Supporting Information for

"Quantitative Proteomic Analysis Reveals the Perturbation of Multiple Cellular Pathways in HL-60 Cells Induced by Arsenite Treatment"

by

Lei Xiong and Yinsheng Wang

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Figure S1. Western blotting analysis of histones H2A, H2B, H3, H4 with lysates of arsenite-treated (“+$NaAsO_2$”) and untreated (“Control”) HL-60 cells. Actin was used as the loading control. Quantification results (based on Western analysis) showed that histones H2A, H2B, H3 and H4 were upregulated by 1.56, 1.55, 1.52, and 1.44 folds, respectively.

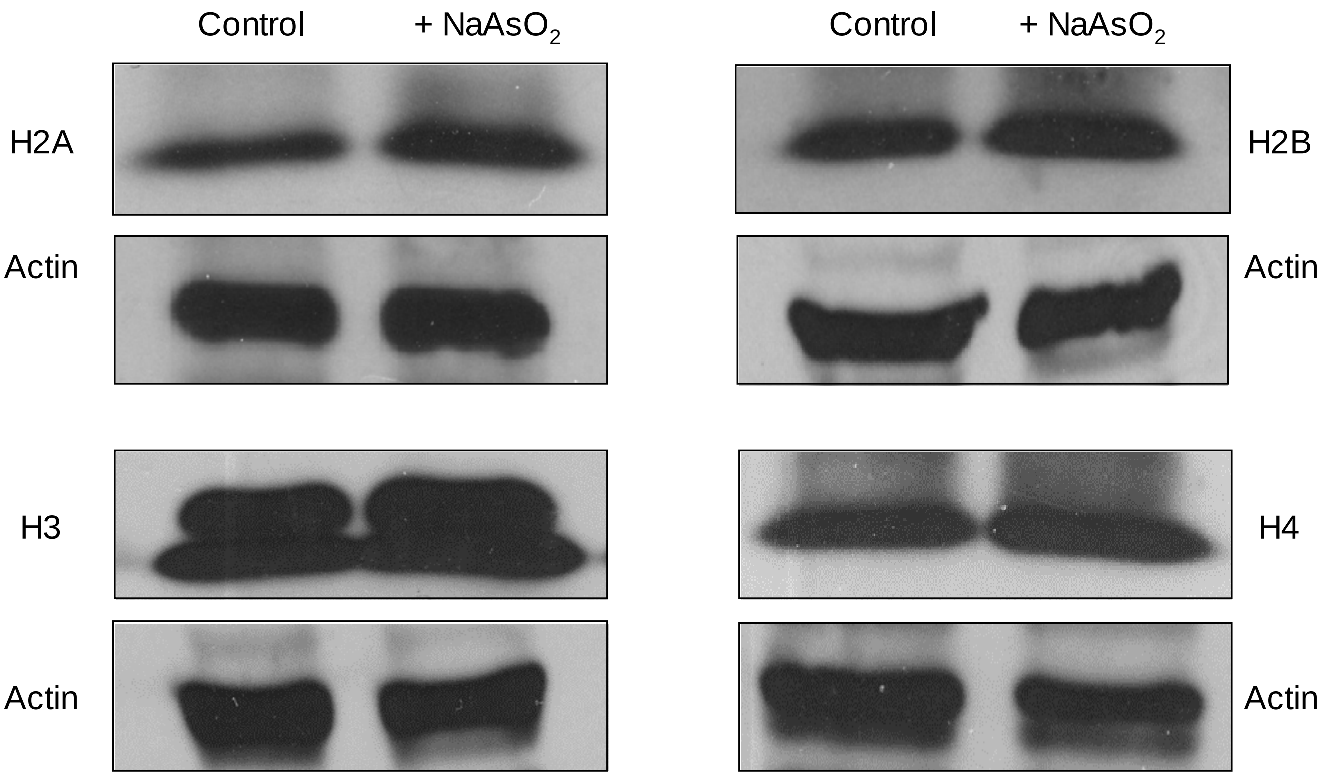

Table S1. Detailed results for all proteins quantified in this study

	GI Number and Protein Name	Forward, set1	Forward, set2	Reverse, set3	Pepide Number	Average Ratio	S.D.
gi|21755073	unnamed protein product	0.442	0.416	0.403	1	0.420	0.020
gi|119587276	hCG19802, isoform CRA_a	0.621	0.551	0.243	1	0.472	0.201
gi|35570	unnamed protein product	0.552	0.521	0.411	2	0.495	0.074
gi|386547	d(TTAGGG)n-binding protein B39	0.652	0.592	0.25	1	0.498	0.217
gi|13477237	ZNF607 protein	0.555		0.486	2	0.521	0.049
gi|181969	elongation factor 2	0.447	0.545	0.636	3	0.543	0.095
gi|531202	spermidine synthase	0.466	0.465	0.773	2	0.568	0.178
gi|35844	unnamed protein product	0.442	0.551	0.739	1	0.577	0.150
gi|119597533	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A), isoform CRA_b	0.583	0.582	0.602	1	0.589	0.011
gi|38202255	threonyl-tRNA synthetase	0.552	0.728	0.512	2	0.597	0.115
gi|114645930	PREDICTED: nucleosome assembly protein 1-like 1 isoform 9	0.583	0.615	0.599	3	0.599	0.016
gi|431422	Ran/TC4 Binding Protein	0.673	0.769	0.358	2	0.600	0.215
gi|2580550	dead box, X isoform	0.602	0.71	0.512	3	0.608	0.099
gi|41584442	fatty acid synthase	0.704	0.612	0.512	5	0.609	0.096
gi|122168	HLA class I histocompatibility antigen, B-58 α chain	0.731	0.724	0.375	2	0.610	0.204
gi|21754758	unnamed protein product	0.684	0.615	0.547	3	0.615	0.069
gi|19353009	Similar to Elongation factor 2b	0.55	0.65	0.651	2	0.617	0.058
gi|193788267	unnamed protein product	0.681	0.658	0.538	3	0.626	0.077
gi|801893	leucine-rich PPR-motif containing protein	0.547	0.595	0.742	3	0.628	0.102
gi|5107666	importin β	0.59	0.453	0.849	5	0.631	0.201
gi|181486	DNA-binding protein B	0.592	0.716	0.587	1	0.632	0.073
gi|1235727	unnamed protein product	0.562		0.71	2	0.636	0.105
gi|1230564	Gu protein	0.743	0.693	0.489	2	0.642	0.135
gi|66392203	NME1-NME2 protein	0.704	0.441	0.78	5	0.642	0.178
gi|4506707	ribosomal protein S25	0.552	0.615	0.771	1	0.646	0.113
gi|40225729	FUBP1 protein	0.706		0.589	1	0.648	0.083
gi|2661039	alpha enolase	0.564	0.689	0.691	5	0.648	0.073
gi|119571409	hCG1643342, isoform CRA_a	0.682	0.635	0.627	1	0.648	0.030
gi|386777	transplantation antigen	0.716	0.636	0.618	2	0.657	0.052
gi|1136741	KIAA0002	0.731	0.812	0.438	3	0.660	0.197
gi|190281	protein phosphatase I alpha subunit	0.683	0.657	0.643	1	0.661	0.020
gi|55958547	heterogeneous nuclear ribonucleoprotein K	0.773	0.724	0.489	3	0.662	0.152
gi|23712	myoblast antigen 24.1D5	0.574	0.704	0.71	3	0.663	0.077
gi|13569879	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E isoform 1	0.616	0.753	0.629	3	0.666	0.076
gi|4507789	ubiquitin-conjugating enzyme E2L 3 isoform 1	0.614	0.657	0.734	5	0.668	0.061
gi|14124984	Chaperonin containing TCP1, subunit 3 (gamma)	0.719	0.75	0.551	4	0.673	0.107
gi|20071957	ZC3HAV1 protein	0.719	0.753	0.551	1	0.674	0.108
gi|40675359	EIF3A protein	0.565	0.691	0.774	3	0.677	0.105

gi|119628379	chaperonin containing TCP1, subunit 6A (zeta 1), isoform CRA_b	0.719	0.762	0.551	2	0.677	0.112
gi|15779184	FLNA protein	0.495	0.834	0.706	5	0.678	0.171
gi|119610575	eukaryotic translation initiation factor 4A, isoform 1, isoform CRA_c	0.646	0.693	0.697	3	0.679	0.028
gi|1322019	uroporphyrinogen decarboxylase	0.827	0.538	0.678	1	0.681	0.145
gi|4506669	ribosomal protein P1 isoform 1	0.625	0.706	0.729	2	0.687	0.055
gi|5006420	ribonucleotide reductase M1 subunit	0.737	0.662	0.661	3	0.687	0.044
gi|4503475	eukaryotic translation elongation factor 1 alpha 2	0.684	0.652	0.726	1	0.687	0.037
gi|7108915	glucocorticoid receptor AF-1 specific elongation factor	0.685	0.677	0.703	3	0.688	0.013
gi|119390147	Chain A, Crystal Structure Of The Heterodimeric Complex Of Human Rgs10 And Activated Gi Alpha 3	0.755	0.687	0.628	1	0.690	0.064
gi|119631661	Sjogren syndrome antigen B (autoantigen La), isoform CRA_a	0.764	0.611	0.707	2	0.694	0.077
gi|119616807	hCG2043493	0.687	0.733	0.663	1	0.694	0.036
gi|4506661	ribosomal protein L7a	0.702	0.649	0.734	2	0.695	0.043
gi|15809590	hnRNP Q1	0.743	0.736	0.61	5	0.696	0.075
gi|169172618	hCG2041218	0.708	0.696	0.687	2	0.697	0.011
gi|119623684	FLJ45422 protein, isoform CRA_b	0.706	0.718	0.672	1	0.699	0.024
gi|33356163	eukaryotic translation initiation factor 1A, Y chromosome	0.745	0.59	0.762	3	0.699	0.095
gi|62089002	RAB40B, member RAS oncogene family variant	0.732	0.589	0.777	1	0.699	0.098
gi|5031635	cofilin 1 (non-muscle)	0.688	0.886	0.526	1	0.700	0.180
gi|550021	ribosomal protein S5	0.458	0.815	0.829	4	0.701	0.210
gi|67464424	Chain A, 14-3-3 Protein Epsilon (Human) Complexed To Peptide	0.774	0.729	0.6	3	0.701	0.090
gi|23397696	copine I isoform a	0.74	0.802	0.562	2	0.701	0.125
gi|2914385	Chain C, Human Pcna	0.573	0.761	0.771	2	0.702	0.112
gi|56789234	TARS protein	0.593	0.681	0.831	3	0.702	0.120
gi|38014625	RPL8 protein	0.573	0.768	0.774	3	0.705	0.114
gi|76825391	ST13 protein	0.831	0.721	0.566	2	0.706	0.133
gi|23304751	MHC class I antigen	0.712	0.789	0.631	5	0.711	0.079
gi|577295	KIAA0088	0.57	0.733	0.831	5	0.711	0.132
gi|7513316	ribosomal protein L14 - human	0.758	0.652	0.726	5	0.712	0.054
gi|485388	eukaryotic initiation factor 4AII	0.646	0.718	0.775	2	0.713	0.065
gi|119616611	cold shock domain protein A, isoform CRA_c	0.724	0.677	0.738	2	0.713	0.032
gi|1431788	Chain A, Determination Of The Nmr Solution Structure Of The Cyclophilin A-Cyclosporin A Complex	0.703	0.709	0.732	5	0.715	0.015
gi|31092	unnamed protein product	0.687	0.733	0.728	5	0.716	0.025
gi|1931584	eIF-3 p110 subunit	0.688	0.683	0.784	3	0.718	0.057
gi|19923193	heat shock 70kD protein binding protein	0.837	0.735	0.589	2	0.720	0.125
gi|66933016	inosine monophosphate dehydrogenase 2	0.748	0.701	0.718	5	0.722	0.024
gi|4504327	mitochondrial trifunctional protein, beta subunit precursor	0.614	0.75	0.813	3	0.726	0.102
gi|4503471	eukaryotic translation elongation factor 1 alpha 1	0.684	0.652	0.841	2	0.726	0.101
gi|119614929	tripartite motif-containing 25, isoform CRA_a	0.742		0.714	1	0.728	0.020
gi|2623761	Aac11	0.707		0.75	2	0.729	0.030
gi|62897525	eukaryotic translation elongation factor 1 alpha 1 variant	0.789	0.722	0.68	3	0.730	0.055
gi|36796	t-complex polypeptide 1	0.74	0.835	0.618	2	0.731	0.109

gi|181484	DNA-binding protein A	0.801	0.657	0.738	2	0.732	0.072
gi|4503481	eukaryotic translation elongation factor 1 gamma	0.729	0.637	0.834	2	0.733	0.099
gi|119587829	ribosomal protein S25, isoform CRA_a		0.634	0.835	3	0.735	0.142
gi|119592244	myosin, heavy polypeptide 14, isoform CRA_a	0.756	0.732	0.722	3	0.737	0.017
gi|182994	Ga subunit	0.878	0.711	0.628	1	0.739	0.127
gi|4506685	ribosomal protein S13	0.789	0.586	0.845	2	0.740	0.136
gi|116284394	myosin, heavy chain 14 isoform 2	0.767	0.732	0.722	5	0.740	0.024
gi|1498227	PHAPI2b protein	0.706	0.74	0.776	5	0.741	0.035
gi|32189	HLA-Bw72 antigen	0.667	0.763	0.792	3	0.741	0.065
gi|34222512	Full=HLA class I histocompatibility antigen, B-73 alpha chain	0.705	0.726	0.804	3	0.745	0.052
gi|119610572	eukaryotic translation initiation factor 4A, isoform 1, isoform CRA_a	0.859	0.715	0.663	4	0.746	0.102
gi|74723863	RecName: Full=60S acidic ribosomal protein P0-like	0.76	0.923	0.558	3	0.747	0.183
gi|4759212	tubulin-specific chaperone a	0.851	0.745	0.647	5	0.748	0.102
gi|1215669	JTV-1	0.74	0.812	0.694	1	0.749	0.059
gi|37547	unnamed protein product	0.731	0.718	0.798	2	0.749	0.043
gi|4885417	ubiquitin-conjugating enzyme E2-25K isoform 1	0.868		0.63	2	0.749	0.168
gi|5453607	chaperonin containing TCP1, subunit 7 isoform a	0.778	0.82	0.654	2	0.751	0.086
gi|3041664	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	0.669	0.7	0.898	2	0.756	0.124
gi|5031601	actin related protein 2/3 complex subunit 1B	0.931	0.6	0.738	2	0.756	0.166
gi|433344	p37 AUF1	0.752	0.75	0.77	3	0.757	0.011
gi|88988289	hypothetical protein LOC648000 isoform 3	0.706	0.824	0.746	4	0.759	0.060
gi|2632123	Xeroderma Pigmentosum Group E Complementing protein	0.731		0.788	3	0.760	0.040
gi|4758256	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	0.793		0.736	1	0.765	0.040
gi|5453740	myosin regulatory light chain MRCL3	0.826	0.771	0.698	5	0.765	0.064
gi|284040	chitobiase-related protein, G protein gamma subunit	0.863		0.67	1	0.767	0.136
gi|553254	NADH cytochrome b5 reductase (EC 1.6.2.2)	0.667	0.945	0.688	2	0.767	0.155
gi|32158	HLA-A2902	0.731	0.787	0.791	2	0.770	0.034
gi|913148	calreticulin=calcium binding protein	0.873	0.61	0.829	5	0.771	0.141
gi|5031753	heterogeneous nuclear ribonucleoprotein H1	0.752	0.855	0.709	3	0.772	0.075
gi|4758516	hepatoma-derived growth factor isoform a	0.75		0.797	1	0.774	0.033
gi|862457	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein	0.716	0.753	0.853	5	0.774	0.071
gi|307066	inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	0.752	0.742	0.83	3	0.775	0.048
gi|5032051	ribosomal protein S14	0.793	0.763	0.769	3	0.775	0.016
gi|4503915	phosphoribosylglycinamide formyltransferase	0.757	0.902	0.676	5	0.778	0.115
gi|28416899	phosphoribosylaminoimidazole synthetase isoform 2	0.759	0.9	0.676	5	0.778	0.113
gi|27754056	tubulin, beta 6	0.831		0.73	3	0.781	0.071
gi|36138	ribosomal protein L6	0.816	0.763	0.766	2	0.782	0.030
gi|119602640	eukaryotic translation elongation factor 1 delta, isoform CRA_e	0.729	0.743	0.874	5	0.782	0.080
gi|693937	polyadenylate binding protein II	0.791	0.728	0.827	1	0.782	0.050
gi|1200184	stimulator of TAR RNA binding	0.864	0.89	0.593	3	0.782	0.164
gi|4583153	cytosolic inorganic pyrophosphatase	0.882	0.674	0.791	5	0.782	0.104
gi|4929739	CGI-135 protein	0.776	0.849	0.724	1	0.783	0.063

