PK
gil13177775	glutamate dehydrogenase 2	61395.4	H	84.9	14.1		33.4	0.9	33.5	mitochondrion	electron transport, glutamate metabolism	ALASLMTYK
gil33286420	pyruvate kinase 3 isoform 2	58024.9	H	22.5	81.8	47.3	49.6	56.4	43.2	cytoplasm	glycolysis	GSGTAEVELK
gil9507135	beta-spectrin 3	270768.9	R				81.5			cytoplasm, cytoskeleton, membrane, nucleus	barbed-end actin filament capping, vesicle-mediated transport	ALAQEDQSAGEVER
gil7305305	N-myc downstream regulated gene 2	40763.2	M	80.4	27.6		48.5		1.2		cell differentiation, nervous system development	TASLTSAA SIDGSR
gil109506410	PREDICTED: similar to myosin-VIIb	304679.2	R		79.0	58.3	60.3	60.4	66.5			DLTDYLMK
gil4506367	RAB3A, member RAS oncogene family	24968.1	H		24.4		78.0		58.8	membrane, cytoplasm	exocytosis, neurotransmitter secretion, small GTPase mediated signal transduction	QLADHLGFEFF EASAK
gil117935064	triosephosphate isomerase 1	26903.8	R	28.6		50.9	19.8	77.3	15.9		fatty acid biosynthesis, gluconeogenesis,	HIFGESDELIGQK
gil29788785	tubulin, beta polypeptide	49639.0	H	27.5	49.3	75.1	62.8	48.3	52.9	cytoplasm, cytoskeleton, protein complex	microtubule-based movement, natural killer cell mediated cytotoxicity	ISVYYNEATGGK
gil62641274	PREDICTED: similar to Tu translation elongation factor, mitochondrial	49391.0	R	20.9	74.7		12.6					AEAGDNLGALVR
gil6753428	creatine kinase, mitochondrial 1, ubiquitous	46974.2	M		62.3	9.0	74.7	66.8	1.6	mitochondrion		GTG GVDTAATG SVF DIS NLDR
gil27369581	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	74522.7	M	25.1	48.5	5.3	72.3	74.4		membrane, mitochondrion		GTGSVVGELMYK
gil13929094	guanine deaminase	50983.8	R		71.7			19.8	3.3	extracellular region, intracellular	nervous system development, nucleotide and nucleic acid metabolism	DHLLGVSDSGK
gil13386272	citrate synthase-like protein	52319.9	M	28.6	0.8	35.4	41.7	71.5	53.8	cytoplasm	tricarboxylic acid cycle	GYSIPECQK
gil62651904	PREDICTED: tumor rejection antigen gp96 (predicted)	92713.4	R	35.4	70.9	33.0						ELISNASDALDK
gil109472265	PREDICTED: similar to CD207 antigen, langerin	61380.7	R	69.6	44.0	50.5		37.9	53.7			IVSNASCTTNCLAPLAK
gil6679651	enolase 3, beta muscle	46995.3	M	69.0	69.1		33.7	18.6		cytoplasm		VNQIGSVTESIQACK
gil29789026	neurofilament, heavy polypeptide	115279.3	R	68.9			1.0	4.6		axon, cytoskeleton, mitochondrion	intermediate filament cytoskeleton organization and biogenesis, nervous system development	WEMAAQLR
gil6981654	thymus cell antigen 1, theta	18160.7	R			13.8	66.6	10.0	32.1	cell surface, cytoplasm, growth cone, membrane	angiogenesis, cell-cell adhesion, cytoskeleton organization and biogenesis, focal adhesion formation, positive regulation of GTPase activity, positive regulation of peptidyl-tyrosine phosphorylation	DEGDYMCEL R
gil119874213	heat shock 70kDa protein 12A	74848.0	H	19.3	38.8		66.2	21.8	4.5			ETAPT SAYSSPAR
gil21464101	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	28284.9	O	57.2	47.1	52.3	42.9	64.0	52.9	cytoplasm	cytoskeleton organization and biogenesis, negative regulation of protein kinase activity, regulation of neuron differentiation	YLAEVATGEK
gil12963799	ATPase, H+ transporting, V1 subunit D	28351.4	M				63.3			cytoplasm	ATP synthesis coupled proton transport	FTAGDFSTTVIQNVNK
gil4507951	tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypeptide	28201.0	H	40.9	35.6	8.6	50.9	62.7	53.5	cytoplasm	glucocorticoid receptor signaling pathway, regulation of dendrite morphogenesis, negative regulation of protein kinase activity, regulation of mitosis, regulation of neuron differentiation	NCNDFQYESK
gil89030116	PREDICTED: similar to tubulin, beta 8 isoform 1	53635.0	H	29.1	43.3	29.8	32.1	61.6	38.5			FPGQLNADLR
gil56605812	sirtuin (silent mating type information regulation 2 homolog) 2	39293.8	R	61.3	32.5		41.9			cytoplasm, cytoskeleton, nucleus	cell cycle, histone deacetylation, negative regulation of striated muscle development, redox signal response	EHANIDAQSGSQASNPSA TVSPR
gil62665891	PREDICTED: similar to pyruvate kinase (EC 2.7.1.40) isozyme M2 - rat	57840.1	R	17.7	25.4	27.8	61.2	24.5	14.7			VNLAMNVGK
gil19526818	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	39606.5	M	9.0	28.6		20.4	13.1	60.5	membrane, mitochondrion	transport	GSTASQVLQR

gil6754012	guanine nucleotide binding protein, alpha o	40058.9	M	25.2	21.8	4.6	60.5	0.6	18.9	membrane	dopamine receptor signaling pathway,locomotory behavior	IIHEDGFSGEDVK
gil88953559	PREDICTED: similar to Prostate, ovary, testis expressed protein on chromosome 2 isoform 1	121366.7	O	53.5	47.2	26.0	59.4	59.3	55.0			AGFAGDDAPR
gil4503571	enolase 1	47139.3	H	52.9	59.0			41.8		cytoplasm, nucleus	glycolysis, regulation of transcription, DNA-dependent, transcription	YNQLLR
gil39930503	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit	32975.1	R			37.6	32.5	22.6	58.9	mitochondrion, intracellular	ion transport, oxidative phosphorylation, proton transport	THSDQFLVSFK
gil13591874	guanine nucleotide-binding protein, beta-1 subunit	37363.0	R				57.7			membrane	acetylcholine receptor signaling, Ras protein signal transduction, sensory perception of taste	ACADATLSQITNIDPVG
gil4885063	fructose-bisphosphate aldolase C	39431.2	H	38.8	57.5		33.8	57.5	43.5		fructose metabolism	R DNAGAATEEFIK
gil33469051	tubulin polymerization-promoting protein	23560.2	M		3.3		56.6	7.7				VDLVDESGYVPGYK
gil76559899	glutamine synthetase 1	46456.4	R	30.6	56.6	16.8	39.0	36.1		mitochondrion	ammonia assimilation cycle, regulation of neurotransmitter levels	DIVEAHYR
gil62644670	PREDICTED: hypothetical protein XP_579688	284462.3	R	46.3	21.2	18.6	55.5					VNEVNQFAAK
gil73486658	aspartate aminotransferase 2 precursor	47487.3	H				54.0	19.1		mitochondrion	aspartate catabolism, biosynthesis	ASAELALGENSEVLK
