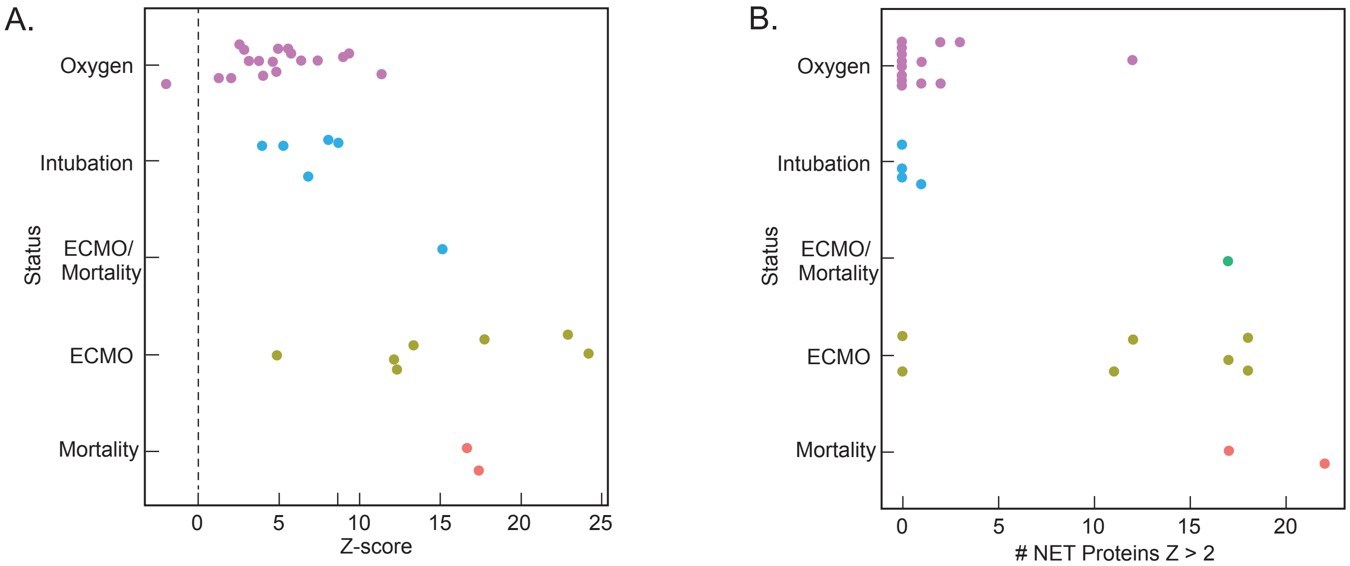
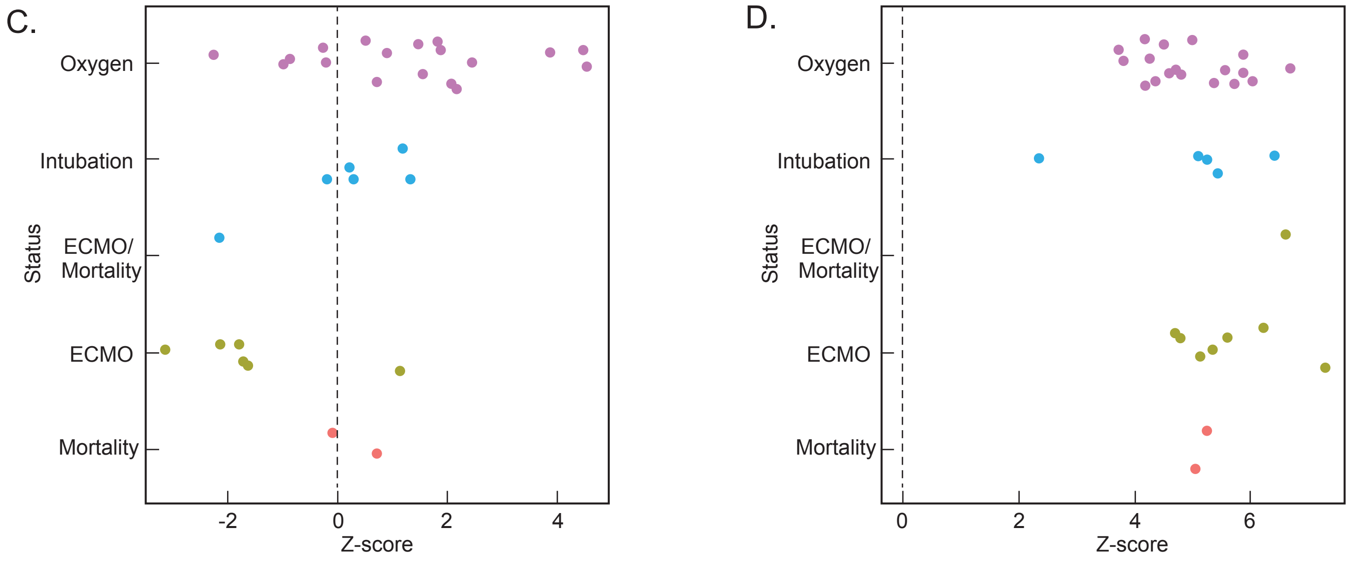
Supplemental Figure 1



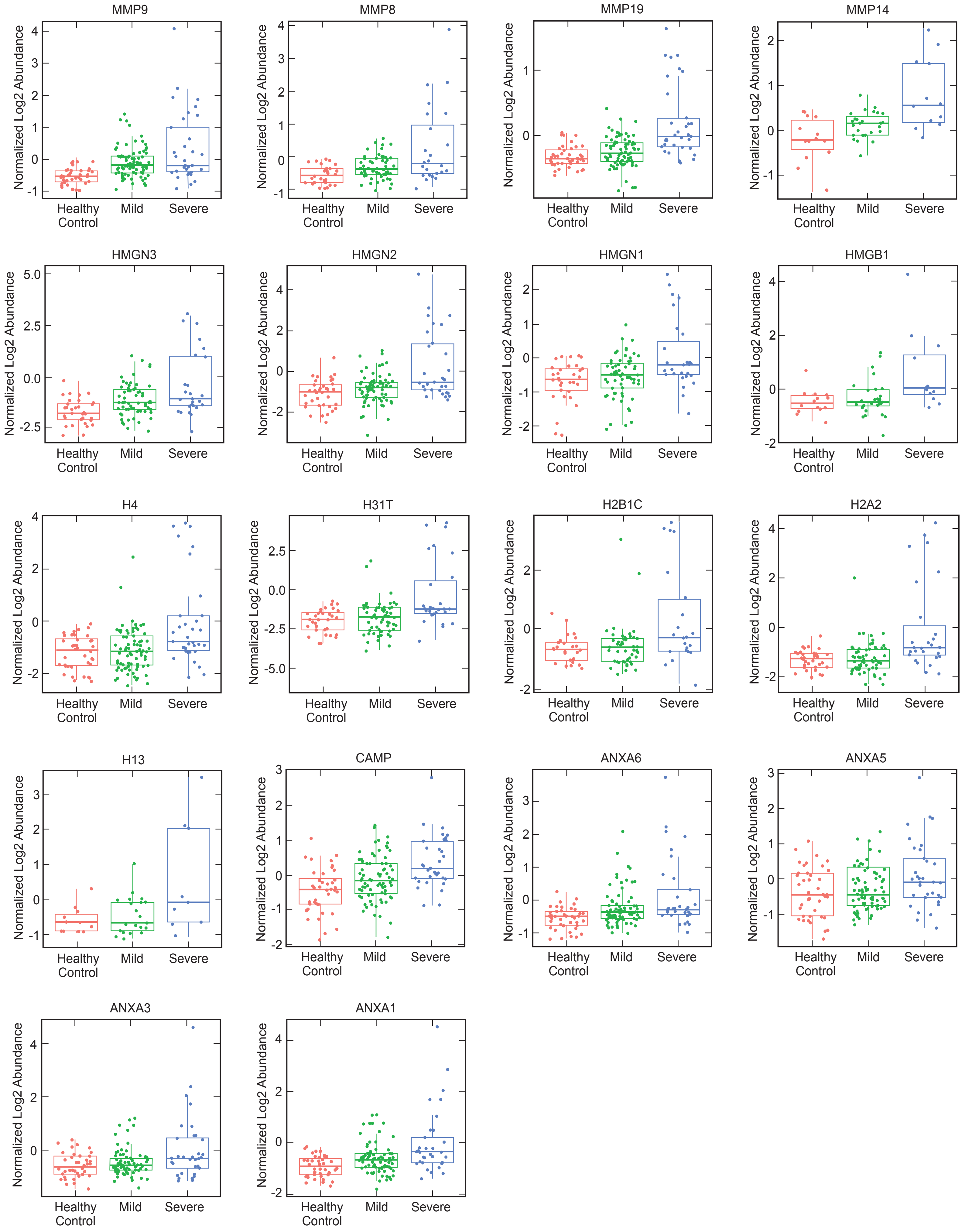
PSPB



CNDP1

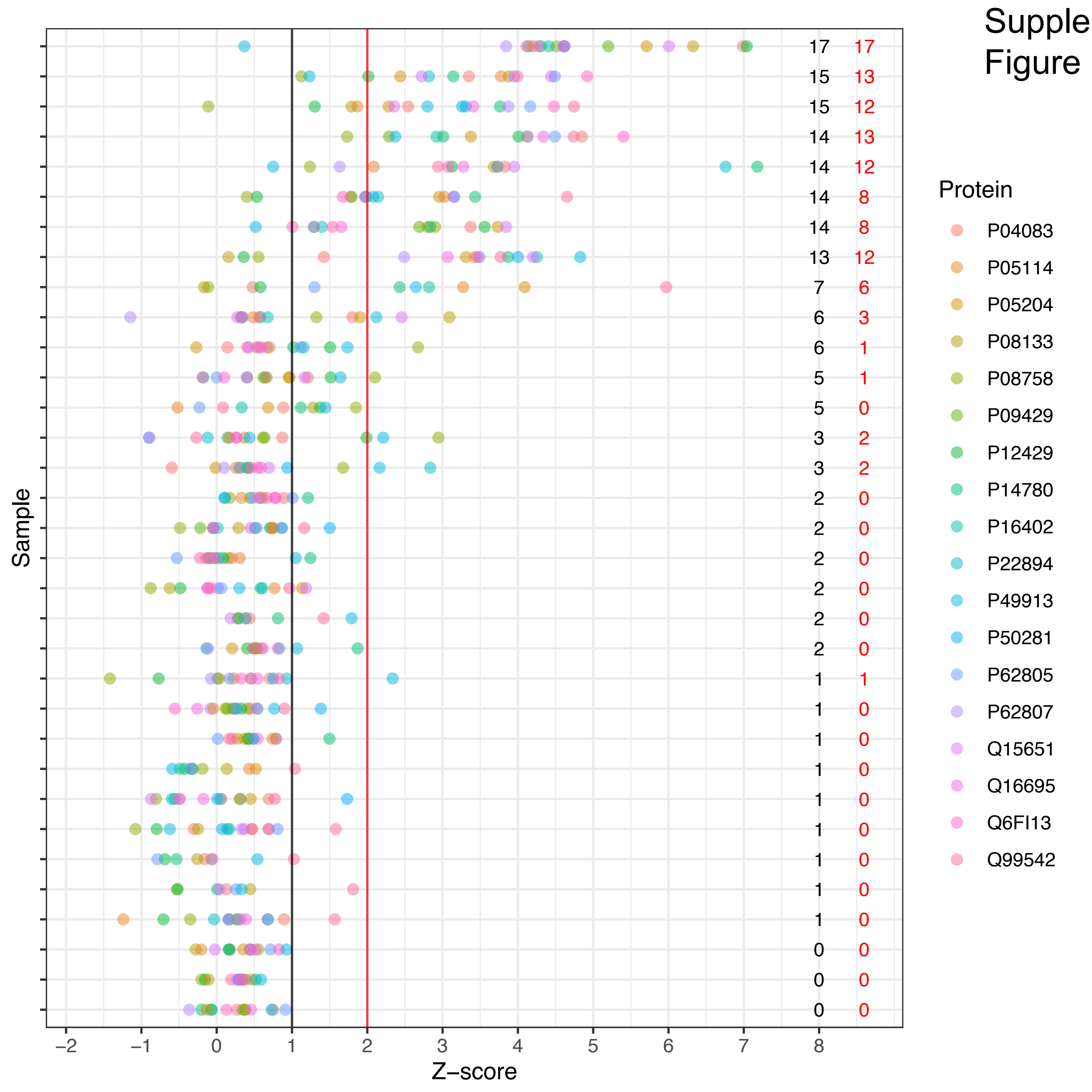
L-cystine

Supplemental Figure 2

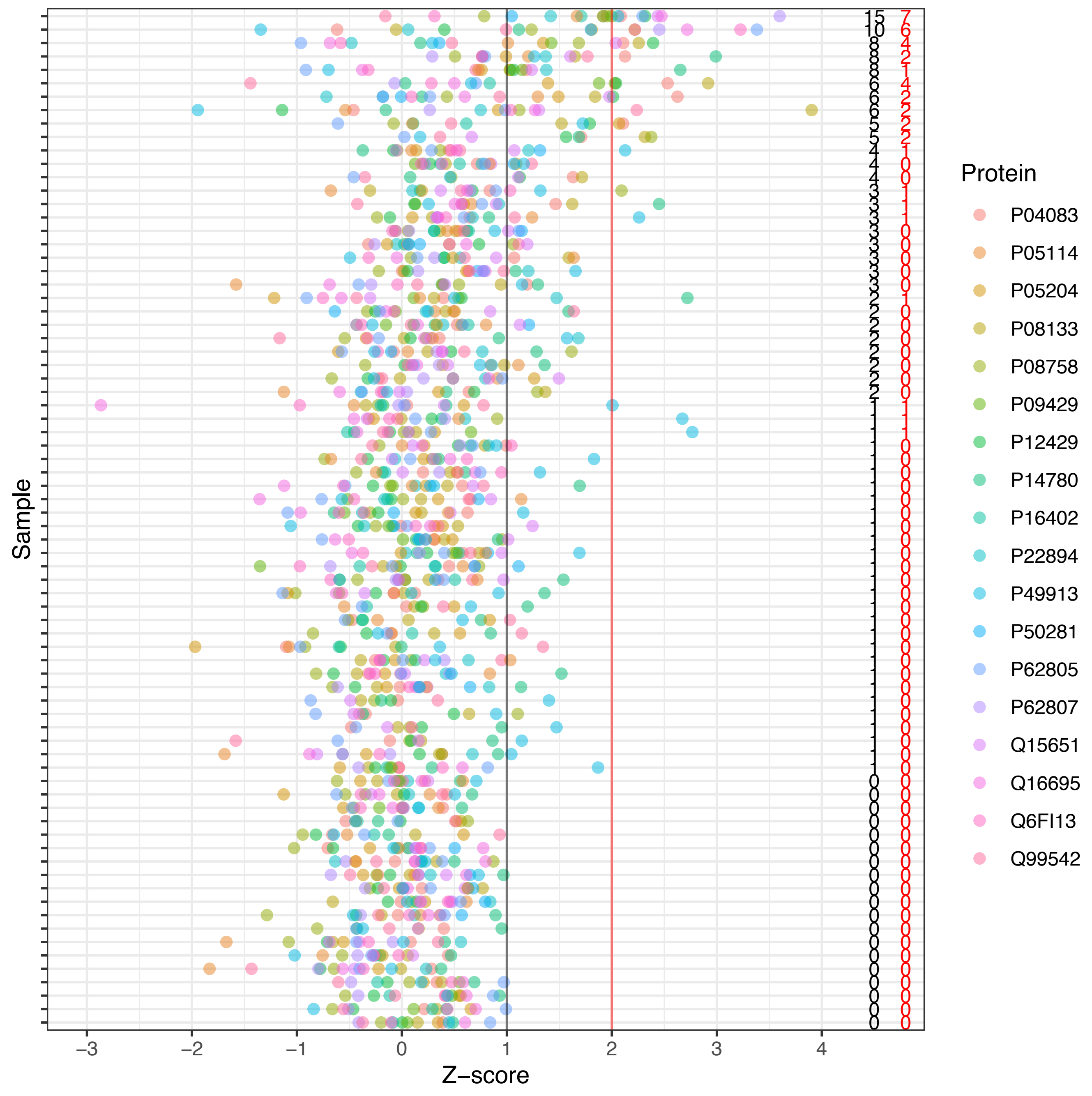


Supplemental Figure 3

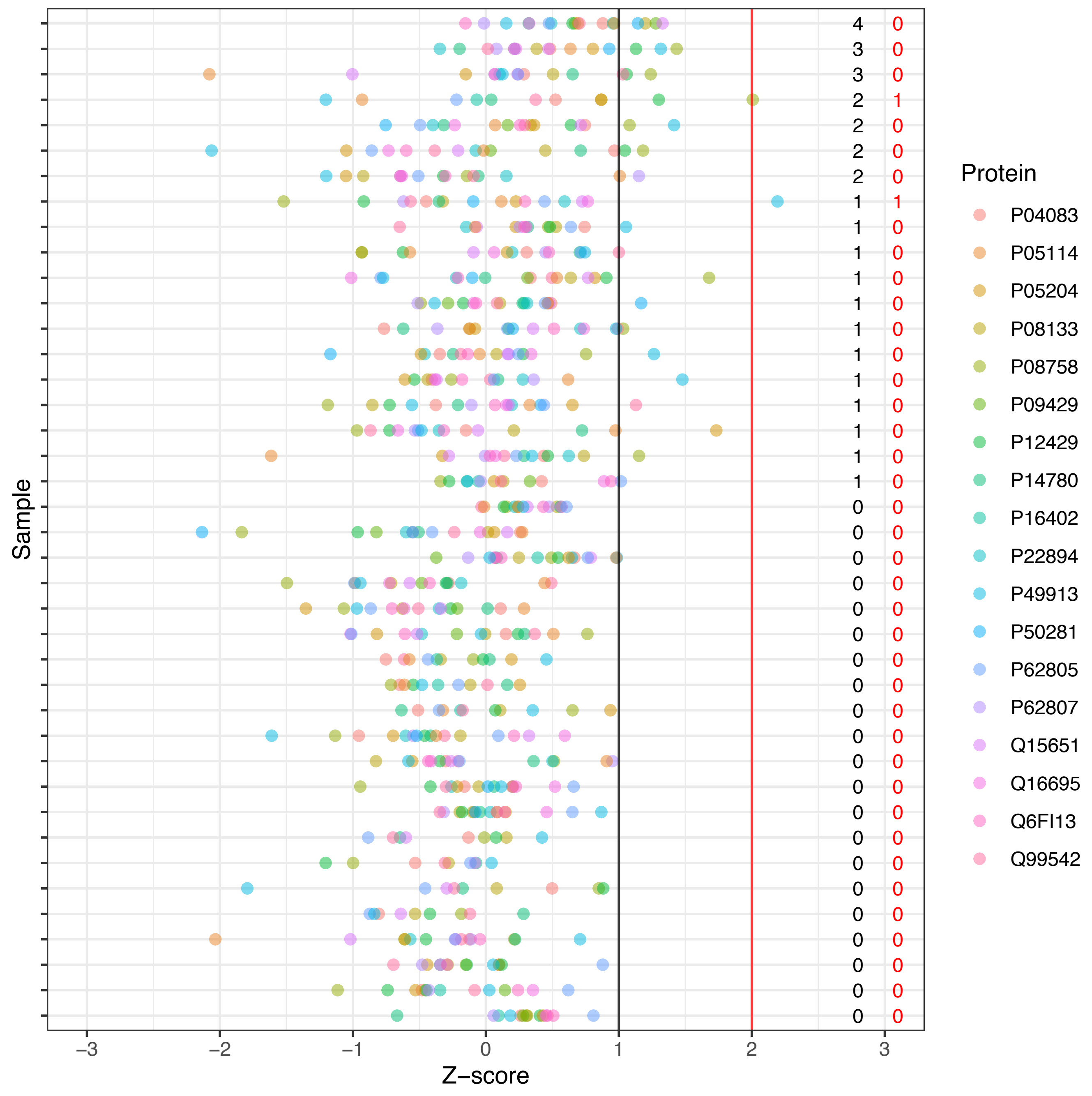
Severe



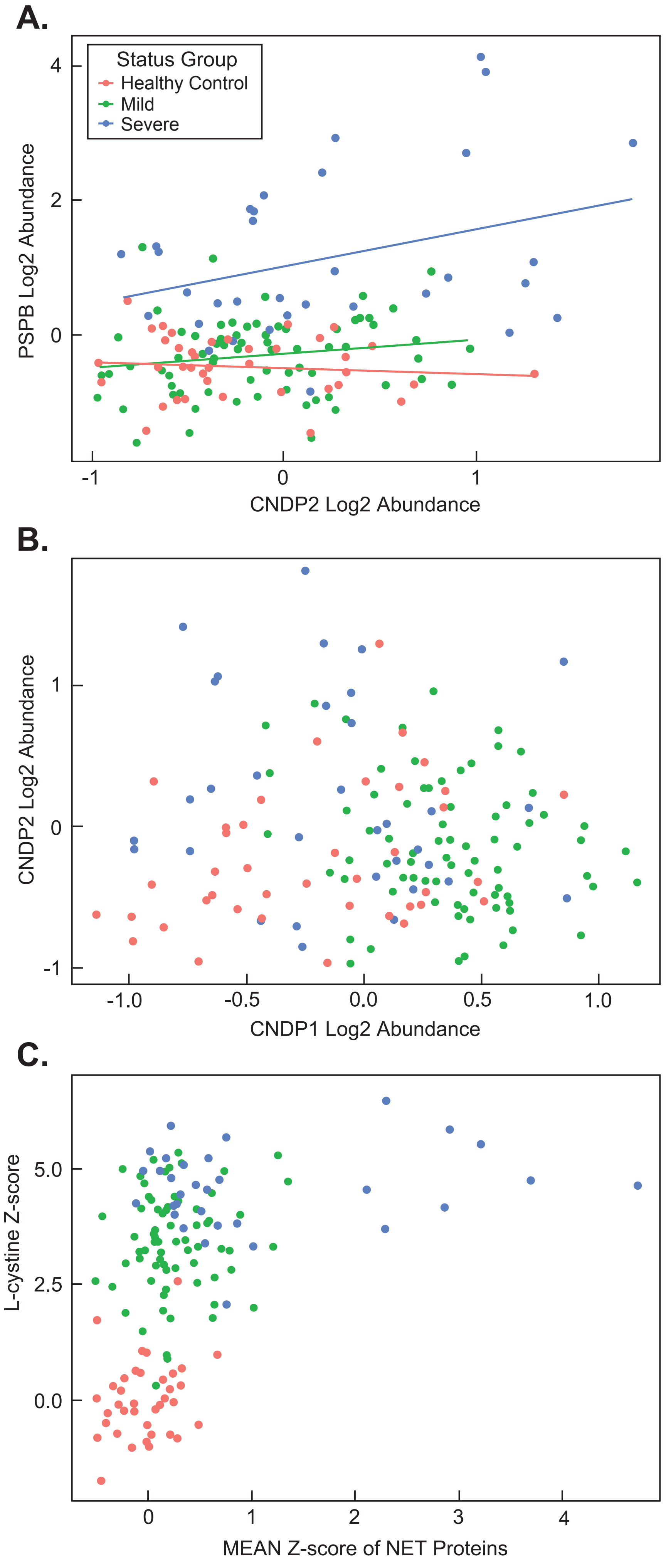
Mild



Healthy Controls



Supplemental Figure 4

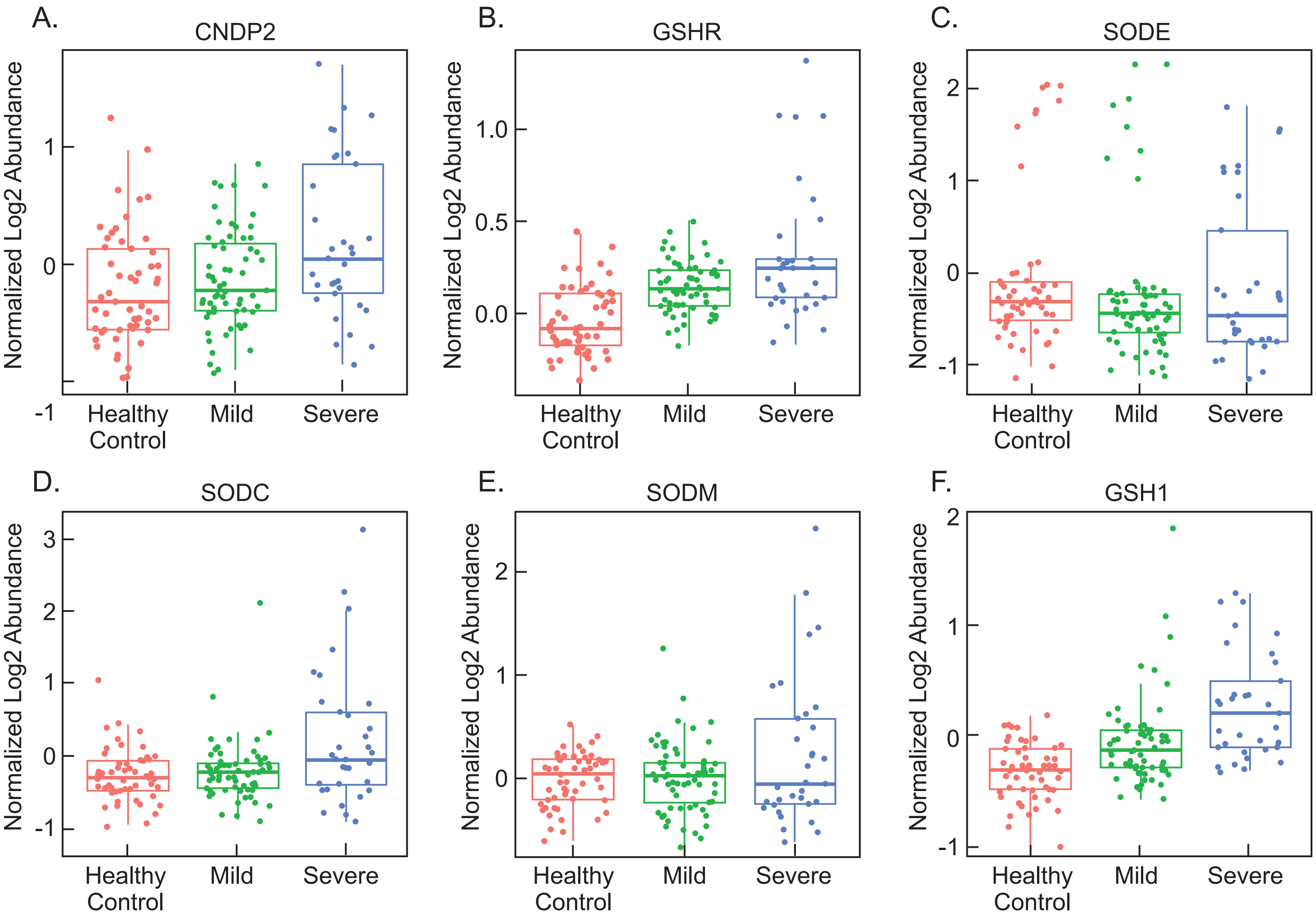


Supplemental Figure 5

>sp|Q96KN2|CNDP1_HUMAN Beta-Ala-His dipeptidase OS=Homo sapiens OX=9606 GN=CNDP1 PE=1 SV=4
MDPKLGRMAASLLAVLLLLLERGMFS**SPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPR**FRQELFR**MMAVAADTLQR**LGA
R**VASVDMGPQQLPDGQSLPIPPIILAELGSDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGK**LYGRGATDNK**GPVLAWINAVSAF**
RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQR**KPAITYGTRGNSYFMVEVK**CRDQDFHSGTFGGILH
EPMADLVALLGSLVDSSGH**ILVPGIYDEVVPLTEEEINTYKAIHLDLEEYR**NSSRVEKFLFDTK**EEILMHLWRYPSLSIHGIEGAFDEPG**
TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR**HLEDVFSK**RNSSNK**MVVSMTLGLHPWIANIDDTQYLAAK**RAIR**TVFGTEPDMIRDGST**
IPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINR**WNYIEGTKLFAAFFLEMAQLH**