gi|15431301	ribosomal protein L7	0.767	0.782	0.801	4	0.783	0.017
gi|11056044	pyrophosphatase 1	0.677	0.745	0.929	3	0.784	0.130
gi|4506753	RuvB-like 1	0.799		0.772	2	0.786	0.019
gi|194385190	unnamed protein product		0.658	0.913	5	0.786	0.180
gi|5174613	nucleosome assembly protein 1-like 4	0.81	0.844	0.705	2	0.786	0.072
gi|6755901	tubulin, alpha 1	0.865	0.781	0.714	2	0.787	0.076
gi|119612312	hCG2008737	0.73	0.831	0.806	3	0.789	0.053
gi|9755861	human leucocyte antigen	0.77	0.746	0.852	1	0.789	0.056
gi|88900491	alpha glucosidase II alpha subunit isoform 3	0.805	0.733	0.831	5	0.790	0.051
gi|4503529	eukaryotic translation initiation factor 4A isoform 1	0.859	0.715	0.796	5	0.790	0.072
gi|4502599	carbonyl reductase 1	0.639	0.86	0.876	3	0.792	0.132
gi|36036	GTPase	0.826	0.708	0.85	2	0.795	0.076
gi|28416956	GTPase, IMAP family member 8	0.826	0.708	0.85	2	0.795	0.076
gi|11513833	Chain B, Core Of The Alu Domain Of The Mammalian Srp	0.75	0.766	0.87	2	0.795	0.065
gi|89573879	ribosomal protein L18	0.726	0.942	0.719	1	0.796	0.127
gi|119572747	ribosomal protein L18, isoform CRA_d	0.726	0.942	0.719	1	0.796	0.127
gi|194374113	unnamed protein product	0.734	0.769	0.888	1	0.797	0.081
gi|347964	TARBP-b gene product	0.831	0.831	0.73	2	0.797	0.058
gi|197304951	Chain B, Dopamine Quinone Conjugation To Dj-1	0.711	0.845	0.841	5	0.799	0.076
gi|5174447	guanine nucleotide binding protein, beta polypeptide 2-like 1	0.686	0.841	0.871	4	0.799	0.099
gi|4759224	programmed cell death 5	0.866		0.734	1	0.800	0.093
gi|4503535	eukaryotic translation initiation factor 4E isoform 1	0.865		0.736	2	0.801	0.091
gi|15277236	TC4	0.788	0.81	0.812	2	0.803	0.013
gi|14591909	ribosomal protein L5	0.843	0.744	0.826	3	0.804	0.053
gi|37258	Tpr	0.813	0.775	0.826	2	0.805	0.027
gi|47123412	RPLP0 protein	0.76	0.923	0.734	5	0.806	0.102
gi|194388520	unnamed protein product		0.886	0.726	1	0.806	0.113
gi|4504041	guanine nucleotide binding protein, alpha inhibiting activity polypeptide 2	0.878	0.846	0.697	4	0.807	0.097
gi|404722	guanine nucleotide regulatory protein	0.878	0.846	0.697	1	0.807	0.097
gi|119593150	filamin A, alpha (actin binding protein 280), isoform CRA_a	0.597	0.902	0.923	5	0.807	0.182
gi|4506667	ribosomal protein P0	0.76	0.923	0.742	5	0.808	0.100
gi|194388444	unnamed protein product		0.859	0.763	2	0.811	0.068
gi|10835067	autoantigen La	0.843	0.826	0.767	5	0.812	0.040
gi|119575628	hCG2043275	0.77	0.716	0.951	2	0.812	0.123
gi|119593154	filamin A, alpha (actin binding protein 280), isoform CRA_e	0.597	0.902	0.94	5	0.813	0.188
gi|16876910	HNRPF protein	0.761	0.866	0.812	5	0.813	0.053
gi|181965	elongation factor 1 alpha		0.897	0.731	1	0.814	0.117
gi|119622042	hCG37214, isoform CRA_a	0.809	0.81	0.826	1	0.815	0.010
gi|34783731	AQR protein	0.774	0.739	0.937	2	0.817	0.106
gi|2697005	cell cycle protein p38-2G4 homolog	0.792	0.783	0.876	3	0.817	0.051
gi|4759158	small nuclear ribonucleoprotein D2 isoform 1	0.797	0.83	0.824	5	0.817	0.018
gi|10433717	unnamed protein product	0.831	0.815	0.813	5	0.820	0.010

gi|609342	nucleophosmin-anaplastic lymphoma kinase fusion protein	0.875	0.732	0.853	3	0.820	0.077
gi|4506697	ribosomal protein S20	0.81	0.93	0.724	5	0.821	0.103
gi|3721864	Ste24p	0.932		0.711	1	0.822	0.156
gi|4503545	eukaryotic translation initiation factor 5A isoform B	0.757	0.821	0.889	2	0.822	0.066
gi|2119276	beta-tubulin (fragment)	0.801	0.838	0.828	5	0.822	0.019
gi|194239729	eukaryotic translation elongation factor 1 delta isoform 4	0.797	0.764	0.907	5	0.823	0.075
gi|7106439	tubulin, beta 5	0.801	0.838	0.829	5	0.823	0.019
gi|3929617	alpha SNAP	0.805	0.821	0.846	3	0.824	0.021
gi|4557241	actinin, alpha 3	0.868	0.884	0.722	3	0.825	0.089
gi|51873036	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform 1 precursor	0.89	0.92	0.668	1	0.826	0.138
gi|4389379	Chain A, Cdc42hs-Gdp Complex	0.888	0.942	0.651	1	0.827	0.155
gi|14165469	ribosomal protein S15a	0.763	0.795	0.928	5	0.829	0.088
gi|7705813	ribosomal protein L26-like 1	0.774	0.826	0.886	5	0.829	0.056
gi|12655179	Dipeptidyl-peptidase 3	0.875	0.987	0.626	3	0.829	0.185
gi|41393545	RAB5C, member RAS oncogene family isoform b	0.798	0.821	0.87	5	0.830	0.037
gi|6912634	ribosomal protein L13a	0.82	1.048	0.621	2	0.830	0.214
gi|30582781	tubulin, beta, 4	0.864	0.838	0.788	3	0.830	0.039
gi|4758118	death-associated protein 3	0.791	0.982	0.718	1	0.830	0.136
gi|180663	c-myc binding protein	0.749	0.809	0.934	2	0.831	0.094
gi|169170622	hypothetical protein	0.952	0.946	0.594	4	0.831	0.205
gi|4929854	Chain A, Structure Of Human Placental S-Adenosylhomocysteine Hydrolase	0.727	0.677	1.089	3	0.831	0.225
gi|119609848	splicing factor, arginine/serine-rich 2, isoform CRA_c	0.914		0.75	5	0.832	0.116
gi|38455427	chaperonin containing TCP1, subunit 4 (delta)	0.809	0.728	0.96	2	0.832	0.118
gi|73959145	40S ribosomal protein S2 isoform 4	0.987	0.791	0.719	1	0.832	0.139
gi|33341692	FP585	0.993		0.674	3	0.834	0.226
gi|83318444	HSP90AA1 protein	0.742	0.996	0.764	2	0.834	0.141
gi|4758340	phenylalanyl-tRNA synthetase, alpha subunit		0.84	0.828	2	0.834	0.008
gi|119615473	ribosomal protein L11, isoform CRA_a	0.875	0.847	0.783	3	0.835	0.047
gi|5454002	putative c-Myc-responsive isoform 1	0.885		0.785	2	0.835	0.071
gi|119605048	ribosomal protein L18a, isoform CRA_b	0.774	0.762	0.97	3	0.835	0.117
gi|6755368	ribosomal protein S18	0.908	0.673	0.925	5	0.835	0.141
gi|641958	non-muscle myosin B	0.826	0.812	0.869	2	0.836	0.030
gi|33869643	EEF2 protein	0.78	0.82	0.907	5	0.836	0.065
gi|31615803	Chain A, Synthetic Ubiquitin With Fluoro-Leu At 50 And 67	0.795	0.851	0.863	2	0.836	0.036
gi|3126984	CAG-isl 7	0.862	0.873	0.774	1	0.836	0.054
gi|4506597	ribosomal protein L12	0.777	0.819	0.913	5	0.836	0.070
gi|4502891	chloride channel, nucleotide-sensitive, 1A	0.894	0.706	0.909	1	0.836	0.113
gi|971270	proteasome subunit p40 / Mov34 protein	0.821	0.905	0.784	2	0.837	0.062
gi|10434147	unnamed protein product	0.88	0.859	0.776	3	0.838	0.055
gi|113420096	hCG1994130	0.763	0.826	0.928	3	0.839	0.083
gi|11128019	cytochrome c	0.879	0.882	0.76	2	0.840	0.070

gi|292435	ribosomal protein L26	0.756	0.826	0.941	5	0.841	0.093
gi|4757880	budding uninhibited by benzimidazoles 3 isoform a	0.799	0.954	0.77	4	0.841	0.099
gi|112490659	Chain A, Structure Of U2af65 Variant With Polyuridine Tract	0.817	0.858	0.849	1	0.841	0.022
gi|927065	eukaryotic translation elongation factor 1 alpha 1-like 14	0.789	0.827	0.909	3	0.842	0.061
gi|21750187	unnamed protein product	0.874	0.867	0.784	5	0.842	0.050
gi|2736256	aflatoxin aldehyde reductase AFAR	0.815	0.889	0.824	5	0.843	0.040
gi|119609240	potassium voltage-gated channel, shaker-related subfamily, member 6	1.043	0.693	0.793	1	0.843	0.180
gi|33874520	SYNCRIP protein	0.875	0.875	0.78	2	0.843	0.055
gi|263098	Tat binding protein 1, TBP-1=transcriptional activator	0.903	0.748	0.881	2	0.844	0.084
gi|169171114	hypothetical protein	0.989	0.827	0.717	4	0.844	0.137
gi|15010550	heat shock protein gp96 precursor	0.819	0.877	0.838	5	0.845	0.030
gi|4432750	ribosomal protein L11	0.866	0.833	0.836	1	0.845	0.018
gi|338039	set	0.85	0.897	0.789	2	0.845	0.054
gi|4503253	defender against cell death 1	0.903	0.873	0.762	1	0.846	0.074
gi|10835256	PYD and CARD domain containing isoform a	0.865	0.85	0.825	4	0.847	0.020
gi|2627129	polyubiquitin	0.844	0.834	0.863	2	0.847	0.015
gi|57999481	hypothetical protein	1.009	0.661	0.871	2	0.847	0.175
gi|35068	Nm23 protein	0.837	0.847	0.859	2	0.848	0.011
gi|799177	100 kDa coactivator	0.826	0.776	0.942	5	0.848	0.085
gi|7765076	S3 ribosomal protein	0.971		0.726	5	0.849	0.173
gi|7710086	RAB10, member RAS oncogene family	0.837	0.794	0.915	5	0.849	0.061
gi|1944352	IgG Fc binding protein		0.886	0.812	2	0.849	0.052
gi|5690431	prefoldin subunit 2	0.926	0.725	0.897	1	0.849	0.109
gi|32358	hnRNP U protein	0.837	0.953	0.76	3	0.850	0.097
gi|170785039	Chain A, The Crystal Structure Of P18, Human Translation Elongation Factor 1 Epsilon 1	0.759	0.954	0.839	3	0.851	0.098
gi|35830	ubiquitin activating enzyme E1	0.896	0.844	0.822	5	0.854	0.038
gi|4261795	eukaryotic initiation factor 5A		1	0.708	1	0.854	0.206
gi|4758774	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	0.755		0.954	2	0.855	0.141
gi|4884343	hypothetical protein	0.865		0.844	1	0.855	0.015
gi|825671	B23 nucleophosmin (280 AA)	0.79	0.877	0.897	5	0.855	0.057
gi|35431	unnamed protein product	0.869	0.898	0.798	2	0.855	0.051
gi|18104989	protein tyrosine phosphatase, non-receptor type 6 isoform 1	0.851	0.934	0.78	3	0.855	0.077
gi|603074	ATP:citrate lyase	0.867	0.67	1.03	1	0.856	0.180
gi|4507793	ubiquitin-conjugating enzyme E2N	0.892	0.965	0.715	2	0.857	0.129
gi|338043	Human pre-mRNA splicing factor SF2p32, complete sequence.	0.93		0.785	2	0.858	0.103
gi|1263196	AICAR formyltransferase/IMP cyclohydrolase bifunctional enzyme	0.853	0.919	0.801	5	0.858	0.059
gi|5107637	Chain C, Structure Of The Karyopherin Beta2-Ran Gppnhp Nuclear Transport Complex	0.877	0.886	0.81	5	0.858	0.042
gi|4885287	guanine nucleotide binding protein (G protein), gamma 5	0.878	0.846	0.849	3	0.858	0.018
gi|190447	prosomal protein P30-33K	0.886	1.044	0.643	3	0.858	0.202
gi|32187319	SHUJUN-1	0.833	0.877	0.865	1	0.858	0.023

gi|183353	glycogen phosphorylase (EC 2.4.1.1)	0.76		0.957	2	0.859	0.139
gi|187281	M4 protein	0.857	0.836	0.884	5	0.859	0.024
gi|40353734	nucleophosmin 1 isoform 2	0.885	0.849	0.845	5	0.860	0.022
gi|1041969	17 kda cyclophilin A {internal fragment}	0.853	0.87	0.857	3	0.860	0.009
gi|4502171	adenine phosphoribosyltransferase isoform a	0.897	0.855	0.828	5	0.860	0.035
gi|4827050	ubiquitin specific protease 14 isoform a	0.917	0.889	0.775	5	0.860	0.075
gi|339878	tripeptidyl peptidase II	0.921	0.749	0.913	4	0.861	0.097
gi|114606879	ribosomal protein isoform 2	0.866	0.905	0.813	3	0.861	0.046
gi|4506613	ribosomal protein L22 proprotein	0.826	0.75	1.009	2	0.862	0.133
gi|114572020	small nuclear ribonucleic protein isoform 2		0.872	0.852	1	0.862	0.014
gi|495126	ribosomal protein L11	0.766	0.975	0.845	3	0.862	0.106
gi|531171	Csa-19	0.719	0.834	1.036	5	0.863	0.160
gi|292160	heat shock protein 70	0.865	0.772	0.952	1	0.863	0.090
gi|5453539	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase isoform 2	0.805	0.847	0.937	5	0.863	0.067
gi|4501867	aconitase 2 precursor	0.887	0.913	0.79	5	0.863	0.065
gi|5174529	methionine adenosyltransferase II, alpha	0.719	0.851	1.022	2	0.864	0.152
gi|5031755	heterogeneous nuclear ribonucleoprotein R isoform 2	0.861	0.973	0.764	3	0.866	0.105
gi|126030593	Chain A, Crystal Structure Of Human Paics, A Bifunctional Carboxylase And Synthetase In Purine Biosynthesis	0.805	0.847	0.948	5	0.867	0.074
gi|119620390	chaperonin containing TCP1, subunit 4 (delta), isoform CRA_a	0.809	0.831	0.96	2	0.867	0.082
gi|5031512	NSAP1 protein	0.841	0.859	0.9	2	0.867	0.030
gi|7341255	brain acetylcholinesterase putative membrane anchor	0.83	0.94	0.831	2	0.867	0.063
gi|159162145	Chain A, Rotamer Strain As A Determinant Of Protein Structural Specificity	0.911	0.828	0.863	2	0.867	0.042
gi|63055057	actin, beta-like 2	0.878	0.827	0.897	5	0.867	0.036
gi|119570260	hCG1642531	0.757	0.811	1.036	3	0.868	0.148
gi|6677809	ribosomal protein S6	0.921	0.879	0.804	3	0.868	0.059
gi|57209813	tubulin, beta	0.825		0.912	3	0.869	0.062
gi|119619571	proteasome (prosome, macropain) subunit, alpha type, 4, isoform CRA_b	0.921	0.932	0.756	2	0.870	0.099
gi|24485	unnamed protein product	0.869	1.02	0.723	2	0.871	0.149
gi|56204904	synaptotagmin binding, cytoplasmic RNA interacting protein	0.861	0.973	0.78	2	0.871	0.097
gi|158259895	unnamed protein product	0.819	0.931	0.865	3	0.872	0.056
gi|7739447	hnRNP 2H9D	0.925	0.803	0.887	1	0.872	0.062
gi|4506723	ribosomal protein S3a		0.953	0.792	5	0.873	0.114
gi|4506185	proteasome alpha 4 subunit isoform 1	0.958	0.923	0.739	2	0.873	0.118
gi|40807091	GANAB protein	0.924		0.823	5	0.874	0.071
gi|119592221	ribosomal protein S4, X-linked, isoform CRA_a		0.863	0.884	3	0.874	0.015
gi|25777600	proteasome 26S non-ATPase subunit 1	0.941	0.904	0.778	1	0.874	0.085
gi|4826659	F-actin capping protein beta subunit	0.992	0.924	0.708	3	0.875	0.148
gi|33875631	ANP32A protein	0.847	0.971	0.806	3	0.875	0.086

gi|5174735	tubulin, beta, 2	0.864	0.838	0.922	5	0.875	0.043
gi|221040138	unnamed protein product	0.883	0.804	0.938	3	0.875	0.067
gi|904032	p48	0.895	0.886	0.845	5	0.875	0.027
gi|4505585	platelet-activating factor acetylhydrolase, isoform Ib, beta subunit	0.88	0.844	0.903	2	0.876	0.030
gi|4503483	eukaryotic translation elongation factor 2	0.862	0.811	0.956	5	0.876	0.074
gi|79160090	NME1-NME2 protein	0.909	0.877	0.844	3	0.877	0.033
gi|169213772	actin alpha 1 skeletal muscle protein	0.946	0.963	0.723	1	0.877	0.134
gi|150261226	Chain B, Crystal Structure Of Human Gins Complex	0.774	0.923	0.937	3	0.878	0.090
gi|4758416	golgi-specific brefeldin A resistant guanine nucleotide exchange factor 1	0.774	0.923	0.937	5	0.878	0.090
gi|169165130	predicted protein	0.774	0.923	0.937	2	0.878	0.090
gi|5106785	HSPC027	0.855	0.843	0.937	5	0.878	0.051
gi|2981743	Chain A, Secypa Complexed With Hagpia (Pseudo-Symmetric Monomer)	0.97	0.831	0.835	5	0.879	0.079
gi|190238	nucleolar phosphoprotein B23	0.798	1.028	0.811	5	0.879	0.129
gi|37928159	Chain A, X-Ray Structure Of Human Nucleoside Diphosphate Kinase A Complexed With Adp At 2 A Resolution	0.817	0.873	0.95	3	0.880	0.067
gi|4503327	cytochrome b5 reductase isoform m	0.907	0.801	0.932	1	0.880	0.070
gi|6841170	HSPC260	0.857	0.906	0.878	2	0.880	0.025
gi|40788877	KIAA0139	0.737	0.945	0.961	5	0.881	0.125
gi|60552225	SHMT2 protein	0.97	0.795	0.88	3	0.882	0.088
gi|5901922	cell division cycle 37 protein	0.967	0.621	1.059	1	0.882	0.231
gi|119587078	hCG1983504, isoform CRA_f	0.801	0.838	1.009	3	0.883	0.111
gi|7020147	unnamed protein product	0.736	0.961	0.952	1	0.883	0.127
gi|58761496	heterogeneous nuclear ribonucleoprotein A1-like	0.875		0.891	3	0.883	0.011
gi|6714232	lymphocyte antigen	0.77	1.028	0.852	1	0.883	0.132
gi|31418053	CCT8 protein	0.847	0.943	0.861	5	0.884	0.052
gi|4826760	heterogeneous nuclear ribonucleoprotein F	0.805	0.855	0.992	5	0.884	0.097
gi|5453603	chaperonin containing TCP1, subunit 2	0.879	1.106	0.668	5	0.884	0.219
gi|1905998	nuclear RNA helicase	0.992	0.921	0.742	2	0.885	0.129
gi|119625894	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase, isoform CRA_a	0.805	0.914	0.937	2	0.885	0.071
gi|4506607	ribosomal protein L18	0.921	0.937	0.799	2	0.886	0.561
gi|14251209	chloride intracellular channel 1	0.903	0.867	0.889	5	0.886	0.018
gi|7656952	calcyclin binding protein isoform 1	0.951	1	0.708	4	0.886	0.156
gi|4506715	ribosomal protein S28	0.717	0.928	1.015	3	0.887	0.153
gi|2662291	cytochrome b5	0.916		0.858	2	0.887	0.041
gi|33413400	esterase D/formylglutathione hydrolase	0.858	0.998	0.809	8	0.888	0.098
gi|36142	ribosomal protein homologous to yeast S24	0.766	0.918	0.982	1	0.889	0.111
gi|6841532	HSPC155	0.886	0.901	0.884	1	0.890	0.009
gi|348012	neutral amino acid transporter	0.942	0.92	0.811	3	0.891	0.070
gi|9836652	BSCv	0.892		0.891	1	0.892	0.001