gil82801095	PREDICTED: similar to Fructose-bisphosphate aldolase A (Muscle-type aldolase)	11133.8	M		53.9		23.4		1.5			FSNEEIAMATVTALR
gil31982681	sirtuin 2 (silent mating type information regulation 2, homolog 2)	43238.5	M	53.7	47.8		43.0			cytoplasm, cytoskeleton	cell division, histone deacetylation, mitosis, negative regulation of striated muscle development, redox signal response	FFSCMQSDFSK
gil8394331	superoxide dismutase 2	24658.6	R				53.0	36.6	31.9	mitochondrion	regulation of transcription from RNA polymerase II promoter,response to superoxide	AIWNVINWENVSQR
gil57977273	phosphofructokinase, platelet	85665.4	R	52.7	35.5					cytoplasm		NVLGHMQQGAPSPFD
gil40556608	heat shock protein 1, beta	83229.1	M	52.7		25.7			3.5	mitochondrion	protein folding, response to heat	R IDIIPNPQER
gil88947784	PREDICTED: similar to Triosephosphate isomerase (TIM) (Triose-phosphate isomerase) isoform 3	26982.0	O	39.2	41.7	52.5	41.9	45.3	39.2			IHYGGSVTGATCK
gil31981722	heat shock 70kD protein 5 (glucose-regulated protein)	72378.4	M	18.7	45.8	51.9	36.3	0.9		endoplasmic reticulum	ER overload response, protein folding, response to unfolded protein	NQLTSNPENTVFDAK
gil41281685	guanine nucleotide binding protein, alpha activating polypeptide O	40047.1	H		6.9	3.7	18.5	23.5	51.9		muscle contraction, nervous system development	IGAADYQPTEQDILR
gil11693170	2-oxoglutarate carrier	34221.9	R			9.5	51.8		18.8	membrane, mitochondrion	transport	GIYTGLSAGLLR
gil6715568	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)	58650.3	O		34.5	32.6	17.4	51.7		protein complex, nucleus	protein amino acid dephosphorylation	GLTPTGMPLSPGVLSGGK
gil34856315	PREDICTED: similar to ATPase, H+ transporting, V1 subunit B, isoform 1	56814.7	R	25.8	12.1			51.4	6.8			TPVSEMDLGR
gil13928706	neural cell adhesion molecule 1	94599.2	R	5.3		0.5	51.0	16.2		extracellular region, growth cone, membrane	calcium-independent cell-cell adhesion, synaptic transmission	FFLCQVAGDAK
gil25453412	glutathione S-transferase, pi 2	23424.1	R				49.7					EAAALVDMVNDGVEDLR
gil62655013	PREDICTED: hypothetical protein XP_579451	60967.3	R		27.8		49.5		13.9			ISSVQSIVPALEIANHR
gil21704020	NADH dehydrogenase (ubiquinone) Fe-S protein 1	79697.5	M	49.2			2.0			mitochondrion		GNDMQVGTYIEK
gil14149619	glycoprotein M6A isoform 1	31188.4	H	18.3	3.9	32.1	34.8	48.9	19.7	cell surface, membrane		SKEEQELHDIHSTR
gil109505185	PREDICTED: similar to tubulin, alpha-like 3 solute carrier family 1 (glial high affinity glutamate transporter), member 2 isoform a	74401.0	R		48.7							SFGGGTGSFGFTSLLMER
gil78126167	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic dynactin 1	62079.7	O	20.1	43.6	14.6	48.2	29.5	35.3	dendrite, membrane, synapse	glutamate transport	SELTIDSQHR
gil6679939	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	47412.1	M	41.6	34.9	47.0	48.2	43.2	32.8	flagellum (sensu Eukaryota)	positive regulation of glycolysis, sperm motility	VPTPNVSVDLTCR
gil13162302	dynactin 1	141842.0	R	48.1						cytoskeleton	microtubule-based process	AEITDAEGLGLK
gil61098212	ubiquitin carboxy-terminal hydrolase L1	24822.4	R	48.0	27.8	42.4	18.5	34.0	5.6	axon, cell soma, cytoplasm	adult walking behavior, eating behavior, protein deubiquitination, response to stress, sensory perception of pain, ubiquitin cycle	MQLKPMEINPEMLNK

gil25742568	dihydropyrimidinase-like 3	61928.0	R	47.7	40.7							growth cone, vesicle	axon guidance, neurite development, vesicle-mediated transport	SAADLISQAR
gil48255951	plasma membrane calcium ATPase 2 isoform a	136789.4	H					47.7	1.1			membrane		ADVGFAMGIAGTDVAK
gil34869154	PREDICTED: similar to ATPase, H+ transporting, V1 subunit A, isoform 1	68221.6	R	11.9	10.5	2.4	47.6							LSMVQVWPVR
gil16418379	syntaxin 1B2	33223.8	H	47.5			11.5					membrane	neurotransmitter transport	QALNEIETR
gil51944966	ATPase, H+/K+ exchanging, alpha polypeptide	114045.2	H	47.5					43.2			membrane	potassium ion transport	VDNSSLTGESEPQTR
gil113199771	myelin oligodendrocyte glycoprotein	28252.8	M	47.5			28.4	26.4				membrane		ALVGDEAELPCR
gil109480990	PREDICTED: similar to SH3-domain binding protein 1 (3BP-1)	95625.6	R							47.3				TPGTGSLAAAVETASGR
gil70794816	hypothetical protein LOC433182	47111.2	M		47.1	27.1	11.5	37.2	36.4					YITPDQLADLYK
gil10092608	glutathione S-transferase, pi 1	23594.1	M				47.0						glutathione metabolism	FEDGDLTYQSNAILR
gil17105366	synaptic vesicle glycoprotein 2a	82652.0	R	46.8			12.0					membrane, synapse	neurotransmitter transport	GGLSDGEGPPGGR
gil4504067	aspartate aminotransferase 1	46218.5	H	46.7	8.8		7.0	32.0	25.4			cytoplasm	aspartate catabolism, biosynthesis	VGGVQSLGGTGALR
gil21735621	mitochondrial malate dehydrogenase precursor	35480.7	H			46.4						mitochondrion	glycolysis, malate metabolism, tricarboxylic acid cycle	VDFPQDQLTALTGR
gil28460695	eukaryotic translation elongation factor 1 alpha 2	50118.1	R	45.6	26.2		28.8	20.5	15.2					MDSTEPYSQK
gil31560513	neurochondrin	78860.7	M	37.6	44.7		16.1	19.4				cellular_component	bone resorption	LLSTSPALQGTPASR
gil61556754	B-cell receptor-associated protein 37	33291.9	R	44.7					3.9			membrane, mitochondrion, nucleus	regulation of transcription, DNA-dependent, signal transduction	IVQAEGEAAEAAK
gil51948476	ubiquinol-cytochrome c reductase core protein I	52815.4	R	44.7	19.6	30.6	36.6	19.2				mitochondrion, protein complex	mitochondrial electron transport, ubiquinol to cytochrome c	MVLAAAGGVK
gil51766670	PREDICTED: similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin	61016.5	O	34.1	44.3		37.6	42.1						VGGTSDVEVNEK
gil51708092	PREDICTED: similar to phosphoglycerate kinase 1	44522.0	M	44.2	44.2		8.2	43.5						SLMDEVVK
gil4505621	prostatic binding protein	21043.7	H		30.1		43.7							LYTLVLTDPDAPSR
gil28467005	heat shock protein 1, alpha	84761.8	R	43.7				0.8				cytoplasm	protein folding, response to unfolded protein	HIYFITGETK