>sp|Q96KP4|CNDP2_HUMAN Cytosolic non-specific dipeptidase OS=Homo sapiens OX=9606 GN=CNDP2
PE=1 SV=2
MAALTTLFK**YIDENQDR**YIKKLAK**WVAIQSVSAWPEK**RGEIRR**MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGR**LGSDPQ
KKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLYGRGSTDDKGPVAGWINALEAYQK**TGQEIPVNVR**FCLEGMEESGSEGLDELIFAR
KDTFFK**DVDYVCISDNYWLGK**KKPCITYGLRGICYFFIEVECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGINEAVAAVT
EEEHKLYDDIDFDIEEFAK**DVGAQILLHSHK**KDILMHRWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPEVVGEQVTSY
LTKKFAELRSPNEFK**VYMGHGGK**PWVSDFSHPHYLAGRRAMK**TVFGVEPDLTREGGSIPVTLTFQEATGK**NVMLLPVGSADDGAHSQNEK
LNRYNYIEGTK**MLAAYLYEVSQLK**D

Supplemental Figure 6



Supplemental Table I:

Protein	N_Peptides	N_HC	N_Mild	N_Severe	Mean_HC	Mean_Mild	Mean_Severe	Log2FC_MvsHC	Log2FC_SvsHC	Log2FC_SvsM	Adj_Pvalue_MvsHC	Adj_Pvalue_SvsHC	Adj_Pvalue_SvsM
sp|O15144|ARPC2_HUMAN	1	40	76	33	-0.02259	-0.06989545	0.20023523	-0.047303905	0.222826775	0.27013068	0.884546227	0.158120539	0.033549362
sp|Q99460|PSMD1_HUMAN	2	8	14	6	-0.11791	0.131884021	0.196822009	0.249796968	0.314734955	0.064937988	0.686891423	0.669587503	0.978954397
sp|O75882|ATRN_HUMAN	1	40	76	33	0.307815	0.192497743	0.02580914	-0.115317339	-0.282005942	-0.166688603	0.000526847	3.15E-12	1.92E-06
sp|P05976|MYL1_HUMAN	2	40	76	33	-2.04317	-2.246505281	-1.624210698	-0.203333813	0.418960771	0.622294583	0.480489602	0.120498268	0.003249631
sp|Q9NZP8|C1RL_HUMAN	2	40	76	33	0.183327	0.296293903	0.224965777	0.112967172	0.041639046	-0.071328125	0.003708868	0.575604385	0.131255072
sp|P05155|IC1_HUMAN	2	40	76	33	0.514166	0.480501436	0.604067741	-0.033664368	0.089901937	0.123566305	0.82524314	0.391527087	0.108174834
sp|P08697|A2AP_HUMAN	2	40	76	33	0.346401	0.310272943	0.093929984	-0.036128008	-0.252470968	-0.216342959	0.3167739	1.30E-13	4.87E-13
sp|Q8NI99|ANGL6_HUMAN	1	40	76	33	0.061497	0.142930088	-0.094752306	0.081433506	-0.156248889	-0.237682395	0.045414294	0.000541769	2.33E-09
sp|P02765|FETUA_HUMAN	36	40	76	33	0.522453	0.459110354	0.094100381	-0.063342935	-0.428352908	-0.365009973	0.30702339	2.65E-13	1.42E-12
sp|P0C0L5|CO4B_HUMAN	3	40	76	33	0.324434	0.375437291	0.244924753	0.051003073	-0.079509464	-0.130512538	0.565479717	0.385950352	0.04119814
sp|P19971|TYPH_HUMAN	2	40	76	33	-0.19728	-0.064090235	0.266718914	0.133187548	0.463996698	0.33080915	0.308394405	0.000110372	0.002322349
sp|P04217|A1BG_HUMAN	1	40	76	33	0.545594	0.513080348	0.407083746	-0.032513941	-0.138510543	-0.105996601	0.348069992	6.77E-06	0.000111899
sp|P01008|ANT3_HUMAN	4	40	76	33	0.483673	0.419441126	0.152338465	-0.064231988	-0.331334648	-0.26710266	0.107486331	5.64E-14	1.61E-12
sp|P05154|IPSP_HUMAN	6	40	76	33	0.266019	0.008342897	-0.073441734	-0.257675996	-0.339460627	-0.081784631	0.05317804	0.030390871	0.765790244
sp|P05543|THBG_HUMAN	1	40	76	33	0.279287	0.270144321	0.0098842	-0.009142869	-0.26940299	-0.260260121	0.969332834	1.08E-07	8.07E-09
sp|P36955|PEDF_HUMAN	2	40	76	33	0.318915	0.28045577	0.32161474	-0.038458994	0.002699976	0.04115897	0.467593663	0.997397407	0.465628761
sp|P00734|THRB_HUMAN	4	40	76	33	0.279823	0.248218247	0.007346056	-0.031604851	-0.272477042	-0.240872191	0.464349479	1.08E-13	1.18E-13
sp|P07357|CO8A_HUMAN	7	40	76	33	0.507877	0.480397854	0.404315724	-0.027479207	-0.103561336	-0.07608213	0.628664363	0.012659583	0.047778113
sp|Q9Y6R7|FCGBP_HUMAN	5	40	76	33	0.138323	0.220596563	0.447576704	0.082273767	0.309253908	0.226980141	0.274749238	1.10E-05	0.000312078
sp|Q2TV78|MST1L_HUMAN	11	40	76	33	0.15427	0.196031405	0.031882211	0.04176125	-0.122387944	-0.164149194	0.258062595	0.000527314	1.10E-07
sp|P00450|CERU_HUMAN	1	40	76	33	0.479359	0.518844654	0.384616701	0.039485218	-0.094742735	-0.134227954	0.562410496	0.105765613	0.003884347
sp|P09668|CATH_HUMAN	2	40	76	33	-0.09716	0.070885582	0.121576627	0.168040705	0.21873175	0.050691045	0.01079464	0.005214021	0.685491849
sp|P00918|CAH2_HUMAN	2	40	76	33	-0.23811	0.01430173	0.38264692	0.252412759	0.620757949	0.36834519	0.029359064	1.48E-06	0.001641871
sp|P62258|1433E_HUMAN	2	40	76	33	-0.08382	-0.138649778	0.347601151	-0.054832939	0.43141799	0.486250929	0.857868947	0.002112534	6.52E-05
sp|P02671|FIBA_HUMAN	2	40	76	33	0.135583	0.28042221	0.599116108	0.14483939	0.463533288	0.318693897	0.131792411	2.46E-06	0.000299489
sp|Q14624|ITIH4_HUMAN	4	40	76	33	0.65837	0.674030345	0.666827681	0.015660468	0.008457803	-0.007202665	0.884556113	0.975589431	0.977451359
sp|P08123|CO1A2_HUMAN	3	40	76	33	-0.01324	-0.038838481	0.310930369	-0.02559618	0.32417267	0.34976885	0.912115741	9.21E-05	1.70E-06
sp|P03952|KLKB1_HUMAN	6	40	76	33	0.503356	0.471927505	0.183779574	-0.031428425	-0.319576356	-0.288147931	0.748631082	2.33E-08	1.38E-08
sp|P00751|CFAB_HUMAN	4	40	76	33	0.236259	0.29120378	0.234919116	0.054944655	-0.001340009	-0.056284665	0.340552262	0.999552936	0.37034438
sp|P00748|FA12_HUMAN	2	40	76	33	0.231376	0.271177443	-0.004988407	0.039801727	-0.236364123	-0.27616585	0.759715504	0.001853044	2.73E-05
sp|P00742|FA10_HUMAN	3	40	76	33	0.218106	0.235792075	0.156493905	0.0176859	-0.06161227	-0.07929817	0.814997213	0.185187289	0.03051772
sp|P00740|FA9_HUMAN	22	40	76	33	0.249501	0.260068143	0.294564302	0.01056695	0.045063109	0.034496159	0.909627851	0.308821758	0.415238237
sp|P02751|FINC_HUMAN	3	40	76	33	0.625746	0.790995647	0.825774037	0.165249927	0.200028316	0.03477839	0.161416338	0.158280195	0.930299472
sp|P06396|GELS_HUMAN	5	40	76	33	0.522895	0.372026377	-0.003807242	-0.150868314	-0.526701934	-0.37583362	0.012312934	1.63E-13	1.01E-09
sp|P15291|B4GT1_HUMAN	1	40	76	33	0.009626	0.052458421	0.451220814	0.042831997	0.44159439	0.398762393	0.820356411	2.61E-06	1.70E-06
sp|P19827|ITIH1_HUMAN	57	40	76	33	0.625391	0.53613162	0.292288999	-0.089259218	-0.33310184	-0.243842621	0.01794115	8.62E-14	1.89E-10
sp|Q15063|POSTN_HUMAN	5	40	76	33	0.16417	0.117024309	0.122426851	-0.0471452	-0.041742658	0.005402542	0.811372998	0.892989916	0.997587612
sp|O00391|QSOX1_HUMAN	4	40	76	33	0.116624	0.090302507	0.135055549	-0.026321437	0.018431605	0.044753042	0.698653079	0.885472491	0.404581119
sp|P04114|APOB_HUMAN	2	40	76	33	0.764763	0.593495285	0.644518911	-0.171268201	-0.120244575	0.051023626	5.11E-06	0.011626374	0.34758575
sp|P22792|CPN2_HUMAN	5	40	76	33	0.275923	0.261397545	0.1685504	-0.014525886	-0.10737303	-0.092847145	0.884534912	0.011979902	0.014721229
sp|Q04756|HGFA_HUMAN	7	40	76	33	0.327763	0.24824213	-0.013154084	-0.079521164	-0.340917378	-0.261396214	0.174192042	5.99E-09	4.21E-07
sp|P02766|TTHY_HUMAN	4	40	76	33	0.285327	-0.078269826	-0.203788827	-0.363597196	-0.489116197	-0.125519001	6.68E-07	3.08E-08	0.187374208
sp|Q15582|BGH3_HUMAN	17	40	76	33	0.196206	0.237746952	0.155471904	0.041540528	-0.040734521	-0.082275049	0.707724296	0.794816346	0.30723364
sp|P15144|AMPN_HUMAN	15	40	76	33	0.097444	0.122107804	0.089799532	0.024663599	-0.007644673	-0.032308272	0.788024509	0.984295227	0.698756887
sp|Q96PD5|PGRP2_HUMAN	95	40	76	33	0.468645	0.336146306	0.032219974	-0.132499165	-0.436425497	-0.303926332	0.017971025	1.36E-11	6.43E-08
sp|P11047|LAMC1_HUMAN	4	40	76	33	-0.07942	-0.064538859	0.362251723	0.014885473	0.441676055	0.426790582	0.978990622	9.84E-06	1.42E-06
sp|P02655|APOC2_HUMAN	1	40	76	33	-0.10338	-0.255339291	0.181230468	-0.151955475	0.284614284	0.436569759	0.446702006	0.14546601	0.003831977
sp|P01019|ANGT_HUMAN	23	40	76	33	0.209328	0.220829991	0.123063076	0.011501634	-0.08626528	-0.097766914	0.97693301	0.407622709	0.232675296
sp|P10619|PPGB_HUMAN	2	40	76	33	0.003333	0.117193034	0.398990218	0.113859851	0.395657035	0.281797184	0.282591261	6.15E-05	0.001578439
sp|P41222|PTGDS_HUMAN	12	40	76	33	0.007307	-0.02519492	0.344469488	-0.032501893	0.337162515	0.369664407	0.91637922	0.002245293	0.000114912
sp|Q9UM47|NOTC3_HUMAN	12	40	76	33	0.116058	0.036273832	0.20083903	-0.079784309	0.084780889	0.164565198	0.174861681	0.255641092	0.001974784
sp|P02774|VTDB_HUMAN	32	40	76	33	0.7797	0.777676996	0.558558683	-0.002022528	-0.221140841	-0.219118312	0.997911497	3.19E-07	1.27E-08
sp|O94985|CSTN1_HUMAN	43	40	76	33	0.174248	0.123637023	-0.074112735	-0.050610882	-0.24836064	-0.197749758	0.178577228	5.99E-11	3.04E-09
sp|O43827|ANGL7_HUMAN	1	33	62	27	-0.00785	-0.042841294	-0.230260532	-0.034994054	-0.222413292	-0.187419238	0.844301465	0.011346637	0.017453082
sp|Q16610|ECM1_HUMAN	11	40	76	33	0.298802	0.258875681	0.083662517	-0.039926576	-0.21513974	-0.175213165	0.683638502	0.00080924	0.002312339
sp|P10643|CO7_HUMAN	1	40	76	33	0.220765	0.187521107	0.284261797	-0.033243508	0.063497181	0.09674069	0.752402755	0.490238103	0.125472078
sp|P0DOY3|IGLC3_HUMAN	1	40	76	33	-0.11017	-0.02962129	0.270139853	0.080549902	0.380311045	0.299761143	0.626220882	0.001163323	0.004466706
sp|A0A0C4DH67|KV108_HUMAN	79	40	76	33	0.072986	-0.068703187	-0.095495275	-0.141689306	-0.168481393	-0.026792088	0.451570564	0.460348447	0.975150532
sp|P35968|VGFR2_HUMAN	6	40	76	33	0.006248	0.052659445	-0.096338148	0.046411168	-0.102586425	-0.148997593	0.386705111	0.04366469	0.000330702
sp|P01042|KNG1_HUMAN	2	40	76	33	0.325089	0.337270891	0.195915881	0.012181988	-0.129173022	-0.141355011	0.899066337	0.000475246	1.26E-05
sp|P35443|TSP4_HUMAN	8	40	76	33	0.052356	0.163083237	0.126440982	0.110727623	0.074085369	-0.036642254	0.386859274	0.744243263	0.911970175
sp|P02649|APOE_HUMAN	2	40	76	33	-0.04666	0.062792736	0.380080261	0.109450463	0.426737988	0.317287525	0.14251754	2.10E-08	2.38E-06
sp|O75015|FCG3B_HUMAN	3	40	76	33	-0.10371	0.060623943	0.170453655	0.164338234	0.274167946	0.109829712	0.143176778	0.025543207	0.462255368
sp|Q9Y490|TLN1_HUMAN	5	40	76	33	-0.05974	-0.023726581	0.199546356	0.036009732	0.259282669	0.223272937	0.96868686	0.324687269	0.345722001
sp|P35858|ALS_HUMAN	10	40	76	33	0.3977	0.445965567	-0.030986087	0.048265556	-0.428686099	-0.476951655	0.681054832	1.90E-08	4.46E-12
sp|P35590|TIE1_HUMAN	2	40	76	33	0.093968	0.154126458	0.238795436	0.060158289	0.144827268	0.084668978	0.290972302	0.008545329	0.119176482
sp|P01031|CO5_HUMAN	14	40	76	33	0.302942	0.292839972	0.315227315	-0.010102285	0.012285057	0.022387343	0.931563648	0.930221537	0.737199253
sp|P06744|G6PI_HUMAN	23	40	76	33	-0.20999	-0.126265148	0.382625296	0.083729685	0.592620129	0.508890444	0.744725388	8.98E-05	0.000152915
sp|P01344|IGF2_HUMAN	4	40	76	33	0.096826	0.141707901	-0.142457832	0.044882348	-0.239283385	-0.284165733	0.498986958	5.02E-06	1.36E-09
sp|P48740|MASP1_HUMAN	1	40	76	33	0.20667	0.2373887	0.137660039	0.030719091	-0.069009569	-0.09972866	0.509916319	0.099711933	0.002712488
sp|P08294|SODE_HUMAN	11	40	76	33	-0.06067	-0.229638895	-0.094398501	-0.16896513	-0.033724736	0.135240393	0.546712468	0.983436333	0.71134692
sp|P05160|F13B_HUMAN	1	40	76	33	0.275354	0.197442907	0.074794826	-0.07791103	-0.200559111	-0.122648081	0.0791257	2.20E-05	0.004677605
sp|P15529|MCP_HUMAN	3	40	76	33	0.022636	-0.055177392	0.099139303	-0.07781321	0.076503484	0.154316695	0.217498087	0.359564794	0.006211887
sp|P02760|AMBP_HUMAN	1	40	76	33	0.301556	0.251846477	0.261650951	-0.049709873	-0.039905398	0.009804474	0.166619839	0.447031444	0.939567264
sp|P26927|HGFL_HUMAN	2	40	76	33	0.148903	0.187457604	0.028786606	0.038554646	-0.120116351	-0.158670997	0.259228242	0.000218014	3.03E-08
sp|P24821|TENA_HUMAN	13	40	76	33	-0.13175	-0.028445605	0.459526656	0.103305028	0.591277289	0.487972261	0.368014001	4.96E-09	4.64E-08
sp|P08603|CFAH_HUMAN	2	40	76	33	0.29547	0.315600982	0.298575461	0.020131062	0.00310554	-0.017025521	0.690407417	0.993911622	0.792157033
sp|P05156|CFAI_HUMAN	6	40	76	33	0.173447	0.176639496	0.162732118	0.003191998	-0.010715379	-0.013907377	0.993565329	0.951067199	0.898098973
sp|P00747|PLMN_HUMAN	3	40	76	33	0.365463	0.378233991	0.178147637	0.012770849	-0.187315505	-0.200086354	0.904377674	1.93E-06	1.15E-08
sp|Q16288|NTRK3_HUMAN	1	40	76	33	0.237847	0.074861321	-0.053768319	-0.162985549	-0.291615189	-0.12862964	0.000274199	5.10E-08	0.009646469
sp|O14498|ISLR_HUMAN	1	40	76	33	-0.04108	0.002942074	0.163535087	0.044022148	0.204615161	0.160593013	0.67629675	0.003957242	0.012455354
sp|P16035|TIMP2_HUMAN	6	40	76	33	0.227487	0.189866543	0.164991461	-0.03761998	-0.062495062	-0.024875083	0.64000817	0.429063968	0.842137804
sp|P01033|TIMP1_HUMAN	3	40	76	33	-0.13396	-0.026942589	0.488656665	0.10701433	0.622613585	0.515599254	0.399382936	1.18E-08	9.13E-08
sp|P01178|NEU1_HUMAN	10	33	62	27	-0.16851	-0.048725533	-0.027342676	0.119782337	0.141165194	0.021382857	0.560154358	0.573972601	0.983890232
sp|P07237|PDIA1_HUMAN	11	40	76	33	0.02636	0.073571361	0.313516422	0.047211228	0.287156289	0.239945061	0.763638492	0.00155774	0.003084264
sp|P19823|ITIH2_HUMAN	1	40	76	33	0.609194	0.524105858	0.338820419	-0.085088125	-0.270373564	-0.185285438	0.057453732	2.73E-08	1.66E-05
sp|Q9BWP8|COL11_HUMAN	60	40	76	33	0.023695	0.117462369	0.004304475	0.093767607	-0.019390287	-0.113157895	0.055992336	0.91614955	0.025812497
sp|P14625|ENPL_HUMAN	38	40	76	33	0.0737	0.079618312	0.442221621	0.00591826	0.368521568	0.362603308	0.993508484	2.78E-07	1.35E-08
sp|Q8IWV2|CNTN4_HUMAN	17	40	76	33	0.291558	0.179401088	-0.065423176	-0.112157019	-0.356981283	-0.244824264	0.029383595	7.04E-10	1.44E-06
sp|Q9HD45|TM9S3_HUMAN	6	26	48	20	-0.09869	-0.094890539	-0.036207433	0.00380286	0.062485966	0.058683106	0.999268044	0.876120673	0.864465605
sp|P02768|ALBU_HUMAN	15	40	76	33	-0.10454	0.058820025	0.435763937	0.163355136	0.540299048	0.376943912	0.48569911	0.005477203	0.03735157
sp|P05546|HEP2_HUMAN	1	40	76	33	0.359524	0.471067465	0.222903632	0.111543504	-0.136620329	-0.248163833	0.07446438	0.068144199	2.85E-05
sp|Q08380|LG3BP_HUMAN	6	40	76	33	-0.14116	0.070112323	0.274407307	0.211271496	0.41556648	0.204294984	0.034334016	0.000191711	0.061757539
sp|A1L4H1|SRCRL_HUMAN	1	40	76	33	0.209399	0.237918461	0.511397979	0.028519495	0.301999013	0.273479518	0.785841394	1.06E-07	5.74E-08
sp|P0C0L4|CO4A_HUMAN	7	40	76	33	0.191429	0.184627922	0.096938076	-0.006800634	-0.094490481	-0.087689847	0.988395858	0.216552904	0.187472908
sp|Q9UKX3|MYH13_HUMAN	9	40	76	33	-0.06614	-0.283020888	-0.075950718	-0.216884327	-0.009814156	0.207070171	0.022892902	0.994465886	0.047585705
sp|Q12907|LMAN2_HUMAN	2	40	76	33	-0.14019	-0.095541129	0.36384128	0.044646673	0.504029082	0.459382409	0.81371094	1.58E-07	7.21E-08
sp|P14209|CD99_HUMAN	40	40	76	33	0.052839	0.057374594	0.471837022	0.00453547	0.418997898	0.414462428	0.997820584	1.03E-05	8.40E-07
sp|Q9BWV1|BOC_HUMAN	7	40	76	33	0.077498	0.026060644	0.148844169	-0.05143694	0.071346584	0.122783525	0.393141181	0.290721332	0.011077619
sp|P43652|AFAM_HUMAN	5	40	76	33	0.385067	0.253051375	0.122744654	-0.132015748	-0.262322468	-0.13030672	0.036938472	0.000195323	0.058725572
sp|Q86WI1|PKHL1_HUMAN	7	40	76	33	0.261613	0.138643501	-0.016939501	-0.122969889	-0.278552891	-0.155583002	0.034926853	1.61E-05	0.009527171
sp|P0DJI8|SAA1_HUMAN	3	40	76	33	-1.49496	-1.407497905	-0.298253885	0.087458983	1.196703003	1.10924402	0.927021245	0.000128249	5.95E-05
sp|P06727|APOA4_HUMAN	15	40	76	33	0.476604	0.293984127	0.20275537	-0.182619551	-0.273848308	-0.091228758	0.009055007	0.000801025	0.343088035
sp|P10646|TFPI1_HUMAN	16	40	76	33	0.047449	0.049878758	0.307139095	0.002429759	0.259690097	0.257260338	0.998206756	3.61E-06	2.31E-07