gi|9845297	diablo isoform 1 precursor	0.82	0.866	0.99	2	0.892	0.088
gi|36038	rho GDP dissociation inhibitor (GDI)	0.8	0.918	0.96	2	0.893	0.083
gi|763130	YPT3	0.964	0.913	0.801	5	0.893	0.083
gi|4506675	ribophorin I precursor	0.96	0.848	0.871	2	0.893	0.059
gi|119618535	hCG2016250, isoform CRA_d	1.006		0.78	2	0.893	0.160
gi|38014635	SFPQ protein	0.878	0.9	0.904	5	0.894	0.014
gi|10441901	unknown	0.837	0.794	1.053	2	0.895	0.139
gi|34147513	RAB7, member RAS oncogene family	0.911	0.917	0.856	5	0.895	0.034
gi|15928389	Unknown (protein for IMAGE:4158571)	0.885	0.827	0.976	2	0.896	0.075
gi|83699649	heat shock 90kDa protein 1, alpha	0.975	0.929	0.784	5	0.896	0.100
gi|1419567	dynactin	0.848	0.966	0.874	1	0.896	0.062
gi|23879	40kDa protein kinase	0.993	0.737	0.962	2	0.897	0.140
gi|114794171	Chain A, Crystal Structure Of Rab11 In Complex With Rab11-Fip2	0.777	1.168	0.748	3	0.898	0.235
gi|32532	unnamed protein product	0.892	0.91	0.891	5	0.898	0.011
gi|4501893	actinin, alpha 2	0.868	0.884	0.942	5	0.898	0.039
gi|550023	ribosomal protein S9	0.872	0.906	0.916	5	0.898	0.023
gi|13097759	Unknown (protein for IMAGE:3544292)		0.954	0.843	5	0.899	0.078
gi|2246558	talin-related protein	1.008	0.949	0.739	3	0.899	0.141
gi|553640	ribosomal protein S13	1.073	0.723	0.904	1	0.900	0.175
gi|4588526	nuclear chloride channel	0.869	0.954	0.878	3	0.900	0.047
gi|157838211	Chain A, Human Platelet Profilin Complexed With The L-Pro10 Peptide	0.951	0.945	0.805	5	0.900	0.083
gi|4929561	CGI-46 protein	0.913	0.882	0.908	3	0.901	0.017
gi|4506691	ribosomal protein S16	0.704	1.115	0.885	5	0.901	0.206
gi|5454154	peptidylprolyl isomerase H	0.97	0.899	0.836	5	0.902	0.067
gi|7706322	homeobox prox 1	0.895		0.909	1	0.902	0.010
gi|119577215	actinin, alpha 4, isoform CRA_c		0.973	0.832	5	0.903	0.100
gi|55958333	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	0.819	0.957	0.932	1	0.903	0.074
gi|4505999	protein phosphatase 1G	0.907	0.739	1.062	1	0.903	0.162
gi|5803225	tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon polypeptide	0.793	0.967	0.949	5	0.903	0.096
gi|75709200	glutathione peroxidase 4 isoform A precursor	0.831		0.975	2	0.903	0.102
gi|21956645	myotrophin	0.898	0.954	0.858	1	0.903	0.048
gi|4757756	annexin A2 isoform 2	0.927	0.737	1.047	1	0.904	0.156
gi|4506703	ribosomal protein S24 isoform c	0.804	1.019	0.891	3	0.905	0.108
gi|119575011	ribosomal protein S24, isoform CRA_i	0.804	1.019	0.891	3	0.905	0.108
gi|1065361	Chain A, Human Adp-Ribosylation Factor 1 Complexed With Gdp, Full Length Non-Myristoylated	0.822	0.866	1.026	1	0.905	0.107
gi|119616784	hCG22922	0.858	0.934	0.923	1	0.905	0.041
gi|1060888	human 26S proteasome subunit p97	0.811	1.04	0.867	5	0.906	0.119
gi|187302	epithelial cell marker protein 1	0.834	0.958	0.928	5	0.907	0.065
gi|74762505	Protein FAM10A4	0.94	1.074	0.706	2	0.907	0.186
gi|4502303	mitochondrial ATP synthase, O subunit precursor	0.78	0.858	1.083	3	0.907	0.157

gi|83674986	rcTPM3	0.857	0.865	1.002	5	0.908	0.082
gi|21104402	IMR-90 ribosomal protein S3	0.914	0.905	0.906	5	0.908	0.005
gi|5803187	transaldolase 1	0.884	1.051	0.793	2	0.909	0.131
gi|35493916	ribophorin II isoform 1 precursor	0.95	1.056	0.723	3	0.910	0.170
gi|2959876	synaptogyrin 2	0.896	0.828	1.006	1	0.910	0.090
gi|54696890	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	0.91	0.961	0.861	5	0.911	0.050
gi|112490030	Chain A, Charged And Uncharged Trnas Adopt Distinct Conformations When Complexed With Human Tryptophanyl-Trna Synthetase	0.837	1.06	0.838	3	0.912	0.128
gi|4557581	fatty acid binding protein 5 (psoriasis-associated)	0.762	0.869	1.105	3	0.912	0.175
gi|551638	SSR alpha subunit	0.985		0.839	1	0.912	0.103
gi|4506679	ribosomal protein S10	1.014	0.834	0.888	3	0.912	0.092
gi|4506181	proteasome alpha 2 subunit	0.919	0.899	0.918	2	0.912	0.011
gi|4506743	ribosomal protein S8	0.91	0.922	0.905	5	0.912	0.009
gi|20149594	heat shock 90kDa protein 1, beta	0.943	0.923	0.871	5	0.912	0.037
gi|32177	HLA-B27	0.862		0.966	1	0.914	0.074
gi|1296662	plectin	0.861	0.945	0.936	3	0.914	0.046
gi|14110407	heterogeneous nuclear ribonucleoprotein D-like	0.771	0.963	1.009	3	0.914	0.126
gi|4507949	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	0.834	0.981	0.928	5	0.914	0.074
gi|119572749	ribosomal protein L18, isoform CRA_f	1.035	0.924	0.785	5	0.915	0.125
gi|35438	unnamed protein product	0.693	0.986	1.067	5	0.915	0.197
gi|5454052	stratifin	0.883	0.914	0.949	5	0.915	0.033
gi|4826898	profilin 1	0.939	1.024	0.783	2	0.915	0.122
gi|55859728	CAP, adenylate cyclase-associated protein 1 (yeast)	1.008	0.673	1.066	1	0.916	0.212
gi|4557361	BH3 interacting domain death agonist isoform 2	0.824		1.008	2	0.916	0.130
gi|95113651	glutaredoxin 3	0.984	0.928	0.836	1	0.916	0.075
gi|1498488	osteoclast stimulating factor	0.749	0.966	1.034	3	0.916	0.149
gi|6110350	Traf2 and NCK interacting kinase, splice variant 2	0.896	0.881	0.973	2	0.917	0.049
gi|5453599	capping protein (actin filament) muscle Z-line, alpha 2	0.924	0.869	0.957	1	0.917	0.044
gi|4507947	tyrosyl-tRNA synthetase	0.925	0.842	0.983	3	0.917	0.071
gi|48257056	TALDO1 protein	0.974	1.005	0.772	5	0.917	0.127
gi|4507785	ubiquitin-conjugating enzyme E2I	0.854	1.022	0.876	5	0.917	0.091
gi|8922331	mago-nashi homolog B	0.884	0.929	0.94	5	0.918	0.030
gi|24119203	tropomyosin 3 isoform 2	0.936	0.865	0.952	5	0.918	0.046
gi|4501887	actin, gamma 1 propeptide	0.868	0.931	0.957	5	0.919	0.046
gi|8922699	CNDP dipeptidase 2	0.933	0.898	0.925	4	0.919	0.018
gi|10834730	PP856	0.933	0.898	0.925	4	0.919	0.018
gi|114578542	Methionine adenosyltransferase II, alpha isoform 4	0.969	0.833	0.954	1	0.919	0.075
gi|913159	neuropolypeptide h3	0.852	0.91	0.995	5	0.919	0.072
gi|4506003	protein phosphatase 1, catalytic subunit, alpha isoform 1	0.863	0.933	0.964	3	0.920	0.052
gi|119620366	malate dehydrogenase 1, NAD (soluble), isoform CRA_b	0.903		0.937	1	0.920	0.024

gi|729422	Alpha-enolase, lung specific (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (HLE1)	0.92	1.039	0.802	3	0.920	0.119
gi|4505591	peroxiredoxin 1	0.821	0.89	1.051	5	0.921	0.118
gi|194375974	unnamed protein product	0.821	0.89	1.051	5	0.921	0.118
gi|4757768	Rho GDP dissociation inhibitor (GDI) alpha	1.048	0.907	0.807	3	0.921	0.121
gi|58652133	tropomyosin 3	0.826	0.894	1.045	5	0.922	0.112
gi|1633054	Chain A, Cyclophilin A Complexed With Dipeptide Gly-Pro	0.908	0.905	0.953	3	0.922	0.027
gi|119596301	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide, isoform CRA_b	0.834	0.981	0.955	5	0.923	0.078
gi|437363	14-3-3n	0.865	0.956	0.949	5	0.923	0.051
gi|1478281	neutral amino acid transporter B	0.907	0.884	0.98	2	0.924	0.050
gi|194379742	unnamed protein product	0.97	1.041	0.76	1	0.924	0.146
gi|52545896	hypothetical protein	0.883	0.887	1.003	5	0.924	0.068
gi|119613432	hCG20693, isoform CRA_a	0.936	0.869	0.968	2	0.924	0.051
gi|119574084	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, isoform CRA_h	0.967	0.871	0.936	3	0.925	0.049
gi|4506381	ras-related C3 botulinum toxin substrate 2	0.861	0.901	1.017	5	0.926	0.081
gi|307383	RNA helicase A	0.905	0.921	0.953	5	0.926	0.024
gi|18379349	vesicle amine transport protein 1	1.024	0.987	0.768	1	0.926	0.138
gi|197099116	signal recognition particle 14kDa	1.049	0.774	0.956	5	0.926	0.140
gi|5453595	adenylyl cyclase-associated protein	0.971	1.035	0.774	3	0.927	0.136
gi|119590106	hCG27371	0.928	1.02	0.833	2	0.927	0.094
gi|119614893	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor), isoform CRA_b	0.916	0.921	0.947	5	0.928	0.017
gi|207080252	DKFZP468I0328 protein	0.928	1.024	0.833	5	0.928	0.096
gi|546518	stearoyl-CoA desaturase; delta-9-desaturase	1.016		0.841	1	0.929	0.124
gi|23491733	ribosomal protein S2	0.865	0.901	1.021	5	0.929	0.082
gi|169216555	hypothetical protein	0.989	0.827	0.972	1	0.929	0.089
gi|119627559	peptidylprolyl isomerase H (cyclophilin H), isoform CRA_d	1.084	0.667	1.037	2	0.929	0.228
gi|113404817	TRIMCyp	1.084	0.667	1.037	3	0.929	0.228
gi|190359598	Putative heat shock protein HSP 90-beta 2	0.924	0.925	0.941	5	0.930	0.010
gi|13376840	WD repeat domain 61	0.971		0.891	1	0.931	0.057
gi|693933	2-phosphopyruvate-hydratase alpha-enolase; carbonate dehydratase	0.794	0.942	1.058	5	0.931	0.132
gi|4758112	HLA-B associated transcript 1	0.888	0.763	1.146	3	0.932	0.195
gi|119619008	phosphoglycerate kinase 1, isoform CRA_a	0.938	0.96	0.901	2	0.933	0.030
gi|1008542	ubiquitin isopeptidase T	0.898	0.972	0.929	2	0.933	0.037
gi|4507181	sialophorin	0.933	0.966	0.901	5	0.933	0.033
gi|3157976	alpha actinin	0.864	0.933	1.004	5	0.934	0.070
gi|114682581	p21-Arc isoform 3	0.969	0.936	0.896	5	0.934	0.037
gi|4504169	glutathione synthetase	0.899	0.881	1.022	2	0.934	0.077
gi|914957	Ash-m	0.887	0.969	0.947	3	0.934	0.042
gi|4506695	ribosomal protein S19	0.972		0.897	3	0.935	0.053
gi|6005842	proline synthetase co-transcribed homolog		0.893	0.977	2	0.935	0.059

gi|4506749	ribonucleoside-diphosphate reductase M1 chain	1.003		0.868	1	0.936	0.095
gi|15088795	phosphatidylinositol glycan anchor biosynthesis, class S	1.068		0.803	1	0.936	0.187
gi|4506183	proteasome alpha 3 subunit isoform 1	0.857	0.983	0.967	3	0.936	0.069
gi|8099350	33 kDa Vamp-associated protein	0.889	0.952	0.966	1	0.936	0.041
gi|19923264	Ras-related protein Rab-27A	0.939	0.908	0.961	2	0.936	0.027
gi|119609127	triosephosphate isomerase 1, isoform CRA_a	0.926	1.077	0.811	2	0.938	0.133
gi|1421609	Chain A, X-Ray Structure Of Nm23 Human Nucleoside Diphosphate Kinase B Complexed With Gdp At 2 Angstroms Resolution	0.837	0.906	1.072	5	0.938	0.121
gi|48145663	RPL7	1.014	0.811	0.99	5	0.938	0.111
gi|4507149	superoxide dismutase 1, soluble	1.033	1.075	0.709	1	0.939	0.200
gi|558528	proteasome subunit Y	0.835	0.914	1.068	4	0.939	0.118
gi|930063	neurone-specific enolase	0.949	1.102	0.767	5	0.939	0.168
gi|5730031	secretory carrier membrane protein 2	1.072	0.816	0.93	1	0.939	0.128
gi|40889610	Chain A, Crystal Structure Of Human Tryptophanyl-Trna Synthetase	0.894	1.009	0.917	3	0.940	0.061
gi|7661922	RAB21, member RAS oncogene family		0.908	0.973	1	0.941	0.046
gi|4507797	ubiquitin-conjugating enzyme E2v2	0.989	0.962	0.871	3	0.941	0.062
gi|306553	ribosmal protein small subunit	0.893	0.84	1.091	2	0.941	0.132
gi|5730023	RuvB-like 2	0.98	0.948	0.897	3	0.942	0.042
gi|12653279	ACAT2 protein	0.906	0.957	0.963	2	0.942	0.031
gi|4505257	moesin	0.956	0.986	0.884	5	0.942	0.052
gi|433308	capping protein alpha	0.924	0.947	0.957	2	0.943	0.017
gi|5453597	F-actin capping protein alpha-1 subunit	0.924	0.947	0.957	4	0.943	0.017
gi|4502205	ADP-ribosylation factor 4	0.858	1.008	0.963	5	0.943	0.077
gi|183182	guanine nucleotide-binding regulatory protein alpha-inhibitory subunit	0.966	0.907	0.957	2	0.943	0.032
gi|5031595	actin related protein 2/3 complex subunit 4 isoform a	0.907	0.942	0.982	5	0.944	0.038
gi|10436409	unnamed protein product	0.907	0.942	0.982	5	0.944	0.038
gi|119590239	ADP-ribosylation factor 1, isoform CRA_b	0.858	1.011	0.963	3	0.944	0.078
gi|15431303	ribosomal protein L9	0.84	0.942	1.051	4	0.944	0.106
gi|7018426	hypothetical protein	0.952	0.946	0.935	3	0.944	0.009
gi|2739119	BAT1	0.896	0.904	1.037	4	0.946	0.079
gi|39645256	MYH14 protein	0.766		1.126	5	0.946	0.255
gi|494066	Chain A, Three-Dimensional Structure Of Class Pi Glutathione S-Transferase From Human Placenta In Complex With S-Hexylglutathione At 2.8 Angstroms Resolution	0.798	0.989	1.051	5	0.946	0.132
gi|895845	p64 CLCP	1.025	1.098	0.715	1	0.946	0.203
gi|4826998	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	0.858	0.985	0.997	2	0.947	0.077
gi|1871210	T-complex protein 1, Beta subunit (TCP-1-BETA)	0.929	0.939	0.972	1	0.947	0.023
gi|114651523	L-plastin isoform 3	0.989	0.902	0.95	2	0.947	0.044
gi|9910460	nitrilase family, member 2	0.973	1.063	0.807	2	0.948	0.130
gi|34616	beta-2 microglobulin	0.756	0.816	1.272	2	0.948	0.282