gil55926203	isocitrate dehydrogenase 3 (NAD+) beta	42326.8	R	43.6			23.3					extracellular region, mitochondrion,	metabolism, tricarboxylic acid cycle	HPFAQAVGR
gil20357529	guanine nucleotide-binding protein, beta-2 subunit	37307.1	H			14.2	43.2	32.8	16.4				signal transduction	TFVSGACDASIK
gil11055998	guanine nucleotide-binding protein, beta-4 subunit	37543.0	H	25.2	29.0	43.1	42.6		26.2				signal transduction	LLVSASQDGK
gil15991831	hexokinase 1 isoform HKI-ta/tb	102672.2	H	42.9			4.2	16.1				membrane	glycolysis	FNTSDVSAIEK
gil16923964	contactin 1	113423.1	R	42.5			33.2	2.1	19.2			extracellular region, membrane,	cell adhesion, DNA methylation, Notch signaling pathway	IVESYQIR
gil83030206	PREDICTED: similar to tubulin, beta 3	49969.9	M	28.6	21.5		42.4	30.3						EVDEQMLAIQSK
gil82534351	microtubule-associated protein tau isoform 1	78853.8	H	42.1					6.8			axon, cytoskeleton, cytoplasm, growth cone, membrane	generation of neurons, negative regulation of microtubule depolymerization, positive regulation of axon extension	TPSLPTPTR
gil88957916	PREDICTED: similar to 14-3-3 protein epsilon (14-3-3E) (Mitochondrial import stimulation factor L s	29584.7	O	7.5	34.0	5.0	41.9	9.2	35.4					IISIEQK
gil114326546	phosphoglycerate mutase 1	28918.9	M	16.9	14.6		41.8						glycolysis, metabolism	FSGWYDADLSPAGHEEA K
gil6678551	vesicle-associated membrane protein 2	12682.7	M						41.6			membrane, cytoplasm, synapse, synaptosome	calcium ion-dependent exocytosis	ADALQAGASQFETSAK
gil11321585	guanine nucleotide-binding protein, beta-1 subunit	37353.0	H	25.3	21.7	21.9	41.3	14.9	22.0				signal transduction	LFVSGACDASAK
gil5174735	tubulin, beta, 2	49799.0	H	30.4	41.2	26.6	35.9	34.3	26.0			cytoplasm, cytoskeleton, protein complex	natural killer cell mediated cytotoxicity, protein polymerization	INVYYNEATGGK
gil6756039	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	27760.8	O		39.5		41.0	12.6	36.2			cellular_component	small GTPase mediated signal transduction	AVTEQGAELSNEER
gil9507115	solute carrier family 1 (glial high affinity glutamate transporter), member 3	59644.7	R				39.3		41.0			cell projection, cell soma, dendrite, membrane, synapse	dicarboxylic acid transport, neurotransmitter uptake	IVQVTAADAFLDLIR

gil117938759	guanine nucleotide binding protein, alpha stimulating activity polypeptide 1 isoform c	97700.5	O		40.6	14.8	31.5	13.9	21.6	cytoplasm, extracellular region, membrane	G-protein coupled receptor protein signaling pathway, pregnancy, protein secretion	LLLLGAGESGK
gil6978771	dynamain 2	98169.1	R	2.7	40.6		18.3	31.9	4.2	cytoplasm, cytoskeleton, membrane	endocytosis, G2/M transition of mitotic cell cycle, synaptic vesicle transport	GYIGVVNR
gil13591886	microtubule-associated protein 1 A	299348.3	R	40.6						cytoplasm, cytoskeleton	negative regulation of microtubule depolymerization, sensory perception of sound	DTDLQQTQATEPR
gil77917546	inner membrane protein, mitochondrial	67135.2	R	38.8						mitochondrion		SLEDALNQTATVTR
gil62657757	PREDICTED: similar to pyruvate kinase 3	84872.1	R	1.3	38.7	2.5	31.3	10.0				IQLINNMLDK
gil82973377	PREDICTED: synaptojanin 1	187522.9	M	7.4			38.6					VSEQTLQSASSK
gil21361657	protein disulfide isomerase-associated 3 precursor	56746.8	H	38.6			6.6			endoplasmic reticulum	protein import into nucleus, protein retention in ER, signal transduction	DGEEAGAYDGPR
gil78711838	adaptor-related protein complex 2, beta 1 subunit isoform a	105654.6	M		8.0			38.6		cytoplasm	intracellular protein transport, protein complex assembly	LHDINAQMVEDQGFLDS LR
gil62645998	PREDICTED: similar to N-ethylmaleimide sensitive fusion protein attachment protein beta	39865.8	O		38.1		1.6		26.3			VAAYAAQLEQYQK
gil19705465	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	28850.5	R	23.2	37.4			14.9	6.7	mitochondrion, intracellular	ion transport, proton transport	HVIQSISAQQEK
gil54020666	isocitrate dehydrogenase 3, gamma	42823.2	R				37.4			mitochondrion	negative regulation of growth, tricarboxylic acid cycle	LGDGLFLQCCR
gil89035672	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-d	28831.8	O				37.3					ALPFWNEEIVPQIK
gil8393502	glutathione S-transferase, mu 1	25897.1	R		37.2	13.8		6.3	11.6	extracellular region	sensory perception, sensory perception of smell	LLLEYTDSSYEEK
gil8394027	alpha isoform of regulatory subunit A, protein phosphatase 2	65280.9	M				37.1			cytoplasm		IGPILDNSTLQSEVKPILE K
gil67078422	thioredoxin domain containing 1	31414.7	R	36.7							electron transport	VDVTEQTGLSGR
gil62638908	PREDICTED: similar to tweety 1	49001.1	R						36.6			TELTITLEEVLSEIR
gil34866853	PREDICTED: similar to cytochrome c-1	35412.0	R				35.8					GLLSSLDHTSIR
gil34538601	cytochrome c oxidase subunit II	25959.0	M					35.7	22.6			ILYMMDEINNPNVLTVK
gil82917120	PREDICTED: similar to cytoplasmic beta-actin isoform 2	26448.2	M			35.5						QEYDESGPSIVHR
gil109465389	PREDICTED: similar to Moloney leukemia virus 10	113629.0	R				35.0		5.3			LLLNNNDNLLR
gil82942469	PREDICTED: similar to tubulin, alpha 1	54777.3	M		13.5	18.7	34.9	19.0	13.5			QLFHPEQLITGK
gil32189355	solute carrier family 25, member 4	32968.2	R		21.8	18.0	21.0	34.6	3.3	membrane, mitochondrion	ADP transport, ATP transport, glutamate uptake during transmission of nerve impulse, mitochondrial genome maintenance, transport	AAYFGVYDTAK
gil9507167	synaptogyrin 1	25652.3	R	21.0	8.7	4.9	34.5	9.9		membrane, synapse	protein targeting	DNPLNEGTDAAAR
gil62234487	plasma membrane calcium ATPase 1	134661.9	M	34.4	7.7		19.4	15.2		membrane		QVVAVTGDGTNDGPALK
gil27702072	PREDICTED: similar to NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor (Compl	30207.6	O			34.3			3.8			SLADLTAVDVPTR
gil31377489	dynein, cytoplasmic, heavy chain 1	531915.8	R	34.1			7.0			cytoskeleton	microtubule-based movement, proteolysis	VQGLTVEQAEAVAR