sp|Q96GW7|PGCB_HUMAN	8	19	34	15	0.142379	0.045962672	0.297592569	-0.096416448	0.155213449	0.251629897	0.632457668	0.44441364	0.077305113
sp|P23142|FBLN1_HUMAN	2	40	76	33	0.171948	0.131944157	0.189187651	-0.040003496	0.017239998	0.057243494	0.560052504	0.928028662	0.354448728
sp|P80108|PHLD_HUMAN	11	40	76	33	0.224388	0.191833943	0.010829548	-0.032554367	-0.213558763	-0.181004396	0.873924571	0.021277925	0.029284466
sp|P10720|PF4V_HUMAN	3	40	76	33	-0.20378	0.094783359	0.113452321	0.298564675	0.317233636	0.018668962	0.008776218	0.024082417	0.983077694
sp|P04155|TFF1_HUMAN	16	18	34	16	-0.01114	-0.020211569	0.18852687	-0.009071029	0.19966741	0.208738439	0.99836213	0.56811451	0.453693795
sp|P02656|APOC3_HUMAN	5	40	76	33	0.221771	0.162782576	0.4740876	-0.058988509	0.252316515	0.311305025	0.807551893	0.07201966	0.006893779
sp|P55290|CAD13_HUMAN	1	40	76	33	0.333972	0.140759437	-0.207260745	-0.193212257	-0.541232438	-0.348020181	0.000938589	7.99E-14	1.51E-08
sp|P01009|A1AT_HUMAN	2	40	76	33	-1.91531	-1.925159911	-1.359917513	-0.009849232	0.555393166	0.565242397	0.999129388	0.153587816	0.085909041
sp|P13533|MYH6_HUMAN	15	40	76	33	0.112691	-0.09842701	0.277521771	-0.211117759	0.164831022	0.375948781	0.111642746	0.392842808	0.002787167
sp|Q9UKX2|MYH2_HUMAN	1	40	76	33	0.173455	-0.025016859	0.138616476	-0.198471738	-0.034838403	0.163633335	0.164007068	0.961597347	0.337190016
sp|P04004|VTNC_HUMAN	12	40	76	33	0.21222	0.288935156	0.05230798	0.076715254	-0.159911922	-0.236627177	0.066549873	0.000437951	3.58E-09
sp|Q07654|TFF3_HUMAN	32	40	76	33	-0.41037	-0.215905465	0.115910997	0.194461453	0.526277915	0.331816461	0.310879888	0.003542831	0.053262113
sp|P02753|RET4_HUMAN	3	40	76	33	0.196101	0.143449374	0.094783459	-0.052651599	-0.101317514	-0.048665915	0.482983321	0.15915836	0.578715956
sp|P69905|HBA_HUMAN	6	40	76	33	-1.04551	-0.791892941	0.079772118	0.253621312	1.125286372	0.871665059	0.439388525	3.75E-05	0.000354536
sp|P02790|HEMO_HUMAN	10	40	76	33	0.423362	0.385298989	0.085124151	-0.038062587	-0.338237426	-0.300174839	0.684449438	2.29E-08	2.22E-08
sp|P13667|PDIA4_HUMAN	29	40	76	33	-0.09626	-0.024321028	0.40313688	0.071943903	0.499401812	0.427457909	0.576811532	1.32E-07	3.42E-07
sp|P20851|C4BPB_HUMAN	5	40	76	33	0.053194	0.156823727	0.170295658	0.103629974	0.117101904	0.013471931	0.104588563	0.136073962	0.966287641
sp|P04278|SHBG_HUMAN	23	40	76	33	0.101983	0.191028486	-0.077847375	0.08904516	-0.179830702	-0.268875862	0.648594635	0.298674747	0.034670739
sp|Q01524|DEF6_HUMAN	13	12	20	9	-0.06602	0.246062121	0.667489404	0.312085555	0.733512838	0.421427283	0.909945022	0.701405933	0.867441954
sp|P09871|C1S_HUMAN	4	40	76	33	0.241875	0.221825844	0.19190511	-0.020049246	-0.049969981	-0.029920735	0.657011264	0.169509586	0.441355296
sp|P03951|FA11_HUMAN	13	40	76	33	0.221177	0.192625627	0.01123571	-0.02855118	-0.209941097	-0.181389917	0.693617638	5.16E-06	8.97E-06
sp|P17813|EGLN_HUMAN	1	40	76	33	0.214475	0.130168854	-0.128369124	-0.084306448	-0.342844426	-0.258537978	0.048102541	8.27E-13	5.77E-10
sp|Q13508|NAR3_HUMAN	3	40	76	33	0.132532	0.021468105	-0.01286212	-0.11106406	-0.145394285	-0.034330225	0.233063062	0.179517423	0.883456331
sp|A0A0C4DH38|HV551_HUMAN	3	31	55	23	-0.26932	-0.261574446	0.203326677	0.007740612	0.472641735	0.464901123	0.997544543	0.003426684	0.001275641
sp|P02743|SAMP_HUMAN	5	40	76	33	0.188159	0.242545292	0.166038375	0.054386396	-0.022120521	-0.076506917	0.691742133	0.958665302	0.528096233
sp|P02776|PLF4_HUMAN	3	40	76	33	-0.58204	-0.096470592	-0.010707919	0.48556528	0.571327954	0.085762674	0.002579096	0.003320988	0.840999745
sp|P01011|AACT_HUMAN	20	40	76	33	0.236646	0.280630269	0.506864728	0.043984666	0.270219125	0.226234459	0.736588288	0.000603493	0.001282076
sp|Q96KN2|CNDP1_HUMAN	19	40	76	33	-0.22405	0.367072691	-0.132794291	0.591119663	0.091252681	-0.499866982	6.12E-11	0.621036187	1.45E-07
sp|P02741|CRP_HUMAN	2	40	76	33	-1.59979	-1.206699544	-0.157644791	0.393095333	1.442150086	1.049054753	0.270229787	1.58E-05	0.000462012
sp|P12821|ACE_HUMAN	7	40	76	33	0.183914	0.084674064	-0.042393981	-0.099239882	-0.226307927	-0.127068045	0.176173141	0.002552868	0.083738505
sp|P19320|VCAM1_HUMAN	3	40	76	33	-0.01759	0.043719901	0.388243903	0.061308299	0.405832301	0.344524003	0.623898377	3.11E-06	8.07E-06
sp|Q9UIQ6|LCAP_HUMAN	2	30	56	24	-0.10896	0.073283857	0.079709963	0.182247515	0.18867362	0.006426106	0.025795297	0.066672697	0.995908679
sp|Q6P179|ERAP2_HUMAN	2	40	76	33	-0.09493	0.021851096	-0.040336698	0.116776789	0.054588996	-0.062187793	0.428242078	0.879104589	0.808484771
sp|P25311|ZA2G_HUMAN	3	40	76	33	0.343441	0.27863225	0.292038591	-0.064808752	-0.051402411	0.013406341	0.204325344	0.498679806	0.941166429
sp|P10909|CLUS_HUMAN	5	40	76	33	0.165864	0.196900202	0.155073487	0.031036237	-0.010790478	-0.041826715	0.455511158	0.936048703	0.287134249
sp|Q96IY4|CBPB2_HUMAN	5	40	76	33	0.270286	0.212007721	0.165369505	-0.058278214	-0.10491643	-0.046638216	0.104646263	0.007343349	0.277444623
sp|P02748|CO9_HUMAN	62	40	76	33	0.10426	0.223412757	0.37799522	0.119152462	0.273734924	0.154582463	0.249140859	0.007565817	0.130054584
sp|P10912|GHR_HUMAN	6	40	76	33	0.107297	0.138367675	-0.229596634	0.03107107	-0.33689324	-0.367964309	0.895504557	0.000260525	5.57E-06
sp|P02788|TRFL_HUMAN	1	40	76	33	-0.30832	-0.091070038	0.23328419	0.217250021	0.54160425	0.324354228	0.138094139	0.000335126	0.022300813
sp|Q01518|CAP1_HUMAN	19	40	76	33	-0.13564	-0.21508362	0.212788239	-0.079439276	0.348432583	0.427871858	0.84953234	0.119981886	0.018464195
sp|P17936|IBP3_HUMAN	2	40	76	33	0.141168	0.227785605	-0.23011564	0.086617658	-0.371283587	-0.457901245	0.258451498	2.83E-07	3.01E-12
sp|P60709|ACTB_HUMAN	2	40	76	33	0.237027	0.039583762	0.33664864	-0.197442777	0.099622102	0.297064878	0.107104581	0.670294183	0.012960373
sp|P02452|CO1A1_HUMAN	12	40	76	33	0.058498	0.071492318	0.513427475	0.012994686	0.454929843	0.441935157	0.983715655	4.45E-06	4.96E-07
sp|P55103|INHBC_HUMAN	59	40	76	33	0.011943	0.06850657	0.21263051	0.056563678	0.200687617	0.14412394	0.444630234	0.001308926	0.011671729
sp|Q8N149|LIRA2_HUMAN	18	40	76	33	-0.15294	-0.005983735	0.132762011	0.14695934	0.285705086	0.138745746	0.330116406	0.058495665	0.419146608
sp|O60493|SNX3_HUMAN	1	40	76	33	0.168679	0.158764672	0.444420389	-0.009914419	0.275741298	0.285655717	0.995160238	0.080323216	0.032957274
sp|Q6EMK4|VASN_HUMAN	6	40	76	33	0.201135	0.17227202	0.262538896	-0.028863394	0.061403483	0.090266876	0.549938871	0.158356952	0.007352571
sp|P08185|CBG_HUMAN	1	40	76	33	0.268934	0.35380291	0.051572744	0.084869127	-0.217361039	-0.302230166	0.282585922	0.004167405	3.30E-06
sp|P04180|LCAT_HUMAN	9	40	76	33	0.297369	0.187365324	0.132396678	-0.110003311	-0.164971958	-0.054968647	0.00485323	0.000317361	0.295867272
sp|P05019|IGF1_HUMAN	3	40	76	33	0.019512	0.18531131	-0.221431234	0.165798946	-0.240943598	-0.406742544	0.050695889	0.013729169	6.86E-07
sp|P20930|FILA_HUMAN	2	40	76	33	-0.27641	-0.441185323	-0.364450302	-0.164773203	-0.088038181	0.076735022	0.488588649	0.867669453	0.871773445
sp|Q8N6C8|LIRA3_HUMAN	2	40	76	33	0.15619	-0.156127833	-0.574352068	-0.312317567	-0.730541802	-0.418224235	0.352749162	0.021870188	0.195850565
sp|O14793|GDF8_HUMAN	1	40	76	33	0.237663	0.061276731	-0.339960324	-0.176386175	-0.577623229	-0.401237054	0.034889837	6.40E-10	9.89E-07
sp|O14960|LECT2_HUMAN	1	40	76	33	-0.06441	0.044816637	-0.059175919	0.109229584	0.005237029	-0.103992555	0.311851408	0.998130602	0.394708186
sp|P55854|SUMO3_HUMAN	2	40	76	33	-0.28427	-0.249271797	0.261246645	0.035002597	0.545521039	0.510518442	0.947932039	0.000259733	0.000108735
sp|P20160|CAP7_HUMAN	18	36	70	30	-0.57776	-0.447710242	0.019108455	0.130054229	0.596872927	0.466818697	0.609082819	0.001203984	0.00473791
sp|O75023|LIRB5_HUMAN	11	40	76	33	0.360687	0.391278458	0.306958696	0.030591692	-0.053728071	-0.084319763	0.759711187	0.558236778	0.164681596
sp|P02042|HBD_HUMAN	11	40	76	33	-1.30185	-1.121303744	-0.074072849	0.180545029	1.227775924	1.047230895	0.734887705	0.000121476	0.000226089
sp|P00746|CFAD_HUMAN	46	40	76	33	0.818716	0.803912318	0.905619649	-0.014803848	0.086903482	0.10170733	0.924500948	0.160050256	0.042830876
sp|P00738|HPT_HUMAN	4	40	76	33	-1.2273	-0.770042817	-0.442344916	0.457259866	0.784957767	0.327697902	0.173159885	0.030135194	0.449916211
sp|P07360|CO8G_HUMAN	3	40	76	33	0.216168	0.196732118	0.130749923	-0.019435722	-0.085417917	-0.065982195	0.775132099	0.037289824	0.080694446
sp|P07225|PROS_HUMAN	2	40	76	33	0.11409	0.181690018	0.163605324	0.067600115	0.049515421	-0.018084695	0.114147387	0.442689347	0.869949445
sp|P02675|FIBB_HUMAN	4	40	76	33	0.025417	0.158020323	0.308707445	0.132603476	0.283290598	0.150687122	0.130608293	0.002129923	0.100106426
sp|P04003|C4BPA_HUMAN	3	40	76	33	0.633682	0.757206224	0.757715697	0.123523792	0.124033265	0.000509473	0.056196178	0.132578508	0.999955686
sp|O00533|NCHL1_HUMAN	1	40	76	33	0.268685	0.17453486	-0.019263519	-0.094150124	-0.287948503	-0.19379838	0.129122816	6.07E-06	0.000722078
sp|Q92954|PRG4_HUMAN	3	40	76	33	0.08497	0.077784073	0.130829934	-0.007185867	0.045859994	0.053045861	0.990911406	0.774217312	0.647367757
sp|P00739|HPTR_HUMAN	9	40	76	33	-1.62603	-1.125860984	-0.718688342	0.500169478	0.90734212	0.407172642	0.185484346	0.02362249	0.372511091
sp|P02652|APOA2_HUMAN	14	40	76	33	-0.1989	-0.144776494	0.317291289	0.054123694	0.516191478	0.462067784	0.866158476	0.000245718	0.000211242
sp|Q9UK55|ZPI_HUMAN	4	40	76	33	0.268548	0.305477679	0.347612865	0.036930007	0.079065193	0.042135186	0.654359739	0.264877484	0.616067045
sp|Q02809|PLOD1_HUMAN	1	40	76	33	-0.05562	-0.017286833	0.180829571	0.038330804	0.236447207	0.198116403	0.760516436	0.001190867	0.002347623
sp|P29622|KAIN_HUMAN	18	40	76	33	0.434602	0.345553386	0.086601537	-0.089048728	-0.348000578	-0.258951849	0.135563766	1.31E-08	1.63E-06
sp|O15031|PLXB2_HUMAN	8	40	76	33	0.045856	0.080321344	0.15566624	0.034465635	0.10981053	0.075344896	0.45473795	0.00512898	0.039797634
sp|P40199|CEAM6_HUMAN	2	40	76	33	-0.03592	-0.090815561	0.295536417	-0.054896018	0.33145596	0.386351978	0.683522071	0.000150248	5.20E-07
sp|P04075|ALDOA_HUMAN	1	40	76	33	0.105665	0.006184584	0.282817789	-0.099479951	0.177153255	0.276633205	0.446964704	0.174698348	0.005373369
sp|P0DP58|LYNX1_HUMAN	1	40	76	33	0.145454	0.081168272	0.304881029	-0.064286025	0.159426732	0.223712757	0.710162315	0.237952146	0.029573822
sp|O95274|LYPD3_HUMAN	4	40	76	33	0.256415	0.19889304	0.013323547	-0.057521996	-0.243091488	-0.185569492	0.508378716	0.000423561	0.002837779
sp|Q08830|FGL1_HUMAN	1	40	76	33	-0.25487	-0.103852066	0.169516982	0.151018458	0.424387506	0.273369048	0.515374528	0.029989488	0.152180095
sp|Q6UXG3|CLM9_HUMAN	8	28	56	25	0.08453	0.086446592	0.176109581	0.001916283	0.091579272	0.089662989	0.999853786	0.790133384	0.744341458
sp|P00488|F13A_HUMAN	13	40	76	33	0.317704	0.24272329	0.013630564	-0.074981149	-0.304073875	-0.229092726	0.343033735	1.63E-05	0.000282261
sp|P05067|A4_HUMAN	4	40	76	33	0.016022	0.314741441	0.428218449	0.298719648	0.412196656	0.113477007	0.005028624	0.001060048	0.495245505
sp|P18428|LBP_HUMAN	2	40	76	33	-0.21929	-0.065429402	0.382062514	0.153863522	0.601355437	0.447491915	0.283544691	6.25E-06	0.000166843
sp|P06276|CHLE_HUMAN	26	40	76	33	0.225733	0.214939508	-0.131891973	-0.010793668	-0.357625149	-0.346831481	0.980177982	1.61E-06	1.60E-07
sp|Q9UHI8|ATS1_HUMAN	9	29	55	23	-0.35231	-0.324055165	0.290309574	0.028251171	0.642615911	0.614364739	0.968745574	5.51E-05	1.43E-05
sp|P15169|CBPN_HUMAN	3	40	76	33	0.234439	0.222964711	0.127038383	-0.011474384	-0.107400711	-0.095926327	0.933258193	0.018164174	0.017137539
sp|P06681|CO2_HUMAN	4	40	76	33	0.257948	0.269237325	0.232042223	0.011289163	-0.025905939	-0.037195102	0.905503455	0.697912676	0.391538956
sp|Q14019|COTL1_HUMAN	29	40	76	33	-0.12622	-0.108411016	0.279818169	0.017806708	0.406035893	0.388229185	0.988717309	0.020055713	0.010888462
sp|Q8N6Q3|CD177_HUMAN	1	36	69	30	-0.15533	-0.153645902	0.051699652	0.001688895	0.207034449	0.205345554	0.999893181	0.333999825	0.253050528
sp|P01023|A2MG_HUMAN	4	40	76	33	-0.07644	0.063439071	-0.074415787	0.139874833	0.002019974	-0.137854858	0.698392459	0.999948148	0.736160161
sp|O15394|NCAM2_HUMAN	6	40	76	33	0.256714	0.215811827	-0.041094738	-0.040902549	-0.297809114	-0.256906565	0.655963732	1.25E-06	2.38E-06
sp|P54108|CRIS3_HUMAN	9	40	76	33	0.18653	0.120707831	-0.152836664	-0.065822346	-0.339366841	-0.273544495	0.46072347	3.12E-06	2.32E-05
sp|P55899|FCGRN_HUMAN	12	40	76	33	0.009076	-0.0424877	-0.025923963	-0.051563984	-0.035000247	0.016563737	0.675356636	0.882377034	0.964933352
sp|P20333|TNR1B_HUMAN	9	40	76	33	-0.36902	-0.274144495	0.237347694	0.094875861	0.60636805	0.511492189	0.586700494	1.68E-06	5.23E-06
sp|Q15485|FCN2_HUMAN	10	40	76	33	-0.19451	-0.015030303	0.228479485	0.17947547	0.422985258	0.243509788	0.05694457	3.60E-05	0.01052918
sp|P35542|SAA4_HUMAN	6	40	76	33	-0.13964	-0.023872265	0.361113266	0.115762853	0.500748385	0.384985532	0.420096667	3.65E-05	0.000387728
sp|P55145|MANF_HUMAN	3	40	76	33	-0.47527	-0.319106945	0.032883602	0.156162951	0.508153498	0.351990547	0.446045571	0.003635656	0.03013312
sp|Q07954|LRP1_HUMAN	23	40	76	33	0.128293	0.193142263	0.358311952	0.064849537	0.230019226	0.165169688	0.129246258	1.60E-07	2.21E-05
sp|P13591|NCAM1_HUMAN	49	40	76	33	0.372043	0.241018327	-0.015935957	-0.131024737	-0.387979021	-0.256954284	0.001914771	8.40E-14	6.23E-09
sp|O00115|DNS2A_HUMAN	9	32	62	27	0.140401	0.044778938	0.180659758	-0.095622073	0.040258746	0.13588082	0.249031773	0.840688616	0.084637686
sp|P06865|HEXA_HUMAN	6	40	76	33	0.026034	-0.009466199	0.222623866	-0.035499969	0.196590096	0.232090066	0.704520101	0.000973447	7.77E-06
sp|P23528|COF1_HUMAN	2	40	76	33	-0.12173	-0.156557967	0.220751276	-0.034831769	0.342477474	0.377309244	0.973123653	0.167993506	0.06532846
sp|Q9Y287|ITM2B_HUMAN	2	40	76	33	-0.01076	0.101328262	0.336154917	0.112092871	0.346919527	0.234826655	0.080069071	3.48E-07	0.000108944
sp|P05062|ALDOB_HUMAN	19	40	76	33	-0.14971	0.064768901	0.198475965	0.214477543	0.348184606	0.133707063	0.148071743	0.032716014	0.516665838
sp|P06733|ENOA_HUMAN	6	40	76	33	-0.07376	0.026964738	0.270491384	0.10072595	0.344252596	0.243526646	0.598562448	0.018492999	0.075951998
sp|Q9UGM5|FETUB_HUMAN	7	40	76	33	0.132667	0.308372085	-0.043334702	0.175704616	-0.176002171	-0.351706787	0.00635172	0.028572533	1.02E-07
sp|P18206|VINC_HUMAN	1	40	76	33	0.13035	-0.086466733	0.280668598	-0.216816696	0.150318635	0.367135331	0.094420788	0.451314624	0.003204322