gi|197725116	Chain A, A Regulatable Switch Mediates Self-Association In An Immunoglobulin Fold	0.756	0.816	1.272	4	0.948	0.282
gi|4505587	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit 29kDa	0.907	1.177	0.76	1	0.948	0.212
gi|5902134	coronin, actin binding protein, 1A	0.889	0.953	1.003	5	0.948	0.057
gi|9507245	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	0.883	0.914	1.05	5	0.949	0.089
gi|4557032	L-lactate dehydrogenase B	0.897	0.981	0.971	5	0.950	0.046
gi|119625804	moesin, isoform CRA_b	0.871	0.963	1.022	5	0.952	0.076
gi|1718502	mitochondrial aconitase		0.899	1.005	2	0.952	0.075
gi|4507133	small nuclear ribonucleoprotein polypeptide G	0.969	0.898	0.993	3	0.953	0.049
gi|18466808	cervical cancer 1 proto-oncogene-binding protein KG19	0.883	1.184	0.793	1	0.953	0.205
gi|190875	ras-like protein	1.002	0.883	0.976	4	0.954	0.063
gi|4758984	Ras-related protein Rab-11A	0.803	1.023	1.036	2	0.954	0.131
gi|438069	thiol-specific antioxidant protein	0.871	1.019	0.972	2	0.954	0.076
gi|183709	small G protein	1.002	0.885	0.976	3	0.954	0.061
gi|4503571	enolase 1	0.945	0.867	1.052	5	0.955	0.093
gi|5822569	Chain A, Crystal Structure Of Hgstp1-1[v104] Complexed With The Gsh Conjugate Of (+)-Anti-Bpde	0.798	0.989	1.08	5	0.956	0.144
gi|7524346	adenylate kinase 2 isoform b	0.887	1.065	0.916	5	0.956	0.096
gi|5031593	actin related protein 2/3 complex subunit 5	0.913	1	0.957	3	0.957	0.044
gi|5453549	thioredoxin peroxidase	0.9	0.965	1.006	2	0.957	0.053
gi|4507953	tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypeptide	0.981	0.96	0.931	5	0.957	0.025
gi|5803181	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	1.025	0.897	0.952	5	0.958	0.064
gi|7657176	canopy 2 homolog	0.879	0.991	1.006	5	0.959	0.069
gi|62897413	pyruvate kinase 3 isoform 1 variant	0.971	1.031	0.877	5	0.960	0.078
gi|82407989	Chain A, Crystal Structure Of Human Tyrosine Phosphatase Shp-1	1.015	0.996	0.868	2	0.960	0.080
gi|4506193	proteasome beta 1 subunit	0.861	0.899	1.12	5	0.960	0.140
gi|511635	delta3, delta2-enoyl-CoA isomerase	1.085		0.835		0.960	0.177
gi|74739412	Kappa-actin	0.985	0.978	0.918	5	0.960	0.037
gi|2804273	alpha actinin 4	0.894	0.943	1.046	5	0.961	0.078
gi|28334	unnamed protein product	0.871	0.966	1.047	5	0.961	0.088
gi|5031599	actin related protein 2/3 complex subunit 2	0.98	0.97	0.935	2	0.962	0.024
gi|825728	ubiquitin precursor	0.911	0.986	0.992	5	0.963	0.045
gi|425553	beta-fodrin	1.032	0.826	1.031	2	0.963	0.119
gi|56966036	Chain A, Three Crystal Structures Of Human Coactosin-Like Protein	0.927	1.059	0.907	5	0.964	0.083
gi|7705433	eukaryotic translation initiation factor 3 subunit 6 interacting protein	0.895		1.034		0.965	0.098
gi|251370	acid phosphatase isoenzyme Af	1.021	1.001	0.873	5	0.965	0.080
gi|460789	transformation upregulated nuclear protein	0.925	0.777	1.193	1	0.965	0.211
gi|221042722	unnamed protein product	0.848	1.036	1.013	3	0.966	0.103
gi|4504067	aspartate aminotransferase 1	1.037	1.105	0.757	3	0.966	0.184
gi|4505701	pyridoxal kinase	1.019	0.942	0.94	4	0.967	0.045

gi|1096024	isoAsp protein carboxyl methyltransferase	1.158		0.777	3	0.968	0.269
gi|9802306	DNA-binding protein TAXREB107	0.76	1.039	1.104	3	0.968	0.183
gi|14625824	moesin/anaplastic lymphoma kinase fusion protein	0.866	1.035	1.003	5	0.968	0.090
gi|62087548	L-plastin variant	0.882	1.032	0.991	2	0.968	0.078
gi|16758368	RAB14, member RAS oncogene family	0.995	0.966	0.954	2	0.972	0.021
gi|5031597	actin related protein 2/3 complex subunit 3	0.969	0.936	1.011	3	0.972	0.038
gi|5114051	HSPC029		0.891	1.053	3	0.972	0.115
gi|4092058	proteasome subunit HSPC	0.898	0.895	1.123	5	0.972	0.131
gi|6005942	valosin-containing protein	0.922	0.962	1.033	5	0.972	0.056
gi|119578807	valosin-containing protein, isoform CRA_a	0.922	0.962	1.033	2	0.972	0.056
gi|35505	pyruvate kinase	0.971	1.031	0.915	5	0.972	0.058
gi|194382944	unnamed protein product	0.966		0.979	2	0.973	0.009
gi|4507791	ubiquitin-conjugating enzyme E2M	0.85	0.976	1.092	5	0.973	0.121
gi|3095186	cargo selection protein TIP47	0.978	0.95	0.99	2	0.973	0.021
gi|119593417	hCG31916	1.175		0.771	2	0.973	0.286
gi|4507357	transgelin 2	0.824	0.823	1.277	4	0.975	0.262
gi|221039844	unnamed protein product	0.819	1.099	1.006	3	0.975	0.143
gi|14488680	Chain A, Crystal Structure Of Human Phosphoglucose IsomeraseNEUROLEUKINAUTOCRINE MOTILITY FACTORMATURATION Factor	1.012	1	0.913	5	0.975	0.054
gi|609308	cytoplasmic chaperonin hTRiC5	0.924	1.17	0.833	1	0.976	0.174
gi|37492	alpha-tubulin	0.968	1.016	0.943	5	0.976	0.037
gi|312005	small nuclear ribonucleoprotein E		0.971	0.982	1	0.977	0.008
gi|178027	alpha-actin	0.682	1.193	1.055	2	0.977	0.264
gi|157831085	Chain A, Atomic Structure Of The Rapamycin Human Immunophilin Fkbp- 12 Complex	0.865	0.94	1.125	5	0.977	0.134
gi|169163387	peptidyl-Pro cis trans isomerase	0.938	0.996	0.997	1	0.977	0.034
gi|119594429	eukaryotic translation elongation factor 1 gamma, isoform CRA_a	0.977	0.998	0.956	3	0.977	0.021
gi|4506031	palmitoyl-protein thioesterase 1 isoform 1 precursor	0.917	0.93	1.085	2	0.977	0.093
gi|114631695	alpha-smooth muscle actin isoform 2	1.021	1.003	0.908	5	0.977	0.061
gi|189036	nonmuscle myosin heavy chain (NMHC)	0.851		1.105	2	0.978	0.180
gi|825667	phospholipid hydroperoxide glutathione peroxidase	0.851		1.105	2	0.978	0.180
gi|4505185	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	0.89	0.962	1.082	5	0.978	0.097
gi|999892	Chain A, Crystal Structure Of Recombinant Human Triosephosphate Isomerase At 2.8 Angstroms Resolution. Triosephosphate Isomerase Related Human Genetic Disorders And Comparison With The Trypanosomal Enzyme	0.928	1.007	0.999	5	0.978	0.043
gi|16740986	FAM49B protein	1.058	0.979	0.897	5	0.978	0.081
gi|62088022	hypothetical protein FLJ41407 variant	1.035	0.924	0.976	2	0.978	0.056
gi|50514025	Chain A, Structure Of T70n Human Lysozyme	0.991	0.996	0.949	3	0.979	0.026
gi|41406084	glutathione peroxidase 1 isoform 1	0.991	0.869	1.078	3	0.979	0.105

gi|157835340	Chain A, Contribution Of Hydrophobic Effect To The Conformational Stability Of Human Lysozyme	0.972	0.907	1.061	5	0.980	0.077
gi|62896495	ribosomal protein P0 variant	1.094	0.762	1.085	3	0.980	0.189
gi|194388126	unnamed protein product	1.094	0.762	1.085	3	0.980	0.189
gi|46309463	vitamin K epoxide reductase complex, subunit 1-like 1	0.837	1.026	1.079	1	0.981	0.127
gi|4502013	adenylate kinase 2 isoform a	0.887	1.065	0.992	5	0.981	0.089
gi|119590453	EDAR-associated death domain, isoform CRA_a	0.994	1.029	0.921	2	0.981	0.055
gi|193785841	unnamed protein product	1.002	0.992	0.952	5	0.982	0.026
gi|74757451	Galectin-9C	1.041		0.923	2	0.982	0.083
gi|169161841	hCG1795719	1.041		0.923	1	0.982	0.083
gi|180637	L-isoaspartyl/D-aspartyl protein carboxyl methyltransferase	1.013	0.99	0.944	5	0.982	0.035
gi|4506635	ribosomal protein L32	1.047	0.904	0.996	1	0.982	0.072
gi|386758	GRP78 precursor	0.978	0.978	0.992	5	0.983	0.008
gi|1220311	elongation factor-1 alpha	0.911	0.829	1.209	3	0.983	0.200
gi|10863927	peptidylprolyl isomerase A	0.988	0.967	0.994	5	0.983	0.014
gi|119624305	splicing factor, arginine/serine-rich 3, isoform CRA_c	0.919	1.011	1.02	5	0.983	0.056
gi|68533125	ACLY variant protein	1.09	0.854	1.01	2	0.985	0.120
gi|285975	human rab GDI	0.824	0.969	1.162	4	0.985	0.170
gi|4960030	Rab GDP dissociation inhibitor beta	0.824	0.969	1.162	3	0.985	0.170
gi|4504165	gelsolin isoform a precursor	0.938		1.032	2	0.985	0.066
gi|27734452	Ras-related protein Rab-15	0.938	0.967	1.053	3	0.986	0.060
gi|434753	KIAA0030	1.133		0.839	5	0.986	0.208
gi|60593722	Chain A, The Crystal Structure Of Human Coactosin-Like Protein At 1.9 A Resolution	0.927	1.124	0.907	5	0.986	0.120
gi|23272533	ACTR2 protein	0.822	1.05	1.087	3	0.986	0.144
gi|996057	gp25l2	0.952	1.036	0.972	3	0.987	0.044
gi|2340104	Very similar and perhaps identical to Hs-CUL-4B.; 80-100% similarity to partial sequence U58091 (PID:g1381150).	0.959	1.129	0.872	2	0.987	0.131
gi|13129092	transmembrane protein 109	1.044	1.023	0.895	2	0.987	0.081
gi|7106387	proteasome (prosome, macropain) subunit, alpha type 5	0.871	1.14	0.955	5	0.989	0.138
gi|234746	RAS-related protein MEL	0.943	0.969	1.055	4	0.989	0.059
gi|12052930	hypothetical protein	1.002		0.976	2	0.989	0.018
gi|6005854	prohibitin 2	1.074	1.159	0.738	5	0.990	0.223
gi|1002923	coronin-like protein	0.932	1.061	0.98	1	0.991	0.065
gi|20127454	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	1.004	0.966	1.003	5	0.991	0.022
gi|4885281	glutamate dehydrogenase 1	0.811	1.177	0.986	3	0.991	0.183
gi|4502101	annexin I	0.995	0.989	0.992	5	0.992	0.003
gi|13385872	interleukin enhancer binding factor 2	0.904	1.039	1.035	2	0.993	0.077
gi|508285	Rab5c-like protein, similar to Canis familiaris Rab5c protein, PIR Accession Number S38625	0.933	1.177	0.868	4	0.993	0.163
gi|6006515	spliceosomal protein SAP 130	0.778	1.226	0.975	5	0.993	0.225
gi|1015321	alanyl-tRNA synthetase	0.989	1.034	0.957	5	0.993	0.039

gi|67464043	Chain O, Crsytal Structure Of Human Liver Gapdh	1.095	0.82	1.065	5	0.993	0.151
gi|5803135	RAB35, member RAS oncogene family	0.962	0.967	1.053	3	0.994	0.051
gi|4507651	tropomyosin 4 isoform 2	0.936	0.997	1.051	5	0.995	0.058
gi|5531851	homologous yeast-44.2 protein	1.056	0.89	1.04	3	0.995	0.092
gi|31170	unnamed protein product	0.942	0.995	1.051	5	0.996	0.055
gi|194387964	unnamed protein product	0.971	1.031	0.986	5	0.996	0.031
gi|38522	human elongation factor-1-delta	0.911	0.868	1.209	5	0.996	0.186
gi|860986	protein disulfide isomerase	1.013	0.963	1.013	5	0.996	0.029
gi|178152	poly(ADP-ribose) polymerase	1.156	1.045	0.789	1	0.997	0.188
gi|2392338	Chain A, Human Glyoxalase I With Benzyl-Glutathione Inhibitor	0.895	1.074	1.021	3	0.997	0.092
gi|6063143	ezrin	0.942	1.023	1.026	3	0.997	0.048
gi|296736	macropain subunit iota	1.002		0.993	5	0.998	0.006
gi|1218024	frataxin	1.062	0.986	0.945	1	0.998	0.059
gi|62087882	heat shock 70kDa protein 4 isoform a variant	1.212	0.755	1.026	3	0.998	0.230
gi|31615313	Chain A, Molecular Mechanism For The Regulation Of Human Mitochondrial Nad(P)+-Dependent Malic Enzyme By Atp And Fumarate	0.959	1.015	1.021	1	0.998	0.034
gi|113408761	hypothetical protein isoform 4	1.046		0.951	3	0.999	0.067
gi|6912594	phosphatidylinositol transfer protein, beta	1.062	0.98	0.954	3	0.999	0.056
gi|40674640	IQGAP1 protein	1.066	0.893	1.039	5	0.999	0.093
gi|62420949	actin-like protein	0.931	1.006	1.062	3	1.000	0.066
gi|119602173	heat shock protein 90kDa alpha (cytosolic), class A member 1, isoform CRA_b	0.951	1.005	1.045	3	1.000	0.047
gi|307375	multidrug resistance protein	1.04		0.961	2	1.001	0.056
gi|28876	ash protein	0.888	1.044	1.07	2	1.001	0.098
gi|31283	unnamed protein product	0.898	1.031	1.073	5	1.001	0.091
gi|21465651	Chain J, Crystal Structure Of The Mammalian 20s Proteasome At 2.75 A Resolution	0.951	1.016	1.036	3	1.001	0.044
gi|478813	nonhistone chromosomal protein HMG-1 - human	0.978	0.736	1.291	5	1.002	0.278
gi|7634785	HDCMC29P	1.014	0.978	1.013	3	1.002	0.021
gi|298588	tropomyosin, P40 {peak 47}	0.863	1.108	1.035	1	1.002	0.126
gi|338695	beta-tubulin	1.169	1.006	0.831	3	1.002	0.169
gi|72534660	splicing factor, arginine/serine-rich 7	0.919	1.011	1.08	5	1.003	0.081
gi|224052	transferase,HG phosphoribosyl	0.932	0.979	1.099	5	1.003	0.086
gi|6680045	guanine nucleotide-binding protein, beta-1 subunit	1.133		0.874	2	1.004	0.183
gi|6694937	nudix hydrolase NUDT5	1.265	0.922	0.824	3	1.004	0.232
gi|4505753	phosphoglycerate mutase 1 (brain)	0.892	1.011	1.108	5	1.004	0.108
gi|4506681	ribosomal protein S11	1.169	0.912	0.931	5	1.004	0.143
gi|4507677	heat shock protein 90kDa beta, member 1	1.037	0.981	0.996	5	1.005	0.029
gi|29888	unnamed protein product	1.089	0.846	1.079	3	1.005	0.138
gi|35959	tubulin 5-beta	1.151	0.888	0.975	5	1.005	0.134
gi|4506179	proteasome alpha 1 subunit isoform 2	0.952	1.005	1.058	5	1.005	0.053
gi|5825608	70 kDa SHP-1L protein		0.941	1.07	5	1.006	0.091

gi|6912388	grancalcin, EF-hand calcium binding protein	1.09	0.93	0.997	5	1.006	0.080
gi|338443	beta-spectrin	0.761	1.236	1.021	3	1.006	0.238
gi|405230	I-plastin	0.943	1.035	1.042	3	1.007	0.055
gi|6457378	cytovillin 2	0.949	1.079	0.992	5	1.007	0.066
gi|89574029	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit	1.046	1.036	0.94	5	1.007	0.059
gi|181250	cyclophilin	0.824	0.901	1.298	5	1.008	0.254
gi|4335941	leucine aminopeptidase	1.051	1.013	0.959	5	1.008	0.046
gi|4758440	glia maturation factor, gamma	0.998	1.101	0.925	3	1.008	0.088
gi|119623396	RAN binding protein 1, isoform CRA_e	1.004	0.802	1.218	1	1.008	0.208
gi|136066	Triosephosphate isomerase	1.01	1.008	1.006	3	1.008	0.002
gi|226529917	triosephosphate isomerase 1 isoform 2	1.01	1.013	1.002	5	1.008	0.006
gi|532313	NF45 protein	0.911	1.069	1.045	5	1.008	0.085
gi|37256	unnamed protein product	0.816	1.038	1.172	2	1.009	0.180
gi|119582950	annexin A1, isoform CRA_b	0.927	1.052	1.047	5	1.009	0.071
gi|542850	heterogeneous nuclear ribonucleoprotein G - human	1.116	0.982	0.93	5	1.009	0.096
gi|10433073	unnamed protein product	1.055	0.984	0.99	1	1.010	0.039
gi|31426	five-lipoxygenase activating protein (FLAP)	1.002	1.025	1.003	1	1.010	0.013
gi|4557305	fructose-bisphosphate aldolase A	1.019	1.064	0.948	5	1.010	0.058
gi|203282367	Chain A, Crystal Structure Of Human Enolase 1	0.953	0.995	1.084	5	1.011	0.067
gi|28395033	ras homolog gene family, member C precursor	1.064	1.018	0.951	2	1.011	0.057
gi|7661678	RAP1B, member of RAS oncogene family	0.978	1.087	0.972	3	1.012	0.065
gi|154146191	heat shock protein 90kDa alpha (cytosolic), class A member 1 isoform 2	0.954	1.021	1.064	5	1.013	0.055
gi|74722491	Putative heat shock protein HSP 90-beta 4	0.954	1.021	1.064	5	1.013	0.055
gi|229532	ubiquitin	1.026	0.943	1.071	5	1.013	0.065
gi|67191208	ubiquitin C	1.026	0.943	1.071	5	1.013	0.065
gi|194375179	unnamed protein product	0.908	1.008	1.125	5	1.014	0.109
gi|15620780	glutamate carboxypeptidase		0.979	1.049	2	1.014	0.049
gi|16507237	heat shock 70kDa protein 5	1.016	1.045	0.982	2	1.014	0.032
gi|114651555	L-plastin isoform 2	0.983	1.02	1.042	5	1.015	0.030
gi|13366090	ribosomal protein L7a	1.054	1.142	0.849	2	1.015	0.150
gi|4503519	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa	1.078	1.186	0.783	1	1.016	0.209
gi|4758796	developmentally regulated GTP binding protein 1	0.782	1.236	1.031	1	1.016	0.227
gi|73765546	ubiquitin-conjugating enzyme E2 variant 1 isoform d	0.993	1.131	0.926	5	1.017	0.105
gi|533693	mitochondrial glycerol-3-phosphate dehydrogenase	1.112	0.873	1.066	3	1.017	0.127
gi|22538465	proteasome beta 3 subunit	1.046	1.034	0.972	3	1.017	0.040
gi|7019485	programmed cell death 6	0.941	0.992	1.121	5	1.018	0.093
gi|23618867	sideroflexin 1	1.01		1.026	1	1.018	0.011
gi|109082737	heterogeneous nuclear ribonucleoprotein C (C1/C2) isoform 2	0.812	1.061	1.182	5	1.018	0.189
gi|9188646	DNA-PKcs	0.908	0.95	1.197	2	1.018	0.156
gi|189030	nonmuscle myosin heavy chain-A	1.027	1.025	1.005	1	1.019	0.012