gil4505685	pyruvate dehydrogenase (lipoamide) alpha 1	43267.6	H		31.7	11.1	10.5		34.0	mitochondrion	acetyl-CoA metabolism, glycolysis, metabolism	LEEGPPVTTLTR
gil53692187	actin-related protein 2 isoform a	45347.6	H		33.8				16.6	cytoskeleton		LCYVGYNIEQEOK
gil82887201	PREDICTED: similar to Tubulin alpha-2 chain (Alpha-tubulin 2)	28075.8	M						33.7			MVDNEAIYDICR
gil11321583	succinate-CoA ligase, ADP-forming, beta subunit	50285.2	H	33.6	13.6			15.3		mitochondrion	succinyl-CoA pathway	ICNQVLVCER
gil45504359	vacuolar H+ ATPase E1	26140.8	M	11.7	4.9	7.0	33.6		24.5	cytoplasm, mitochondrion, protein complex	ATP synthesis coupled proton transport,	LDLIAQQMMPEVR
gil58743306	alpha-tubulin isotype H2-alpha	49987.7	H				33.2	1.1	21.8	cytoskeleton, protein complex	microtubule-based movement, protein polymerization	LIGQIVSSITASLR

gil6679299	prohibitin	29801.9	M	33.1							membrane, mitochondrion	DNA replication	IYTSIGEDYDER
gil4502855	sarcomeric mitochondrial creatine kinase precursor	47490.4	H		20.4	0.0	33.1	25.8	12.9		mitochondrion	generation of precursor metabolites and energy, muscle contraction	LGYILTCPSNLGTGLR
gil82884325	PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	60279.1	O			16.8	32.7	9.7					DLSSVQTLTK
gil16757994	pyruvate kinase, muscle	57780.9	R	32.5	10.4	5.8	6.2	7.1			cytoplasm, mitochondrion	glycolysis	EAEAAVFHR
gil18543177	citrate synthase	51833.5	R	31.7	32.5		12.9	4.6	13.5		mitochondrion		EGSSIGAIDSK
gil61097906	actinin, alpha 1	103003.6	M				32.3				cytoskeleton, cytoplasm, membrane	cortical cytoskeleton organization and biogenesis	GISQEQMNEFR
gil23346461	NADH dehydrogenase (ubiquinone) Fe-S protein 2	52591.7	M		31.8						mitochondrion	electron transport	APGFAHLAGLDK
gil4506931	SH3-domain GRB2-like 2	39937.1	H		28.5		31.6	2.4	30.8		cytoplasm	central nervous system development	QAVQILQQVTVR
gil9506445	carbonic anhydrase 2	29095.6	R	31.5				2.2			cytoplasm	carbon dioxide transport, morphogenesis of an epithelium, osteoclast differentiation	IGPASQGLQK
gil13786202	voltage-dependent anion channel 2	31725.6	R	1.6		29.3	31.5	30.3	26.0		mitochondrion	anion transport	LTFDITFSPNTGK
gil109487858	PREDICTED: similar to Synaptogyrin 3	24497.4	R	31.1									TAPGPGTAQAGDAAR
gil109475599	PREDICTED: similar to 14-3-3 protein sigma (Stratifin)	36725.0	R		30.7	9.9	29.6	5.8	10.0				NLLSVAYK
gil6679186	claudin 11	22099.3	M	30.0	17.5		30.6				membrane	axon ensheathment, calcium-independent cell-cell adhesion, cell adhesion, spermatogenesis	FYYSSGSSSPTHAK
gil9506411	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	18751.6	R				30.5		7.8		mitochondrion, intracellular	ion transport, proton transport	NCAQFVTGSQAR
gil7657116	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	44472.8	H		30.4			20.4				positive regulation of glycolysis, sperm motility	VPTPDVSVVDLTCR
gil14043072	heterogeneous nuclear ribonucleoprotein A2/B1 isoform B1	37406.7	H			7.9	29.6	11.9	30.1		nucleus	nuclear mRNA splicing	IDTIEITDR
gil34419635	heat shock 70kDa protein 6 (HSP70B')	70984.2	H	12.0	13.8	11.9	13.0	14.4	29.8			protein folding	TTPSYVAFTDTER
gil45598372	brain abundant, membrane attached signal protein 1	22073.6	M	0.0	1.0	23.5	29.1	4.8					ESEPQAAADATEVK
gil16758892	calbindin 2	31384.5	R	28.2							membrane		EMNIQQLTTYR
gil41393608	reticulon 3 isoform b	110583.5	H				27.7		2.7		endoplasmic reticulum, extracellular region, membrane		TQIDHYVGIAR
gil23510338	ubiquitin-activating enzyme E1	117774.3	H	9.3	27.5							DNA replication, ubiquitin cycle	LAGTQPLEVLEAVQR
gil40445397	beta-glo	16027.2	R						27.4				VVAGVASALAHK
gil13591955	guanine nucleotide binding protein, alpha inhibiting 2	40473.1	R		27.4							acetylcholine receptor signaling, adenylate cyclase inhibiting pathway,	LFDSICNNK
gil29788768	tubulin, beta polypeptide paralog	49920.9	H	27.3	8.4			20.7			cytoplasm, cytoskeleton, protein complex	microtubule-based movement	INVYYNEATGNK
gil82884323	PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	147141.8	O	12.7	8.0	27.2	19.7	5.1					EELYQNLTR
gil109507853	PREDICTED: similar to vacuolar protein sorting 35	91668.8	R	27.1									EDGPGIPAEIK
gil45827776	reticulon 1 isoform C	23560.6	H				26.8				endoplasmic reticulum, membrane	neuron differentiation	SQAIDLLYWR
gil82884343	PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	235125.0	O	26.4	4.2								DLTNVQNLQK
gil15147224	sideroflexin 1	35626.3	M						26.3		membrane, mitochondrion	cation transport, erythrocyte differentiation	NILLTNEQLENAR
gil11560135	brain abundant, membrane attached signal protein 1	21777.4	R				20.3		25.8		membrane, nucleus	regulation of transcription	AGEASAESTGAADGAPQ
gil4758788	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	30222.7	H				25.7				membrane, mitochondrion	mitochondrial electron transport, NADH to ubiquinone	VVAEPVELAQEFR
gil8567390	pyruvate kinase liver and red blood cell	62269.6	M		25.5								GDLGIEIPA EK
gil9257192	adducin 2 isoform a	80803.4	H				25.3				cytoskeleton, membrane		VNVADEVQR

gil4503875	glutamate decarboxylase 2 PREDICTED: similar to Carcinoembryonic antigen-related cell adhesion molecule 1 precursor (Biliary glycoprotein 1) (BGP-1) (Murine hepatitis virus receptor) (MHV-R) (Biliarv glycoprotein D)	65368.5	H	25.1						membrane	glutamate decarboxylation to succinate	HYDLSYDTGDK
gil94380294		108834.8	M	25.0								EIDGGLETLR
gil62654759	PREDICTED: phosphoglycerate kinase 2 (predicted)	44981.3	R	3.7	24.7		11.7	24.9	16.0			VDFNVPMK
gil4507191	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	284107.1	H	24.8	0.8					cytoskeleton, membrane	barbed-end actin filament capping	LSDDNITIGKEEIQQR
gil82999838	PREDICTED: similar to zinc finger protein 161	33185.2	M				24.5					LTLSALLDGK