sp|P10451|OSTP_HUMAN	1	40	76	33	-0.46963	-0.42325956	0.212183335	0.046374177	0.681817072	0.635442895	0.927180052	3.69E-05	1.39E-05
sp|P13671|CO6_HUMAN	1	40	76	33	0.268222	0.292828394	0.192802361	0.024606565	-0.075419468	-0.100026033	0.696417936	0.100461276	0.006704118
sp|P00736|C1R_HUMAN	7	40	76	33	0.263002	0.278652434	0.206691652	0.015650655	-0.056310127	-0.071960782	0.776728213	0.10961565	0.011227609
sp|P08493|MGP_HUMAN	6	40	76	33	-0.09021	-0.133145379	0.30744763	-0.042930582	0.397662427	0.440593009	0.799246921	7.14E-06	2.24E-08
sp|P05164|PERM_HUMAN	4	40	76	33	-0.02845	0.16398756	0.755639835	0.192440151	0.784092425	0.591652274	0.187003801	5.57E-08	3.57E-06
sp|P21333|FLNA_HUMAN	6	40	76	33	0.147181	0.423527811	0.675556589	0.276347163	0.52837594	0.252028777	0.088828977	0.002744037	0.168677358
sp|P13796|PLSL_HUMAN	4	40	76	33	-0.01179	0.127697593	0.329261749	0.139487722	0.341051878	0.201564155	0.051847071	1.27E-05	0.004990522
sp|Q9H2G2|SLK_HUMAN	5	4	7	3	0.098117	0.24747819	-0.114534379	0.149361201	-0.212651368	-0.362012569	0.818073492	0.761660575	0.402947891
sp|P04275|VWF_HUMAN	4	40	76	33	-0.07417	0.040139918	0.739250711	0.114305854	0.813416647	0.699110793	0.476963056	4.98E-10	1.50E-09
sp|P43251|BTD_HUMAN	1	40	76	33	0.373401	0.23459162	-0.028390258	-0.13880981	-0.401791688	-0.262981878	0.000882448	4.55E-14	2.49E-09
sp|P02679|FIBG_HUMAN	1	40	76	33	0.036672	0.18714675	0.348800995	0.150475116	0.312129361	0.161654245	0.114617239	0.002074144	0.111437757
sp|P02786|TFR1_HUMAN	85	40	76	33	0.219743	-0.047019844	-0.065312901	-0.266763267	-0.285056324	-0.018293057	0.055946135	0.101707369	0.987807052
sp|P26038|MOES_HUMAN	3	40	76	33	0.096381	0.078402148	0.292072805	-0.017979244	0.195691413	0.213670657	0.961594421	0.045034603	0.009739573
sp|P25786|PSA1_HUMAN	6	40	76	33	-0.2358	-0.035786028	0.594118143	0.200014532	0.829918702	0.629904171	0.207745046	8.53E-08	4.35E-06
sp|Q9BYE9|CDHR2_HUMAN	2	40	76	33	-0.81147	-0.475053696	0.603392965	0.336420213	1.414866874	1.078446661	0.068436003	3.04E-12	1.15E-09
sp|O95810|CAVN2_HUMAN	1	40	76	33	-0.19948	-0.345327676	-0.086786429	-0.145850259	0.112690988	0.258541247	0.675789397	0.850600235	0.341864424
sp|P02750|A2GL_HUMAN	2	40	76	33	-0.32463	-0.077311582	0.427606841	0.247318626	0.752237048	0.504918423	0.165443353	2.61E-05	0.001847175
sp|P08118|MSMB_HUMAN	2	40	76	33	-0.011	-0.118385122	0.069963078	-0.107385252	0.080962949	0.188348201	0.284999754	0.608780051	0.03619074
sp|P30101|PDIA3_HUMAN	2	40	76	33	0.084196	0.127754601	0.215235621	0.043558663	0.131039682	0.08748102	0.801015178	0.254425101	0.457917963
sp|Q06033|ITIH3_HUMAN	18	40	76	33	0.042838	0.110589409	0.421313948	0.067751879	0.378476418	0.310724539	0.631664305	0.00011367	0.000379249
sp|P46531|NOTC1_HUMAN	364	40	76	33	0.196245	0.202482781	0.093114619	0.006237937	-0.103130225	-0.109368162	0.978193302	0.018493055	0.003626976
sp|P07358|CO8B_HUMAN	2	40	76	33	0.614161	0.590249516	0.528524949	-0.023911672	-0.085636239	-0.061724567	0.72154008	0.05995803	0.152837286
sp|P07359|GP1BA_HUMAN	4	40	76	33	0.16117	0.105910799	0.128622191	-0.055259357	-0.032547965	0.022711392	0.452727914	0.826205294	0.888362771
sp|Q9UNW1|MINP1_HUMAN	1	40	76	33	0.086723	0.136121968	0.082891529	0.049399103	-0.003831337	-0.053230439	0.231418684	0.993850036	0.225021468
sp|P02745|C1QA_HUMAN	12	40	76	33	0.154021	0.295186171	0.167036695	0.14116556	0.013016085	-0.128149476	0.162742766	0.989203379	0.267011398
sp|O00187|MASP2_HUMAN	7	40	76	33	0.271055	0.384985026	0.387277349	0.113929943	0.116222266	0.002292324	0.032290116	0.083007146	0.99873613
sp|Q86VB7|C163A_HUMAN	2	40	76	33	-0.1016	0.041289818	0.315158087	0.142894041	0.416762309	0.273868268	0.151870562	3.70E-05	0.002904192
sp|Q9UBV2|SE1L1_HUMAN	4	4	6	3	0.10389	-0.002173201	1.141139113	-0.106062726	1.037249588	1.143312314	0.979379051	0.28664279	0.184709389
sp|Q03591|FHR1_HUMAN	1	40	76	33	0.108033	0.141331317	0.107886347	0.03329873	-0.00014624	-0.03344497	0.353197122	0.999985996	0.397352279
sp|Q9UN70|PCDGK_HUMAN	7	40	76	33	0.00834	0.033538145	0.098508344	0.025197975	0.090168174	0.064970199	0.83180425	0.201328195	0.344762164
sp|Q6UX71|PXDC2_HUMAN	26	40	76	33	0.145115	0.086980075	0.177022739	-0.058135241	0.031907423	0.090042664	0.211743178	0.72118351	0.0401906
sp|P11226|MBL2_HUMAN	4	40	76	33	-0.06025	-0.165551903	-0.03387612	-0.105304554	0.026371229	0.131675783	0.746356527	0.987383117	0.66955235
sp|P04196|HRG_HUMAN	3	40	76	33	0.235597	0.211578539	-0.068086744	-0.024018191	-0.303683473	-0.279665282	0.89774752	2.20E-05	1.02E-05
sp|Q6UWW8|EST3_HUMAN	21	33	62	27	0.024089	-0.065266881	-0.196851971	-0.089356077	-0.220941167	-0.13158509	0.326991903	0.0108173	0.123394775
sp|Q8TDL5|BPIB1_HUMAN	1	36	69	30	-0.09242	0.015488018	0.318556108	0.1079037	0.41097179	0.30306809	0.403625948	0.000223697	0.002511844
sp|P04070|PROC_HUMAN	1	40	76	33	0.197748	0.158685115	-0.008921721	-0.039062865	-0.206669701	-0.167606836	0.455331422	1.42E-06	1.05E-05
sp|P07711|CATL1_HUMAN	7	40	76	33	0.019604	0.067083537	0.182751159	0.047479851	0.163147473	0.115667621	0.490135204	0.0039612	0.027160839
sp|P61626|LYSC_HUMAN	6	40	76	33	-0.0277	0.160130659	0.29527066	0.187826766	0.322966767	0.135140001	0.009006456	0.000100498	0.111273872
sp|P08571|CD14_HUMAN	1	40	76	33	0.057528	0.091927644	0.221708771	0.034399561	0.164180688	0.129781127	0.752027168	0.013604476	0.031866415
sp|Q71U36|TBA1A_HUMAN	1	40	76	33	-0.33333	-0.10018792	0.185740916	0.233140711	0.519069548	0.285928837	0.158319043	0.002372396	0.088962793
sp|P54289|CA2D1_HUMAN	13	40	76	33	0.293177	0.101622661	-0.343494878	-0.19155469	-0.63667223	-0.445117539	0.00716122	1.10E-13	1.37E-09
sp|P01024|CO3_HUMAN	9	40	76	33	0.43664	0.381683772	0.46079642	-0.054956372	0.024156276	0.079112648	0.353820881	0.869502842	0.153526056
sp|P02747|C1QC_HUMAN	9	40	76	33	-0.04302	0.130909731	-0.039021824	0.173926879	0.003995324	-0.169931555	0.089472039	0.999098964	0.131194997
sp|P02749|APOH_HUMAN	1	40	76	33	0.164332	0.123430789	0.130778943	-0.040900738	-0.033552584	0.007348154	0.645296304	0.815538845	0.987607159
sp|P01034|CYTC_HUMAN	29	40	76	33	0.017167	0.030203224	0.421950703	0.013035913	0.404783392	0.391747479	0.974370367	3.12E-07	2.56E-08
sp|P21589|5NTD_HUMAN	1	40	76	33	-0.23397	-0.060258289	0.001660226	0.173715419	0.235633934	0.061918515	0.083567385	0.043708342	0.753274355
sp|P16109|LYAM3_HUMAN	3	40	76	33	-0.13254	0.007615598	0.236750321	0.14015271	0.369287434	0.229134724	0.044463159	1.33E-06	0.000885245
sp|P81605|DCD_HUMAN	1	40	76	33	-0.3149	-0.205176813	0.045615448	0.109723568	0.360515829	0.250792261	0.667177367	0.053082296	0.16063097
sp|Q96FE7|P3IP1_HUMAN	1	40	76	33	-0.2316	-0.223841487	0.121530272	0.007759444	0.353131203	0.345371759	0.995287676	0.001782797	0.000495074
sp|P17301|ITA2_HUMAN	5	40	76	33	0.042222	0.005627789	-0.056083548	-0.036594206	-0.098305542	-0.061711337	0.682152165	0.15337395	0.387005437
sp|P27487|DPP4_HUMAN	1	40	76	33	0.180163	0.07497484	-0.148465078	-0.105188053	-0.328627971	-0.223439918	0.088026318	4.54E-07	0.000119937
sp|Q12884|SEPR_HUMAN	11	40	76	33	0.141339	0.020234233	-0.102345695	-0.121105142	-0.24368507	-0.122579928	0.297594955	0.03639829	0.335681681
sp|Q9UHG3|PCYOX_HUMAN	1	40	76	33	0.102564	0.034863907	0.067183132	-0.067699989	-0.035380765	0.032319224	0.489598145	0.873351368	0.866085645
sp|P22891|PROZ_HUMAN	1	40	76	33	0.331102	0.264003263	0.02611638	-0.067098424	-0.304985308	-0.237886884	0.554722539	0.000403518	0.002139633
sp|P23381|SYWC_HUMAN	10	40	76	33	-0.22304	0.085538542	0.32735786	0.308581832	0.550401151	0.241819318	0.000515219	1.89E-07	0.014744249
sp|Q92484|ASM3A_HUMAN	3	40	76	33	0.127148	0.100277248	0.055475213	-0.026870298	-0.071672333	-0.044802034	0.943764735	0.753188324	0.868363641
sp|P24593|IBP5_HUMAN	6	40	76	33	0.138379	0.124468836	-0.026795904	-0.013909876	-0.165174616	-0.15126474	0.936955962	0.002565408	0.00175853
sp|P22692|IBP4_HUMAN	1	40	76	33	-0.00633	0.0247718	0.32296957	0.031097955	0.329295725	0.29819777	0.875726307	8.53E-05	5.87E-05
sp|P08833|IBP1_HUMAN	7	40	76	33	-0.34916	-0.264298895	-0.12441712	0.084863499	0.224745274	0.139881775	0.800221624	0.343403008	0.58866805
sp|O00462|MANBA_HUMAN	5	40	76	33	0.114045	0.072253824	0.017346314	-0.041791301	-0.096698811	-0.05490751	0.511291614	0.087791271	0.36313032
sp|P49747|COMP_HUMAN	1	40	76	33	0.281967	0.17946943	-0.001261265	-0.102497161	-0.283227856	-0.180730695	0.24655805	0.000933086	0.023953692
sp|P05452|TETN_HUMAN	34	40	76	33	0.262959	0.167538308	-0.200176567	-0.09542031	-0.463135186	-0.367714876	0.038308186	3.81E-14	4.47E-14
sp|Q9BQ66|KR412_HUMAN	2	4	7	3	-0.03261	0.424495419	-0.303638452	0.457103314	-0.271030556	-0.72813387	0.807766606	0.949959205	0.645717021
sp|Q16627|CCL14_HUMAN	55	40	76	33	-0.07359	0.042166955	0.233119044	0.115759137	0.306711226	0.190952089	0.133006623	0.000109732	0.009179766
sp|Q8NBP7|PCSK9_HUMAN	1	40	76	33	0.025581	0.071592863	0.159083844	0.046011622	0.133502603	0.087490981	0.67085432	0.102933569	0.284839
sp|P28799|GRN_HUMAN	47	40	76	33	0.081921	0.142670847	0.246905849	0.060749914	0.164984916	0.104235002	0.420546446	0.0141627	0.109950933
sp|P27918|PROP_HUMAN	6	40	76	33	0.264207	0.185625664	-0.087743494	-0.078581222	-0.35195038	-0.273369158	0.127278396	5.96E-11	6.88E-09
sp|P60900|PSA6_HUMAN	28	40	76	33	-0.37737	-0.196698568	0.414974314	0.180673333	0.792346215	0.611672882	0.242407195	7.85E-08	2.78E-06
sp|P01597|KV139_HUMAN	8	33	62	27	-0.08079	-0.051727863	0.146442986	0.029060675	0.227231525	0.198170849	0.921879056	0.036909361	0.041473818
sp|P01602|KV105_HUMAN	9	15	27	13	0.233609	0.071514271	0.541900981	-0.162095029	0.308291681	0.47038671	0.485313876	0.158690982	0.00658136
sp|P02746|C1QB_HUMAN	5	40	76	33	0.102249	0.224281676	0.111355924	0.12203228	0.009106529	-0.112925752	0.119226415	0.991678655	0.200366623
sp|Q8IZF2|AGRF5_HUMAN	1	40	76	33	0.034451	0.057947183	-0.008128922	0.02349629	-0.042579815	-0.066076104	0.860111027	0.711224807	0.35468399
sp|P07998|RNAS1_HUMAN	7	40	76	33	-0.21894	-0.225801972	0.33843286	-0.006866442	0.55736839	0.564234832	0.996532611	9.86E-07	2.56E-08
sp|P20061|TCO1_HUMAN	3	40	76	33	0.081197	0.058705437	0.080363783	-0.022491797	-0.000833451	0.021658346	0.9426749	0.999944036	0.953070713
sp|Q14520|HABP2_HUMAN	3	40	76	33	0.344825	0.373591071	0.191400362	0.028766305	-0.153424404	-0.182190709	0.700920469	0.001428838	1.29E-05
sp|P03950|ANGI_HUMAN	1	40	76	33	0.059573	0.099438059	0.118266448	0.039865437	0.058693825	0.018828389	0.590350766	0.455620851	0.901507353
sp|A0A0B4J1V0|HV315_HUMAN	30	18	35	16	-0.13195	-0.114151981	0.093513322	0.017801955	0.225467259	0.207665304	0.988535998	0.276237608	0.243801688
sp|P01780|HV307_HUMAN	5	40	76	33	-0.23515	-0.102847561	0.078555412	0.13229961	0.313702582	0.181402973	0.293239759	0.010072465	0.134190096
sp|P01782|HV309_HUMAN	1	11	21	10	0.178613	0.022240117	0.158157508	-0.156372619	-0.020455228	0.135917391	0.188709486	0.978497181	0.301588547
sp|P36980|FHR2_HUMAN	6	40	76	33	0.045723	0.090525465	0.098000108	0.044802169	0.052276812	0.007474643	0.412932882	0.435461773	0.978421789
sp|P33908|MA1A1_HUMAN	1	40	76	33	0.134441	0.146438124	0.244298381	0.011996936	0.109857193	0.097860257	0.945112731	0.042349785	0.041106361
sp|Q8TDQ0|HAVR2_HUMAN	7	40	76	33	-0.44603	-0.30194773	0.353334152	0.144078346	0.799360228	0.655281882	0.329170936	2.34E-09	2.91E-08
sp|Q9Y6L7|TLL2_HUMAN	8	40	76	33	0.043821	0.071359603	-0.020750971	0.027539055	-0.06457152	-0.092110575	0.830817895	0.496967219	0.166978049
sp|Q9BXR6|FHR5_HUMAN	2	40	76	33	-0.08285	0.031326602	0.25947352	0.114173463	0.342320382	0.228146918	0.146879471	1.83E-05	0.001615099
sp|Q9P0K1|ADA22_HUMAN	2	16	27	12	0.12312	0.019448222	0.323606755	-0.103671838	0.200486695	0.304158533	0.733444823	0.457168231	0.120429534
sp|Q24JP5|T132A_HUMAN	13	40	76	33	0.114078	0.101882807	0.097020514	-0.012195124	-0.017057418	-0.004862293	0.931834291	0.909122463	0.990188276
sp|Q7Z7M0|MEGF8_HUMAN	3	40	76	33	0.215984	0.205832873	0.240832167	-0.010151449	0.024847845	0.034999295	0.916774828	0.69895758	0.406960501
sp|Q12860|CNTN1_HUMAN	12	40	76	33	0.268409	0.116935509	-0.226334612	-0.151473153	-0.494743274	-0.343270121	0.011292911	1.71E-12	1.67E-08
sp|Q6WN34|CRDL2_HUMAN	46	40	76	33	-0.00182	-0.085963626	-0.02648536	-0.084142321	-0.024664054	0.059478266	0.611464465	0.971119128	0.80538571
sp|P00338|LDHA_HUMAN	3	40	76	33	0.085971	0.191778806	0.491394197	0.105808121	0.405423513	0.299615392	0.362199307	7.73E-05	0.001171411
sp|P20062|TCO2_HUMAN	5	40	76	33	0.097667	0.104297099	0.132543198	0.006630525	0.034876625	0.028246099	0.988102097	0.79615121	0.826673256
sp|P07333|CSF1R_HUMAN	1	40	76	33	0.10416	0.115408268	0.168399204	0.011247855	0.06423879	0.052990935	0.975142591	0.569353307	0.61379054
sp|Q96BZ4|PLD4_HUMAN	3	40	76	33	0.083522	0.175415268	-0.159824835	0.091893334	-0.243346769	-0.335240103	0.317724562	0.004904053	5.77E-06
sp|Q13740|CD166_HUMAN	20	40	76	33	0.146701	0.145581555	0.209696039	-0.001119874	0.06299461	0.064114484	0.999485401	0.329362558	0.23257142
sp|Q12805|FBLN3_HUMAN	5	40	76	33	0.394228	0.342202985	0.568874388	-0.052025508	0.174645895	0.226671403	0.557793258	0.012705551	0.000128998
sp|P51884|LUM_HUMAN	30	40	76	33	0.299395	0.171154296	0.174242487	-0.128240775	-0.125152584	0.003088191	0.025485391	0.086999934	0.998060805
sp|P07996|TSP1_HUMAN	27	40	76	33	-0.46147	0.294608877	0.313293822	0.756078135	0.774763081	0.018684945	2.92E-06	7.45E-05	0.992302024
sp|P01762|HV311_HUMAN	19	21	41	19	-0.20471	-0.065753011	0.304878582	0.138958508	0.509590101	0.370631593	0.63302784	0.01564055	0.053910154
sp|P08519|APOA_HUMAN	4	40	76	33	0.252977	0.27721209	0.207015594	0.024234698	-0.045961798	-0.070196496	0.933527301	0.843226305	0.603910562
sp|P02787|TRFE_HUMAN	25	40	76	33	-0.22504	-0.54259436	-0.786448147	-0.317553246	-0.561407032	-0.243853787	0.167454761	0.02291042	0.393156849
sp|Q15113|PCOC1_HUMAN	10	40	76	33	0.156016	0.15873871	0.113395942	0.002722258	-0.042620511	-0.045342769	0.997405444	0.645750333	0.533344161
sp|P05362|ICAM1_HUMAN	1451	40	76	33	-0.14869	-0.04022184	0.464941221	0.108470285	0.613633346	0.50516306	0.176402795	1.40E-13	3.06E-12
sp|Q9H1U4|MEGF9_HUMAN	75	40	76	33	0.115668	0.16397621	-0.000309358	0.048308503	-0.115977066	-0.164285568	0.358437539	0.019083888	6.91E-05
sp|P14543|NID1_HUMAN	13	40	76	33	-0.08648	0.070955607	0.37537689	0.157438219	0.461859503	0.304421284	0.018499778	1.31E-09	5.37E-06
sp|Q9UBX1|CATF_HUMAN	152	40	76	33	0.095495	0.104295631	0.061377427	0.008800198	-0.034118005	-0.042918204	0.987505523	0.877892346	0.769618644

sp|P24387|CRHBP_HUMAN	29	40	76	33	0.058584	0.045870225	0.180745087	-0.012713623	0.122161239	0.134874862	0.941443412	0.024695644	0.003580685
sp|O43278|SPIT1_HUMAN	12	40	76	33	-0.10861	-0.040181795	0.428777395	0.068429615	0.537388805	0.468959191	0.552807327	8.08E-10	1.41E-09
sp|P07093|GDN_HUMAN	2	40	76	33	-0.39523	-0.093272093	0.106135517	0.301961559	0.501369169	0.19940761	0.00774394	0.000136801	0.146983056
sp|Q9NY15|STAB1_HUMAN	35	40	76	33	0.241415	0.213948281	0.1580146	-0.027466267	-0.083399947	-0.05593368	0.579960688	0.034537353	0.141639431
sp|Q14118|DAG1_HUMAN	29	40	76	33	0.052365	0.016311737	0.367380646	-0.036052869	0.315016039	0.351068909	0.822055341	8.10E-05	6.39E-07
sp|Q9UBQ7|GRHPR_HUMAN	11	40	76	33	-0.15371	-0.099147765	0.180291889	0.054566785	0.334006439	0.279439654	0.824888114	0.008663327	0.014257821
sp|Q6UXB8|PI16_HUMAN	621	40	76	33	0.854951	0.773050443	0.493662266	-0.081900532	-0.36128871	-0.279388178	0.570420983	0.000858229	0.004268681
sp|Q9UNN8|EPCR_HUMAN	340	40	76	33	0.107174	0.08388722	0.079238061	-0.023287237	-0.027936396	-0.004649159	0.869506404	0.870359119	0.995111653
sp|P20933|ASPG_HUMAN	133	40	76	33	0.053938	-0.027349533	0.0266917	-0.081287418	-0.027246186	0.054041233	0.348720015	0.920800931	0.662589563
sp|Q96CX2|KCD12_HUMAN	97	40	76	33	0.092534	0.014977797	0.027606074	-0.077555824	-0.064927547	0.012628277	0.14138827	0.384443201	0.954598041
sp|P12259|FA5_HUMAN	126	40	76	33	0.135399	0.200156794	0.25871773	0.064758095	0.123319031	0.058560935	0.18184469	0.015614506	0.292300457
sp|P25789|PSA4_HUMAN	140	40	76	33	-0.35443	-0.162137042	0.343397042	0.192288765	0.697822849	0.505534084	0.149765672	2.43E-07	2.51E-05
sp|P13727|PRG2_HUMAN	47	40	76	33	0.056493	0.015470379	0.119503124	-0.041022863	0.063009881	0.104032744	0.804074712	0.701561991	0.295738334
sp|Q76LX8|ATS13_HUMAN	699	40	76	33	0.201634	0.204882409	-0.115553754	0.003248829	-0.317187334	-0.320436163	0.996812752	1.90E-08	2.17E-10
sp|Q9Y5Y7|LYVE1_HUMAN	263	40	76	33	0.051896	0.104096326	0.142162671	0.052200632	0.090266978	0.038066345	0.710087573	0.494770633	0.852007419
sp|P10586|PTPRF_HUMAN	538	40	76	33	0.060004	0.131567008	0.263114763	0.071562788	0.203110544	0.131547755	0.257680711	0.000812075	0.01986941
sp|P14151|LYAM1_HUMAN	6	40	76	33	0.054749	0.164041472	-0.206571303	0.10929236	-0.261320416	-0.370612775	0.120399002	0.000374831	1.01E-08
sp|Q02985|FHR3_HUMAN	44	40	76	33	-0.01389	-0.07095263	-0.055590104	-0.057065936	-0.04170341	0.015362526	0.346654362	0.674923209	0.934143609
sp|P30043|BLVRB_HUMAN	32	40	76	33	-0.36905	-0.084450829	0.167175277	0.284596505	0.53622261	0.251626106	0.013913481	4.90E-05	0.051160093
sp|P23468|PTPRD_HUMAN	8	40	76	33	0.100514	0.091979236	-0.000133862	-0.008534674	-0.100647772	-0.092113098	0.959993357	0.023078616	0.018182086
sp|P98160|PGBM_HUMAN	6	40	76	33	0.388557	0.339729505	0.379861454	-0.048827714	-0.008695765	0.040131949	0.376389245	0.978629845	0.55879314
sp|P55268|LAMB2_HUMAN	335	40	76	33	0.121033	0.110980082	0.222593517	-0.010052444	0.101560991	0.111613436	0.954117222	0.040732692	0.007915108
sp|P68871|HBB_HUMAN	149	40	76	33	-1.49187	-1.130994485	-0.067617905	0.36087498	1.42425156	1.06337658	0.267043287	2.98E-06	9.08E-05
sp|Q9UHD8|SEPT9_HUMAN	453	4	7	3	0.245954	0.078410929	-0.09573579	-0.167543178	-0.341689897	-0.174146719	0.515087637	0.185933983	0.551440516
sp|P09493|TPM1_HUMAN	264	40	76	33	0.046251	-0.318040714	0.031803931	-0.364291873	-0.014447229	0.349844645	0.022940224	0.995748836	0.046041229
sp|Q6E0U4|DMKN_HUMAN	207	40	76	33	-0.2014	-0.329819302	-0.012565616	-0.128422205	0.18883148	0.317253686	0.203158977	0.094539585	0.000330609
sp|P08670|VIME_HUMAN	273	40	76	33	-1.00632	-0.799528945	-0.061507213	0.206794096	0.944815828	0.738021732	0.202748064	3.36E-09	1.60E-07
sp|P00915|CAH1_HUMAN	913	40	76	33	-0.25181	0.072081735	0.351532431	0.32388705	0.603337745	0.279450695	0.008394358	2.01E-05	0.041795473
sp|P27169|PON1_HUMAN	15	40	76	33	0.40943	0.213537105	0.058614977	-0.195893176	-0.350815304	-0.154922128	0.009087949	5.01E-05	0.071674696
sp|P68366|TBA4A_HUMAN	41	40	76	33	-0.32623	-0.067447938	0.048296921	0.258781264	0.374526123	0.115744859	0.063548424	0.019533334	0.60919296
sp|Q07960|RHG01_HUMAN	3	40	76	33	-0.11493	-0.046918472	0.143329737	0.068009613	0.258257823	0.19024821	0.666381884	0.020339564	0.065746932
sp|Q86UX2|ITIH5_HUMAN	2	40	76	33	0.003459	-0.07717917	-0.03079829	-0.080637921	-0.034257041	0.04638088	0.077394316	0.721673527	0.468907669
sp|Q8NHM4|TRY6_HUMAN	3	40	76	33	0.120517	-0.005474735	-0.128784244	-0.125991548	-0.249301057	-0.123309509	0.0004668	6.91E-09	0.001472358
sp|O75636|FCN3_HUMAN	435	40	76	33	0.067236	0.193359997	0.031358961	0.126124308	-0.035876729	-0.162001037	0.10424066	0.878888259	0.039069151
sp|P07602|SAP_HUMAN	2	40	76	33	-0.21912	-0.116828449	0.41299935	0.102293754	0.632121553	0.529827799	0.345121921	1.03E-10	8.31E-10
sp|P14314|GLU2B_HUMAN	27	40	76	33	-0.1373	-0.13471165	0.313552341	0.002586103	0.450850094	0.448263991	0.998854056	2.08E-09	2.87E-11
sp|P22105|TENX_HUMAN	9	40	76	33	0.362	0.289604448	0.051228037	-0.07239508	-0.310771491	-0.238376411	0.1885986	1.23E-08	7.38E-07
sp|P37840|SYUA_HUMAN	15	40	76	33	-0.07674	-0.19611775	0.203360604	-0.119382182	0.280096172	0.399478354	0.385016716	0.029305124	0.000167878
sp|Q86UX7|URP2_HUMAN	2	40	76	33	0.035739	-0.165911529	-0.015045061	-0.201650346	-0.050783878	0.150866468	0.38486826	0.958684137	0.623960547
sp|P63098|CANB1_HUMAN	3	36	70	30	0.027884	0.14056918	0.440877701	0.112685129	0.41299365	0.300308521	0.382422795	0.000266906	0.003254415
sp|Q14766|LTBP1_HUMAN	1	40	76	33	-0.32866	-0.001228572	0.238439923	0.327435745	0.56710424	0.239668494	0.001257862	2.17E-06	0.038800996
sp|P49908|SEPP1_HUMAN	2	40	76	33	0.234509	0.211184037	0.002596856	-0.023325353	-0.231912534	-0.208587181	0.82113298	6.21E-06	4.52E-06
sp|P20742|PZP_HUMAN	5	40	76	33	-0.04039	0.148065212	-0.175624183	0.18845853	-0.135230865	-0.323689395	0.559874709	0.813107424	0.225819133
sp|Q9NPY3|C1QR1_HUMAN	3	40	76	33	0.067231	3.95E-05	0.17631598	-0.067191735	0.10908472	0.176276455	0.615539165	0.415282043	0.057238114
sp|P12955|PEPD_HUMAN	1	40	76	33	0.289395	0.221733471	0.062976468	-0.067661746	-0.226418749	-0.158757003	0.090455598	8.15E-08	2.20E-05
sp|Q02487|DSC2_HUMAN	24	40	76	33	0.048635	0.024423056	0.390832463	-0.024212095	0.342197312	0.366409407	0.929205475	9.71E-05	2.19E-06
sp|Q07075|AMPE_HUMAN	3	40	76	33	0.175578	0.26325343	-0.014735199	0.087675652	-0.190312977	-0.277988629	0.037154144	4.38E-05	3.21E-11
sp|P05556|ITB1_HUMAN	6	40	76	33	0.230416	0.199440531	0.102158433	-0.030975875	-0.128257973	-0.097282098	0.558657406	0.001521189	0.008009051
sp|P08709|FA7_HUMAN	3	40	76	33	0.162604	0.182994487	0.063210834	0.020390523	-0.099393129	-0.119783652	0.745388317	0.00997029	0.00026773
sp|P12111|CO6A3_HUMAN	2	40	76	33	0.259411	0.248207361	0.436117517	-0.011203398	0.176706758	0.187910157	0.966518255	0.003982036	0.000417269
sp|P33241|LSP1_HUMAN	1	7	14	6	0.160112	0.089628174	0.148445503	-0.070484254	-0.011666925	0.058817329	0.836596497	0.99659437	0.893906491
sp|Q13683|ITA7_HUMAN	2	40	76	33	0.175567	0.116525728	-0.141681897	-0.059040987	-0.317248612	-0.258207625	0.454923808	9.62E-07	6.91E-06
sp|P22352|GPX3_HUMAN	3	40	76	33	0.186247	0.076020428	-0.000133185	-0.110226496	-0.186380109	-0.076153613	0.036800153	0.001794656	0.243861448
sp|Q6UWP8|SBSN_HUMAN	3	40	76	33	0.128392	0.032471539	0.192044829	-0.095920271	0.06365302	0.15957329	0.184206814	0.594283244	0.018057812
sp|Q15942|ZYX_HUMAN	1	40	76	33	0.061643	-0.061582917	0.184657447	-0.123226381	0.123013982	0.246240364	0.472700885	0.596610487	0.075980886
sp|P16112|PGCA_HUMAN	2	40	76	33	0.120408	0.047411085	-0.195512166	-0.072996963	-0.315920214	-0.242923251	0.305892765	1.24E-06	2.70E-05
sp|P34096|RNAS4_HUMAN	1	40	76	33	0.031062	0.107663423	0.310186705	0.076601313	0.279124595	0.202523282	0.126452331	6.40E-08	9.30E-06
sp|Q13822|ENPP2_HUMAN	6	40	76	33	0.295282	0.286834707	0.146039511	-0.008447639	-0.149242836	-0.140795196	0.987241725	0.067973209	0.048115253
sp|P09172|DOPO_HUMAN	1	40	76	33	0.290453	0.200814238	-0.105175728	-0.089639231	-0.395629197	-0.305989966	0.563874607	0.00074341	0.00380853
sp|Q6GTS8|P20D1_HUMAN	25	40	76	33	-0.09134	-0.258556455	-0.090769695	-0.167213667	0.000573094	0.167786761	0.568455506	0.999995394	0.60673456
sp|O00299|CLIC1_HUMAN	12	40	76	33	-0.0897	-0.03383157	0.19268642	0.055869176	0.282387165	0.22651799	0.905713895	0.179775514	0.244248481
sp|Q13093|PAFA_HUMAN	8	40	76	33	0.015804	0.173443181	0.327285946	0.157639409	0.311482174	0.153842765	0.141615454	0.006091946	0.194011659
sp|Q6MZM0|HPHL1_HUMAN	18	40	76	33	0.195469	0.136686713	0.009204251	-0.058782485	-0.186264948	-0.127482463	0.592876829	0.029863111	0.119699429
sp|P62937|PPIA_HUMAN	14	40	76	33	0.047132	-0.01032778	0.296061682	-0.057459705	0.248929756	0.306389462	0.786867244	0.049030685	0.003477209
sp|P19961|AMY2B_HUMAN	9	40	76	33	0.112982	0.052298145	-0.013164419	-0.06068389	-0.126146454	-0.065462564	0.650019805	0.280017892	0.643999468
sp|P55056|APOC4_HUMAN	23	40	76	33	0.151037	0.163588342	0.321396634	0.012551147	0.170359439	0.157808292	0.991763055	0.353488527	0.321638583
sp|O95445|APOM_HUMAN	14	40	76	33	6.60E-05	0.157382891	0.269164552	0.157316881	0.269098542	0.111781661	0.095288475	0.009680759	0.347758579
sp|P04040|CATA_HUMAN	3	40	76	33	-0.3043	-0.143744511	0.415261567	0.160558665	0.719564743	0.559006078	0.286100499	2.48E-07	6.08E-06
sp|Q9UBP4|DKK3_HUMAN	9	40	76	33	0.161028	0.069602965	0.255097449	-0.091425042	0.094069443	0.185494485	0.097747448	0.18095635	0.000351814
sp|P32119|PRDX2_HUMAN	8	40	76	33	-0.58948	-0.128517254	0.159956042	0.460961013	0.749434309	0.288473296	0.001117724	7.25E-06	0.087155125
sp|P08195|4F2_HUMAN	4	40	76	33	0.183861	0.170959865	-0.123327291	-0.012901402	-0.307188558	-0.294287155	0.942769619	4.20E-09	2.73E-10
sp|O95479|G6PE_HUMAN	6	40	76	33	0.06481	0.115900505	0.093070966	0.051090099	0.02826056	-0.022829539	0.500465961	0.863302075	0.885066694
sp|Q9NQ79|CRAC1_HUMAN	1	40	76	33	0.336198	0.09688913	-0.232195412	-0.239308813	-0.568393355	-0.329084542	0.009921138	9.55E-08	0.000580454
sp|P00325|ADH1B_HUMAN	6	40	76	33	-0.64119	-0.185372139	0.108082933	0.455819687	0.749274759	0.293455072	0.005056872	7.68E-05	0.13683369
sp|P17927|CR1_HUMAN	3	40	76	33	0.0459	0.023309832	0.131353698	-0.022589822	0.085454044	0.108043866	0.896896565	0.345231254	0.117745772
sp|Q05682|CALD1_HUMAN	35	40	76	33	-0.00316	-0.204837093	0.091389226	-0.20167694	0.094549379	0.296226319	0.25311529	0.809825982	0.076512644
sp|P35527|K1C9_HUMAN	17	40	76	33	0.176197	-0.23809524	-0.096666351	-0.41429183	-0.272862941	0.141428889	0.044877985	0.386752946	0.72115239
sp|O75083|WDR1_HUMAN	71	40	76	33	0.060336	-0.096188077	0.160208288	-0.156524261	0.099872104	0.256396365	0.456555359	0.801263201	0.160901771
sp|Q15848|ADIPO_HUMAN	5	40	76	33	0.300206	0.110273796	-0.12455343	-0.189931849	-0.424759075	-0.234827226	0.136656748	0.001412907	0.070441972
sp|Q9P232|CNTN3_HUMAN	29	40	76	33	0.201044	0.144140838	0.050048263	-0.056903518	-0.150996093	-0.094092575	0.358341803	0.008249638	0.088221724
sp|Q86SQ4|AGRG6_HUMAN	5	40	76	33	0.148435	0.142274496	0.230045076	-0.006160929	0.081609651	0.08777058	0.985514228	0.176450578	0.079479931
sp|P33151|CADH5_HUMAN	2	40	76	33	0.090081	0.06494014	0.025264428	-0.025140511	-0.064816223	-0.039675712	0.834302099	0.438164688	0.673522042
sp|Q93070|NAR4_HUMAN	11	40	76	33	0.032825	0.05717212	0.176530064	0.02434696	0.143704903	0.119357944	0.822990708	0.011330683	0.019185535
sp|P35442|TSP2_HUMAN	2	40	76	33	-0.233	-0.011957165	0.332073861	0.22104313	0.565074156	0.344031026	0.010074737	1.10E-08	8.73E-05
sp|Q8N0V5|GNT2A_HUMAN	15	40	76	33	0.162236	0.153063753	0.135955021	-0.009172628	-0.026281361	-0.017108732	0.984616367	0.915993373	0.953765358
sp|Q4LDE5|SVEP1_HUMAN	10	40	76	33	0.137834	0.151828983	0.52186932	0.013995076	0.384035412	0.370040336	0.976513767	1.54E-05	2.54E-06
sp|P01833|PIGR_HUMAN	22	40	76	33	0.017303	0.022464695	0.246101514	0.005161803	0.228798622	0.223636819	0.996489646	0.01058296	0.004172384
sp|Q9H8L6|MMRN2_HUMAN	112	40	76	33	0.203427	0.187945729	0.09173017	-0.015481737	-0.111697296	-0.096215559	0.902014162	0.028087017	0.034060433
sp|Q92859|NEO1_HUMAN	60	40	76	33	0.111223	0.061831967	0.132792414	-0.049390585	0.021569862	0.070960447	0.508695023	0.914384022	0.295836777
sp|Q92820|GGH_HUMAN	20	40	76	33	0.085644	0.153018049	0.156866068	0.067374406	0.071222425	0.003848019	0.456316762	0.545483101	0.99773675
sp|Q16706|MA2A1_HUMAN	45	40	76	33	0.081935	0.080933999	0.146692621	-0.001000737	0.064757885	0.065758622	0.999490774	0.234758156	0.150660634
sp|Q0VAF6|SYCN_HUMAN	76	40	76	33	-0.0353	0.170438759	0.087870676	0.205741467	0.123173384	-0.082568083	0.025523983	0.393328544	0.585200264
sp|P35555|FBN1_HUMAN	318	40	76	33	0.207734	0.179025223	0.213203324	-0.02870883	0.005469271	0.034178102	0.686911793	0.990603124	0.626962558
sp|Q16651|PRSS8_HUMAN	340	36	69	30	-0.04841	-0.014901028	0.323886007	0.03350902	0.372296055	0.338787035	0.866210511	1.76E-05	9.94E-06
sp|P80370|DLK1_HUMAN	306	40	76	33	-0.02948	-0.171330001	0.156193703	-0.141849109	0.185674595	0.327523704	0.209764962	0.158668785	0.000978893
sp|P0DJI9|SAA2_HUMAN	3	40	76	33	-0.38527	-0.243882966	0.691680725	0.141388073	1.076951763	0.93556369	0.671016748	8.13E-07	1.34E-06
sp|O60613|SEP15_HUMAN	25	36	69	31	-0.07045	0.048812934	0.262461868	0.119266667	0.332915601	0.213648935	0.268196594	0.001104419	0.024253923
sp|Q9Y6N6|LAMC3_HUMAN	43	32	62	27	-0.08799	-0.038351018	0.357720183	0.049634525	0.445705726	0.396071201	0.886018189	0.001845245	0.001696888
sp|Q9HDC9|APMAP_HUMAN	64	40	76	33	0.059906	-0.028625964	0.255373682	-0.088531641	0.195468005	0.283999646	0.544367636	0.133263285	0.005297249
sp|Q07092|COGA1_HUMAN	62	25	48	21	-0.04618	-0.073542672	0.391115453	-0.027357838	0.437300287	0.464658125	0.94213055	9.28E-05	2.74E-06
sp|Q6UWV6|ENPP7_HUMAN	107	40	76	33	-0.25785	-0.238858132	-0.043384553	0.018992429	0.214466009	0.19547358	0.981933165	0.206429795	0.188941339
sp|Q8TER0|SNED1_HUMAN	51	40	76	33	0.091365	0.091052041	0.073581941	-0.000312854	-0.017782954	-0.0174701	0.999957058	0.908797107	0.889211855
sp|P08174|DAF_HUMAN	256	40	76	33	0.172999	0.116370625	0.331494508	-0.0566288	0.158495082	0.215123883	0.540714877	0.039396504	0.000684937
sp|Q8TCZ2|C99L2_HUMAN	323	40	76	33	-0.24977	-0.26842974	0.313390369	-0.018657663	0.563162446	0.581820109	0.981698347	2.82E-05	1.00E-06
sp|P52566|GDIR2_HUMAN	51	40	76	33	-0.24108	-0.240339212	0.251484798	0.000736473	0.492560483	0.49182401	0.999986123	0.016499966	0.005780129