gi|4505595	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	1.058	1.015	0.984	3	1.019	0.037
gi|34740335	tubulin, alpha 1B	0.845	1.183	1.03	5	1.019	0.169
gi|17389815	Triosephosphate isomerase 1	0.946	1.063	1.052	2	1.020	0.065
gi|4506195	proteasome beta 2 subunit	1.004	0.985	1.073	3	1.021	0.046
gi|190613420	Chain A, Structural Basis Of Human Triosephosphate Isomerase Deficiency. Mutation E104d And Correlation To Solvent Perturbation.	0.946	1.065	1.052	5	1.021	0.065
gi|13786129	RAB33B, member RAS oncogene family	1.105	0.979	0.979	1	1.021	0.073
gi|4757900	calreticulin precursor	0.927	1.068	1.07	5	1.022	0.082
gi|4758012	clathrin heavy chain 1	1.038	1.026	1.004	5	1.023	0.017
gi|114653233	Proteasome (prosome, macropain) subunit, alpha type, 3 isoform 1	1.046	1.008	1.015	5	1.023	0.020
gi|4758988	RAB1A, member RAS oncogene family isoform 1	0.964	1.054	1.053	3	1.024	0.052
gi|56203163	ubiquitin-conjugating enzyme E2 variant 1	0.975	1.006	1.09	2	1.024	0.060
gi|1082886	tumor necrosis factor type 1 receptor associated protein TRAP-1	0.998	0.951	1.122	2	1.024	0.088
gi|546901	cytosolic acetoacetyl-coenzyme A thiolase; CT	0.958		1.09	1	1.024	0.093
gi|194373841	unnamed protein product	1.037	1.04	0.996	3	1.024	0.025
gi|312137	fructose bisphosphate aldolase	1.005	1.121	0.949	5	1.025	0.088
gi|73948356	40S ribosomal protein S16	0.964	1.038	1.075	5	1.026	0.057
gi|33620739	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	1.1	0.943	1.034	4	1.026	0.079
gi|6563212	putative peroxisomal antioxidant enzyme	1.122	1.043	0.912	5	1.026	0.106
gi|6678271	TAR DNA binding protein	1.183	0.892	1.002	1	1.026	0.147
gi|337930	scar protein	0.795	1.035	1.251	5	1.027	0.228
gi|119593214	signal sequence receptor, delta (translocon-associated protein delta), isoform CRA_b	1.075	0.973	1.033	2	1.027	0.051
gi|114155144	tropomyosin 3 isoform 4	0.938	1.108	1.035	3	1.027	0.085
gi|11559925	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	0.984	0.996	1.102	2	1.027	0.065
gi|4206368	placental protein 17a2; PP17a2	0.996	1.047	1.04	5	1.028	0.028
gi|49168498	TXNRD1	1.125	1.011	0.948	4	1.028	0.090
gi|13543618	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	1.121	1.088	0.876	3	1.028	0.133
gi|3660040	Chain A, Fkbp Mutant F36v Complexed With Remodeled Synthetic Ligand	1.11		0.947	2	1.029	0.115
gi|13384630	stathmin-like 2		0.889	1.168	2	1.029	0.197
gi|12804891	TUBB protein	1.093	1.162	0.831	4	1.029	0.175
gi|473947	KIAA0115	0.885	1.047	1.158	3	1.030	0.137
gi|29725611	protein phosphatase 2A, regulatory subunit B' isoform b	1.11	0.75	1.23	1	1.030	0.250
gi|3255965	U5 snRNP-specific 200kD protein	1.119	1.153	0.818	2	1.030	0.184
gi|4758484	glutathione-S-transferase omega 1	0.888	1.164	1.04	5	1.031	0.138
gi|119602776	GrpE-like 1, mitochondrial (E. coli), isoform CRA_a	0.971	1.062	1.06	5	1.031	0.052
gi|1339989	dihydrolipoamide dehydrogenase	0.935	1.185	0.974	2	1.031	0.135
gi|12248755	mono ATP-binding cassette protein	1.058	1.136	0.901	3	1.032	0.120
gi|13569962	RAB1B, member RAS oncogene family	0.998	1.045	1.053	3	1.032	0.030
gi|292059	MTHSP75	0.982	1.004	1.112	5	1.033	0.070

gi|167614506	L-plastin	1.003	1.098	0.999	5	1.033	0.056
gi|221043698	unnamed protein product	0.954	1.021	1.127	5	1.034	0.087
gi|50593002	small nuclear ribonucleoprotein polypeptide A'	0.979	1.206	0.92	3	1.035	0.151
gi|179106	nonerythroid alpha-spectrin	1.019	1.193	0.893	5	1.035	0.151
gi|1491714	rab-related GTP-binding protein	1.073	0.979	1.054	1	1.035	0.050
gi|119612723	actin, alpha, cardiac muscle, isoform CRA_b	1.084	1.068	0.955	5	1.036	0.070
gi|157830335	Chain A, The Crystal Structure Of The Human Dna Repair Endonuclease Hap1 Suggests The Recognition Of Extra-Helical Deoxyribose At Dna Abasic Sites	0.92	0.831	1.357	3	1.036	0.282
gi|40889633	Chain A, Structure Of Arf1-Gdp Bound To Sec7 Domain Complexed With Brefeldin A	1.095	0.933	1.08	5	1.036	0.090
gi|194382070	unnamed protein product	1.095	0.933	1.08	5	1.036	0.090
gi|220702506	Chain A, TapasinERP57 HETERODIMER	0.915	1.091	1.102	5	1.036	0.105
gi|197692221	14-3-3 protein beta/alpha	0.981	0.96	1.168	5	1.036	0.115
gi|193506632	Chain A, Crystal Structure Of Human Phosphoglycerate Kinase Bound To D-Adp	1.131	0.913	1.065	5	1.036	0.112
gi|178663	medium tumor antigen-associated 61-kD protein	1.025	1.1	0.986	1	1.037	0.058
gi|119598291	pyruvate kinase, muscle, isoform CRA_b	1.083	0.967	1.062	2	1.037	0.062
gi|21068652	apoA-I binding protein	0.961	1.095	1.062	2	1.039	0.070
gi|3318841	Chain A, Horf6 A Novel Human Peroxidase Enzyme	0.978	1.121	1.019	5	1.039	0.074
gi|218511895	Putative uncharacterized protein FLJ45840		1.187	0.893	1	1.040	0.208
gi|1483511	3-hydroxyacyl-CoA dehydrogenase	1.131	1.127	0.864	2	1.041	0.153
gi|31543380	Parkinson disease protein 7	0.941	1.13	1.053	5	1.041	0.095
gi|169216498	hypothetical LOC389901	0.969	1.363	0.792	3	1.041	0.292
gi|179074	alternative	1.035	1.074	1.015	4	1.041	0.030
gi|20664358	Chain A, Crystal structure of a recombinant glutathione transferase, created by replacing The Last Seven Residues Of Each Subunit Of The Human Class Pi Isoenzyme With The Additional C-Terminal Helix Of Human Class Alpha Isoenzyme	1.069	1.025	1.032	5	1.042	0.024
gi|1655596	ribosomal protein L31	1.078	1.037	1.012	3	1.042	0.033
gi|183777	HLA-Bw62 antigen	1.21	0.986	0.931	3	1.042	0.148
gi|31543397	phosphoglycerate kinase 2	1.131	0.945	1.052	5	1.043	0.093
gi|194381612	unnamed protein product	0.915	1.091	1.123	5	1.043	0.112
gi|4503609	electron-transfer-flavoprotein, beta polypeptide isoform 1	0.898	1.184	1.049	5	1.044	0.143
gi|16307468	LRPPRC protein		0.855	1.233	5	1.044	0.267
gi|4759160	small nuclear ribonucleoprotein polypeptide D3	1.032	1.144	0.962	1	1.046	0.092
gi|2506545	78 kDa glucose-regulated protein	0.998	1.077	1.064	5	1.046	0.042
gi|1843434	KM-102-derived reductase-like factor	1.073	1.095	0.972	3	1.047	0.066
gi|119595229	nuclear mitotic apparatus protein 1, isoform CRA_c	1.065		1.029	2	1.047	0.025
gi|4505763	phosphoglycerate kinase 1	1.131	0.945	1.065	5	1.047	0.094
gi|5031973	protein disulfide isomerase-associated 6	1.075	1.061	1.007	5	1.048	0.036
gi|3355455	R33729_1	0.962	1.092	1.09	4	1.048	0.074
gi|194388374	unnamed protein product	1.012	0.993	1.141	5	1.049	0.081

gi|55958543	heterogeneous nuclear ribonucleoprotein K	0.935	1.01	1.207	3	1.051	0.140
gi|7023366	unnamed protein product	0.863	1.414	0.876	5	1.051	0.314
gi|24234688	heat shock 70kDa protein 9 precursor	0.958	1.066	1.132	5	1.052	0.088
gi|194382176	unnamed protein product	0.827	1.318	1.014	4	1.053	0.248
gi|596140	proteasome subunit LMP7	0.994	1.067	1.098	2	1.053	0.053
gi|159162689	Chain A, Human Protein Disulfide Isomerase, Nmr, 40 Structures	1.022	1.105	1.032	5	1.053	0.045
gi|5453559	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d isoform a	1.037	1.008	1.115	5	1.053	0.055
gi|4557317	annexin A11	0.942	0.814	1.405	2	1.054	0.311
gi|5803023	lectin, mannose-binding 2 precursor	1.029	1.023	1.112	3	1.055	0.050
gi|4506243	polypyrimidine tract-binding protein 1 isoform a	0.947	0.952	1.268	5	1.056	0.184
gi|13129018	gamma-glutamyl cyclotransferase	0.966	1.142	1.061	3	1.056	0.088
gi|5174539	cytosolic malate dehydrogenase	0.999	1.065	1.106	5	1.057	0.054
gi|558596	prolyl oligopeptidase	1.099	1.164	0.907	2	1.057	0.134
gi|119599627	hCG1646871	1.037	1.142	0.992	5	1.057	0.077
gi|5262681	hypothetical protein	1.03	1.048	1.093	2	1.057	0.032
gi|62898171	L-plastin variant	1.013	1.092	1.067	3	1.057	0.040
gi|183351	glycogen phosphorylase type IV	1.068	1.056	1.048	3	1.057	0.010
gi|3153908	liver glycogen phosphorylase	1.068	1.056	1.048	3	1.057	0.010
gi|704416	elongation factor Tu	1.149	1.043	0.98	5	1.057	0.085
gi|28178825	isocitrate dehydrogenase 1 (NADP+), soluble	1.076	1.141	0.956	5	1.058	0.094
gi|36146	ribosomal protein S12	1.216	1.037	0.922	5	1.058	0.148
gi|13477319	RPL14 protein		1.068	1.049	3	1.059	0.013
gi|8394076	proteasome (prosome, macropain) subunit, alpha type 6	1.17	0.983	1.027	5	1.060	0.098
gi|3327110	KIAA0648 protein	1.036	1.1	1.045	1	1.060	0.035
gi|165761145	Chain A, Structure Of A104t Dj-1	1.086		1.035	3	1.061	0.036
gi|5803013	endoplasmic reticulum protein 29 isoform 1 precursor	0.937	1.068	1.179	5	1.061	0.121
gi|1924954	galectin	1.03		1.093	1	1.062	0.045
gi|1065111	Chain A, High Resolution Solution Nmr Structure Of Mixed Disulfide Intermediate Between Mutant Human Thioredoxin And A 13 Residue Peptide Comprising Its Target Site In Human Nfkb	1.144	1.203	0.838	2	1.062	0.196
gi|4235275	talin	1.231	0.983	0.971	5	1.062	0.147
gi|169213873	Glucose phosphate isomerase	1.087	1.025	1.075	2	1.062	0.033
gi|189238	neuroleukin	0.942	1.008	1.239	2	1.063	0.156
gi|306875	C protein	0.967		1.159	2	1.063	0.136
gi|169208088	glyceraldehyde-3-phosphate dehydrogenase-like 6	1.117	1.042	1.03	3	1.063	0.047
gi|1552242	hRlf beta subunit (p102 protein)	0.996	0.931	1.264	5	1.064	0.177
gi|2815604	Opa-interacting protein OIP2	1.293	0.796	1.104	1	1.064	0.251
gi|133254	Heterogeneous nuclear ribonucleoprotein A1	1.024	0.962	1.208	5	1.065	0.128
gi|2624694	Chain A, Human Mitochondrial Single-Stranded Dna Binding Protein	1.052	1.212	0.931	2	1.065	0.141
gi|306891	90kDa heat shock protein	1.048	0.993	1.155	2	1.065	0.082
gi|31291	unnamed protein product	1.005	1.098	1.099	2	1.067	0.054
gi|5729953	nuclear distribution gene C homolog	1.056	1.036	1.11	1	1.067	0.038

gi|61104919	heat shock protein 90Bf	1.091	0.989	1.123	5	1.068	0.070
gi|56204418	heat shock protein 90kDa alpha (cytosolic), class B member 1	1.091	0.989	1.123	5	1.068	0.070
gi|847724	methylthioadenosine phosphorylase	1.213	0.811	1.179	3	1.068	0.223
gi|6841176	HSPC263	1.094	1.017	1.094	3	1.068	0.044
gi|4503097	casein kinase 2, alpha prime polypeptide	1.144	1.055	1.007	2	1.069	0.070
gi|1401034	hyaluronan synthase	0.97	1.156	1.083	3	1.070	0.094
gi|194389892	unnamed protein product	1.093	1.03	1.087	3	1.070	0.035
gi|31615966	Chain A, Crystal Structure Of Familial Als Mutant S134n Of Human Cu, Zn Superoxide Dismutase (Cuznsod) To 1.3a Resolution	1.023	1.164	1.024	2	1.070	0.081
gi|7706495	DnaJ (Hsp40) homolog, subfamily B, member 11 precursor	0.901	1.109	1.203	2	1.071	0.155
gi|169160753	mCG50656	1.093	1.043	1.078	4	1.071	0.026
gi|2098347	Chain A, Physiological Dimer Hpp Precursor	1.095		1.05	1	1.073	0.032
gi|88953571	protein expressed in prostate, ovary, testis, and placenta 2 isoform 2	1.299	1.009	0.91	5	1.073	0.202
gi|4501885	beta actin	0.986	1.004	1.23	5	1.073	0.136
gi|4218034	GTP-binding regulatory protein Gi alpha-2 chain	0.992	1.096	1.134	5	1.074	0.074
gi|219478	apurinic/apyrimidinic endonuclease	0.789	1.184	1.253	2	1.075	0.250
gi|6518533	adenylate kinase 3 alpha	1.204	0.926	1.096	1	1.075	0.140
gi|4758304	protein disulfide isomerase-associated 4	0.97	1.028	1.231	3	1.076	0.137
gi|54304028	glyceraldehyde-3-phosphate dehydrogenase	1.084	1.077	1.068	2	1.076	0.008
gi|2282013	GAPDH-2 like	1.095	1.072	1.065	2	1.077	0.016
gi|194388808	unnamed protein product	1.095	1.072	1.065	5	1.077	0.016
gi|15082234	lactate dehydrogenase A-like 6B	1.01	1.137	1.087	1	1.078	0.064
gi|5031857	L-lactate dehydrogenase A isoform 1	1.01	1.137	1.087	5	1.078	0.064
gi|13431875	Putative S100 calcium-binding protein H_NH0456N16.1	1.12	1.203	0.912	5	1.078	0.150
gi|33286420	pyruvate kinase, muscle isoform M1	1.083	1.091	1.062	3	1.079	0.015
gi|7634779	HDCMA39P	0.896	1.118	1.223	1	1.079	0.167
gi|23308751	3-hydroxyisobutyrate dehydrogenase	1.045	0.857	1.335	1	1.079	0.241
gi|56676393	Rho GDP dissociation inhibitor (GDI) beta	1.048	1.384	0.807	5	1.080	0.290
gi|28336	mutant beta-actin (beta'-actin)	1.299	1.009	0.931	5	1.080	0.194
gi|134133226	protein expressed in prostate, ovary, testis, and placenta 2	1.299	1.009	0.931	5	1.080	0.194
gi|221043300	unnamed protein product	1.299	1.009	0.931	5	1.080	0.194
gi|16877746	Similar to mannose-6-phosphate receptor (cation dependent)		1.257	0.903	1	1.080	0.250
gi|189545	plasminogen activator inhibitor	1.237	1.015	0.99	2	1.081	0.136
gi|5031571	actin-related protein 2 isoform b	1.103	1.075	1.066	3	1.081	0.019
gi|435756	lysosomal membrane glycoprotein lamp-2 homolog	1.202		0.961	1	1.082	0.170
gi|34719	unnamed protein product	1.067	1.049	1.129	5	1.082	0.042
gi|31417921	TKT protein	1.062	1.175	1.008	3	1.082	0.085
gi|38013966	TKT protein	1.12	1.059	1.066	5	1.082	0.033
gi|2689608	UEV1Bs	0.995	1.066	1.187	3	1.083	0.097
gi|4503729	FK506 binding protein 52	1.024	1.383	0.841	1	1.083	0.276
gi|32488	unnamed protein product	1.146	1.051	1.052	4	1.083	0.055
gi|414587	ribosomal protein L10	1.008	1.062	1.179	5	1.083	0.087