gil4506713	ubiquitin and ribosomal protein S27a precursor	17953.5	H				11.1		24.5	cytoplasmic small ribosomal subunit	protein biosynthesis, protein modification	TITLEVEPSDTIENVK
gil62642907	PREDICTED: similar to Phosphoglycerate kinase 1	43148.3	R				24.1	20.6				ALESPERPFMAILGGAK
gil5031857	lactate dehydrogenase A	36665.4	H				24.0		5.1	cytoplasm, cytosol	tricarboxylic acid	SADTLWGIQK
gil62662610	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	31224.5	R		24.0							VVDLMSYMASK
gil6679599	RAB7, member RAS oncogene family	23543.9	M				23.8			Golgi apparatus, cytoplasm, membrane cytoskeleton	small GTPase mediated signal transduction, transport	EAINVEQAFQTIAR
gil5031573	ARP3 actin-related protein 3 homolog	47341.0	H	23.6							cell motility	LPACVVDCGTGYTK
gil11125772	myristoylated alanine-rich protein kinase C substrate	31525.8	H	19.1			23.6	7.3	6.6	cytoskeleton, membrane		GEAAAERPGEAAVASSPSK
gil12711692	dihydropyrimidinase-like 5	61501.2	R		23.4					cell soma, cytoplasm, dendrite, protein complex	axon guidance, nervous system development	TPYLGDVAVVVNPGK
gil109506701	PREDICTED: similar to Gamma-soluble NSF attachment protein (SNAP-gamma) (N-ethylmaleimide-sensitive	144886.5	O				23.2					LPEAVQLIEK
gil14165437	heterogeneous nuclear ribonucleoprotein K isoform a	50996.4	H	23.0				13.0		nucleus, ribonucleoprotein complex	DNA-dependent, transcription	TDYNASVSVPDSSGPER
gil6671664	calnexin	67235.7	M	23.0						endoplasmic reticulum, membrane	protein folding	IADPDVAVKPPDDWDEDAPSK
gil109510373	PREDICTED: similar to NF-kappaB repressing factor	143912.0	O		14.0		22.8					VNIIPIIAK
gil62639687	PREDICTED: similar to Adapter-related protein complex 2 alpha 1 subunit (Alpha-adaptin A) (Adaptor	107597.9	O	7.5			22.8					YLETADYAIR
gil13591900	4-aminobutyrate aminotransferase	56418.5	R	4.9				22.4		mitochondrion, protein complex	behavior, gamma-aminobutyric acid catabolism	ESLMSVAPK
gil34859236	PREDICTED: similar to Proteasome subunit beta type 3 (Proteasome theta chain) (Proteasome chain 13)	23030.5	O				22.4					FGPYYTEPVIAGLDPK
gil33563256	guanine nucleotide binding protein, alpha inhibiting 3	40512.2	M				20.1	22.3	10.4	cytoplasm, Golgi apparatus, membrane	G-protein coupled receptor protein signaling pathway, regulation of heart contraction	TTGIVETHFTFK
gil6753966	glycerol-3-phosphate dehydrogenase 1 (soluble)	37548.4	M	22.3						cytoplasm, protein complex	glycerol-3-phosphate metabolism	FCETTIGCK
gil5032007	purine-rich element binding protein A	34889.4	H		2.3	2.1		22.1	0.9	nucleus	G1/S transition checkpoint, DNA-dependent, transcription	FFFDVGSNK
gil6754658	Golli-mbp isoform 1	27151.4	M	21.8			15.2				myelination	TTHYGSLPQK
gil62653460	PREDICTED: similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M)	36489.3	O	0.5		8.3	12.4		21.8			VTLTPEDEAR
gil10946936	adenylate kinase 1	23101.8	M		21.7		15.2			cytoplasm, mitochondrion, membrane	ATP metabolism, cell cycle arrest	IIFVVGGPGSGK

gil14210536	tubulin, beta 6	49825.0	H		6.1		21.6			cytoplasm, cytoskeleton, protein complex	microtubule-based movement, protein polymerization	GHYTEGAELVDAVLDVVR
gil62650366	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	76910.9	R	3.7		5.9	21.2	14.7	15.0			VVDLMAYMASK
gil62665162	PREDICTED: ATPase, H+ transporting, V0 subunit D isoform 1 (predicted)	51009.9	R	21.2	12.8	16.7	5.9		4.7			LLFEGAGSNPGDK
gil82996621	PREDICTED: similar to Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)	23903.1	M				21.1					VVLAYELVWAIGTGK
gil6752952	actin, gamma 2, smooth muscle, enteric	42852.3	M		7.1	2.9	21.1	2.7		cytoskeleton	cytoskeleton organization and biogenesis	YPIEHGIITNWDDMEK
gil47933379	N-ethylmaleimide-sensitive factor attachment protein, alpha	33211.3	H	21.1					3.0	endoplasmic reticulum, Golgi apparatus	ER to Golgi vesicle-mediated transport	TIQGDEEDLR
gil69885032	myelin basic protein isoform 1	21489.0	M	20.8							myelination	GAYDAQGTLSK
gil53850628	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa	79361.6	R	20.6	1.9					mitochondrion	NADH oxidation	VAGMLQSFEGK
gil21328448	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	28064.8	O	18.3			20.5	16.5	16.7	cytoplasm		YLSEVASGDNK
gil6980972	glutamate oxaloacetate transaminase 2	47284.1	R		20.1	16.2				cell surface, extracellular region, mitochondrion	aspartate catabolism, fatty acid transport	EYLPIGGLADFCCK
gil4503971	GDP dissociation inhibitor 1	50550.1	H	20.0		2.2		12.0		cytoplasm	protein transport, regulation of GTPase activity	TFEGVDPQITSMR
gil5032009	glycogen phosphorylase	97030.6	H					19.9			glycogen metabolism	YEFGIFNQK
gil31560560	laminin receptor 1 (ribosomal protein SA)	32893.5	M				19.9			intracellular, ribosome	protein biosynthesis	AIVAIENPADVSVISSR
gil31542559	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	67902.7	O				12.3	19.9		mitochondrion, cytoplasm	acetyl-CoA biosynthesis from pyruvate	VVDGAVGAQWLAEFK
gil62661722	PREDICTED: similar to succinate-Coenzyme A ligase, ADP-forming, beta subunit	50274.2	R	19.5	2.5		1.1					ILACDDLDEAAK
gil31982030	Rho GDP dissociation inhibitor (GDI) alpha	23392.8	M		8.6		19.5	3.4	2.2	membrane	Rho protein signal transduction	VAVSADPNVPNVIVTR
gil62642537	PREDICTED: similar to mKIAA0417 protein	74783.5	R	16.2			19.5					LDLTGTSGAAVPAR
gil8393742	myelin-associated glycoprotein	69308.9	R	19.3						extracellular region, membrane	cell adhesion	SNPEPSVAFELPSR
gil71534276	guanosine diphosphate dissociation inhibitor 1	50504.2	R	3.8	5.2	0.4			19.3	membrane	small GTPase mediated signal transduction	KQNDVFGEADQ
gil109464792	PREDICTED: similar to PDZ domain containing 6	186746.7	R	18.0			19.1	11.0				YFPTQALNFAFK
gil62653546	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase	35760.1	R		19.0	1.2			14.3			LVNNGKPITIFQER
gil6679066	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1	33342.0	M						18.8	mitochondrion	biological_process	AGPNIYELR