sp|P49257|LMAN1_HUMAN	1677	40	76	33	-0.10139	0.013108577	-0.010789061	0.114500545	0.090602907	-0.023897638	0.291653348	0.584928698	0.953398409
sp|P06312|KV401_HUMAN	190	40	76	33	-0.22804	-0.037852202	0.227069582	0.190187765	0.455109549	0.264921784	0.107231539	0.000245748	0.023625917
sp|P01615|KVD28_HUMAN	292	10	21	9	-0.07677	0.185804633	0.065648376	0.262577648	0.142421391	-0.120156257	0.167997136	0.68166969	0.695588426
sp|P01860|IGHG3_HUMAN	7	40	76	33	-0.40038	-0.335915716	-0.060101479	0.06446906	0.340283296	0.275814237	0.864286945	0.06529972	0.10111371
sp|P06310|KV230_HUMAN	252	32	62	27	-0.29067	-0.202347706	-0.304109303	0.088326579	-0.013435018	-0.101761598	0.537887714	0.990020831	0.480708491
sp|O14791|APOL1_HUMAN	28	40	76	33	-0.2087	0.037393493	0.143414573	0.246090777	0.352111857	0.10602108	0.008710675	0.001386032	0.447198991
sp|O00241|SIRB1_HUMAN	123	36	69	30	-0.12119	-0.143336145	0.250726036	-0.022144709	0.371917472	0.394062181	0.962308553	0.000954283	6.10E-05
sp|P78324|SHPS1_HUMAN	1	40	76	33	-0.07951	0.016233511	0.276750168	0.095746535	0.356263193	0.260516658	0.37506575	0.000169713	0.002344793
sp|Q9H4B7|TBB1_HUMAN	631	40	76	33	-0.28316	-0.09068047	0.03890709	0.192475176	0.322062737	0.129587561	0.178090913	0.037613461	0.499477496
sp|P04433|KV311_HUMAN	21	32	62	27	-0.08358	0.01381066	0.042045839	0.0973916	0.125626779	0.028235179	0.358980834	0.307137719	0.925304518
sp|P01619|KV320_HUMAN	7	40	76	33	0.005591	0.038841551	0.357811861	0.033250529	0.352220839	0.31897031	0.920426958	0.002377726	0.001855212
sp|Q86YD3|TMM25_HUMAN	39	40	76	33	0.157941	0.065713533	-0.150530981	-0.092226986	-0.3084715	-0.216244513	0.101269879	1.65E-07	3.58E-05
sp|Q02325|PLGB_HUMAN	77	40	76	33	0.183319	0.217555616	0.045242553	0.034236655	-0.138076408	-0.172313063	0.56783938	0.002454732	1.19E-05
sp|Q15195|PLGA_HUMAN	62	29	56	24	-2.97275	-3.094563362	-3.070406165	-0.121816065	-0.097658867	0.024157198	0.958336961	0.981370551	0.998528692
sp|O14594|NCAN_HUMAN	729	40	76	33	0.089593	0.02599	-0.162109576	-0.063602755	-0.251702331	-0.188099576	0.425036411	0.000190564	0.001982686
sp|Q14767|LTBP2_HUMAN	6	40	76	33	-0.31773	-0.405660703	0.388531702	-0.087929074	0.706263332	0.794192406	0.60192488	5.40E-09	5.10E-13
sp|P16070|CD44_HUMAN	7	40	76	33	0.10818	0.094760603	0.206753098	-0.013419067	0.098573429	0.111992495	0.938467685	0.099338186	0.023799429
sp|Q13103|SPP24_HUMAN	1	40	76	33	0.065319	0.165311551	-0.032769947	0.0999921	-0.098089398	-0.198081498	0.687667519	0.779613652	0.278635192
sp|O95980|RECK_HUMAN	25	40	76	33	0.177645	0.148928799	-0.080807647	-0.028716078	-0.258452524	-0.229736446	0.703091814	4.74E-08	4.38E-08
sp|Q58FF3|ENPLL_HUMAN	140	7	14	6	0.313298	0.171936538	0.340892539	-0.141361138	0.027594864	0.168956001	0.421674854	0.976602852	0.333437195
sp|Q8N3T6|T132C_HUMAN	326	40	76	33	0.181032	0.135252286	0.086119931	-0.045779954	-0.094912308	-0.049132354	0.455170363	0.100492672	0.45118186
sp|P06702|S10A9_HUMAN	3	40	76	33	-0.71468	-0.409084213	0.370249465	0.305592403	1.084926081	0.779333678	0.165734223	8.84E-07	7.34E-05
sp|O43895|XPP2_HUMAN	8	40	76	33	0.012251	-0.11402998	-0.198241656	-0.126281266	-0.210492942	-0.084211676	0.583613058	0.358068355	0.809779194
sp|P20023|CR2_HUMAN	372	40	76	33	0.017651	0.14266669	-0.224836922	0.12501561	-0.242488003	-0.367503612	0.217497384	0.020935203	2.49E-05
sp|P48551|INAR2_HUMAN	379	37	69	29	-0.21305	-0.15747271	0.353901664	0.055579051	0.566953425	0.511374374	0.809918608	2.32E-06	1.81E-06
sp|Q86YW5|TRML1_HUMAN	55	40	76	33	-0.29076	-0.051606418	0.150221234	0.23915136	0.440979012	0.201827652	0.04162989	0.000768404	0.133745607
sp|P16562|CRIS2_HUMAN	4	40	76	33	0.060521	-0.03674567	0.010118699	-0.097266987	-0.050402619	0.046864369	0.165928494	0.713235372	0.689605315
sp|Q9UIB8|SLAF5_HUMAN	11	40	76	33	0.063807	0.127551895	0.234294002	0.063744747	0.170486855	0.106742108	0.273903212	0.002265526	0.043794982
sp|P15085|CBPA1_HUMAN	30	40	76	33	-0.13251	-0.123465113	0.006449819	0.009043266	0.138958198	0.129914932	0.996088646	0.530373799	0.4941946
sp|P07737|PROF1_HUMAN	75	40	76	33	0.130939	-0.003353463	0.350405248	-0.134292294	0.219466416	0.353758711	0.5894748	0.379310393	0.043547763
sp|Q9Y6Z7|COL10_HUMAN	39	40	76	33	0.087338	0.176788009	0.116578377	0.089450285	0.029240654	-0.060209632	0.085540467	0.830552049	0.370413406
sp|P39060|COIA1_HUMAN	7	40	76	33	-0.02142	0.067809576	0.391590075	0.089231641	0.413012139	0.323780498	0.257701347	3.10E-08	9.05E-07
sp|Q15084|PDIA6_HUMAN	13	40	76	33	-0.08837	-0.026439989	0.379272558	0.061933696	0.467646243	0.405712547	0.825435815	0.000873733	0.001155566
sp|B2RNN3|C1T9B_HUMAN	2	32	63	27	0.117717	0.056655354	-0.028265152	-0.061061431	-0.145981937	-0.084920506	0.85462065	0.540016789	0.763194694
sp|Q9H2A7|CXL16_HUMAN	2674	40	76	33	-0.06122	-0.023393325	0.160473956	0.037822931	0.221690212	0.183867281	0.822639534	0.01191498	0.020277065
sp|Q9Y279|VSIG4_HUMAN	3	40	76	33	-0.69033	-0.622211852	0.294831233	0.06811592	0.985159005	0.917043085	0.882456386	1.70E-07	4.20E-08
sp|O00585|CCL21_HUMAN	2	40	76	33	-0.09226	0.110073337	0.451612559	0.202332084	0.543871305	0.341539222	0.019994034	3.15E-08	9.19E-05
sp|P69849|NOMO3_HUMAN	7	40	76	33	0.059133	0.099883598	0.203753252	0.040750274	0.144619928	0.103869653	0.508601394	0.003739019	0.023837694
sp|P51693|APLP1_HUMAN	9	40	76	33	0.155975	0.004386748	-0.174401974	-0.151587796	-0.330376519	-0.178788722	0.019576832	6.43E-06	0.008527466
sp|P81172|HEPC_HUMAN	32	36	69	30	0.025926	-0.032810453	0.120257848	-0.05873678	0.094331521	0.153068301	0.716037665	0.552028317	0.139684832
sp|Q01459|DIAC_HUMAN	246	40	76	33	0.14634	0.138140988	-0.081077499	-0.008199079	-0.227417566	-0.219218487	0.98394502	0.000357816	9.44E-05
sp|O96019|ACL6A_HUMAN	3	8	14	5	0.013447	-0.486654504	-0.366623781	-0.500101815	-0.380071092	0.120030723	0.078971701	0.385469541	0.888439943
sp|P02654|APOC1_HUMAN	304	40	76	33	0.447107	0.200978877	0.561456897	-0.246128541	0.114349479	0.36047802	0.077783237	0.677692435	0.009037536
sp|P40306|PSB10_HUMAN	2	40	76	33	-0.36068	-0.215363302	0.1967591	0.145313965	0.557436368	0.412122402	0.290800497	1.15E-05	0.000290107
sp|Q99436|PSB7_HUMAN	1	40	76	33	-0.41317	-0.231017016	0.417760503	0.182156932	0.830934451	0.648777519	0.299516637	2.56E-07	5.60E-06
sp|P43121|MUC18_HUMAN	40	40	76	33	0.336822	0.131489729	-0.008136233	-0.205332612	-0.344958574	-0.139625962	1.08E-05	1.14E-09	0.007198892
sp|Q969E1|LEAP2_HUMAN	1	40	76	33	-0.53768	-0.429433881	0.280206067	0.108248658	0.817888606	0.709639948	0.70093474	3.90E-06	6.27E-06
sp|Q02747|GUC2A_HUMAN	381	40	76	33	-0.0344	-0.131053044	0.205266188	-0.096657833	0.239661399	0.336319232	0.41779866	0.027344055	0.000185176
sp|Q8WWA0|ITLN1_HUMAN	72	40	76	33	0.0891	-0.195517499	-0.099601003	-0.284617341	-0.188700845	0.095916496	0.066705509	0.432873405	0.758110403
sp|Q9Y4D7|PLXD1_HUMAN	2	40	76	33	0.096034	0.088971213	0.099455263	-0.007063216	0.003420835	0.01048405	0.968589254	0.99484667	0.940150907
sp|P29401|TKT_HUMAN	7	40	76	33	-0.23076	-0.097539221	0.449098999	0.133223384	0.679861604	0.54663822	0.344189065	6.30E-08	8.74E-07
sp|P60174|TPIS_HUMAN	34	40	76	33	-0.07552	-0.015742368	0.279393454	0.059773455	0.354909277	0.295135822	0.792630668	0.004682691	0.00866387
sp|Q8IXL6|FA20C_HUMAN	26	40	76	33	0.124104	0.105862179	0.089258629	-0.018241769	-0.034845319	-0.01660355	0.723962316	0.445285903	0.790435098
sp|Q9UJJ9|GNPTG_HUMAN	1	40	76	33	0.008504	0.045360364	0.223888238	0.036856087	0.215383961	0.178527875	0.555755428	4.30E-06	1.77E-05
sp|P08253|MMP2_HUMAN	8	40	76	33	0.206613	0.171547436	0.182229219	-0.035065234	-0.024383452	0.010681782	0.698529778	0.886914266	0.971091777
sp|O00151|PDLI1_HUMAN	2	40	76	33	-0.05322	-0.319696054	0.042158885	-0.266477613	0.095377326	0.361854939	0.207086893	0.868221613	0.080118779
sp|P53004|BIEA_HUMAN	7	40	76	33	-0.2009	-0.055552402	0.207292025	0.145352138	0.408196565	0.262844427	0.145358996	5.96E-05	0.00475167
sp|P02775|CXCL7_HUMAN	13	40	76	33	-0.38681	0.072136497	0.01250033	0.458950643	0.399314476	-0.059636167	0.000399416	0.014524234	0.88221253
sp|P04066|FUCO_HUMAN	4	40	76	33	0.198694	0.132220063	0.315989101	-0.06647394	0.117295099	0.183769039	0.431428157	0.167280075	0.004580844
sp|Q9BYH1|SE6L1_HUMAN	3	40	76	33	0.214811	0.162457878	0.041650306	-0.052352781	-0.173160352	-0.120807572	0.380056245	0.001026333	0.012678206
sp|Q9HBB8|CDHR5_HUMAN	7	40	76	33	0.179966	0.218424572	0.137772142	0.03845872	-0.042193709	-0.08065243	0.712336716	0.754361969	0.273474114
sp|Q9BY67|CADM1_HUMAN	2	40	76	33	0.205371	0.189052077	0.204181075	-0.016319255	-0.001190258	0.015128997	0.934836197	0.999752524	0.950415926
sp|P54802|ANAG_HUMAN	1	40	76	33	0.183583	0.156264978	0.092865613	-0.027318064	-0.090717428	-0.063399365	0.872879119	0.358886182	0.527565855
sp|Q9UBR2|CATZ_HUMAN	32	40	76	33	-0.1116	-0.092029363	0.152892575	0.01956672	0.264488658	0.244921938	0.927182402	0.00015953	7.67E-05
sp|P55058|PLTP_HUMAN	5	40	76	33	0.033958	0.067737381	0.247699168	0.033779156	0.213740944	0.179961788	0.723708233	0.000260305	0.000554064
sp|P49641|MA2A2_HUMAN	24	40	76	33	0.229657	0.136487844	0.006255797	-0.093169136	-0.223401183	-0.130232047	0.004312322	4.93E-09	0.000119683
sp|P19021|AMD_HUMAN	52	40	76	33	0.122059	0.091245029	0.067717084	-0.030813775	-0.05434172	-0.023527945	0.58553884	0.319436533	0.759777901
sp|P16233|LIPP_HUMAN	31	40	76	33	-0.03807	-0.039231146	-0.012433026	-0.001161393	0.025636727	0.02679812	0.999898437	0.966440904	0.953654328
sp|O14786|NRP1_HUMAN	5	40	76	33	0.132241	0.151239894	0.189070175	0.018999202	0.056829483	0.037830282	0.87221883	0.432706806	0.622394511
sp|P24043|LAMA2_HUMAN	28	40	76	33	0.084055	0.040992944	0.319790479	-0.04306184	0.235735695	0.278797535	0.779825863	0.007430505	0.000217135
sp|Q9GZT8|NIF3L_HUMAN	12	40	76	33	0.019476	0.084843433	0.176357678	0.065367569	0.156881813	0.091514244	0.26432877	0.006158915	0.10357709
sp|P29322|EPHA8_HUMAN	22	7	13	7	-0.00917	0.167092477	0.044197972	0.176259661	0.053365156	-0.122894505	0.048379492	0.784452174	0.207115064
sp|P00533|EGFR_HUMAN	24	40	76	33	0.133033	0.092741898	-0.265504985	-0.040291562	-0.398538446	-0.358246883	0.462088984	3.97E-14	3.85E-14
sp|P08567|PLEK_HUMAN	2	40	76	33	-0.12313	-0.074909353	0.024248095	0.048221176	0.147378625	0.099157449	0.936623893	0.656794627	0.78458032
sp|P05109|S10A8_HUMAN	3	40	76	33	-1.64433	-1.198553667	-0.239993561	0.445776803	1.404336908	0.958560105	0.079569605	2.09E-07	6.80E-05
sp|P14618|KPYM_HUMAN	23	40	76	33	-0.02364	-0.015859804	0.140065177	0.007777287	0.163702268	0.155924981	0.996205035	0.317191551	0.26629493
sp|P48304|REG1B_HUMAN	55	40	76	33	-0.69405	-0.573973476	-0.036266062	0.120074137	0.657781551	0.537707415	0.800599931	0.012153332	0.022961451
sp|P12829|MYL4_HUMAN	262	28	55	25	-1.62706	-1.797625782	-1.24207553	-0.170566999	0.384983253	0.555550253	0.672567715	0.241946654	0.023946523
sp|P13497|BMP1_HUMAN	297	40	76	33	0.070552	0.144236187	0.068264082	0.073684144	-0.002287961	-0.075972105	0.274283387	0.99912792	0.298656905
sp|Q53GG5|PDLI3_HUMAN	243	4	6	3	0.192592	0.170532917	1.277432168	-0.022059216	1.084840035	1.106899252	0.999335272	0.356939479	0.293655555
sp|O75106|AOC2_HUMAN	4	40	76	33	0.361579	0.277276374	0.26161398	-0.084302504	-0.099964898	-0.015662394	0.242448274	0.252762468	0.957363661
sp|P31948|STIP1_HUMAN	47	40	76	33	-0.23306	-0.216422222	0.212838496	0.016635062	0.44589578	0.429260718	0.990577014	0.011315892	0.005271534
sp|P20810|ICAL_HUMAN	2	40	76	33	-0.5702	-0.321648471	0.224364351	0.248553667	0.794566489	0.546012822	0.028134151	4.78E-10	1.06E-06
sp|Q9NVA2|SEP11_HUMAN	4	29	55	23	0.004605	-0.075392948	0.437237399	-0.079997705	0.432632643	0.512630347	0.893830359	0.115561936	0.023463582
sp|Q99733|NP1L4_HUMAN	20	40	76	33	-0.22323	-0.235556183	0.169852464	-0.012321358	0.393087289	0.405408647	0.995632728	0.050822941	0.018470508
sp|P14555|PA2GA_HUMAN	3	36	69	30	-0.69869	-0.629444372	0.299465217	0.069245873	0.998155463	0.92890959	0.886390621	3.39E-07	8.55E-08
sp|Q01813|PFKAP_HUMAN	3	40	76	33	0.095332	-0.025858808	0.226809188	-0.121190402	0.131477594	0.252667996	0.519670925	0.587281579	0.086162147
sp|P06753|TPM3_HUMAN	38	40	76	33	-0.00734	-0.207415191	0.31793214	-0.200071219	0.325276111	0.525347331	0.482334442	0.266746458	0.014172686
sp|P07954|FUMH_HUMAN	1	40	76	33	-0.49362	-0.304354305	0.037638865	0.189267829	0.531260999	0.34199317	0.081803154	4.15E-06	0.001035777
sp|P27824|CALX_HUMAN	4	40	76	33	-0.20648	-0.253629497	0.337030801	-0.047151814	0.543508483	0.590660297	0.827714605	2.90E-07	4.87E-10
sp|Q86VP6|CAND1_HUMAN	2	40	76	33	-0.22863	-0.048789506	0.267043164	0.179835956	0.495668626	0.31583267	0.065049061	2.26E-06	0.000834426
sp|Q15293|RCN1_HUMAN	10	40	76	33	0.001307	-0.020955957	-0.039302323	-0.022262706	-0.040609073	-0.018346366	0.860605924	0.708984099	0.914327416
sp|Q9UPZ6|THS7A_HUMAN	5	40	76	33	0.125812	-0.077984934	0.018810434	-0.203797292	-0.107001925	0.096795368	0.000350919	0.199683367	0.187043768
sp|P80723|BASP1_HUMAN	63	40	76	33	-0.1464	-0.167955149	0.390172519	-0.02155475	0.536572918	0.558127668	0.971995847	1.82E-05	4.77E-07
sp|Q01995|TAGL_HUMAN	157	40	76	33	-0.13773	-0.198935341	0.369203109	-0.06120706	0.50693139	0.56813845	0.694724781	3.05E-07	1.66E-10
sp|P29966|MARCS_HUMAN	364	40	76	33	-0.31838	-0.160840707	0.396898105	0.157540496	0.715279308	0.557738812	0.343636322	1.38E-06	2.25E-05
sp|P63316|TNNC1_HUMAN	37	14	27	13	-1.60155	-1.827927083	-1.167331434	-0.226380882	0.434214766	0.660595648	0.849153619	0.645964938	0.27509754
sp|P02585|TNNC2_HUMAN	12	10	20	9	0.07487	0.028474087	0.472774962	-0.04639558	0.397905295	0.444300875	0.983142775	0.421099548	0.249155781
sp|P35908|K22E_HUMAN	5	40	76	33	0.681383	0.384533818	0.213165653	-0.296848905	-0.46821707	-0.171368165	0.160895975	0.045253862	0.581665048
sp|Q12882|DPYD_HUMAN	28	40	76	33	-0.29597	-0.10486398	0.152873433	0.19110546	0.448842873	0.257737414	0.002014477	9.41E-10	6.76E-05
sp|P52758|RIDA_HUMAN	4	37	69	30	-0.26391	-0.120206083	0.354199816	0.143701002	0.618106901	0.474405899	0.370277453	1.17E-05	0.000171888
sp|P28838|AMPL_HUMAN	7	40	76	33	-0.3537	-0.08399013	0.279576916	0.269706784	0.63327383	0.363567046	0.078023271	0.00011117	0.018139065
sp|Q96RW7|HMCN1_HUMAN	6	40	76	33	-0.11237	0.016240674	0.302969563	0.128612788	0.415341676	0.286728889	0.031985878	6.57E-10	1.17E-06
sp|Q5JRA6|TGO1_HUMAN	9	40	76	33	-0.71869	-0.617746316	0.166067747	0.100946278	0.884760341	0.783814063	0.647143994	3.89E-09	3.98E-09
sp|P05386|RLA1_HUMAN	104	40	76	33	-0.40935	-0.191317515	0.462402182	0.218035132	0.87175483	0.653719697	0.086116519	1.56E-10	4.42E-08