gi|134105063	Chain B, Crystal Structure And Solution Nmr Studies Of Lys48-Linked Tetraubiquitin At Neutral Ph	1.093	1.086	1.071	5	1.083	0.011
gi|117167827	ACTB protein	1.299	1.009	0.943	3	1.084	0.189
gi|22538467	proteasome beta 4 subunit	1.084	1.232	0.936	4	1.084	0.148
gi|5902102	small nuclear ribonucleoprotein D1 polypeptide 16kDa	0.895	1.212	1.145	2	1.084	0.167
gi|54696200	RAP1A, member of RAS oncogene family	0.993	1.193	1.067	3	1.084	0.101
gi|179832	calnexin	0.993	1.238	1.022	5	1.084	0.134
gi|71042476	Chain A, Crystal Structure Of Human Potassium Channel Kv Beta-Subunit (Kcnab2)	1.04	1.166	1.048	3	1.085	0.071
gi|48145549	PGK1	1.108	1.078	1.071	5	1.086	0.020
gi|2780871	Chain B, Proteasome Activator Reg(Alpha)	1.112	1.24	0.905	4	1.086	0.169
gi|197724894	Chain A, Crystal Structure Of E60q Mutant Of Fkbp12	1.116		1.056	2	1.086	0.042
gi|4503423	deoxyuridine triphosphatase isoform 2	1.216	1.12	0.923	5	1.086	0.149
gi|8671754	DAZ associated protein 1	0.983	1.068	1.21	2	1.087	0.115
gi|339647	thyroid hormone binding protein precursor	1.084	1.15	1.027	2	1.087	0.062
gi|18375501	APEX nuclease 1	1.116		1.058	5	1.087	0.041
gi|16579885	ribosomal protein L4	1.219		0.957	3	1.088	0.185
gi|23510338	ubiquitin-activating enzyme E1	1.09	1.021	1.154	5	1.088	0.067
gi|3170190	antigen NY-CO-25	1.109	1.097	1.061	1	1.089	0.025
gi|940536	P1 Cdc21 protein	1.121	1.056	1.091	2	1.089	0.033
gi|28940	unnamed protein product	1.184	1.069	1.015	5	1.089	0.086
gi|189306	nucleolin	1.08	1.088	1.101	2	1.090	0.011
gi|38197252	MCM2 protein	1.104	1.118	1.048	2	1.090	0.037
gi|13676857	heat shock 70kDa protein 2	1.118	1.045	1.108	5	1.090	0.040
gi|13775198	SH3 domain binding glutamic acid-rich protein like 3	1.188	1.162	0.922	5	1.091	0.147
gi|10716563	calnexin precursor	0.995	1.062	1.216	5	1.091	0.113
gi|17391477	Annexin A5	1.061	1.138	1.078	3	1.092	0.040
gi|221041984	unnamed protein product	0.982	1.004	1.292	5	1.093	0.173
gi|457436	basic transcription factor 3a	1.088	1.128	1.062	2	1.093	0.033
gi|7669492	glyceraldehyde-3-phosphate dehydrogenase	1.1	1.079	1.099	2	1.093	0.012
gi|157833780	Chain A, Human Annexin V With Proline Substitution By Thioproline	1.025	1.233	1.022	5	1.093	0.121
gi|509291	H+-ATP synthase subunit b	1.131	1.21	0.946	2	1.096	0.136
gi|21758578	unnamed protein product	0.866	1.011	1.411	5	1.096	0.282
gi|7023323	unnamed protein product	1.015	1.234	1.039	2	1.096	0.120
gi|188492	heat shock-induced protein	1.059	1.07	1.16	3	1.096	0.055
gi|36059	RING12	1.14	1.099	1.051	2	1.097	0.045
gi|4759112	solute carrier family 16, member 3	1.172	1.158	0.962	3	1.097	0.117
gi|55669744	Chain A, Nmr Structure Of Rrm2 From Human Polypyrimidine Tract Binding Protein Isoform 1 (Ptb1)	1.237	0.972	1.083	3	1.097	0.133
gi|5174741	ubiquitin carboxyl-terminal esterase L3	0.899	1.067	1.328	5	1.098	0.216
gi|21730367	Chain A, Ca2+-Binding Mimicry In The Crystal Structure Of The Eu3+-Bound Mutant Human Macrophage Capping Protein Cap G	1.036	1.117	1.142	2	1.098	0.055
gi|194373703	unnamed protein product	0.978	0.996	1.324	5	1.099	0.195

gi|33987931	HSP90AB1 protein	1.049	1.105	1.144	2	1.099	0.048
gi|4502111	annexin VII isoform 1	1.036	1.155	1.11	1	1.100	0.060
gi|21752646	unnamed protein product	0.88	1.011	1.411	5	1.101	0.277
gi|1942609	Chain A, Human Rap1a, Residues 1-167, Double Mutant (E30d,K31e) Complexed With Gppnhp And The Ras-Binding-Domain Of Human C-Raf1, Residues 51-131	0.993	1.193	1.118	3	1.101	0.101
gi|194381006	unnamed protein product		1.107	1.098	2	1.103	0.006
gi|62898285	heat shock 70kDa protein 6 (HSP70B') variant	1.022	1.127	1.159	4	1.103	0.072
gi|5729877	heat shock 70kDa protein 8 isoform 1	1.022	1.127	1.159	5	1.103	0.072
gi|23271312	HSPA2 protein	1.022	1.127	1.16	5	1.103	0.072
gi|49168580	MDH2	1.114	1.086	1.11	4	1.103	0.015
gi|8922601	ADP-ribosylation factor-like 10C	1.051	0.926	1.335	5	1.104	0.210
gi|20270343	ADP-ribosylation factor-like 8A	1.051	0.926	1.335	5	1.104	0.210
gi|1314308	nucleophosmin-retinoic acid receptor alpha fusion protein NPM-RAR long form	0.995	1.06	1.263	5	1.106	0.140
gi|7705696	endoplasmic reticulum thioredoxin superfamily member, 18 kDa	1.119	1.099	1.1	2	1.106	0.011
gi|1710248	protein disulfide isomerase-related protein 5	1.075	1.061	1.186	5	1.107	0.068
gi|181184	stomatin peptide	1.141	1.298	0.883	2	1.107	0.210
gi|24234686	heat shock 70kDa protein 8 isoform 2	1.095	1.048	1.18	5	1.108	0.067
gi|438639	lamin B receptor	1.269	1.054	1	1	1.108	0.142
gi|62089422	membrane alanine aminopeptidase precursor variant	1.12		1.096	5	1.108	0.017
gi|205277465	transketolase isoform 2	1.055	1.062	1.208	5	1.108	0.086
gi|13569956	actin related protein 2/3 complex, subunit 5-like	0.898		1.32	1	1.109	0.298
gi|88992455	hypothetical protein isoform 1	1.095	1.054	1.179	5	1.109	0.064
gi|189067253	unnamed protein product	1.296	0.942	1.09	5	1.109	0.178
gi|42734438	hypothetical protein LOC51571	1.211	1.054	1.066	5	1.110	0.087
gi|1545813	KNP-Ia	1.224	1.03	1.078	1	1.111	0.101
gi|181914	DNA-binding protein	1.294	1.077	0.962	2	1.111	0.169
gi|109157100	Chain A, Structure Of Human Purine Nucleoside Phosphorylase H257g Mutant	0.915	1.011	1.411	5	1.112	0.263
gi|387033	purine nucleoside phosphorylase	0.915	1.011	1.411	5	1.112	0.263
gi|20070125	prolyl 4-hydroxylase, beta subunit precursor	1.157	1.124	1.056	5	1.112	0.052
gi|145309046	POTE-2 alpha-actin	1.131	0.943	1.264	5	1.113	0.161
gi|4557395	carbonic anhydrase II	1.13	1.369	0.842	2	1.114	0.264
gi|145579602	Chain A, Crystallographic And Kinetic Studies Of Human Mitochondrial Acetoacetyl-Coa Thiolase (T2): The Importance Of Potassium And Chloride For Its Structure And Function	1.042	1.128	1.178	5	1.116	0.069
gi|4757810	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit precursor	1.188	1.335	0.826	5	1.116	0.262
gi|3860002	unknown	0.989	1.35	1.01	1	1.116	0.203
gi|1575607	FUSE binding protein 2	1.104	1.183	1.066	4	1.118	0.060
gi|194386896	unnamed protein product	1.175	0.89	1.289	5	1.118	0.206
gi|33337556	citrate synthase	0.896	1.163	1.298	3	1.119	0.205

gi|433938	ERGIC53	1.067	1.203	1.087	2	1.119	0.073
gi|194379304	unnamed protein product	1.132	1.107	1.119	5	1.119	0.013
gi|25453472	eukaryotic translation elongation factor 1 delta isoform 2	1.105	1.243	1.013	5	1.120	0.116
gi|35222	unnamed protein product	1.045	1.078	1.239	5	1.121	0.104
gi|55670364	Chain A, Human Peroxiredoxin 5, C47s Mutant	1.16	1.176	1.026	5	1.121	0.082
gi|4502297	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit precursor	1.084	1.126	1.155	2	1.122	0.036
gi|14016	cytochrome C oxidase II subunit	1.069	1.119	1.18	3	1.123	0.056
gi|7243107	KIAA1363 protein	1.09	1.231	1.053	2	1.125	0.094
gi|187399	myeloblastin	0.956	1.047	1.375	1	1.126	0.220
gi|35193	unnamed protein product	0.956	1.047	1.375	5	1.126	0.220
gi|21759781	Heat shock 70kDa protein 1-like	1.088	1.045	1.246	4	1.126	0.106
gi|119587946	heat shock 70kDa protein 8, isoform CRA_c	1.088	1.045	1.246	3	1.126	0.106
gi|194389734	unnamed protein product	1.088	1.045	1.246	3	1.126	0.106
gi|4502673	CD47 antigen isoform 1 precursor	1.204	1.177	1	2	1.127	0.111
gi|20149675	EF-hand domain family, member D2		0.993	1.264	2	1.129	0.192
gi|12653415	Heat shock 70kDa protein 9 (mortalin)	1.089	1.052	1.248	5	1.130	0.104
gi|34419635	heat shock 70kDa protein 6 (HSP70B')	1.022	1.127	1.243	2	1.131	0.111
gi|21361181	Na+/K+ -ATPase alpha 1 subunit isoform a proprotein	0.966	1.214	1.213	5	1.131	0.143
gi|123079	Beta-hexosaminidase subunit alpha	1.205	1.113	1.078	1	1.132	0.066
gi|5031573	ARP3 actin-related protein 3 homolog	0.91	1.074	1.418	3	1.134	0.259
gi|4503037	cellular repressor of E1A-stimulated genes	1.115	1.234	1.053	1	1.134	0.092
gi|10439505	unnamed protein product	1.128		1.142	1	1.135	0.010
gi|119577375	biliverdin reductase B (flavin reductase (NADPH)), isoform CRA_c	1.096	1.273	1.037	2	1.135	0.123
gi|6755448	SEC22 vesicle trafficking protein-like 1	1.118		1.153	1	1.136	0.025
gi|5174731	translin-associated factor X	0.887	1.071	1.449	2	1.136	0.287
gi|7448823	adenosine kinase	0.861	1.142	1.406	2	1.136	0.273
gi|5453990	proteasome activator subunit 1 isoform 1	1.141	1.24	1.033	5	1.138	0.104
gi|57162629	vinculin	1.011	1.14	1.272	3	1.141	0.131
gi|4506609	ribosomal protein L19	1.058	1.063	1.306	5	1.142	0.142
gi|194374345	unnamed protein product	1.19	1.103	1.142	3	1.145	0.044
gi|192228	7 enoyl-CoA hydratase	1.095		1.198	1	1.147	0.073
gi|28614	aldolase A	1.073	1.293	1.074	5	1.147	0.127
gi|194378468	unnamed protein product	1.073	1.293	1.074	5	1.147	0.127
gi|21624607	coactosin-like 1	1.069	1.173	1.199	2	1.147	0.069
gi|62088804	minichromosome maintenance deficient protein 5 variant	1.03	1.145	1.268	2	1.148	0.119
gi|119617399	serine hydroxymethyltransferase 2 (mitochondrial), isoform CRA_a	1.199	1.056	1.192	5	1.149	0.081
gi|5453980	DnaJ (Hsp40) homolog, subfamily C, member 3	1.244		1.054	1	1.149	0.134
gi|62897129	heat shock 70kDa protein 8 isoform 1 variant	1.119	1.133	1.197	5	1.150	0.042
gi|31545	valyl-tRNA synthetase	1.13	1.178	1.142	5	1.150	0.025
gi|12667788	myosin, heavy polypeptide 9, non-muscle	0.979	0.975	1.496	5	1.150	0.300
gi|62088286	ARP3 actin-related protein 3 homolog variant	1.159	1.177	1.115	3	1.150	0.032
gi|62898960	transketolase variant	1.106	1.189	1.157	5	1.151	0.042

gi|6465985	quiescent cell proline dipeptidase	1.046	1.137	1.271	2	1.151	0.113
gi|729433	Protein disulfide-isomerase A3	1.114	1.091	1.249	5	1.151	0.085
gi|2906146	malate dehydrogenase precursor	1.121	1.176	1.157	5	1.151	0.028
gi|42794622	zinc finger protein 784		1.182	1.121	1	1.152	0.043
gi|119614877	myeloperoxidase, isoform CRA_b	1.194	1.161	1.109	5	1.155	0.043
gi|36102	unnamed protein product	1.363	0.885	1.221	5	1.156	0.245
gi|62898103	aspartate aminotransferase 2 precursor variant	1.105	1.169	1.203	5	1.159	0.050
gi|189617	protein PP4-X	1.126	1.247	1.112	5	1.162	0.074
gi|307141	lysozyme precursor (EC 3.2.1.17)	1.459	0.884	1.145	5	1.163	0.288
gi|71042395	Chain A, Crystal Structure Of Human Dihydrolipoamide Dehydrogenase Complexed To Nad+	1.073	1.257	1.161	5	1.164	0.092
gi|118674	Dihydrolipoyl dehydrogenase, mitochondrial	1.073	1.257	1.161	5	1.164	0.092
gi|37267	transketolase	1.017	1.175	1.303	5	1.165	0.143
gi|238427	Porin 31HM	1.365	1.051	1.083	2	1.166	0.173
gi|5032027	retinoblastoma binding protein 4 isoform a	1.404	0.961	1.134	3	1.166	0.223
gi|10436946	unnamed protein product	1.098	1.004	1.401	1	1.168	0.207
gi|1478503	SCG10	1.424	1.042	1.039	3	1.168	0.221
gi|5031851	stathmin 1	1.424	1.042	1.039	5	1.168	0.221
gi|6653226	sperm antigen-36	1.084	1.15	1.272	3	1.169	0.095
gi|193506758	Chain A, Crystal Structure Of E18q Dj-1	0.941	1.13	1.442	2	1.171	0.253
gi|133854601	cytochrome c oxidase subunit II	1.06	1.318	1.14	3	1.173	0.132
gi|30451	cytochrome P450 db1	1.169	1.169	1.181	3	1.173	0.007
gi|7656991	coronin, actin binding protein, 1C isoform 1	1.13	1.258	1.134	1	1.174	0.073
gi|5771523	3-phosphoglycerate dehydrogenase	1.016	1.287	1.221	3	1.175	0.141
gi|34709	manganese superoxide dismutase (MnSOD)	1.301	1.43	0.799	2	1.177	0.333
gi|5802974	peroxiredoxin 3 isoform a precursor	1.231	1.194	1.114	5	1.180	0.060
gi|14327942	HSP90B1 protein	1.386	1.228	0.925	2	1.180	0.234
gi|40068518	phosphogluconate dehydrogenase	1.21	1.202	1.131	5	1.181	0.043
gi|809185	Chain A, The Effect Of Metal Binding On The Structure Of Annexin V And Implications For Membrane Binding	1.124	1.252	1.168	5	1.181	0.065
gi|4503841	ATP-dependent DNA helicase II, 70 kDa subunit	1.154	1.167	1.228	3	1.183	0.040
gi|31746	glutathione-insulin transhydrogenase (216 AA)	1.146	1.327	1.076	2	1.183	0.130
gi|4759140	sodium/hydrogen exchanger regulatory factor 1	1.016	1.449	1.09	1	1.185	0.232
gi|1419374	alpha-mannosidase	1.253	1.174	1.133	5	1.187	0.061
gi|178045	gamma-actin	1.215	1.173	1.179	5	1.189	0.023
gi|4504061	glucosamine (N-acetyl)-6-sulfatase precursor	1.263	1.252	1.054	2	1.190	0.118
gi|6912586	6-phosphogluconolactonase	0.843	1.326	1.404	1	1.191	0.304
gi|7669550	vinculin isoform meta-VCL	0.946	1.14	1.497	5	1.194	0.279
gi|4507877	vinculin isoform VCL	0.946	1.14	1.497	5	1.194	0.279
gi|2065179	unnamed protein product	1.109	1.017	1.457	3	1.194	0.232
gi|73983054	Cofilin-1 isoform 2	1.132	1.538	0.915	3	1.195	0.316
gi|20520997	KIAA0320	1.219	1.216	1.163	5	1.199	0.032
gi|4505773	prohibitin	1.42	1.184	1.001	4	1.202	0.210