gil62945278	hypothetical protein LOC360975	116221.4	R			18.8						VIPEDGPAAQNPKD
gil31543974	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	28068.9	O	18.7	13.5		7.8			cellular_component	protein targeting	AVTEQGHELSNEER
gil41399285	chaperonin	61016.4	H		18.6					cytoplasm, mitochondrion	protein import into mitochondrial matrix, regulation of apoptosis	LVQDVANNTNEEAGDGT TTATVLAR
gil4759080	succinate dehydrogenase complex, subunit A, flavoprotein precursor	72643.3	H	18.6						mitochondrion	tricarboxylic acid cycle	GEGGILINSQGER
gil11230802	actinin alpha 4	104911.4	M			0.6		18.5		cytoskeleton, cytoplasm, pseudopodium	actin filament bundle formation, positive regulation of pinocytosis	LASDLLEWIR
gil30795227	histidyl-tRNA synthetase 2	23409.0	H	18.4						cytoplasm	D-amino acid catabolism	SASSGAEGDVSSEREP
gil77404242	synapsin 2 isoform 1	63416.8	R		18.4				15.8	synapse	regulation of neurotransmitter secretion, synaptic transmission	TPALSPQRPLTTQQPSG TLK
gil34858950	PREDICTED: brain glycogen phosphorylase	96676.5	R	18.1				13.5	3.7			VEDVEALDQK
gil82894424	PREDICTED: similar to heat shock protein 1 (chaperonin)	67369.3	M					18.0				LSDGVAVLK
gil89060515	PREDICTED: similar to Phosphoglycerate kinase 1	10241.4	H		17.9							ALESERPFLAILGGAK
gil16758840	crystallin, mu	33533.1	R			17.8					visual perception	FASSVQGDVR
gil34873499	PREDICTED: aminopeptidase puromycin sensitive	103278.8	R	17.8				4.8				YTTPAGEVR

gil83700235	eukaryotic translation initiation factor 4A isoform 2	46372.8	H	3.8		17.6			cytoplasm	protein biosynthesis, regulation of translational initiation	VLITTDLLAR	
gil13994177	synaptosomal-associated protein, 91kDa homolog	93460.3	R			17.5			membrane		ATNSSWVVVFK	
gil19913426	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1	56796.8	H	17.3	0.9		4.4	5.3	cytoplasm, membrane, intracellular	regulation of pH, sensory perception of sound	QIYPINVLPSLSR	
gil15042957	RAB3D, member RAS oncogene family	24400.9	M			2.3		17.2	intracellular, membrane, cytoplasm	exocytosis, small GTPase mediated signal transduction	LLLIGNSSVGK	
gil63530505	predicted gene, EG433923	33050.3	O	16.9	11.5	12.1	1.2	12.0			LLLQVQHASK	
gil121583768	RAB5B, member RAS oncogene family	23544.0	R				16.8		cytoplasm,	regulation of endocytosis	TAMNVNDLFLAIK	
gil62664637	PREDICTED: similar to solute carrier family 25, member 5	33155.4	R	0.1			16.7				GAWSNVLR	
gil89024803	PREDICTED: similar to heat shock protein 8	72696.0	H			13.2	6.2	16.5	4.4		LLQDFFNGK	
gil6981182	microtubule-associated protein 2	198445.6	R	3.5			16.1		cytoplasm, cytoskeleton, dendrite	microtubule bundle formation	FAAPVQPEEER	
gil12025532	ATPase, H+ transporting, lysosomal V0 subunit a isoform 1	96231.1	M	8.2		0.7	15.8		cytoplasm, membrane, nucleus	brain development, heart development, ion transport, myeloid cell differentiation	ASLYPCPETPQER	
gil61889115	phosphoserine aminotransferase 1	40600.8	R	15.7						L-serine biosynthesis	QVVNFGPGPAK	
gil40254781	GDP dissociation inhibitor 2	50504.7	R	4.0	15.7		2.9		cytoplasm, Golgi apparatus	small GTPase mediated signal transduction, vesicle-mediated transport	MLLFTEVTR	
gil32455264	peroxiredoxin 1	22096.3	H				15.6			cell proliferation, skeletal development	QITVNDLPVGR	
gil13591908	adaptor protein complex AP-2, alpha 2 subunit	103979.1	R	15.3					cytoplasm, Golgi apparatus	endocytosis, intracellular protein transport, vesicle-mediated transport	YGGTFQNVSVK	
gil89034708	PREDICTED: hypothetical protein XP_947819	21260.3	H	15.2			9.9				QNYHQDSEAINR	
gil54607098	succinate dehydrogenase Fp subunit	72539.2	M			13.4		15.1	mitochondrion	electron transport, transport, tricarboxylic acid cycle	TLNEADCATVPPAIR	
gil21311845	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	34648.2	M				15.1		membrane, mitochondrion	glutamate transport, transport	LAANDFFR	
gil61657921	kinesin family member 5B	109483.7	M	15.0					cytoplasm, cytoskeleton	microtubule-based process, mitochondrial transport	GGGSFVQNNQPVGLR	
gil109465638	PREDICTED: similar to Rap1 GTPase-GDP dissociation stimulator 1 (SMG P21 stimulatory GDP/GTP exchange protein) (SMG GDS protein) (Exchange factor smgGDS)	87543.0	R				15.0				SVAQQASLTEQR	
gil11560087	liver glycogen phosphorylase	97421.0	R	13.9	14.8	0.2					VLYPNDNFFEGK	
gil89036204	PREDICTED: similar to Ras-related protein Rab-13	24807.6	H		12.3			12.5	14.7		LLLIGDSGVGK	
gil13399308	related RAS viral (r-ras) oncogene homolog 2	23439.8	M	14.6							QVTQEEGQQLAR	
gil66346706	neuronal growth regulator 1	38694.3	H				14.1		intracellular, membrane	Ras protein signal transduction	VVVNFAPTIQEI	
gil88952640	PREDICTED: similar to ubiquitin and ribosomal protein S27a precursor	17955.4	H					14.0		cell adhesion	ESTLHLVLR	
gil109504977	PREDICTED: similar to Histone H2B 291B	36920.9	R				13.8				VFLENVIR	
gil6678195	synaptophysin	33332.1	M	10.9	12.1	13.8	3.5	12.7	11.0	membrane, synapse, synaptosome	endocytosis, synaptic transmission	MATDPENIIK
gil68303561	proteasome (prosome, macropain) subunit, alpha type, 8 isoform 1	28512.1	H					13.7		cytoplasm, protein complex	ubiquitin-dependent protein catabolism	ALLEVVQSGGK
gil31711992	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	68953.1	O	1.8	13.6	4.3			10.9	mitochondrion, cytoplasm	acetyl-CoA biosynthesis	ILVPEGTR
gil48762932	chaperonin containing TCP1, subunit 8 (theta)	59582.5	H		13.5					cytoplasm	protein folding	LFVTNDAATILR
gil57528682	thiosulfate sulfurtransferase	33385.8	R	10.6			13.3			mitochondrion	cyanate catabolism, iron-sulfur cluster assembly	YLGQTQPEPDAVGLDSGHIR
gil82965326	PREDICTED: similar to Peroxiredoxin 1 (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide re	22248.4	O		13.2							LVQAFQFTDK
gil82950867	PREDICTED: similar to Tubulin beta chain (T beta-15)	38644.1	M		13.1							SGPFGQIFR