sp|Q15833|STXB2_HUMAN	11	40	76	33	0.019239	-0.149283798	-0.006284893	-0.168522833	-0.025523929	0.142998904	0.314275532	0.981627547	0.479504913
sp|Q9UQ80|PA2G4_HUMAN	2	40	76	33	-0.24792	-0.229954693	0.071646855	0.017969167	0.319570715	0.301601547	0.978743111	0.011357274	0.00642988
sp|Q8WUJ3|CEMIP_HUMAN	5	40	76	33	-0.07853	-0.04207654	0.297640268	0.036450108	0.376166917	0.339716808	0.726560064	2.96E-09	1.57E-09
sp|P80511|S10AC_HUMAN	419	36	69	30	-1.39417	-1.11856984	-0.245439346	0.275603294	1.148733789	0.873130494	0.416326916	6.75E-05	0.000704237
sp|P08319|ADH4_HUMAN	3	40	76	33	-0.65984	-0.339475607	-0.091729393	0.320362015	0.568108229	0.247746214	0.057242696	0.002441923	0.218086519
sp|Q8N8Z6|DCBD1_HUMAN	2	40	76	33	-0.01986	0.002329385	0.106028295	0.022191117	0.125890028	0.10369891	0.750121677	0.002422984	0.005300981
sp|O43747|AP1G1_HUMAN	269	29	55	24	0.049718	-0.191307166	-0.181454247	-0.241024694	-0.231171775	0.009852919	0.194226623	0.349698127	0.997540303
sp|P54920|SNAA_HUMAN	27	40	76	33	-0.20573	-0.225879349	0.177602422	-0.020154247	0.383327523	0.40348177	0.976263741	0.003481912	0.00040284
sp|P09417|DHPR_HUMAN	282	40	76	33	0.058336	0.100535837	0.340296879	0.042199519	0.281960562	0.239761043	0.792050432	0.001200737	0.001993975
sp|P08727|K1C19_HUMAN	4	14	28	12	-0.21435	-0.631172412	-0.675206059	-0.416823995	-0.460857642	-0.044033647	0.598206194	0.646845012	0.994790638
sp|P17181|INAR1_HUMAN	1	36	69	30	0.149187	0.053800421	0.081971846	-0.095386824	-0.067215399	0.028171426	0.082172415	0.417279165	0.820623349
sp|Q8N4F0|BPIB2_HUMAN	29	15	28	12	0.01672	-0.19040573	0.865449376	-0.207125826	0.84872928	1.055855106	0.671010857	0.015104739	0.000511432
sp|P25787|PSA2_HUMAN	39	40	76	33	-0.53475	-0.397245882	0.177564758	0.137502617	0.712313257	0.57481064	0.434741215	1.18E-06	9.89E-06
sp|P42765|THIM_HUMAN	3	40	76	33	-0.49653	-0.356524431	0.179779995	0.140009689	0.676314115	0.536304425	0.558596954	0.000174473	0.000884359
sp|Q8N436|CPXM2_HUMAN	35	28	55	24	-1.09592	-1.076525019	-0.5669982	0.019396656	0.528923475	0.509526819	0.987304867	0.00221221	0.00072111
sp|Q13449|LSAMP_HUMAN	32	40	76	33	0.142031	0.030251564	-0.022141601	-0.11177894	-0.164172104	-0.052393164	0.026414641	0.004898706	0.485598936
sp|Q9Y4L1|HYOU1_HUMAN	1	40	76	33	0.009288	0.057160359	0.25878506	0.047872111	0.249496812	0.201624701	0.434607229	1.01E-06	8.42E-06
sp|P08590|MYL3_HUMAN	12	36	69	30	-2.09039	-2.270948972	-1.735967855	-0.180555782	0.354425335	0.534981117	0.54858317	0.205427436	0.011506822
sp|Q9Y639|NPTN_HUMAN	14	4	6	3	0.557826	0.238293572	0.453853222	-0.319532804	-0.103973154	0.215559651	0.230305886	0.879784663	0.54312262
sp|O43508|TNF12_HUMAN	7	15	28	12	0.43171	0.392749971	0.405919376	-0.038959642	-0.025790237	0.013169404	0.949463663	0.984596329	0.994911607
sp|P11216|PYGB_HUMAN	20	40	76	33	-0.04684	-0.10683617	0.339929218	-0.05999741	0.386767977	0.446765388	0.848454047	0.011045911	0.000589517
sp|Q92823|NRCAM_HUMAN	3	40	76	33	0.063941	0.049185724	0.071900354	-0.014755587	0.007959043	0.02271463	0.955221635	0.990842084	0.909132326
sp|O94856|NFASC_HUMAN	13	29	55	24	-0.11245	-0.286263705	-0.07848941	-0.17380926	0.033965035	0.207774295	0.288563917	0.967193863	0.210891739
sp|Q15828|CYTM_HUMAN	7	40	76	33	0.044668	-0.029915717	0.017499344	-0.074583461	-0.027168401	0.047415061	0.246708265	0.878208743	0.605710722
sp|P37837|TALDO_HUMAN	11	40	76	33	-0.16175	-0.063965472	0.501549889	0.097783757	0.663299118	0.565515361	0.525782325	2.64E-08	8.35E-08
sp|P0DN79|CBSL_HUMAN	26	26	48	20	-0.67358	-0.156934884	0.158366731	0.516649794	0.831951408	0.315301614	0.005785066	0.000194087	0.184908616
sp|P12318|FCG2A_HUMAN	11	40	76	33	-0.01777	-0.026964257	0.098989126	-0.009192094	0.116761288	0.125953382	0.986096085	0.215704122	0.10495275
sp|O75071|EFC14_HUMAN	2	20	34	14	-0.09069	-0.044404964	0.437566819	0.046282939	0.528254722	0.481971783	0.96703706	0.066325079	0.065914744
sp|P07942|LAMB1_HUMAN	5	40	76	33	0.036503	0.029714388	0.21193838	-0.006788594	0.175435398	0.182223992	0.985808081	0.002059315	0.000243221
sp|O75112|LDB3_HUMAN	238	10	20	9	-0.74525	-0.825486623	-0.076699257	-0.080238309	0.668549056	0.748787365	0.979747616	0.375696805	0.206204894
sp|Q8WWQ8|STAB2_HUMAN	39	40	76	33	-0.03356	-0.010701659	-0.031147537	0.022856677	0.002410799	-0.020445878	0.815513644	0.998432423	0.866436176
sp|P09525|ANXA4_HUMAN	4	40	76	33	0.425433	0.378029922	0.590869299	-0.047403266	0.165436111	0.212839377	0.903717933	0.429950451	0.1719159
sp|Q9Y3F4|STRAP_HUMAN	14	40	76	33	-0.28398	-0.094416102	0.14044064	0.189559222	0.424415964	0.234856742	0.124219086	0.00102955	0.061382397
sp|P80303|NUCB2_HUMAN	2	40	76	33	0.152503	0.1243417	0.397221615	-0.028161628	0.244718287	0.272879915	0.921504404	0.016804745	0.001791615
sp|P48594|SPB4_HUMAN	5	17	34	16	-0.13451	-0.387044132	-0.656662688	-0.252529594	-0.52214815	-0.269618556	0.591012768	0.201596531	0.562718896
sp|P11766|ADHX_HUMAN	24	40	76	33	-0.0777	-0.04336476	0.240916126	0.034338737	0.318619624	0.284280887	0.913113757	0.005932261	0.005568278
sp|Q8NDA2|HMCN2_HUMAN	35	40	76	33	0.109385	0.111681282	-0.164877719	0.002296298	-0.274262703	-0.276559001	0.99921976	0.000786683	0.00011364
sp|Q9H2X3|CLC4M_HUMAN	3	40	76	33	-0.1489	-0.082870931	0.074736937	0.066031646	0.223639514	0.157607869	0.46081989	0.002951152	0.023338521
sp|P13716|HEM2_HUMAN	311	40	76	33	-0.08511	0.036628935	0.35106773	0.121736565	0.43617536	0.314438794	0.335738177	0.000130089	0.002290035
sp|P07327|ADH1A_HUMAN	290	40	76	33	-0.54792	-0.249229489	0.011009361	0.298687993	0.558926842	0.26023885	0.094130608	0.003962561	0.204395991
sp|Q9Y2E5|MA2B2_HUMAN	36	40	76	33	0.002866	-0.033141523	0.043689117	-0.036007702	0.040822938	0.07683064	0.875846495	0.889065419	0.589980919
sp|Q9HBW9|AGRL4_HUMAN	91	40	76	33	0.051385	-0.04905798	-0.0505373	-0.10044273	-0.101922051	-0.00147932	0.346221606	0.469544752	0.999795726
sp|P04083|ANXA1_HUMAN	29	40	76	33	-0.93261	-0.61537317	0.017196012	0.317241723	0.949810905	0.632569182	0.097516124	2.23E-06	0.00044989
sp|Q9Y623|MYH4_HUMAN	3	40	76	33	0.155193	0.023616799	-0.003813989	-0.131576205	-0.159006993	-0.027430788	0.000497478	0.000471172	0.731779221
sp|Q14563|SEM3A_HUMAN	1	40	76	33	-0.01549	-0.048066891	0.023679955	-0.032577471	0.039169374	0.071746845	0.694897194	0.695538323	0.216307322
sp|P07911|UROM_HUMAN	20	40	76	33	0.17847	0.08228941	-0.045005537	-0.096180624	-0.223475571	-0.127294947	0.464988136	0.06125235	0.309561696
sp|P00558|PGK1_HUMAN	19	40	76	33	-0.05701	-0.010520251	0.379054069	0.046492596	0.436066916	0.38957432	0.890337486	0.001357911	0.001232618
sp|O95393|BMP10_HUMAN	9	40	76	33	0.120323	-0.030459694	-0.037028053	-0.15078288	-0.157351238	-0.006568358	0.010236279	0.030778811	0.992029176
sp|Q9H939|PPIP2_HUMAN	9	40	76	33	-0.49706	-0.434273998	-0.293924571	0.062781623	0.20313105	0.140349427	0.911715413	0.515016915	0.667511662
sp|P21860|ERBB3_HUMAN	7	40	76	33	0.302063	0.311005564	0.043626096	0.008942989	-0.258436479	-0.267379468	0.989311463	0.002925044	0.000410018
sp|Q02763|TIE2_HUMAN	28	40	76	33	0.030214	0.031708326	0.021568467	0.001494624	-0.008645235	-0.010139859	0.998927984	0.975549675	0.957601651
sp|Q14847|LASP1_HUMAN	22	40	76	33	0.005907	-0.032363878	0.231794945	-0.038270434	0.22588839	0.264158823	0.907338404	0.101849862	0.020044994
sp|P22234|PUR6_HUMAN	12	22	42	18	-0.33633	-0.135437843	0.382180622	0.200888131	0.718506596	0.517618465	0.333455596	0.000190838	0.002754873
sp|P49407|ARRB1_HUMAN	26	40	76	33	-0.1131	-0.157744711	0.038413053	-0.044648681	0.151509083	0.196157764	0.943900214	0.633337149	0.379478908
sp|P22897|MRC1_HUMAN	15	40	76	33	0.040948	0.034831908	0.67623928	-0.006116287	0.635291084	0.641407371	0.996951001	5.35E-09	4.78E-11
sp|Q96HD1|CREL1_HUMAN	7	40	76	33	-0.03157	0.034645991	0.407541958	0.066212961	0.439108929	0.372895968	0.579822678	5.11E-07	1.49E-06
sp|P12814|ACTN1_HUMAN	3	40	76	33	0.121978	-0.19590492	0.079079388	-0.317882485	-0.042898177	0.274984309	0.125548844	0.973708055	0.253260602
sp|O43707|ACTN4_HUMAN	19	40	76	33	0.034075	-0.241070796	0.089800531	-0.275145646	0.055725682	0.330871327	0.142457906	0.945287744	0.085343382
sp|P13929|ENOB_HUMAN	32	40	76	33	0.190285	0.224247186	0.281298561	0.03396246	0.091013834	0.057051375	0.866779614	0.494500899	0.702283557
sp|Q9H8J5|MANS1_HUMAN	4	40	76	33	0.035992	0.08162125	0.208510474	0.045629189	0.172518413	0.126889224	0.623880504	0.011492882	0.044319846
sp|O00451|GFRA2_HUMAN	4	40	76	33	-0.02915	-0.034417515	0.077938431	-0.005267311	0.107088636	0.112355946	0.994539478	0.215142749	0.117806351
sp|Q8NHP8|PLBL2_HUMAN	31	36	69	30	0.160471	0.077875425	0.30129576	-0.082595829	0.140824506	0.223420335	0.581522576	0.33845037	0.033495316
sp|Q8WWZ8|OIT3_HUMAN	69	40	76	33	-0.09657	0.078302219	0.30558761	0.174870728	0.402156118	0.227285391	0.011335136	3.51E-07	0.001482724
sp|O15197|EPHB6_HUMAN	7	8	13	6	-0.05621	-0.119656468	0.291999016	-0.063446867	0.348208617	0.411655484	0.926152782	0.223429128	0.090230368
sp|Q6YHK3|CD109_HUMAN	9	40	76	33	0.300341	0.22069223	-0.008263013	-0.079649046	-0.308604289	-0.228955243	0.18612152	2.21E-07	1.46E-05
sp|Q9NY47|CA2D2_HUMAN	10	40	76	33	0.164123	0.011973753	-0.349971488	-0.152149178	-0.514094418	-0.361945241	0.018303233	5.14E-12	2.33E-08
sp|Q8IUL8|CILP2_HUMAN	16	40	76	33	0.07398	0.118471015	-0.52157901	0.044491357	-0.595558667	-0.640050024	0.862613593	1.43E-07	2.81E-10
sp|Q15262|PTPRK_HUMAN	159	40	76	33	0.009958	0.050432487	0.12310627	0.040474697	0.113148479	0.072673782	0.52019835	0.032574475	0.16086125
sp|Q99719|SEPT5_HUMAN	30	40	76	33	-0.27137	-0.181269452	-0.102563725	0.090105034	0.16881076	0.078705726	0.75598484	0.509352459	0.828967562
sp|Q6NUS6|TECT3_HUMAN	2	40	76	33	-0.06935	-0.046805752	-0.001201687	0.022543274	0.068147339	0.045604065	0.79491652	0.239573353	0.440652332
sp|P00441|SODC_HUMAN	2	40	76	33	-0.36056	-0.200358246	0.256677957	0.160203165	0.617239368	0.457036203	0.335688195	3.62E-05	0.000656213
sp|P48739|PIPNB_HUMAN	39	25	48	21	-0.1428	-0.090916424	0.119560259	0.051880558	0.262357241	0.210476683	0.889178649	0.131641539	0.186571616
sp|P61970|NTF2_HUMAN	17	40	76	33	-0.18685	-0.058105199	0.247892214	0.128749335	0.434746748	0.305997412	0.248599979	4.26E-05	0.001423172
sp|P35579|MYH9_HUMAN	6	40	76	33	-0.58797	-0.073992828	0.327624454	0.513978013	0.915595295	0.401617282	2.72E-06	1.05E-11	0.000725557
sp|P00390|GSHR_HUMAN	4	40	76	33	-0.12592	0.149517036	0.329785421	0.27543895	0.455707335	0.180268385	3.73E-09	4.53E-14	0.000316139
sp|P35237|SPB6_HUMAN	15	40	76	33	-0.13208	-0.160262427	0.168018504	-0.02818182	0.300099111	0.328280931	0.923787615	0.002886415	0.000171762
sp|P09622|DLDH_HUMAN	112	40	76	33	0.045724	0.037508694	0.123736235	-0.008214951	0.07801259	0.086227541	0.991932334	0.605691926	0.459709684
sp|Q13231|CHIT1_HUMAN	24	40	76	33	-0.44223	-0.618768446	0.15301586	-0.176536341	0.595247965	0.771784306	0.609277116	0.023337545	0.000437833
sp|P07307|ASGR2_HUMAN	3	40	76	33	-0.19645	-0.103679324	0.252585667	0.092773564	0.449038555	0.356264991	0.530618947	8.31E-05	0.000476496
sp|O00748|EST2_HUMAN	2	40	76	33	0.188686	0.14917813	0.167316555	-0.039507599	-0.021369173	0.018138426	0.593066946	0.899486346	0.907440866
sp|Q09666|AHNK_HUMAN	19	40	76	33	-0.37453	-0.359909737	0.201820575	0.014616801	0.576347114	0.561730313	0.985323021	9.32E-07	7.37E-08
sp|Q13418|ILK_HUMAN	4	40	76	33	0.042332	-0.083490111	-0.012888802	-0.12582217	-0.055220861	0.070601309	0.661287361	0.946320083	0.891641522
sp|O95747|OXSR1_HUMAN	59	27	48	21	-0.22446	-0.100452866	0.106557726	0.124011775	0.331022367	0.207010592	0.57147091	0.071014755	0.271447764
sp|Q99523|SORT_HUMAN	9	40	76	33	-0.12348	-0.135755352	0.168723625	-0.012272531	0.292206446	0.304478977	0.978380596	0.000370915	2.39E-05
sp|P07900|HS90A_HUMAN	2	40	76	33	-0.20665	-0.137328577	0.265674007	0.069323062	0.472325645	0.403002584	0.801342597	0.001297917	0.002060238
sp|P20701|ITAL_HUMAN	28	40	76	33	0.212468	0.266908576	0.34031889	0.054440896	0.12785121	0.073410314	0.318944428	0.014791348	0.163398327
sp|P50453|SPB9_HUMAN	12	40	76	33	-0.17553	-0.048551572	0.162426329	0.126977854	0.337955755	0.210977901	0.324491997	0.005123334	0.068277874
sp|O75635|SPB7_HUMAN	19	4	6	3	-0.13861	0.019646755	-0.078373417	0.15825369	0.060233518	-0.098020172	0.300837134	0.870118448	0.658732711
sp|P30740|ILEU_HUMAN	8	40	76	33	-0.16577	-0.093950031	0.398283623	0.071821327	0.564054981	0.492233654	0.781510497	6.99E-05	9.18E-05
sp|P36871|PGM1_HUMAN	14	40	76	33	-0.10083	-0.063341947	0.157596737	0.037484523	0.258423207	0.220938684	0.876815627	0.015987051	0.021118236
sp|Q86SR1|GLT10_HUMAN	4	40	76	33	0.092325	0.089279731	0.222047595	-0.00304487	0.129722994	0.132767864	0.995920581	0.007679448	0.001670572
sp|Q9UNF0|PACN2_HUMAN	6	40	76	33	-0.16043	-0.398599102	-0.102049236	-0.238172208	0.058377658	0.296549866	0.121678679	0.914671801	0.058115682
sp|P26572|MGAT1_HUMAN	10	40	76	33	-0.10428	0.01666867	0.199753947	0.120947066	0.304032343	0.183085277	0.066670376	1.82E-05	0.004951243
sp|P31146|COR1A_HUMAN	269	40	76	33	-0.12015	-0.17148238	0.290615618	-0.051332141	0.410765856	0.462097997	0.90144065	0.012451079	0.001015054
sp|Q9H4M9|EHD1_HUMAN	30	40	76	33	-0.06358	-0.106563719	0.11604133	-0.042978726	0.179626323	0.222605049	0.925900729	0.39868078	0.168479293
sp|P55285|CADH6_HUMAN	51	40	76	33	0.095758	-0.022815486	0.073636027	-0.118573199	-0.022121686	0.096451513	0.199086011	0.961352764	0.388963853
sp|Q02952|AKA12_HUMAN	5	40	76	33	-0.06091	-0.005610404	0.040470126	0.05530307	0.101383601	0.04608053	0.500123038	0.203600707	0.654697543
sp|Q9Y4E8|UBP15_HUMAN	12	33	62	26	-0.32586	-0.163386554	0.260979896	0.16247421	0.58684066	0.42436645	0.351082973	0.000210762	0.003191925
sp|P48668|K2C6C_HUMAN	48	40	76	33	-0.46462	-0.408574507	-0.404770412	0.056045151	0.059849247	0.003804096	0.931323841	0.945548477	0.999712032
sp|Q16181|SEPT7_HUMAN	9	40	76	33	-0.15983	-0.192410004	0.167021778	-0.03258468	0.326847102	0.359431782	0.96996689	0.125957185	0.042723837
sp|Q9UQP3|TENN_HUMAN	16	40	76	33	0.046036	0.17744678	0.208209622	0.131410936	0.162173778	0.030762842	0.036598314	0.031111286	0.848358201
sp|O43493|TGON2_HUMAN	930	40	76	33	-0.08002	-0.106939609	0.251201405	-0.026918421	0.331222593	0.358141013	0.940020082	0.00229366	0.000149051
sp|P08575|PTPRC_HUMAN	3	40	76	33	-0.02292	0.071836936	0.082330376	0.094760015	0.105253455	0.01049344	0.074876313	0.10915777	0.971739924
sp|Q7RTS7|K2C74_HUMAN	15	4	7	2	0.138993	0.1367658	1.416073771	-0.002227202	1.27708077	1.279307971	0.999967624	0.024327149	0.01587858
sp|P04264|K2C1_HUMAN	22	40	76	33	0.466468	0.240045832	0.186537758	-0.226421918	-0.279929992	-0.053508074	0.343350057	0.324097188	0.948393372