gi|31543	unnamed protein product	1.38	1.356	0.876	4	1.204	0.284
gi|4503513	eukaryotic translation initiation factor 3, subunit 2 beta, 36kDa	1.021		1.389	2	1.205	0.260
gi|28678	unnamed protein product	1.084	1.261	1.271	5	1.205	0.105
gi|4503987	gamma-glutamyl hydrolase precursor	1.191	1.461	0.966	1	1.206	0.248
gi|1197636	p105MCM	1.035	1.069	1.518	2	1.207	0.270
gi|307109	lysosomal membrane glycoprotein-1	1.21	1.248	1.173	5	1.210	0.038
gi|4008131	chaperonin 10	1.216	1.193	1.224	2	1.211	0.016
gi|4507521	transketolase isoform 1	1.017	1.186	1.432	5	1.212	0.209
gi|7706747	transient receptor potential cation channel, subfamily C, member 4 isoform alpha	1.077	1.394	1.181	2	1.217	0.162
gi|386785	heat shock protein	1.408	1.051	1.197	5	1.219	0.179
gi|5032057	S100 calcium binding protein A11	1.255	1.192	1.209	2	1.219	0.033
gi|1582221	prepro-cathepsin C	1.39		1.053	2	1.222	0.238
gi|494395	Chain C, X-Ray Crystal Structure Of Canine Myeloperoxidase At 3 Angstroms Resolution	1.079	1.224	1.365	5	1.223	0.143
gi|1916850	scaffold protein Pbp1	1.139	1.468	1.062	1	1.223	0.216
gi|4432754	ribosomal protein L27a		1.296	1.153	1	1.225	0.101
gi|194384576	unnamed protein product	1.267	1.241	1.171	3	1.226	0.050
gi|178277	S-adenosylhomocysteine hydrolase	1.269	1.226	1.189	2	1.228	0.040
gi|4557817	3-oxoacid CoA transferase 1 precursor	1.268	1.45	0.967	2	1.228	0.244
gi|4884148	hypothetical protein	1.316	1.158	1.217	2	1.230	0.080
gi|119614885	eosinophil peroxidase, isoform CRA_a	1.238	1.24	1.216	3	1.231	0.013
gi|703093	serine hydroxymethyltransferase	1.199	1.056	1.442	5	1.232	0.195
gi|23512215	Chitinase 3-like 1 (cartilage glycoprotein-39)	1.203	1.321	1.178	5	1.234	0.076
gi|196049886	Chain A, Crystal Structure Of Human 3-Oxoacid Coa Transferase 1	1.268	1.395	1.043	2	1.235	0.178
gi|29789195	basic transcription factor 3-like 4	1.394	1.054	1.265	1	1.238	0.172
gi|3043670	KIAA0573 protein		1.091	1.386	1	1.239	0.209
gi|4504523	heat shock 10kDa protein 1	1.245	1.295	1.181	5	1.240	0.057
gi|13562132	catalase	1.23	1.301	1.198	5	1.243	0.053
gi|30047125	Ribosomal protein SA	1.186	1.304	1.245	5	1.245	0.059
gi|157831273	Chain A, Hnrnp A1 (Rbd1,2) From Homo Sapiens	1.295		1.206	4	1.251	0.063
gi|9910280	UDP-glucose ceramide glucosyltransferase-like 1 isoform 1	1.119	1.383	1.251	5	1.251	0.132
gi|565169	early-pregnancy factor	1.245	1.331	1.181	3	1.252	0.075
gi|1942977	Chain A, Macrophage Migration Inhibitory Factor (Mif)	1.31	1.374	1.076	2	1.253	0.157
gi|4826940	prolylcarboxypeptidase isoform 1 preproprotein	0.883	1.366	1.525	1	1.258	0.334
gi|167744990	Chain A, Solution Structure Of The Tandem Hmg Box Domain From Human High Mobility Group Protein B1		1.313	1.213	3	1.263	0.071
gi|11139093	GrpE-like protein cochaperone	1.12	1.503	1.168	5	1.264	0.209
gi|1773227	HP1Hs-gamma	1.225	1.344	1.227	2	1.265	0.068
gi|71773329	annexin VI isoform 1	1.179	1.326	1.309	4	1.271	0.080
gi|194377012	unnamed protein product	1.517	1.054	1.246	3	1.272	0.233
gi|62088648	tumor rejection antigen (gp96) 1 variant	1.319	0.966	1.548	3	1.278	0.293

gi|230867	Chain R, Twinning In Crystals Of Human Skeletal Muscle D-Glyceraldehyde-3-Phosphate Dehydrogenase	1.496	1.244	1.094	5	1.278	0.203
gi|4501881	actin, alpha 1, skeletal muscle	1.548	1.371	0.918	5	1.279	0.325
gi|39644554	LAMP1 protein	1.21	1.458	1.173	3	1.280	0.155
gi|7705925	dicarbonyl/L-xylulose reductase	1.233	1.273	1.345	3	1.284	0.057
gi|6005757	chromatin-specific transcription elongation factor large subunit	1.151	1.354	1.362	3	1.289	0.120
gi|1673514	B-cell receptor associated protein	1.195	1.402	1.271	1	1.289	0.105
gi|494394	Chain A, X-Ray Crystal Structure Of Canine Myeloperoxidase At 3 Angstroms Resolution	1.199	1.268	1.408	5	1.292	0.106
gi|577062	glutathione peroxidase	1.615	1.208	1.053	3	1.292	0.290
gi|119614878	myeloperoxidase, isoform CRA_c	1.194	1.161	1.524	5	1.293	0.201
gi|35655	unnamed protein product	1.242	1.228	1.427	2	1.299	0.111
gi|35218	unnamed protein product	1.295	1.326	1.309	4	1.310	0.016
gi|31183	eosinophil preperoxidase (AA -127 to 575)	1.238	1.24	1.468	4	1.315	0.132
gi|178409	alpha-L-fucosidase precursor (EC 3.2.1.5)	1.285	1.386	1.287	2	1.319	0.058
gi|34527427	unnamed protein product	1.35	1.216	1.4	3	1.322	0.095
gi|19070529	CABLES	1.35	1.216	1.404	2	1.323	0.097
gi|16924265	Enoyl Coenzyme A hydratase 1, peroxisomal	1.295	1.311	1.366	3	1.324	0.037
gi|189067487	unnamed protein product	1.211	1.317	1.446	5	1.325	0.118
gi|4105819	Rab7	1.456	1.333	1.199	5	1.329	0.129
gi|6014895	Cystatin-F	1.319	1.371	1.368	1	1.353	0.029
gi|633073	protein-tyrosine phosphatase	1.382	1.513	1.293	4	1.396	0.111
gi|11345462	signal peptidase complex subunit 3	0.983	1.708	1.548	1	1.413	0.381
gi|7022407	unnamed protein product	1.351	1.278	1.61	1	1.413	0.174
gi|5729810	emopamil binding protein (sterol isomerase)	1.342		1.494	1	1.418	0.107
gi|1703167	AP-1 complex subunit beta-1	1.329		1.509	1	1.419	0.127
gi|74706932	Putative endoplasmin-like protein	1.369	1.402	1.487	1	1.419	0.061
gi|112490564	Chain J, Structure Of Human Ferritin L. Chain	1.41	1.543	1.312	5	1.422	0.116
gi|182516	ferritin light subunit	1.394	1.57	1.336	5	1.433	0.122
gi|32628	ICAM-3	1.43		1.442	1	1.436	0.008
gi|17402893	phosphoserine aminotransferase isoform 1	1.295	1.454	1.679	3	1.476	0.193
gi|4506773	S100 calcium-binding protein A9	1.506	1.571	1.499	1	1.525	0.040
gi|5231228	ribonuclease T2 precursor	1.314	1.567	1.72	3	1.534	0.205
gi|9955206	Rho GDP-dissociation factor 2	1.417	1.46	1.773	3	1.550	0.194
gi|4758504	hydroxysteroid (17-beta) dehydrogenase 10 isoform 1	1.541		1.574	1	1.558	0.023
gi|8037945	prothymosin alpha	1.541		1.574	1	1.558	0.023
gi|11321591	high-mobility group box 2	1.634	1.921	1.396	2	1.650	0.263
gi|4503143	cathepsin D	1.574	1.734	1.655	3	1.654	0.080
gi|119239	Bone marrow proteoglycan	1.626	1.785	1.733	1	1.715	0.081
gi|28375485	unnamed protein product	1.917	1.952	1.548	3	1.806	0.224
gi|968888	HMG-1	1.821	1.924	1.798	2	1.848	0.067
gi|186461558	neutrophil elastase	1.935	1.951	1.957	2	1.948	0.011
gi|627372	alpha-mannosidase precursor	2.291	2.056	1.811	1	2.053	0.240

gi|4506191	proteasome beta 10 subunit proprotein	2.15	2.145	2.323	1	2.206	0.101
gi|4504437	heme oxygenase (decyclizing) 1	3.203	1.713	2.054	2	2.323	0.781
gi|223582	histone H4	2.332	2.388	2.505	5	2.408	0.088
gi|356168	histone H1b	2.929	2.963	2.381	5	2.758	0.327
gi|386772	histone H3	2.64	2.479	3.279	3	2.799	0.423
gi|1568557	histone H2B	2.577	2.888	3.465	4	2.977	0.451
gi|12654715	TXNDC5 protein	3.327	3.353	2.732	5	3.137	0.351
gi|510990	histone H2A	4.592	4.429	3.595	5	4.205	0.535
gi|32111	unnamed protein product	5.999	4.425	4.272	1	4.899	0.956

Table S2. The detailed quantification results for proteins with substantial changes.

name	forward set1	forward set2	reverse set3	No. of Peptides Quantified	Average	S.D.
A. Histone and HMG proteins						
gi|11321591 HMG-2	1.634	1.921	1.396	2	1.65	0.263
K.YEKDIAAYR.A						
K.LKEKYEKDIAAYR.A						
gi|968888 HMG-1	1.821	1.924	1.798	3	1.847	0.067
K.IKGEHPGLSIGDVAK.K						
K.LKEKYEKDIAAYR.A						
K.KHPDASVNFSEFSK.K						
gi|223582 histone H4	2.332	2.388	2.505	5	2.408	0.088
R.DAVTYTEHAK.R						
R.ISGLIYEETR.G						
K.TVTAMDVVYALKR.Q						
K.VFLENVIRDAVTYTEHAK.R						
K.VFLENVIR.D						
gi|386772 histone H3	2.64	2.479	3.279	3	2.799	0.423
K.STELLIR.K						
R.KLPFQR.L						
R.KLPFQR.L						
gi|356168 histone H1b	2.929	2.963	2.381	5	2.758	0.327
K.ATGPPVSELITK.A						
K.ALAAGGYDVEKNNSR.						
K.ALAAAGYDVEK.N						
-.SETAPAAPAAPAPAEKTPVKK.K						
K.GTLVQTK.G						
gi|1568557 histone H2B	2.577	2.888	3.465	5	2.977	0.451
R.LLLPGELAK.H						
R.EIQTAVR.L						
K.AMGIMNSFVNDIFER.I						
R.KESYSVYVYK.V						
K.QVHPDTGISSK.A						
gi|510990 histone H2A	4.592	4.429	3.595	5	4.205	0.535
K.VTIAQGGVLPNIQAVLLPK.K						
R.HLQLAIR.N						
R.HLQLAIRNDEELNK.L						
R.NDEELNKLLGK.V						
R.AGLQFPVGR.V						
B. Translation related proteins						
gi|38202255 threonyl-tRNA synthetase	0.552	0.728	0.512	2	0.597	0.115
K.WPFWLSPR.Q						
R.NELSGALTGLTR.V						

gi|181969 elongation factor 2 **R.ETVSEESNVLCLSK.S** **K.AYLPVNESFGFTADLR.S** **K.EGIPALDNFLDKL.-**	0.447	0.545	0.636	3	0.543	0.094
gi|19353009 Similar to Elongation factor 2b **R.VFSGLVSTGLK.V** **R.TFCQLILDPIFK.V**	0.55	0.65	0.651	2	0.617	0.058
gi|4506707 ribosomal protein S25 **R.AALQELLSK.G**	0.552	0.615	0.771	1	0.646	0.113
C. hnRNP gi|386547 d(TTAGGG)n-binding protein B39 **.IFVGGLSPDTPEEK.I**	0.652	0.592	0.25	1	0.498	0.217
gi|119597533 heterogeneous nuclear ribonucleoprotein U, isoform CRA_b **K.EKPYFPIPEEYTFIQNVPLEDR.V**	0.583	0.582	0.602	1	0.589	0.012
gi|55958547 heterogeneous nuclear ribonucleoprotein K **R.TDYNASVSVPDSSGPER.I** **R.NTDEMVELR.I** **R.SRNTDEMVELR.I**	0.773	0.724	0.489	3	0.662	0.152
D. Enzymes gi|531202 spermidine synthase **R.KVLIIGGGDGGVLR.E** **K.VLIIGGGDGGVLR.E**	0.466	0.465	0.773	2	0.568	0.178
gi|41584442 fatty acid synthase **R.GTPLISPLIK.W** **R.GYAVLGGER.G** **K.TGTVSLEVR.V** **R.LQVVDQPLPVR.G** **R.DNLEFFLAGIGR.L**	0.704	0.612	0.512	5	0.609	0.096
gi|66392203 NME1-NME2 protein **R.GLVGEIIKR.F** **K.DRPFFAGLVK.Y** **K.EHYVDLKDRPFFAGLVK.Y** **R.TFIAIKPDGVQR.G** **K.FMQASEDLLK.E**	0.704	0.441	0.78	5	0.642	0.178
gi|1230564 Gu protein **R.APQVLVLAPTR.E** **K.TFSFAIPLIEK.L**	0.743	0.693	0.489	2	0.642	0.135
gi|2661039 alpha enolase **K.EGLELLK.T**	0.564	0.689	0.691	5	0.648	0.073

R.IGAEVYHNLK.N **R.YISPDQLADLYK.S** **R.AAVPSGASTGIYEALELR.D** **K.LAMQEFMILPVGAANFR.E**						
gi|190281 protein phosphatase I alpha subunit **R.EIFLSQPILLELEAPLK.I**	0.683	0.657	0.643	1	0.661	0.02
gi|4507789 ubiquitin-conjugating enzyme E2L 3 isoform 1 **K.ELEEIR.K** **R.ADLAEEYSK.D** **R.IEINFPAEYPFKPPK.I** **K.GQVCLPVISAENWKPATK** **R.NIQVDEANLLTWQGLIVPDNPPYDK.G**	0.614	0.657	0.734	5	0.668	0.061
gi|5231228 ribonuclease T2 precursor **R.ELDLNSVLLK.L** **HGTCAAQVDALNSQK.K** **K.LQIKPSINYYQVADFK.D**	1.314	1.567	1.72	3	1.533	0.205
gi|4758504 hydroxysteroid (17-beta) dehydrogenase 10 isoform 1 **R.LVGQGASAVLLDLPNSGGEAQAK.K**	1.541		1.574	1	1.557	0.023
gi|4503143 cathepsin D **R.VGFAEAAR.L** **R.VGFAEAARL.-**	1.574	1.734	1.655	2	1.654	0.08
gi|186461558 neutrophil elastase **R.QVFAVQR.I** **R.VVLGAHNLSR.R**	1.935	1.951	1.957	2	1.948	0.011
gi|627372 alpha-mannosidase precursor **R.HLVLLDTAQAAAAGHR.L**	2.291	2.056	1.811	1	2.053	0.24
gi|4504437 heme oxygenase (decyclizing) 1 **R.TEPELLVAHAYTR.Y** **R.YLGDLSGGQVLK.K**	3.203	1.713	2.054	2	2.323	0.781
gi|12654715 TXNDC5 protein **R.GYPTLLLFR.G** **R.GYPTLLWFR.D** **R.DLESLREYVESQLQR.T** **K.ALAPTWEQLALGLEHSETVK.I**	3.327	3.353	2.732	4	3.138	0.351
E. Others						
gi|21755073 unnamed protein product **K.MDLNSEQAEQLER.I**	0.442	0.416	0.403	1	0.42	0.02

gi|119587276 hCG19802, isoform CRA_a **M.AEVQVLVLDGR.G**	0.621	0.551	0.243	1	0.472	0.201
gi|35570 unnamed protein product **K.NLDDGIDDER.L** **R.IVATKPLYVALAQR.K**	0.552	0.521	0.411	2	0.495	0.074
gi|13477237 ZNF607 protein **R.FDAGELITQR.E** **K.SLVARFDAGELITQR.E**	0.555		0.486	2	0.52	0.049
gi|56462484 MHC class I antigen **R.AYLEGLCVEWLR.R** **R.FIAVGYVDDTQFVR.F** **R.APWIEQEGPEYWDGETR.N** **R.DGEDQTQDTELVETRPAGDR.T**	0.703	0.56	0.453	4	0.572	0.125
gi|194374111 unnamed protein product **M.YGCDVGPDGR.L** **K.THVTHHPISDHEATLR.C**	0.663	0.603	0.456	2	0.573	0.1065
gi|35844 unnamed protein product **K.ELSLAGNELGDEGAR.L**	0.442	0.551	0.739	1	0.577	0.151
gi|114645930 PREDICTED: nucleosome assembly protein 1-like 1 isoform 9 **K.GIPEFWLTVFK.N** **K.FYEEVHDLER.K** **R.LDGLVETPTGYIESLPR.V**	0.583	0.615	0.599	3	0.599	0.016
gi|431422 Ran/TC4 Binding Protein **R.FLNAENAQK.F** **K.TLEEDEEELFK.M**	0.673	0.769	0.358	2	0.6	0.215
gi|2580550 dead box, X isoform **K.DLLDLLVEAK.Q** **R.SFLLDLLNATGK.D** **K.TAAFLLPILSQIYSDGPGEALR.A**	0.602	0.71	0.512	3	0.608	0.099
gi|122168 HLA class I histocompatibility antigen, B-58 α chain **R.DGEDQTQDTELVETRPAGDR.T** **R.VAEQLR.A**	0.731	0.724	0.375	2	0.61	0.204
gi|181486 DNA-binding protein B	0.592	0.716	0.587	1	0.632	0.073