gil57114330	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	29427.2	R						8.6	membrane, mitochondrion, protein complex	electron transport	VPDFSDYR
gil6981668	tenascin R	149276.5	R				8.6			cell surface, extracellular matrix, membrane	cell adhesion, extracellular matrix organization and biogenesis	SSLTSTIFTGGR
gil13540707	profilin 2	16103.9	R						8.5	cytoskeleton	regulation of actin filament polymerization	SQGGEPTYNNVAVGR
gil21361370	brain glycogen phosphorylase	96634.5	H				8.5				glycogen catabolism	GLAGLGDVAEVR
gil6981716	mitogen activated protein kinase kinase kinase 12	96247.3	R			6.2	8.5			cytoplasm, cytoplasm, membrane	histone phosphorylation, JNK cascade	LEEELVMRR
gil30520131	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	66957.1	M	8.3						axon, membrane	neurotransmitter transport	VADGQISTEVSEAPVASD KPK
gil62662345	PREDICTED: hypothetical protein XP_577496	71469.2	R	8.3								QTVAVGVIK
gil8393358	fumarate hydratase 1	54429.0	R	8.2						cytoplasm, mitochondrion	fumarate metabolism	AAAEVNQEYGLDPK
gil109465447	PREDICTED: similar to cytochrome c oxidase, subunit VIb polypeptide 1	17710.7	O						8.2			IAEGTFPGK
gil6671672	capping protein (actin filament) muscle Z-line, alpha 2	32946.6	M				8.0			cytoskeleton	actin cytoskeleton organization and biogenesis	FTVTPTSTTVVGILK
gil109948279	hypothetical protein LOC653499	14944.0	H				7.9					LDTSEVVFNBSK
gil94385873	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	57373.8	M		7.9		4.1		3.2			VIIISAPSADAPMFVMGV NHEK
gil54019419	proteasome (prosome, macropain) subunit, beta type 6	25273.4	R					7.8		cytoplasm, nucleus, protein complex	ubiquitin-dependent protein catabolism	LAAIQSGVER
gil30023842	valosin containing protein	89307.8	M	7.8				1.9	1.0	cytoplasm, endoplasmic reticulum, microsome, nucleus	caspase activation, ER-associated protein catabolism	LAGESESNLRL
gil109501680	PREDICTED: similar to Dihydropyrimidinase-related protein 2 (DRP-2)(Turned on after division, 64 kDa protein) (TOAD-64) (Collapsin response mediator protein 2) (CRMP-2)	20767.5	R	7.8					5.8			EALQNIYDQSDR
gil4557515	damage-specific DNA binding protein 2 (48kD)	47833.4	H				7.4			nucleus	nucleotide-excision repair	TSEIVLRPRNK
gil109465364	PREDICTED: similar to Glutathione S-transferase Mu 6 (GST class-mu 6) (Glutathione-S-transferase class M5)	25495.0	R	7.3	1.8							ITQSNAIIR
gil16924002	DJ-1 protein	19961.4	R					1.5	7.3	nucleus	adult locomotory behavior, synaptic transmission, dopaminergic	DVVICPDTSLEEAKE
gil4885377	H1 histone family, member 3	22336.3	H	7.3	6.8					chromosome, nucleus	nucleosome assembly	ALAAAGDYVEK
gil4826655	calbindin 1	30006.0	H						7.0			TFVDQYGQR
gil6980956	glutamate dehydrogenase 1	61377.3	R	7.0	2.4					mitochondrion	long-term memory, transmembrane receptor protein tyrosine kinase signaling pathway	NYTDNELEK
gil32455244	beta isoform of regulatory subunit A, protein phosphatase 2 isoform b	73538.2	H		7.0					cytoplasm, membrane, cytoskeleton, mitochondrion, nucleus	ceramide metabolism, inactivation of MAPK activity, induction of apoptosis, negative regulation of cell growth	TSACGLFSVCYPR
gil42821116	neural cell adhesion molecule 2	93123.4	R	6.9						extracellular region,	axonal fasciculation, cell adhesion, sensory	IIELSQTTAK
gil13929002	phosphofructokinase, muscle	85505.7	R	6.8			2.3			membrane	perception of smell	LPLMECVQVTK
gil11560002	amphiphysin 1	74832.0	R	6.7						cytoplasm,	regulation of glycolysis	
gil33414505	chaperonin subunit 4 (delta)	58062.8	R	6.7						cytoskeleton, cytoplasm	learning, regulation of GTPase activity, synaptic vesicle endocytosis	EATEDVAPQQPAGEK
gil16924010	septin 2	41566.3	R							cytoplasm,	chaperone cofactor-dependent protein folding,	LVIEEAER
gil21264345	peripherin	53618.4	H	6.6					6.6	cytoplasm, synaptosome	chaperonin-mediated tubulin folding	LTVVDTPGYGDAINSR
									0.7	cytoskeleton,	neurite development	AQYESIAAK

gil62660026	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase	40957.0	R				6.6					LIVINGKPTITFQER
gil35215309	neurofascin	137889.2	M	6.5						axon, membrane mitochondrion,	axon guidance	TSGAPPESNPDSVK
gil78365255	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	67123.4	O			1.3	6.4			cytoplasm	acetyl-CoA biosynthesis	AAPAAAAAAPGPR
gil32483416	neurofilament, heavy polypeptide 200kDa	111770.8	H	6.2						axon, cytoskeleton, chromosome, nucleus	nervous system development, nucleosome assembly	SAMGELYER
gil9507177	transcytosis associated protein	107158.8	R	6.2						cytoplasm, Golgi apparatus, microsome	ER to Golgi vesicle-mediated transport	GVMGGQSAGPQHTEAE TIQK
gil4505357	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	9363.9	H					6.1		mitochondrion,		FYSVNVDYSK
gil82907477	PREDICTED: similar to translocase of outer mitochondrial membrane 7 homolog	6200.4	M	6.0								LQLFLR
gil109486463	PREDICTED: similar to Ras-related protein Rab-12	45201.4	R				5.1	5.9	4.5			LQIWDTAGQER
gil57222274	PHD finger protein 8	102075.5	M			5.8						HLCTTDLFKFPSFETICW HV GK
gil31981350	hypothetical protein LOC76820	37318.7	M	5.7								VMLETPEYR
gil21704242	vesicle-associated calmodulin-binding protein	54785.5	M	5.7	5.1							PFGCVTLGD K
gil4757900	calreticulin precursor	48111.8	H	5.4						cytoplasm, endoplasmic reticulum	calcium ion homeostasis, protein export from nucleus, protein folding	HEQNIDCGGGYV K
gil13786204	voltage-dependent anion channel 3	30778.4	R		5.4					mitochondrion	adenine transport, behavioral fear response, learning, nerve-nerve synaptic transmission	LTVD TIFVPNT G K
gil30065645	protein phosphatase 2A, regulatory subunit B' isoform a	40641.4	H					5.2		soluble fraction	protein amino acid dephosphorylation	FGSL LPIHPVT SG
gil14389299	vimentin	53700.0	R		5.0			4.6		cytoplasm, cytoskeleton, nucleus	cell motility, intermediate filament-based process	E E AESTL QSFR