sp|Q969T9|WBP2_HUMAN	271	33	62	27	-0.04655	-0.122013732	0.245844017	-0.075467834	0.292389915	0.367857749	0.709538452	0.032610349	0.001336972
sp|Q8WZ42|TITIN_HUMAN	32	40	76	33	-0.55802	-0.750884428	-0.272877896	-0.192862631	0.285143901	0.478006531	0.320853112	0.181892072	0.002891602
sp|P10721|KIT_HUMAN	4	40	76	33	0.227579	0.153017148	-0.2789374	-0.074561373	-0.506515921	-0.431954548	0.331019549	8.91E-13	4.77E-12
sp|P48163|MAOX_HUMAN	14	40	76	33	0.09831	0.145706107	0.240464727	0.047395807	0.142154427	0.09475862	0.650682698	0.073738804	0.22507563
sp|P01133|EGF_HUMAN	7	37	69	29	0.068944	0.127317933	0.186167797	0.05837423	0.117224094	0.058849864	0.554769359	0.204754788	0.601609074
sp|Q03252|LMNB2_HUMAN	14	4	7	3	0.151853	-0.042170483	1.400324825	-0.194023381	1.248471928	1.442495309	0.949367796	0.276383236	0.139931971
sp|P15086|CBPB1_HUMAN	6	40	76	33	-0.20066	-0.180746662	-0.011190155	0.019911474	0.189467981	0.169556507	0.976982339	0.238539303	0.232201113
sp|Q8TAB3|PCD19_HUMAN	2	7	14	6	-0.05745	0.065943373	0.444724059	0.123391836	0.502172522	0.378780686	0.794581026	0.091842349	0.163106347
sp|Q92619|HMHA1_HUMAN	9	29	55	25	0.031913	0.08511729	0.478210129	0.053204705	0.446297545	0.39309284	0.91984715	0.01919265	0.019695153
sp|O95425|SVIL_HUMAN	1	4	6	3	0.243317	-0.226095433	1.218756274	-0.469412821	0.975438885	1.444851707	0.786055073	0.493217023	0.194515679
sp|P55822|SH3BG_HUMAN	6	8	13	6	-0.72666	-1.103676684	0.510068638	-0.377017995	1.236727327	1.613745322	0.812051649	0.231299955	0.060461466
sp|P09110|THIK_HUMAN	15	40	76	33	-0.83751	-0.665883193	-0.152312728	0.171630225	0.68520069	0.513570465	0.496853652	0.000742053	0.005251133
sp|P11234|RALB_HUMAN	10	24	49	21	-0.01782	0.06399847	0.42918095	0.081820157	0.447002637	0.36518248	0.762044664	0.005253106	0.009680949
sp|Q9UHY7|ENOPH_HUMAN	67	14	27	11	-0.00921	-0.083043997	0.278227283	-0.07383641	0.28743487	0.36127128	0.898392171	0.346426846	0.125750878
sp|P67936|TPM4_HUMAN	21	40	76	33	-0.15415	-0.336857936	0.002000705	-0.18270918	0.156149461	0.338858641	0.595671209	0.769665516	0.212750521
sp|Q14315|FLNC_HUMAN	8	40	76	33	-0.14132	-0.12250901	0.088207162	0.018810572	0.229526744	0.210716172	0.953870361	0.009776602	0.007101676
sp|P29122|PCSK6_HUMAN	2	40	76	33	-0.23033	-0.025988119	0.181342163	0.204345809	0.411676091	0.207330282	0.014715123	1.55E-05	0.021752334
sp|Q9HCK4|ROBO2_HUMAN	12	40	76	33	0.029215	0.063280607	0.052478082	0.034065503	0.023262978	-0.010802525	0.764267313	0.916978794	0.976483166
sp|Q16787|LAMA3_HUMAN	8	40	76	33	0.206064	0.141867202	0.070038279	-0.064197247	-0.13602617	-0.071828923	0.4362144	0.080066578	0.402089397
sp|P53041|PPP5_HUMAN	3	36	69	30	-0.102	0.251524849	0.43397875	0.353521289	0.53597519	0.182453901	0.035700989	0.005549314	0.446258752
sp|Q96QK1|VPS35_HUMAN	2	40	76	33	0.163227	0.144359015	0.517396178	-0.018867881	0.354169282	0.373037163	0.979837771	0.008935615	0.001440755
sp|P04424|ARLY_HUMAN	16	40	76	33	-0.29236	-0.020819213	0.40133875	0.271537154	0.693695117	0.422157963	0.015804415	5.79E-08	0.000215021
sp|Q9UQV4|LAMP3_HUMAN	21	3	7	4	-0.41429	-0.071669337	0.688816876	0.342621705	1.103107918	0.760486213	0.849827861	0.289202172	0.40468055
sp|Q15404|RSU1_HUMAN	13	40	76	33	0.054102	-0.295608353	-0.129337092	-0.349710452	-0.183439191	0.166271261	0.101455773	0.642180073	0.629447057
sp|Q12864|CAD17_HUMAN	1	40	76	33	0.175346	0.007949473	-0.054942274	-0.167396267	-0.230288014	-0.062891747	0.0632174	0.027990518	0.704031935
sp|P07476|INVO_HUMAN	10	40	76	33	-0.13827	-0.042886094	-0.108959783	0.095380699	0.02930701	-0.066073689	0.560873989	0.962822031	0.783091241
sp|Q14515|SPRL1_HUMAN	2	40	76	33	0.152845	0.058465176	0.204251255	-0.094380012	0.051406066	0.145786079	0.190564314	0.708876748	0.033015411
sp|P61088|UBE2N_HUMAN	1	40	76	33	-0.21621	-0.104952424	0.233114272	0.111256158	0.449322854	0.338066696	0.537731506	0.001395246	0.008086088
sp|P34932|HSP74_HUMAN	8	40	76	33	-0.07247	0.031725686	0.429626471	0.104196594	0.50209738	0.397900785	0.342908913	2.96E-07	4.54E-06
sp|P13798|ACPH_HUMAN	13	40	76	33	-0.30688	-0.120009267	0.194618224	0.186872763	0.501500254	0.314627492	0.056589861	2.31E-06	0.001037365
sp|Q04721|NOTC2_HUMAN	16	40	76	33	0.203477	0.191898868	0.061188209	-0.011577701	-0.14228836	-0.130710659	0.895358924	3.01E-05	1.50E-05
sp|Q9BWS9|CHID1_HUMAN	18	40	76	33	0.013346	0.014819768	0.088626403	0.001474092	0.075280728	0.073806635	0.999818703	0.722425474	0.672076086
sp|Q9HCB6|SPON1_HUMAN	2	40	76	33	0.052612	0.012048705	0.311158027	-0.040563643	0.258545679	0.299109322	0.660186967	2.64E-05	4.25E-08
sp|P41226|UBA7_HUMAN	327	40	76	33	0.158238	0.065313936	0.180000888	-0.092924325	0.021762627	0.114686952	0.506924616	0.974441249	0.403966643
sp|Q7L1Q6|BZW1_HUMAN	3	24	49	22	-0.50633	-0.339841256	0.311644147	0.166485403	0.817970805	0.651485402	0.81310533	0.033437326	0.056544734
sp|P35241|RADI_HUMAN	35	40	76	33	-0.43462	-0.430102053	-0.145295017	0.004522718	0.289329753	0.284807036	0.998531173	0.018636873	0.007691953
sp|P31327|CPSM_HUMAN	17	36	69	31	-0.61333	-0.599322572	-0.090528676	0.014006133	0.52280003	0.508793896	0.994333808	0.005180446	0.001780978
sp|Q15365|PCBP1_HUMAN	160	40	76	33	-0.17608	-0.074071722	0.280286387	0.102007618	0.456365726	0.354358109	0.610402388	0.001627995	0.006775224
sp|O95373|IPO7_HUMAN	1396	22	42	17	-0.09793	-0.009602119	0.320215247	0.088328989	0.418146355	0.329817366	0.816841433	0.056049132	0.101834523
sp|P54577|SYYC_HUMAN	1	40	76	33	0.027577	-0.138012767	0.091208695	-0.16558978	0.063631682	0.229221462	0.368774392	0.902477981	0.188895065
sp|Q96G03|PGM2_HUMAN	2	40	76	33	-0.17965	-0.088781556	0.147860337	0.090865898	0.327507791	0.236641893	0.686203609	0.037811015	0.110813005
sp|P53396|ACLY_HUMAN	1	40	76	33	-0.32305	-0.088494737	0.269100612	0.234550605	0.592145954	0.357595349	0.024743861	4.15E-07	0.000682818
sp|P32754|HPPD_HUMAN	1	40	76	33	-0.34233	-0.075399014	0.288466543	0.266929545	0.630795102	0.363865557	0.139270789	0.000738233	0.041728892
sp|P42892|ECE1_HUMAN	1	40	76	33	0.221646	0.225251725	0.292499476	0.00360552	0.070853271	0.067247751	0.995851456	0.334570231	0.285655041
sp|P49189|AL9A1_HUMAN	3	40	76	33	-0.16833	0.001670913	0.22205474	0.170000122	0.390383949	0.220383827	0.050791922	4.01E-05	0.013070996
sp|Q14517|FAT1_HUMAN	43	40	76	33	-0.15107	-0.167552717	0.197348205	-0.016480322	0.348420601	0.364900923	0.962248381	2.28E-05	5.38E-07
sp|P55786|PSA_HUMAN	12	40	76	33	-0.14233	-0.067522893	0.226838498	0.074806436	0.369167828	0.294361391	0.627075501	0.000661838	0.002483991
sp|P08581|MET_HUMAN	5	40	76	33	0.049651	0.085345856	0.035295617	0.035694981	-0.014355259	-0.050050239	0.605971722	0.945381699	0.422581146
sp|P32004|L1CAM_HUMAN	1	40	76	33	0.185866	0.089838635	-0.127188316	-0.096027419	-0.313054371	-0.217026952	0.069245071	3.59E-08	1.59E-05
sp|P05388|RLA0_HUMAN	27	26	48	20	-0.13905	-0.03123449	0.357237361	0.107813005	0.496284856	0.388471851	0.559278961	0.000562317	0.002862651
sp|P09211|GSTP1_HUMAN	4	40	76	33	-0.05107	-0.064108521	0.156521707	-0.013042777	0.207587452	0.220630229	0.988727807	0.143505167	0.06285721
sp|Q99435|NELL2_HUMAN	12	40	76	33	0.062831	-0.000506861	-0.054734127	-0.063338163	-0.117565429	-0.054227266	0.613960468	0.316153133	0.730134927
sp|P09603|CSF1_HUMAN	1	40	76	33	-0.301	-0.144118008	0.234903946	0.156880571	0.535902526	0.379021954	0.107855585	1.37E-07	2.66E-05
sp|Q00610|CLH1_HUMAN	1	40	76	33	-0.29533	-0.212656385	0.219687056	0.082668936	0.515012377	0.432343442	0.772169735	0.001504365	0.002839457
sp|Q9BUJ0|ABHEA_HUMAN	1	7	14	7	-0.01682	-0.067542797	-0.014785491	-0.050719623	0.002037683	0.052757306	0.943966961	0.99993002	0.939528084
sp|Q9UKU6|TRHDE_HUMAN	11	40	76	33	0.144368	0.207204101	0.037725701	0.06283584	-0.10664256	-0.1694784	0.716497675	0.5167209	0.123648227
sp|Q8N392|RHG18_HUMAN	2	40	76	33	0.003341	-0.0781812	0.099175919	-0.081521798	0.095835321	0.177357119	0.813000694	0.820841367	0.425537592
sp|Q9NZT1|CALL5_HUMAN	3	32	61	25	-1.81332	-1.842715555	-2.375624479	-0.029393843	-0.562302766	-0.532908923	0.995696997	0.352871973	0.307264809
sp|P10768|ESTD_HUMAN	2	40	76	33	-0.03104	0.094380244	0.396245757	0.125422764	0.427288277	0.301865513	0.237626504	2.66E-05	0.000988723
sp|P11279|LAMP1_HUMAN	19	40	76	33	0.480463	0.47415684	0.304790057	-0.006305723	-0.175672506	-0.169366784	0.978229724	2.44E-05	4.25E-06
sp|Q9UNZ2|NSF1C_HUMAN	5	40	76	33	-0.05891	-0.026784738	0.463720563	0.032125813	0.522631114	0.490505301	0.9372765	2.34E-05	7.32E-06
sp|P31939|PUR9_HUMAN	11	40	76	33	-0.15128	-0.118870347	0.196780142	0.032404702	0.348055191	0.315650489	0.931069548	0.004589544	0.003618706
sp|P48147|PPCE_HUMAN	13	40	76	33	-0.18641	-0.129781778	0.199814396	0.056632541	0.386228715	0.329596174	0.741128335	0.000145866	0.000266275
sp|O75116|ROCK2_HUMAN	17	37	69	29	-0.41723	-0.156790382	0.062776786	0.260442757	0.480009925	0.219567168	0.276433628	0.055243187	0.45878278
sp|Q96EG1|ARSG_HUMAN	73	29	55	24	0.354634	0.241949898	0.308564388	-0.11268435	-0.04606986	0.066614489	0.37519307	0.891687233	0.737717964
sp|P0DMV8|HS71A_HUMAN	8	40	76	33	-0.16789	-0.092692615	0.309835214	0.075200772	0.477728601	0.402527829	0.717898662	0.000201992	0.000434764
sp|Q16270|IBP7_HUMAN	16	40	76	33	0.192242	0.088750596	0.25673847	-0.103491658	0.064496216	0.167987874	0.098565565	0.531548539	0.005481188
sp|O75019|LIRA1_HUMAN	1	40	76	33	-0.15284	-0.126984028	-0.110902594	0.025851386	0.04193282	0.016081434	0.955594333	0.920878941	0.984681245
sp|O43280|TREA_HUMAN	384	40	76	33	0.058318	-0.007116317	0.022090461	-0.065434471	-0.036227694	0.029206777	0.824773538	0.960011101	0.966808208
sp|P04406|G3P_HUMAN	9	40	76	33	-0.3608	-0.073297389	0.139312173	0.287499638	0.5001092	0.212609561	0.04264793	0.001695214	0.21433787
sp|Q93088|BHMT1_HUMAN	24	40	76	33	-0.08339	0.034062278	0.397010355	0.117447684	0.48039576	0.362948076	0.568857094	0.002126061	0.010667043
sp|P08648|ITA5_HUMAN	16	40	76	33	0.073364	0.105279994	0.12250843	0.031916041	0.049144476	0.017228435	0.475045008	0.297688769	0.825674957
sp|P16278|BGAL_HUMAN	18	40	76	33	0.337721	0.320857767	0.465719458	-0.016863511	0.12799818	0.144861691	0.954979172	0.165702979	0.055203214
sp|O60610|DIAP1_HUMAN	20	40	76	33	-0.51719	-0.274752136	0.186682371	0.24244123	0.703875737	0.461434507	0.082391833	1.98E-06	0.000524117
sp|Q9UP79|ATS8_HUMAN	1	40	76	33	0.091618	-0.030340283	-0.385618772	-0.121958745	-0.477237234	-0.355278489	0.122089209	5.41E-09	8.25E-07
sp|O43396|TXNL1_HUMAN	1	40	76	33	-0.23663	-0.216724662	0.185082291	0.019906549	0.421713502	0.401806953	0.980753329	0.003415118	0.001490585
sp|P29017|CD1C_HUMAN	9	40	76	33	0.093286	0.147193406	-0.366126494	0.05390775	-0.45941215	-0.513319899	0.72789937	8.58E-07	8.16E-10
sp|Q99519|NEUR1_HUMAN	201	32	62	28	0.010008	-0.012996129	0.13729922	-0.02300391	0.127291439	0.150295349	0.954405281	0.368136638	0.168209086
sp|Q9HC56|PCDH9_HUMAN	13	40	76	33	0.11206	0.126033029	0.026808226	0.013972952	-0.085251851	-0.099224803	0.948476588	0.261789739	0.101513546
sp|Q9BXX0|EMIL2_HUMAN	8	29	55	25	-0.28051	-0.254496208	0.295970338	0.026012357	0.576478903	0.550466546	0.962229861	9.24E-06	1.72E-06
sp|P42025|ACTY_HUMAN	43	22	42	18	-0.11528	0.168490075	0.483774653	0.28376954	0.599054118	0.315284578	0.141347822	0.003557035	0.122107474
sp|Q9BY76|ANGL4_HUMAN	59	40	76	33	-0.16339	-0.15057275	0.251985786	0.012812482	0.415371018	0.402558536	0.989080888	0.000616688	0.000162583
sp|P29350|PTN6_HUMAN	3	40	76	33	-0.15981	-0.179895806	0.16420159	-0.020085431	0.324011965	0.344097395	0.984546267	0.065989436	0.021146523
sp|Q9UBW5|BIN2_HUMAN	34	40	76	33	-0.40978	-0.103057665	0.049437503	0.306721219	0.459216387	0.152495168	0.027704283	0.004317658	0.448864921
sp|P02461|CO3A1_HUMAN	10	40	76	33	-0.04054	0.035708122	0.296049134	0.076251676	0.336592688	0.260341012	0.48457503	0.00012623	0.000945185
sp|P09467|F16P1_HUMAN	4	40	76	33	-0.13608	0.061394184	0.383799798	0.19747395	0.519879564	0.322405614	0.184336936	0.000488184	0.020855737
sp|P20618|PSB1_HUMAN	2	40	76	33	-0.25628	-0.117460826	0.416688656	0.138817697	0.672967178	0.534149482	0.356846789	4.19E-07	5.86E-06
sp|Q09327|MGAT3_HUMAN	3	33	62	26	-0.08435	0.036710474	0.037335233	0.121065264	0.121690024	0.000624759	0.542523691	0.658240476	0.999986044
sp|P06732|KCRM_HUMAN	6	40	76	33	0.180023	-0.010653858	-0.206851889	-0.190677139	-0.38687517	-0.196198031	0.102096176	0.001967406	0.119485525
sp|Q13018|PLA2R_HUMAN	28	15	28	11	0.116519	0.035925728	0.01624802	-0.080593492	-0.100271201	-0.019677709	0.536288851	0.534404605	0.970004176
sp|P23526|SAHH_HUMAN	2	40	76	33	-0.34157	-0.115345668	0.306762613	0.226225113	0.648333394	0.422108281	0.021489994	5.69E-09	1.72E-05
sp|O75369|FLNB_HUMAN	63	4	7	3	0.243222	0.337315741	0.135645384	0.094093953	-0.107576404	-0.201670357	0.94037498	0.947284875	0.795112248
sp|P13987|CD59_HUMAN	2	40	76	33	-0.18384	-0.16364271	0.287937978	0.020197958	0.471778646	0.451580687	0.967552228	1.45E-05	2.77E-06
sp|Q6ZMI3|GLDN_HUMAN	6	40	76	33	-0.05835	-0.151138117	0.193218241	-0.092783209	0.251573149	0.344356358	0.301219831	0.002998789	2.33E-06
sp|Q9H2K8|TAOK3_HUMAN	14	26	48	20	0.220982	0.113802958	0.226832761	-0.107179216	0.005850587	0.113029803	0.614159566	0.999019737	0.635030585
sp|P49247|RPIA_HUMAN	19	40	76	33	-0.11327	-0.061257496	0.321700842	0.052016013	0.434974351	0.382958338	0.718212598	8.21E-07	9.74E-07
sp|P52209|6PGD_HUMAN	19	40	76	33	-0.10629	-0.083510472	0.367198996	0.022779106	0.473488574	0.450709468	0.970463133	0.000265556	8.34E-05
sp|Q99439|CNN2_HUMAN	5	40	76	33	-0.10979	-0.076031499	0.166896265	0.03376312	0.276690884	0.242927764	0.953252761	0.114245758	0.118978532
sp|Q86VZ4|LRP11_HUMAN	30	40	76	33	0.047119	0.014138657	0.129338078	-0.032980259	0.082219163	0.115199421	0.698081729	0.218182049	0.02427381
sp|Q99704|DOK1_HUMAN	4	13	28	13	-0.04967	0.144295519	0.278770258	0.193965402	0.328440141	0.134474739	0.444579765	0.188639839	0.674713354
sp|Q9UKY3|CES1P_HUMAN	110	40	76	33	-0.04115	-0.14250131	-0.000903654	-0.101352519	0.040245137	0.141597656	0.589297405	0.943818312	0.405495396
sp|P23141|EST1_HUMAN	13	40	76	33	0.009625	-0.052385076	0.135541358	-0.062010372	0.125916063	0.187926434	0.784786639	0.503489023	0.14661965
sp|Q9UBG0|MRC2_HUMAN	2	40	76	33	0.128336	0.086519123	0.086126825	-0.041816996	-0.042209295	-0.000392298	0.792734123	0.849250706	0.999982008
sp|Q9Y696|CLIC4_HUMAN	4	40	76	33	-0.03251	-0.093029585	0.115542781	-0.060519216	0.14805315	0.208572366	0.828830629	0.462805027	0.146269996
sp|Q9NQR4|NIT2_HUMAN	2	40	76	33	-0.08688	-0.079190033	0.150820248	0.007693557	0.237703839	0.230010281	0.993679924	0.01820326	0.008752256