R.EDGNEEDKENQGDETQGQQPPQR.R						
gi|193788267 unnamed protein product **R.AIRLELQGPR.G** **K.NLPYKVTQDELKEVFEDAAEIR.L** **K.EVFEDAAEIR.L**	0.681	0.658	0.538	3	0.626	0.077
gi|801893 leucine-rich PPR-motif containing protein **K.TVLDQQQTPSR.L** **K.VIEPQYFGLAYLFR.K**	0.547	0.595	0.742	2	0.628	0.101
gi|5107666 importin β **R.VAALQNLVK.I** **R.VLANPGNSQVAR.V** **K.SNEILTAIIQGMR.K** **K.LAATNALLNSLEFTK.A** **R.AAVENLPTFLVELSR.V**	0.59	0.453	0.849	5	0.631	0.201
gi|1235727 unnamed protein product **K.EPLVDVVDPK.Q** **R.ATLYVTAIEDR.Q**	0.562		0.71	2	0.636	0.104
gi|40225729 FUBP1 protein **R.ITGDPYKVQQAK.E** **R.LLDQIVEK.G** **K.IQIAPDSGGLPER.S**	0.706		0.589	1	0.647	0.083
gi|119571409 hCG1643342, isoform CRA_a **K.LLEPVLLLGKER**	0.682	0.635	0.627	1	0.648	0.03
gi|386777 transplantation antigen **R.FDSDAASPR.G** **K.THVTHHPLSDHEATLR.C**	0.716	0.636	0.618	2	0.657	0.052
gi|1136741 KIAA0002 **K.AIADTGANVVVTGGK.V** **K.FAEAFEAIPR.A** **K.TVGATALPR.L**	0.731	0.812	0.438	3	0.661	0.197
gi|23712 myoblast antigen 24.1D5 **R.AVVIVDDR.G** **R.FATHAALSVR.N** **R.NLSPYVSNELLEEAFSQFGPIER.A**	0.574	0.704	0.71	3	0.663	0.077
gi|13569879 acidic (leucine-rich) nuclear phosphoprotein 32 family, member E isoform 1 **K.SLDLFNCEITNLEDYR.E** **K.DLSTVEALQNLK.N**	0.616	0.753	0.629	3	0.666	0.076

K.IKDLSTVEALQNLK.N						
gi|4506773 S100 calcium-binding protein A9 **K.ELPGFLQSGK.D**	1.506	1.571	1.499	1	1.525	0.040
gi|9955206 Rho GDP-dissociation factor 2 **K.TLLGDGPVVTDPK.A** **K.APNVVVTR.L** **R.LTLVCESAPGPITMDLTGDLEALKK.E**	1.417	1.46	1.773	3	1.55	0.194
gi|8037945 prothymosin alpha **K.EVVEEAENGR.D**	1.541		1.574	1	1.557	0.023
gi|119239 Bone marrow proteoglycan **R.GNLVSIHNFNINYR.I**	1.626	1.785	1.733	1	1.714	0.081
gi|28375485 unnamed protein product **K.LKPLEVELR.R**	1.917	1.952	1.548	1	1.806	0.224
gi|4506191 proteasome beta 10 subunit proprotein **R.LPFTALGSGQDAALAVLEDR.F**	2.15	2.145	2.323	1	2.206	0.101
gi|32111 unnamed protein product **R.AGLQFPVGR.V**	5.999	4.425	4.272	1	4.899	0.956

Table S3. The detailed quantification results for histone proteins.

Experiments	histones	Peptide Ratio (treated/untreated)	Protein Ratio (Treated/Untreated)	Standard Deviation
	gi|223582 histone H4			
Set 1	K.VFLENVIR.D	2.28	2.33	0.16
	R.ISGLIYEETR.G	2.51		
	K.TVTAMDVVYALK.R	2.20		
Set 2	R.DAVTYTEHAK.R	2.40	2.39	0.26
	R.ISGLIYEETR.G	2.18		
	K.TVTAMDVVYALKR.Q	2.40		
	K.VFLENVIRDAVTYTEHAK.R	2.83		
	K.VFLENVIR.D	2.09		
	R.DNIQGITKPAIR.R	2.42		
Set 3	K.VFLENVIR.D	2.36	2.51	0.19
	R.ISGLIYEETR.	2.24		
	K.VFLENVIRDAVTYTEHAK.R	2.66		
	K.TVTAMDVVYALKR.Q	2.58		
	K.VFLENVIR.D	2.68		
	gi|510990 histone H2A			
Set 1	R.HLQLAIR.N	2.36	4.59	1.96
	R.VTIAQGGVLPNIQAVLLPK.K	5.43		
	R.AGLQFPVGR.V	5.99		
Set 2	K.VTIAQGGVLPNIQAVLLPK.K	5.86	4.43	1.86
	R.HLQLAIR.N	3.84		
	R.HLQLAIRNDEELNK.L	3.74		
	R.NDEELNKLLGK.V	2.01		
	R.AGLQFPVGR.V	6.70		
Set 3	R.AGLQFPVGR.V	3.56	3.60	0.38
	R.AGLQFPVGR.V	4.06		
	R.HLQLAIR.N	3.90		
	R.HLQLAIRNDEELNK.L	3.16		
	R.HLQLAIRNDEELNKLLGK.V	3.30		
	gi|1568551 histone H2B			
Set 1	K.ESYSIYVYK.V	2.62	2.58	0.04
	R.LLLPGELAK.H	2.55		
	K.QVHPDTGISSK.A	2.56		
Set 2	R.LLLPGELAK.H	2.86	2.89	0.24
	R.EIQTAVR.L	2.67		
	K.AMGIMNSFVNDIFER.I	2.52		
	R.KESYSVYVYK.V	3.21		
	K.QVHPDTGISSK.A	3.00		
	K.ESYSVYVYK.V	2.85		
	K.AMGIMNSFVNDIFER.I	2.71		
	R.KESYSVYVYK.V	3.21		
	K.ESYSIYVYK.V	2.96		
Set 3	K.AMGIMNSFVNDIFER.I	4.21	3.47	0.90
	K.AMGIMNSFVNDIFERIAGEASR.L	4.50		
	K.AMGIMNSFVNDIFER.I	2.92		
	R.EIQTAVR.L	3.39		
	R.KESYSVYVYK.V	2.31		

	gi|386772 histone H3			
Set 1	K.STELLIR.K	2.50	2.64	0.20
	K.DIQLAR.H	2.78		
Set 2	K.STELLIR.K	2.52	2.48	0.06
	R.KLPFQR.L	2.44		
Set 3	K.STELLIR.K	3.06	3.28	0.35
	K.DIQLAR.H	3.68		
	R.YRPGTVALR.E	3.10		
	gi|356168 histone H1b			
Set 1	R.SGVSLAALK.K	2.45	2.93	0.84
	K.ATGPPVSELITK.A	2.439		
	K.ALAAAGYDVEK.N	3.899		
Set 2	K.ATGPPVSELITK.A	2.342	2.96	0.94
	K.ALAAGGYDVEKNNSR.	2.566		
	K.ALAAAGYDVEK.N	1.974		
	.SETAPAAPAAPAPAEKTPVKK.K	3.959		
	K.GTLVQTK.G	3.975		
Set 3	K.ALAAAGYDVEK.N	2.281	2.38	0.14
	K.ATGPPVSELITK.A	2.481		

Table S4. Quantification results for hnRNPs, translation initiation factors, elongation factors and ribosomal proteins.

hnRNPs

	GI Number and Protein Name	**Forward, Set 1**	**Forward, Set 2**	**Reverse, Set 3**	**Peptide Number**	**Average Ratio**	**S.D.**
gi|386547	d(TTAGGG)n-binding protein B39	0.652	0.592	0.25	1	0.50	0.217
gi|133254	Heterogeneous nuclear ribonucleoprotein A1	1.024	0.962	1.208	5	1.07	0.128
gi|58761496	heterogeneous nuclear ribonucleoprotein A1-like	0.875		0.891	3	0.88	0.011
gi|14110407	heterogeneous nuclear ribonucleoprotein D-like	0.771	0.963	1.009	3	0.91	0.126
gi|4826760	heterogeneous nuclear ribonucleoprotein F	0.805	0.855	0.992	5	0.88	0.097
gi|542850	heterogeneous nuclear ribonucleoprotein G - human	1.116	0.982	0.93	5	1.01	0.096
gi|5031753	heterogeneous nuclear ribonucleoprotein H1	0.752	0.855	0.709	3	0.77	0.075
gi|55958547	heterogeneous nuclear ribonucleoprotein K	0.773	0.724	0.489	3	0.66	0.152
gi|55958543	heterogeneous nuclear ribonucleoprotein K	0.935	1.01	1.207	3	1.05	0.140
gi|5031755	heterogeneous nuclear ribonucleoprotein R isoform 2	0.861	0.973	0.764	3	0.87	0.105
gi|119597533	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A), isoform CRA_b	0.583	0.582	0.602	1	0.59	0.012
gi|109082737	PREDICTED: heterogeneous nuclear ribonucleoprotein C (C1/C2) isoform 2	0.812	1.061	1.182	5	1.02	0.189
					Average Ratio	**0.85**	

eukaryotic translation initiation factor

	GI Number and Protein Name	Forward, Set 1	Forward, Set 2	Reverse, Set 3	Peptide Number	Average Ratio	S.D.
gi|119610575	eukaryotic translation initiation factor 4A, isoform 1, isoform CRA_c	0.646	0.693	0.697	3	0.68	0.028
gi|33356163	eukaryotic translation initiation factor 1A, Y chromosome	0.745	0.59	0.762	3	0.70	0.095
gi|485388	eukaryotic initiation factor 4AII	0.646	0.718	0.775	2	0.71	0.065
gi|4503529	eukaryotic translation initiation factor 4A isoform 1	0.859	0.715	0.796	5	0.79	0.072
gi|4261795	eukaryotic initiation factor 5A		1	0.708	1	0.85	0.206
gi|4503545	eukaryotic translation initiation factor 5A isoform B	0.757	0.821	0.889	2	0.82	0.066
gi|4503519	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa	1.078	1.186	0.783	1	1.02	0.209
gi|7705433	eukaryotic translation initiation factor 3 subunit 6 interacting protein	0.895		1.034		0.97	0.099
					Average Ratio	**0.82**	

eukaryotic translation elongation factor

	GI Number and Protein Name	Forward, Set 1	Forward, Set 2	Reverse, Set 3	Peptide Number	Average Ratio	S.D.
gi|181969	elongation factor 2	0.447	0.545	0.636	3	0.54	0.09
gi|19353009	Similar to Elongation factor 2b	0.55	0.65	0.651	2	0.62	0.06
gi|4503475	eukaryotic translation elongation factor 1 alpha 2	0.684	0.652	0.726	1	0.69	0.04
gi|7108915	glucocorticoid receptor AF-1 specific elongation factor	0.685	0.677	0.703	3	0.69	0.01
gi|4503471	eukaryotic translation elongation factor 1 alpha 1	0.684	0.652	0.841	2	0.73	0.10
gi|62897525	eukaryotic translation elongation factor 1 alpha 1 variant	0.789	0.722	0.68	3	0.73	0.06
gi|4503481	eukaryotic translation elongation factor 1 gamma	0.729	0.637	0.834	2	0.73	0.10
gi|119602640	eukaryotic translation elongation factor 1 delta, isoform CRA_e	0.729	0.743	0.874	5	0.78	0.08
gi|194239729	eukaryotic translation elongation factor 1 delta isoform 4	0.797	0.764	0.907	5	0.82	0.08
gi|927065	eukaryotic translation elongation factor 1 alpha 1-like 14	0.789	0.827	0.909	3	0.84	0.06
gi|170785039	Human Translation Elongation Factor 1 Epsilon 1	0.759	0.954	0.839	3	0.85	0.10
gi|4503483	eukaryotic translation elongation factor 2	0.862	0.811	0.956	5	0.88	0.07
gi|181965	elongation factor 1 alpha		0.897	0.731	1	0.81	0.12
gi|119594429	eukaryotic translation elongation factor 1 gamma, isoform CRA_a	0.977	0.998	0.956	3	0.98	0.02
gi|1220311	elongation factor-1 alpha	0.911	0.829	1.209	3	0.98	0.20
gi|38522	human elongation factor-1-delta	0.911	0.868	1.209	5	1.00	0.19
gi|704416	elongation factor Tu	1.149	1.043	0.98	5	1.06	0.09
gi|25453472	eukaryotic translation elongation factor 1 delta isoform 2	1.105	1.243	1.013	5	1.12	0.12
					Average Ratio	**0.82**	

Ribosomal Proteins

GI Number and Protein Name		Forward, Set 1	Forward, Set 2	Reverse, Set 3	Peptide Number	Average Ratio	S.D.
gi|4506707	ribosomal protein S25	0.552	0.615	0.771	1	0.65	0.113
gi|4506669	ribosomal protein P1 isoform 1	0.625	0.706	0.729	2	0.69	0.055
gi|4506661	ribosomal protein L7a	0.702	0.649	0.734	2	0.70	0.043
gi|550021	ribosomal protein S5	0.458	0.815	0.829	4	0.70	0.210
gi|7513316	ribosomal protein L14	0.758	0.652	0.726	5	0.71	0.054
gi|119587829	ribosomal protein S25, isoform CRA_a		0.634	0.835	3	0.73	0.142
gi|4506685	ribosomal protein S13	0.789	0.586	0.845	2	0.74	0.136
gi|74723863	60S acidic ribosomal protein P0-like	0.76	0.923	0.558	3	0.75	0.183
gi|5032051	ribosomal protein S14	0.793	0.763	0.769	3	0.78	0.016
gi|36138	ribosomal protein L6	0.816	0.763	0.766	2	0.78	0.030
gi|15431301	ribosomal protein L7	0.767	0.782	0.801	4	0.78	0.017
gi|89573879	ribosomal protein L18	0.726	0.942	0.719	1	0.80	0.127
gi|119572747	ribosomal protein L18, isoform CRA_d	0.726	0.942	0.719	1	0.80	0.127
gi|14591909	ribosomal protein L5	0.843	0.744	0.826	3	0.80	0.053
gi|4506667	ribosomal protein P0	0.76	0.923	0.742	5	0.81	0.100
gi|4506697	ribosomal protein S20	0.81	0.93	0.724	5	0.82	0.103
gi|7705813	ribosomal protein L26-like 1	0.774	0.826	0.886	5	0.83	0.056
gi|14165469	ribosomal protein S15a	0.763	0.795	0.928	5	0.83	0.088
gi|6912634	ribosomal protein L13a	0.82	1.048	0.621	2	0.83	0.214
gi|113417504	PREDICTED: similar to ribosomal protein L12	0.777	0.804	0.913	3	0.83	0.072
gi|73959145	PREDICTED: similar to 40S ribosomal protein S2 isoform 4	0.987	0.791	0.719	1	0.83	0.139
gi|119615473	ribosomal protein L11, isoform CRA_a	0.875	0.847	0.783	3	0.84	0.047
gi|119605048	ribosomal protein L18a, isoform CRA_b	0.774	0.762	0.97	3	0.84	0.117
gi|4506597	ribosomal protein L12	0.777	0.819	0.913	5	0.84	0.070
gi|292435	ribosomal protein L26	0.756	0.826	0.941	5	0.84	0.093
gi|113429348	PREDICTED: similar to ribosomal protein S10	0.801	0.911	0.812	2	0.84	0.061
gi|4432750	ribosomal protein L11	0.866	0.833	0.836	1	0.85	0.018
gi|7765076	S3 ribosomal protein	0.971		0.726	5	0.85	0.173
gi|114606879	PREDICTED: similar to ribosomal protein isoform 2	0.866	0.905	0.813	3	0.86	0.046
gi|4506613	ribosomal protein L22 proprotein	0.826	0.75	1.009	2	0.86	0.133
gi|495126	ribosomal protein L11	0.766	0.975	0.845	3	0.86	0.106
gi|6677809	ribosomal protein S6	0.921	0.879	0.804	3	0.87	0.059

gi|4506723	ribosomal protein S3a		0.953	0.792	5	0.87	0.114
gi|119592221	ribosomal protein S4, X-linked, isoform CRA_a		0.863	0.884	3	0.87	0.015
gi|4506607	ribosomal protein L18	0.921	0.937	0.799	2	0.89	0.075
gi|4506715	ribosomal protein S28	0.717	0.928	1.015	3	0.89	0.153
gi|36142	ribosomal protein homologous to yeast S24	0.766	0.918	0.982	1	0.89	0.111
gi|14141193	ribosomal protein S9	0.833	0.922	0.916	5	0.89	0.050
gi|553640	ribosomal protein S13	1.073	0.723	0.904	1	0.90	0.175
gi|4506691	ribosomal protein S16	0.704	1.115	0.885	5	0.90	0.206
gi|4506679	ribosomal protein S10	0.992	0.849	0.873	3	0.90	0.077
gi|4506703	ribosomal protein S24 isoform c	0.804	1.019	0.891	3	0.90	0.108
gi|119575011	ribosomal protein S24, isoform CRA_i	0.804	1.019	0.891	3	0.90	0.108
gi|21104402	IMR-90 ribosomal protein S3	0.914	0.905	0.906	5	0.91	0.005
gi|4506743	ribosomal protein S8	0.91	0.922	0.905	5	0.91	0.009
gi|119572749	ribosomal protein L18, isoform CRA_f	1.035	0.924	0.785	5	0.91	0.125
gi|23491733	ribosomal protein S2	0.865	0.901	1.021	5	0.93	0.082
gi|4506695	ribosomal protein S19	0.972		0.897	3	0.93	0.053
gi|15431303	ribosomal protein L9	0.84	0.942	1.051	4	0.94	0.106
gi|62896495	ribosomal protein P0 variant	1.094	0.762	1.085	3	0.98	0.189
gi|4506635	ribosomal protein L32	1.047	0.904	0.996	1	0.98	0.072
gi|4506681	ribosomal protein S11	1.169	0.912	0.931	5	1.00	0.143
gi|13366090	ribosomal protein L7a	1.054	1.142	0.849	2	1.02	0.150
gi|73948356	PREDICTED: similar to 40S ribosomal protein S16	0.964	1.038	1.075	5	1.03	0.057
gi|1655596	ribosomal protein L31	1.078	1.037	1.012	3	1.04	0.033
gi|36146	ribosomal protein S12	1.216	1.037	0.922	5	1.06	0.148
gi|414587	ribosomal protein L10	1.008	1.062	1.179	5	1.08	0.087
gi|4506609	ribosomal protein L19	1.058	1.063	1.306	5	1.14	0.142
gi|4432754	ribosomal protein L27a		1.296	1.153	1	1.22	0.101
gi|30047125	Ribosomal protein SA	1.186	1.304	1.245	5	1.25	0.059
					Average Ratio	**0.88**	