gil109460227	PREDICTED: similar to Alpha-centractin (Centractin)(Centrosome-associated actin homolog) (Actin-RPV) (ARP1)	51309.1	O	4.9								AGFAG D QIP K
gil4505937	polymerase (DNA directed), gamma	139473.4	H					4.8		mitochondrion	base-excision repair, gap-filling, DNA-dependent DNA replication	HCLEQG K
gil4758986	RAB11B, member RAS oncogene family	24558.6	H		4.8					membrane	protein transport, small GTPase mediated signal transduction	STIGVE FAT R
gil62645331	PREDICTED: similar to Nck-associated protein 1 (NAP 1) (p125Nap1) (Membrane-associated protein HEM-2)	141549.4	R	4.8								LSS V DSVL K
gil47132509	septin 5	42848.7	M					4.7		membrane, cytoplasm, synaptosome	cell cycle, regulation of exocytosis	MESI P I PLPL TPDAETE K
gil24308229	protein kinase C and casein kinase substrate in neurons 1	50933.8	H		4.6					cytoplasm	endocytosis	GPQ Y GSLE R
gil16758270	F-box only protein 2	33679.0	R				4.5			cytoplasm	ER-associated protein catabolism, glycoprotein catabolism	EL VD GAP LWLL K
gil31317307	proprotein convertase subtilisin/kexin type 9 preproprotein	74239.1	H					4.4			cholesterol metabolism	MSG DLLELA L K
gil9507125	synuclein, alpha	14506.2	R					4.4		cytoplasm, synaptosome	anti-apoptosis, central nervous system development, dopamine biosynthesis, dopamine metabolism	EGVVHG VT TVA EK
gil31981282	glyoxalase 1 PREDICTED: similar to Serine/threonine-protein phosphatase 2A regulatory subunit B (PP2A, subunit B, PR53 isoform) (Phosphotyrosyl phosphatase activator) (PTPA)	20826.4	M		4.3					cytoplasm	anti-apoptosis	D F LL QQ TM LR
gil109467991	phosphatase 2A regulatory subunit B (PP2A, subunit B, PR53 isoform) (Phosphotyrosyl phosphatase activator) (PTPA)	36486.0	R		4.3							LVALLDTLD R
gil116805788	cytoplasmic FMR1 interacting protein 2	145599.0	H	4.3						cytoplasm, synaptosome		AVGPS ST QL YM VR

gil5729850	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	40506.3	O	4.2							G-protein coupled receptor protein signaling pathway, negative regulation of adenylate cyclase activity	EIYTHFTCATDTK
gil68163411	activated leukocyte cell adhesion molecule	65061.1	H	4.2						membrane		SSNTYTLTDVR
gil32401457	opsin 5	59284.5	R		0.7				4.1			MALNHTALPQDER
gil30409998	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	35265.4	O				4.0			flagellum, membrane, mitochondrion		GNLANVIR
gil110347439	zinc finger protein 225	82382.9	H		3.9					intracellular, nucleus	regulation of transcription, DNA-dependent, transcription	VHMGEK
gil62661476	PREDICTED: similar to N-copine	219591.5	R		3.9							FLVYDYDSSGK
gil70906474	Ca<2+>dependent activator protein for secretion	153906.3	M	3.8						cytoplasm, membrane, synapse	catecholamine secretion, exocytosis, protein transport, transport	AGGGRPSSPSVSEK
gil114326502	paxillin isoform beta	64434.8	M				3.8			cytoskeleton, membrane, lamellipodium		AGPLVK
gil110625946	kinesin family member 2B	79529.1	M				3.7			cytoskeleton	microtubule-based movement	KSQVE
gil62666823	PREDICTED: similar to prohibitin	30973.2	R	3.7								EFTEAVEAK
gil9506941	oligodendrocyte myelin glycoprotein	49252.0	M	3.5						extracellular matrix, membrane	cell adhesion	LESPLAQLPR
gil82697315	rap2 interacting protein x isoform 1	70564.8	H	3.5								TAEGQALSEAR
gil4503725	FK506-binding protein 1A	11943.1	H						3.4		positive regulation of I-kappaB kinase/NF-kappaB cascade, protein folding	GWEEGVAQMSVGQR
gil94388698	PREDICTED: TBP-interacting protein isoform 1	164765.0	M	1.9			3.4					HTVDDGLDIR
gil109489185	PREDICTED: similar to angiotensin I converting enzyme(peptidyl-dipeptidase A) 1 isoform 1	90074.4	R				3.4					SQFMLYFGTR
gil109474831	PREDICTED: similar to Protein KIAA1045	51326.4	R	1.3					3.3			EAEASAPGVQEESNNR
gil62945366	hypothetical protein LOC498407	33397.6	R		3.3							GGGGPGGEQETQELASK
gil62652199	PREDICTED: similar to Inner nuclear membrane protein Man1 (LEM domain containing protein 3)	76201.9	O		3.2							TAVAPLPR
gil29789257	RAB5C, member RAS oncogene family	25335.7	M	3.2	1.6					cytoplasm, membrane	regulation of endocytosis, small GTPase mediated signal transduction, transport	GVDLQESNPASR
gil109475709	PREDICTED: similar to loss of heterozygosity, 11, chromosomal region 2, gene A homolog	134608.0	R				3.2					QPLRQGHPR
gil6981420	pancreatic trypsin 1	25942.7	R	3.0			3.2			extracellular region, mitochondrion	calcium ion binding, peptidase activity, trypsin activity	LGEHNINVLEGDEQFINA AK
gil12621120	sideroflexin 3	35410.6	R						3.1	membrane, mitochondrion	iron ion transport	ELQVGIPVTDEAGQR
gil62990176	thyroid stimulating hormone receptor	86527.4	M				3.1			membrane	adult locomotory behavior, G-protein coupled receptor protein signaling pathway, positive regulation of body size, regulation of locomotion cyclic-nucleotide-mediated signaling,	NPQYNPRDK
gil5729804	nudix-type motif 3	19458.7	H						2.9	intracellular	diadenosine polyphosphate catabolism, regulation of RNA export from nucleus	LVGIFENQER
gil112382252	spectrin, beta, non-erythrocytic 1 isoform 2	251263.2	H	2.7						cytoskeleton, membrane	barbed-end actin filament capping	ALVADSHPESER
gil52317184	olfactory receptor, family 10, subfamily X, member 1	36421.1	H				2.7			membrane	G-protein coupled receptor protein signaling pathway, sensory perception of smell	IPSAEGKQK
gil30519995	sideroflexin 5	37304.9	M						2.6	membrane, mitochondrion	cation transport, ion transport	EAVQLLEDYK
gil7661966	mediator of DNA damage checkpoint 1	226554.8	H	2.5						intracellular, nucleus	cell cycle, DNA repair	VEPAGRSR
gil34868383	PREDICTED: similar to Mrp150 protein	18307.5	R			2.5						AALCVCVR
gil63475897	PREDICTED: similar to ADP/ATP translocase 2 (Adenine nucleotide translocator 2) (ANT 2) (ADP,ATP ca	32854.9	O					2.4				DFLAGGVAAAISK

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