sp|P35609|ACTN2_HUMAN	44	40	76	33	-0.09847	-0.426420381	-0.159514432	-0.32795233	-0.061046381	0.266905949	0.152812557	0.955243152	0.332413192
sp|P06756|ITAV_HUMAN	19	40	76	33	0.19413	-0.020816767	-0.087079336	-0.214947158	-0.281209726	-0.066262568	7.55E-05	1.59E-05	0.422295817
sp|Q10469|MGAT2_HUMAN	162	40	76	33	0.085913	0.107556461	0.05290921	0.021643923	-0.033003328	-0.054647251	0.73613862	0.6123297	0.184577795
sp|Q8WWY7|WFD12_HUMAN	266	10	21	10	0.289357	-0.052992503	-0.095465769	-0.34234992	-0.384823186	-0.042473267	0.254119728	0.277746586	0.978275374
sp|Q9UJ70|NAGK_HUMAN	3	14	28	12	0.000514	0.023857021	0.003010835	0.023342951	0.002496764	-0.020846186	0.969019129	0.999750588	0.977659761
sp|B9A064|IGLL5_HUMAN	5	40	76	33	-0.42722	-0.257397779	0.178249943	0.169824472	0.605472193	0.435647722	0.266256099	2.48E-05	0.000739441
sp|O75340|PDCD6_HUMAN	8	40	76	33	-0.02012	0.006282005	0.057175612	0.026398544	0.077292151	0.050893607	0.774753536	0.22538508	0.437027251
sp|O95965|ITGBL_HUMAN	11	33	62	27	-0.0327	-0.081225937	0.210973	-0.048526448	0.243672489	0.292198937	0.873887715	0.101913165	0.017028137
sp|Q96KG7|MEG10_HUMAN	1	40	76	33	0.124991	0.049293815	-0.123138812	-0.075697079	-0.248129705	-0.172432627	0.30892606	0.000295015	0.005857603
sp|Q15149|PLEC_HUMAN	2	40	76	33	-0.68312	-0.61066582	0.076894138	0.072453639	0.760013596	0.687559958	0.870706464	6.95E-05	4.83E-05
sp|Q9NPG4|PCD12_HUMAN	57	40	76	33	0.06355	0.062622721	0.072046344	-0.000927532	0.008496091	0.009423623	0.999711814	0.983455355	0.974223718
sp|P16930|FAAA_HUMAN	47	40	76	33	-0.11809	0.025671093	0.254566351	0.143762413	0.372657671	0.228895258	0.176374602	0.000504916	0.022780879
sp|P50990|TCPQ_HUMAN	3	40	76	33	-0.28918	-0.169614614	0.262959798	0.119563005	0.552137417	0.432574412	0.497213573	8.00E-05	0.000552122
sp|P08572|CO4A2_HUMAN	16	40	76	33	-0.11298	-0.061217719	0.296989766	0.051765268	0.409972753	0.358207485	0.754837785	1.73E-05	2.30E-05
sp|O15230|LAMA5_HUMAN	1	40	76	33	-0.03641	-0.106388281	0.177101654	-0.069983057	0.213506878	0.283489935	0.417450861	0.004701566	1.15E-05
sp|P0DMN0|ST1A4_HUMAN	8	40	76	33	-0.39284	-0.315369312	-0.034962438	0.077466446	0.35787332	0.280406874	0.860615395	0.114863534	0.182913392
sp|O00461|GOLI4_HUMAN	12	40	76	33	-0.33831	-0.289730713	0.075703403	0.04857445	0.414008565	0.365434116	0.776747416	1.16E-05	1.27E-05
sp|P61201|CSN2_HUMAN	7	37	69	30	-0.45366	-0.207125083	0.140929045	0.246530773	0.594584901	0.348054128	0.037174834	5.82E-06	0.003844503
sp|Q93091|RNAS6_HUMAN	34	40	76	33	-0.17069	-0.168186136	0.335030028	0.002507759	0.505723924	0.503216165	0.99960778	4.65E-05	4.51E-06
sp|O95861|BPNT1_HUMAN	1	40	76	33	-0.18316	-0.082619777	0.317884241	0.100537851	0.50104187	0.400504019	0.405155559	1.12E-06	1.15E-05
sp|Q9H115|SNAB_HUMAN	1	11	21	9	0.048851	-0.268757088	0.524567015	-0.317608517	0.475715587	0.793324103	0.163313521	0.066336341	0.000287042
sp|Q93063|EXT2_HUMAN	1	40	76	33	0.121302	0.062253339	0.104936451	-0.059048386	-0.016365274	0.042683113	0.08516321	0.874782784	0.318029246
sp|P55072|TERA_HUMAN	3	40	76	33	-0.1952	-0.157750125	0.155914264	0.03745201	0.351116399	0.31366439	0.952753136	0.05783132	0.055402919
sp|P08473|NEP_HUMAN	11	40	76	33	0.14022	0.220770701	0.099011956	0.080550636	-0.041208109	-0.121758745	0.583446768	0.906871297	0.341379907
sp|P50502|F10A1_HUMAN	19	40	76	33	-0.25296	-0.148154623	0.222838226	0.104808832	0.475801681	0.370992849	0.479902629	6.97E-05	0.000528908
sp|Q9UJM8|HAOX1_HUMAN	28	8	14	6	-0.20215	-0.329537047	0.258876492	-0.127388659	0.461024881	0.588413539	0.854901461	0.268770359	0.083001561
sp|Q9H4A4|AMPB_HUMAN	4	40	76	33	-0.17052	0.032206884	0.087375042	0.202727478	0.257895637	0.055168158	0.002081016	0.001059042	0.653380372
sp|O00339|MATN2_HUMAN	4	40	76	33	0.10791	0.059344755	0.099630265	-0.048564856	-0.008279347	0.040285509	0.459919945	0.984420331	0.624523279
sp|Q8TDQ7|GNPI2_HUMAN	19	40	76	33	0.018426	0.015852527	0.100826106	-0.002573857	0.082399721	0.084973579	0.998329636	0.311101146	0.207349331
sp|P16949|STMN1_HUMAN	1	33	62	26	-0.35333	-0.251464989	0.370839517	0.101868805	0.724173311	0.622304506	0.64227784	2.04E-06	4.59E-06
sp|P29144|TPP2_HUMAN	54	36	69	31	0.591173	0.5443854	0.800854724	-0.046788065	0.209681259	0.256469325	0.857525311	0.119312746	0.018276234
sp|P48637|GSHB_HUMAN	12	40	76	33	0.019691	0.087446548	0.294691394	0.067755901	0.275000747	0.207244846	0.417145812	0.000105328	0.001149375
sp|O75223|GGCT_HUMAN	28	40	76	33	-0.29014	-0.091838364	0.314999062	0.198305157	0.605142583	0.406837426	0.128844464	6.30E-06	0.000749736
sp|P60520|GBRL2_HUMAN	2	20	42	19	-0.17764	-0.068524771	0.238723404	0.109116738	0.416364913	0.307248176	0.707790872	0.032070434	0.077975059
sp|P07339|CATD_HUMAN	27	40	76	33	-0.00077	-0.001751449	0.523766741	-0.000980613	0.524537576	0.525518189	0.999921007	1.15E-06	4.22E-08
sp|P07148|FABPL_HUMAN	35	40	76	33	-0.32992	-0.212345684	0.282341809	0.117571602	0.612259095	0.494687492	0.535616656	2.50E-05	0.000131319
sp|P21926|CD9_HUMAN	8	40	76	33	-0.62429	-0.028947247	0.057669375	0.595347096	0.681963717	0.086616622	0.000156721	0.000339162	0.837500372
sp|P23471|PTPRZ_HUMAN	12	40	76	33	0.161103	0.12780302	0.042846395	-0.033299801	-0.118256425	-0.084956624	0.591249175	0.012347133	0.053457274
sp|Q9Y646|CBPQ_HUMAN	33	40	76	33	0.09597	0.127063991	-0.034178569	0.031093879	-0.130148681	-0.16124256	0.830383501	0.11083565	0.014854183
sp|Q9BTY2|FUCO2_HUMAN	450	40	76	33	0.200762	0.141108777	0.307139857	-0.059653557	0.106377523	0.166031079	0.507506965	0.228619576	0.011818278
sp|A8MU46|SMTL1_HUMAN	3	4	6	3	0.005489	0.202174101	1.882342508	0.196685121	1.876853529	1.680168407	0.975558479	0.248607165	0.269138602
sp|Q9Y2A7|NCKP1_HUMAN	10	11	21	10	-0.52624	-0.207158459	0.134178389	0.319079113	0.66041596	0.341336847	0.38069723	0.058380668	0.35522514
sp|Q92520|FAM3C_HUMAN	4	40	76	33	0.012301	-0.009011359	0.22772502	-0.021312564	0.215423814	0.236736379	0.912006532	0.002226412	0.000109191
sp|O43242|PSMD3_HUMAN	18	33	62	27	-0.35219	-0.091813365	0.21776263	0.260373915	0.569949909	0.309575995	0.091671895	0.000580702	0.053328618
sp|Q9BT78|CSN4_HUMAN	24	11	21	9	-0.07531	0.055462471	0.116949968	0.130773508	0.192261005	0.061487497	0.56594157	0.433043485	0.894611043
sp|P07951|TPM2_HUMAN	3	40	76	33	0.016833	-0.213330542	0.21036964	-0.230163603	0.193536579	0.423700182	0.246102036	0.502009023	0.017260162
sp|P10253|LYAG_HUMAN	86	40	76	33	0.020955	0.061961673	0.182870371	0.041007163	0.16191586	0.120908697	0.686165791	0.020117797	0.060640887
sp|Q13642|FHL1_HUMAN	44	40	76	33	-0.10269	-0.128245675	0.025586639	-0.025552928	0.128279386	0.153832314	0.9836418	0.751282075	0.593336705
sp|Q9NYU2|UGGG1_HUMAN	18	40	76	33	-0.05899	-0.015703162	0.149449474	0.043282069	0.208434705	0.165152636	0.70471156	0.004881364	0.013633411
sp|O95490|AGRL2_HUMAN	12	7	14	6	0.071898	-0.014092531	0.022744782	-0.085990472	-0.049153159	0.036837313	0.25991128	0.726501411	0.791195542
sp|Q15102|PA1B3_HUMAN	3	40	76	33	-0.06728	0.059956752	0.30899342	0.127232148	0.376268816	0.249036668	0.244071894	0.000344069	0.010128812
sp|P04179|SODM_HUMAN	14	40	76	33	-0.03583	0.007099039	0.249726046	0.042933179	0.285560186	0.242627007	0.875715026	0.020325094	0.027602125
sp|Q13442|HAP28_HUMAN	6	26	48	20	-0.04503	-0.105300241	0.855101522	-0.060271856	0.900129908	0.960401764	0.946956153	0.00064624	4.25E-05
sp|P04080|CYTB_HUMAN	12	40	76	33	-0.52071	-0.323983058	0.434465697	0.196724453	0.955173208	0.758448755	0.168133372	4.56E-11	2.65E-09
sp|P02647|APOA1_HUMAN	48	40	76	33	-0.29901	-0.012075004	0.356317907	0.28693495	0.65532786	0.368392911	0.015033347	9.96E-07	0.00255451
sp|P15907|SIAT1_HUMAN	4	40	76	33	-0.11412	-0.023935516	0.205838075	0.090188019	0.31996161	0.229773591	0.210909379	5.00E-06	0.000248869
sp|Q86SF2|GALT7_HUMAN	9	40	76	33	0.10894	0.145744092	-0.028825527	0.036804531	-0.137765088	-0.174569619	0.458929726	0.000851138	1.23E-06
sp|P00367|DHE3_HUMAN	27	40	76	33	-0.07067	-0.037644892	0.226572513	0.033024555	0.29724196	0.264217405	0.963976082	0.134186672	0.132760411
sp|P07108|ACBP_HUMAN	12	40	76	33	-0.41886	-0.332222241	0.317705236	0.086639971	0.736567448	0.649927477	0.747316545	2.58E-06	2.87E-06
sp|O15511|ARPC5_HUMAN	22	40	76	33	0.010229	-0.061010852	0.290381415	-0.071239864	0.280152402	0.351392266	0.848349403	0.177968989	0.033480808
sp|P52888|THOP1_HUMAN	9	40	76	33	-0.06418	0.086949042	0.304298709	0.151128368	0.368478035	0.217349667	0.064604364	2.93E-05	0.007677479
sp|Q15382|RHEB_HUMAN	15	14	27	12	0.16666	-0.048727528	0.340337528	-0.215387399	0.173677657	0.389065056	0.419482451	0.670097997	0.085463169
sp|P46060|RAGP1_HUMAN	74	4	6	3	-0.03804	0.319981703	0.549037978	0.358018963	0.587075238	0.229056275	0.273059761	0.105597839	0.616931936
sp|Q8NBS9|TXND5_HUMAN	11	40	76	33	-0.41805	-0.354398195	0.495637057	0.063653071	0.913688324	0.850035253	0.822251848	1.42E-10	2.11E-11
sp|O75594|PGRP1_HUMAN	3	40	76	33	-0.02609	0.040662056	0.252454534	0.066749813	0.278542291	0.211792478	0.646431884	0.006722481	0.024062919
sp|Q9NQW7|XPP1_HUMAN	46	40	76	33	-0.11921	-0.20465483	0.142337115	-0.085444964	0.26154698	0.346991944	0.736560991	0.14328445	0.014256487
sp|Q9GZX9|TWSG1_HUMAN	4	40	76	33	0.121155	0.031391639	0.175155552	-0.089763549	0.054000365	0.143763913	0.21241074	0.67596579	0.032633808
sp|P49368|TCPG_HUMAN	52	40	76	33	-0.29872	-0.118215893	0.199508248	0.180502105	0.498226246	0.317724141	0.204088756	0.000388969	0.014861281
sp|P50120|RET2_HUMAN	2	28	56	24	-0.00533	-0.016941607	0.052987418	-0.011612488	0.058316537	0.069929026	0.994213754	0.903762374	0.82784601
sp|Q9NZ08|ERAP1_HUMAN	8	40	76	33	-0.04029	0.026059144	0.275557806	0.066351925	0.315850587	0.249498663	0.710533912	0.006162506	0.016882599
sp|P22061|PIMT_HUMAN	9	40	76	33	-0.1485	-0.011697997	0.315955397	0.136803249	0.464456642	0.327653394	0.122925595	3.73E-07	5.56E-05
sp|P26447|S10A4_HUMAN	42	40	76	33	-0.06978	0.054155033	0.24223408	0.12393306	0.312012107	0.188079047	0.376135533	0.01593105	0.141282169
sp|Q08623|HDHD1_HUMAN	1	7	14	6	-0.08392	0.10165342	0.437205556	0.1855763	0.521128436	0.335552136	0.715063221	0.179365388	0.383261917
sp|Q00796|DHSO_HUMAN	13	40	76	33	-0.37611	-0.0847308	0.234741077	0.291379008	0.610850885	0.319471877	0.041754148	0.00011217	0.035216212
sp|Q93045|STMN2_HUMAN	21	13	28	12	-0.00208	-0.016819324	0.619493188	-0.014737981	0.621574531	0.636312512	0.997177212	0.037991039	0.011283658
sp|P49354|FNTA_HUMAN	17	11	20	9	-0.13625	-0.19752196	0.172266646	-0.061273717	0.30851489	0.369788606	0.901814378	0.1759962	0.049326369
sp|Q9Y617|SERC_HUMAN	7	40	76	33	-0.19524	0.007789921	0.270149565	0.203025681	0.465385326	0.262359644	0.067470705	0.000103195	0.020147578
sp|P13797|PLST_HUMAN	7	40	76	33	0.091354	0.118464415	0.107564645	0.027110496	0.016210726	-0.01089977	0.72536868	0.923657749	0.955326924
sp|Q9NZR1|TMOD2_HUMAN	93	32	62	27	-0.67433	-0.292789853	0.080548603	0.381536635	0.754875092	0.373338456	0.145993323	0.006483687	0.192562305
sp|Q9H008|LHPP_HUMAN	14	8	14	6	-0.03869	0.139624571	0.092903592	0.178311134	0.131590155	-0.046720979	0.480866148	0.760306037	0.958149372
sp|P52848|NDST1_HUMAN	4	40	76	33	0.062463	0.16376741	0.079085368	0.101304062	0.01662202	-0.084682041	0.025203963	0.931472337	0.10122715
sp|Q9NQ36|SCUB2_HUMAN	128	29	55	24	-0.01771	0.021503788	0.057959915	0.03920952	0.075665647	0.036456127	0.908512169	0.781440798	0.929590578
sp|Q99574|NEUS_HUMAN	4	40	76	33	-0.06075	-0.048063286	0.267984914	0.01269117	0.32873937	0.3160482	0.991431792	0.02173768	0.011400455
sp|P25940|CO5A3_HUMAN	4	26	48	20	0.113957	0.166400564	0.0463723	0.05244308	-0.067585184	-0.120028264	0.901677028	0.891188642	0.636670535
sp|P26641|EF1G_HUMAN	13	40	76	33	-0.50936	-0.289480914	0.251297429	0.219879109	0.760657453	0.540778343	0.229015887	1.52E-05	0.000622893
sp|O95372|LYPA2_HUMAN	23	30	55	23	-0.24436	-0.134683983	0.103869424	0.109678526	0.348231933	0.238553407	0.640062689	0.053918838	0.176625331
sp|P08133|ANXA6_HUMAN	24	40	76	33	-0.55289	-0.235239943	0.150436808	0.317648405	0.703325156	0.385676751	0.039802029	3.72E-05	0.016009863
sp|Q7LDG7|GRP2_HUMAN	3	26	48	20	0.024718	-0.154865141	0.082949338	-0.179583012	0.058231467	0.237814479	0.551046	0.958537578	0.418414107
sp|O14818|PSA7_HUMAN	4	40	76	33	-0.30796	-0.107193527	0.504533323	0.200766165	0.812493015	0.61172685	0.208231016	1.75E-07	9.05E-06
sp|Q96MK3|FA20A_HUMAN	7	40	76	33	-0.05417	0.009090109	0.149514645	0.063262963	0.203687499	0.140424536	0.281510238	0.000214772	0.005167454
sp|Q96QR1|SG3A1_HUMAN	4	33	62	28	-0.06526	-0.041371238	0.241983385	0.023893118	0.307247741	0.283354622	0.949211571	0.003428046	0.002205299
sp|Q70J99|UN13D_HUMAN	4	40	76	33	0.116965	-0.03565023	0.300164957	-0.152615667	0.18319952	0.335815187	0.450644697	0.452705493	0.036828241
sp|P08758|ANXA5_HUMAN	2	40	76	33	-0.3783	-0.323756095	0.109804245	0.054541303	0.488101643	0.43356034	0.917474474	0.010615531	0.010433019
sp|Q15043|S39AE_HUMAN	10	40	76	33	-0.03266	-0.000596582	-0.094779252	0.03206117	-0.062121499	-0.094182669	0.831800544	0.621533254	0.252140514
sp|Q8IV08|PLD3_HUMAN	1	37	69	30	0.014164	0.06167774	0.247198276	0.047514216	0.233034752	0.185520536	0.503555537	3.47E-05	0.000231855
sp|P12429|ANXA3_HUMAN	6	40	76	33	-0.56441	-0.461714334	0.028618823	0.10270031	0.593033468	0.490333158	0.746568353	0.001791085	0.0039113
sp|P21549|SPYA_HUMAN	20	40	76	33	-0.33953	-0.221831966	0.1355439	0.117702546	0.475078413	0.357375866	0.56070516	0.00214065	0.011131827
sp|O15467|CCL16_HUMAN	15	40	76	33	-0.12155	-0.078616964	0.293960148	0.042933646	0.415510758	0.372577113	0.724771237	2.08E-08	1.46E-08
sp|Q96RD9|FCRL5_HUMAN	11	40	76	33	-0.04775	-0.021407576	0.180873277	0.026342978	0.228623831	0.202280853	0.944269555	0.055413888	0.056019646
sp|Q12955|ANK3_HUMAN	28	4	7	3	-0.14271	-0.141115913	1.075314516	0.001595662	1.21802609	1.216430428	0.99999699	0.344398275	0.279164132
sp|Q08ET2|SIG14_HUMAN	21	33	61	27	-0.64189	-0.225670917	-0.696001677	0.416215918	-0.054114842	-0.47033076	0.517441228	0.99224484	0.479694635
sp|P30044|PRDX5_HUMAN	1	40	76	33	-0.31445	-0.236694704	0.063155242	0.077759916	0.377609862	0.299849946	0.717983945	0.005905062	0.015645018
sp|Q9NYQ8|FAT2_HUMAN	9	8	14	6	-0.12859	0.136530348	0.2724139	0.265125285	0.401008837	0.135883552	0.525237802	0.376229295	0.867043913
sp|P27816|MAP4_HUMAN	15	14	27	13	-0.11174	-0.010363011	0.470912272	0.101374114	0.582649397	0.481275284	0.799371438	0.007771963	0.012735775
sp|O43488|ARK72_HUMAN	17	36	70	30	-0.244	-0.205852239	0.025645776	0.038150936	0.269648951	0.231498015	0.93386591	0.1007823	0.11377865

sp|P40227|TCPZ_HUMAN	5	34	62	26	-0.16859	0.038327204	0.483995585	0.206918081	0.652586463	0.445668381	0.428658538	0.00469298	0.041256659
sp|O00429|DNM1L_HUMAN	7	40	76	33	-0.12049	-0.172865603	0.080584933	-0.052374711	0.201075825	0.253450535	0.905481915	0.367840205	0.135221217
sp|O00468|AGRIN_HUMAN	28	40	76	33	-0.2517	-0.122949499	0.3056017	0.128751115	0.557302314	0.428551199	0.116288379	9.62E-11	1.40E-08
sp|Q8IZP9|AGRG2_HUMAN	3	40	76	33	0.1653	0.101094477	-0.12465334	-0.064205183	-0.289953001	-0.225747817	0.311410855	5.17E-07	1.05E-05
sp|P54764|EPHA4_HUMAN	3	40	76	33	0.046674	-0.032868684	-0.179679924	-0.079542691	-0.226353931	-0.146811241	0.393792713	0.006767675	0.064862415
sp|P98095|FBLN2_HUMAN	7	40	76	33	0.089558	0.056672562	0.396269519	-0.032885797	0.306711159	0.339596957	0.829911274	3.93E-05	2.65E-07
sp|P30626|SORCN_HUMAN	9	36	69	30	-0.11856	-0.011692335	0.121110607	0.106864436	0.239667377	0.132802942	0.28018823	0.013804766	0.177674466
sp|Q13310|PABP4_HUMAN	18	23	41	18	-0.07995	-0.027345643	0.19214499	0.052605192	0.272095824	0.219490632	0.898968587	0.150127127	0.214920063
sp|P15259|PGAM2_HUMAN	2	40	76	33	-0.06827	0.020353066	0.208435766	0.088623901	0.276706601	0.1880827	0.417881773	0.003719202	0.034644959
sp|O75326|SEM7A_HUMAN	4	40	76	33	-0.0006	0.024316684	0.190044393	0.024912942	0.190640651	0.165727709	0.812470572	0.000419075	0.000553797
sp|P42785|PCP_HUMAN	6	40	76	33	0.012607	0.050361138	0.219722885	0.037753649	0.207115397	0.169361748	0.651980358	0.000269647	0.000851289
sp|P11597|CETP_HUMAN	3	40	76	33	0.291564	0.260833186	-0.242505259	-0.030730921	-0.534069366	-0.503338445	0.943022442	1.69E-05	4.67E-06
sp|Q68BL8|OLM2B_HUMAN	50	3	6	3	-0.38182	-0.544501866	0.691297093	-0.162678344	1.073120614	1.235798958	0.935942624	0.170989376	0.063116169
sp|Q86U17|SPA11_HUMAN	4	40	76	33	0.094263	0.096942429	0.315637702	0.002679897	0.22137517	0.218695273	0.998813427	0.005019306	0.001505408
sp|O43390|HNRPR_HUMAN	1	29	55	24	0.100251	0.032631812	0.340007837	-0.067619487	0.239756538	0.307376025	0.827774005	0.19935564	0.036901199
sp|Q9H9K5|MER34_HUMAN	11	40	76	33	-0.07202	-0.093766047	-0.07294994	-0.021746963	-0.000930856	0.020816107	0.970173113	0.999961708	0.975934076
sp|O94923|GLCE_HUMAN	1	40	76	33	-0.12255	-0.007140733	0.036334079	0.11541122	0.158886033	0.043474812	0.206919327	0.128729507	0.81942481
sp|Q15369|ELOC_HUMAN	1	13	28	12	-0.18299	-0.069459759	0.496090685	0.113528224	0.679078668	0.565550444	0.784114514	0.004452609	0.006138884
sp|P48059|LIMS1_HUMAN	20	40	76	33	-0.01136	-0.148553371	0.013734528	-0.137193103	0.025094797	0.1622879	0.685756216	0.991295105	0.629376073
sp|Q16851|UGPA_HUMAN	4	40	76	33	0.07271	0.212146026	0.66167452	0.139436519	0.588965012	0.449528494	0.416168118	5.12E-05	0.000559526
sp|P49006|MRP_HUMAN	2	10	21	10	-0.66255	-0.250249276	0.600870351	0.412305393	1.26342502	0.851119627	0.355806408	0.002149191	0.017873163
sp|P00491|PNPH_HUMAN	25	40	76	33	-0.12577	-0.099404057	0.193760586	0.026363285	0.319527928	0.293164643	0.963595598	0.026754363	0.020877645
sp|P40121|CAPG_HUMAN	7	40	76	33	-0.19873	-0.034773115	0.308611118	0.163960627	0.50734486	0.343384233	0.099291514	1.11E-06	0.000229151
sp|P21695|GPDA_HUMAN	3	40	76	33	0.093292	0.114783763	0.135897289	0.021491813	0.042605339	0.021113526	0.943617004	0.854535398	0.95200944
sp|Q9Y4C0|NRX3A_HUMAN	3	40	76	33	0.19888	0.064092504	-0.108771128	-0.134787977	-0.30765161	-0.172863633	0.008448457	1.76E-07	0.00115705
sp|Q6V0I7|FAT4_HUMAN	17	40	76	33	0.011107	-0.005523844	0.02986644	-0.016630996	0.018759288	0.035390285	0.837540587	0.855841388	0.496130247
sp|P05186|PPBT_HUMAN	2	40	76	33	0.009176	0.054222123	0.299258201	0.045046371	0.290082448	0.245036077	0.739982208	0.000342512	0.000681072
sp|P25445|TNR6_HUMAN	3	40	76	33	0.024861	0.036219295	0.406860959	0.011358459	0.382000123	0.370641664	0.980350717	1.25E-06	1.18E-07
sp|P58166|INHBE_HUMAN	29	40	76	33	-0.12728	-0.054671731	0.086906784	0.072603801	0.214182316	0.141578514	0.563171133	0.035094251	0.150987193
sp|P29323|EPHB2_HUMAN	1	40	76	33	-0.15002	-0.084396267	-0.043966038	0.065626974	0.106057202	0.040430228	0.264397888	0.09335431	0.639259864
sp|Q02818|NUCB1_HUMAN	9	40	76	33	-0.17067	-0.066582577	0.490714227	0.104082612	0.661379416	0.557296804	0.546181296	3.98E-07	1.42E-06
sp|Q8WWV6|FCAMR_HUMAN	24	36	69	30	-0.30305	-0.1658975	0.185717709	0.137154115	0.488769323	0.351615208	0.322830388	0.000108675	0.001996284
sp|P40189|IL6RB_HUMAN	77	40	76	33	0.415713	0.413234574	0.450129958	-0.002478001	0.034417383	0.036895384	0.99608293	0.594801979	0.468702674
sp|Q9UBQ6|EXTL2_HUMAN	3	40	76	33	0.219135	0.116564195	-0.111923188	-0.102570957	-0.33105834	-0.228487383	0.063441634	2.95E-08	1.52E-05
sp|P15311|EZRI_HUMAN	8	40	76	33	0.038952	0.071725209	0.270827295	0.032773632	0.231875719	0.199102086	0.871878125	0.010826891	0.014159942
sp|Q9Y5Z4|HEBP2_HUMAN	2	36	69	30	-0.3635	-0.343289674	0.185972901	0.02021245	0.549475024	0.529262575	0.985601143	0.001026424	0.000315628
sp|Q7Z7M9|GALT5_HUMAN	23	40	76	33	0.156736	0.064384129	0.038335725	-0.092351483	-0.118399887	-0.026048404	0.263431977	0.220898851	0.909910339
sp|P16284|PECA1_HUMAN	2	40	76	33	0.064787	0.028594324	0.09911359	-0.036192888	0.034326379	0.070519267	0.611502856	0.736487762	0.197905242
sp|Q06323|PSME1_HUMAN	4	40	76	33	-0.24354	-0.026656258	0.397959588	0.216884453	0.6415003	0.424615847	0.058898289	2.42E-07	0.00012607
sp|P00966|ASSY_HUMAN	143	32	62	28	0.167094	0.395494665	0.519292962	0.228400698	0.352198995	0.123798296	0.169757009	0.052739063	0.616545416
sp|P62191|PRS4_HUMAN	52	7	14	5	0.161759	0.164071119	0.537069751	0.002312027	0.375310659	0.372998633	0.99985174	0.110986077	0.06856326
sp|P07384|CAN1_HUMAN	1	40	76	33	-0.04758	-0.031381414	0.335256963	0.016198772	0.382837149	0.366638376	0.980282858	0.000791066	0.000261509
sp|Q11201|SIA4A_HUMAN	1	40	76	33	0.003834	-0.031587704	-0.022430451	-0.035421322	-0.026264069	0.009157254	0.59100741	0.818566719	0.96945156
sp|P49593|PPM1F_HUMAN	1	36	69	31	0.02806	-0.007809086	0.126108097	-0.035869555	0.098047629	0.133917184	0.83149905	0.382034517	0.103120414
sp|P47914|RL29_HUMAN	5	4	7	2	-0.43034	-0.109143119	-0.251347951	0.321192958	0.178988126	-0.142204832	0.479992483	0.880478467	0.910222532
sp|Q9HC84|MUC5B_HUMAN	3	40	76	33	-0.15563	-0.420972686	-0.099118579	-0.265344917	0.056509189	0.321854106	0.195232379	0.949345135	0.122461152
sp|P30049|ATPD_HUMAN	4	4	6	3	0.075098	-0.175264566	0.70643548	-0.250362276	0.63133777	0.881700046	0.861900524	0.52683393	0.258836782
sp|Q3KQU3|MA7D1_HUMAN	10	4	6	3	-0.17913	0.043296157	1.245130275	0.222422095	1.424256213	1.201834118	0.949457095	0.265351138	0.324280735
sp|Q9Y2Q5|LTOR2_HUMAN	43	7	14	6	0.036403	0.251615787	0.56050311	0.215212898	0.524100221	0.308887323	0.308666334	0.015035713	0.123735689
sp|Q99426|TBCB_HUMAN	41	40	76	33	-0.28789	-0.255049674	0.256058937	0.032841904	0.543950515	0.511108611	0.971331616	0.005407908	0.002939302
sp|P98161|PKD1_HUMAN	8	40	76	33	0.007513	-0.007896818	-0.03889864	-0.015409359	-0.046411181	-0.031001822	0.895061523	0.501761289	0.675166167
sp|Q12797|ASPH_HUMAN	8	40	76	33	0.06408	0.044529312	0.115735359	-0.019550377	0.05165567	0.071206047	0.839870347	0.434010659	0.13616992
sp|P55084|ECHB_HUMAN	9	4	7	3	0.190986	0.083987679	1.136182537	-0.1069984	0.945196458	1.052194858	0.96683354	0.215892713	0.112787241
sp|P08582|TRFM_HUMAN	74	40	76	33	0.186066	0.12559503	-0.081956928	-0.060470881	-0.268022838	-0.207551958	0.620546264	0.002223942	0.008874367
sp|P32019|I5P2_HUMAN	9	4	7	3	0.054315	0.115351947	0.495376334	0.061037435	0.441061821	0.380024386	0.826391819	0.012262772	0.016226255
sp|Q9NWV4|CZIB_HUMAN	5	40	76	33	-0.35864	-0.243416817	0.055844732	0.115222619	0.414484168	0.299261549	0.544528138	0.005631433	0.03038409
sp|Q8WWI1|LMO7_HUMAN	3	4	6	3	-0.03253	-0.00327693	0.789274667	0.029257982	0.82180958	0.792551598	0.998097412	0.379490593	0.352376624
sp|P21709|EPHA1_HUMAN	10	40	76	33	-0.03018	-0.009996048	0.279514879	0.02018717	0.309698097	0.289510926	0.879516409	2.08E-08	3.78E-09
sp|P62491|RB11A_HUMAN	497	40	76	33	-0.43209	-0.326782109	0.243005644	0.105307401	0.675095154	0.569787753	0.715706767	0.000162335	0.000347145
sp|P15289|ARSA_HUMAN	589	40	76	33	0.097949	0.098612848	0.242961098	0.000663628	0.145011879	0.144348251	0.999950026	0.198204785	0.131089321
sp|P54578|UBP14_HUMAN	6	40	76	33	-0.12678	-0.051051526	0.276607529	0.075723665	0.403382719	0.327659055	0.580304329	5.92E-05	0.000252865
sp|Q92734|TFG_HUMAN	5	4	7	3	-0.08724	0.055128555	0.637784859	0.142369645	0.72502595	0.582656304	0.892856454	0.183193592	0.250411994
sp|Q9H3S1|SEM4A_HUMAN	41	40	76	33	-0.07658	-0.01603116	0.063473901	0.060548606	0.140053668	0.079505061	0.553031013	0.116342098	0.409090025
sp|Q6Q788|APOA5_HUMAN	18	40	76	33	-0.00753	-0.026630387	0.017907176	-0.019104469	0.025433094	0.044537563	0.962416696	0.954240666	0.833177196
sp|P02545|LMNA_HUMAN	42	40	76	33	-0.35142	-0.264957001	0.403737699	0.08646102	0.75515572	0.6686947	0.646980226	4.33E-09	4.49E-09
sp|O75339|CILP1_HUMAN	5	40	76	33	0.030247	0.031004822	0.223262059	0.000758298	0.193015535	0.192257237	0.999915522	0.026349197	0.010576342
sp|P49773|HINT1_HUMAN	4	40	76	33	-0.37109	-0.155821992	0.222565956	0.215265439	0.593653387	0.378387949	0.085959488	7.64E-06	0.001660531
sp|P41250|GARS_HUMAN	12	40	76	33	-0.35134	-0.191809041	0.174967266	0.159531255	0.526307562	0.366776307	0.46554114	0.004198721	0.03171994
sp|Q7Z6M3|MILR1_HUMAN	23	22	41	18	-0.12239	0.010494837	0.210402145	0.132882107	0.332789414	0.199907308	0.482865843	0.047843941	0.240987578
sp|P78386|KRT85_HUMAN	4	8	13	6	-0.37485	0.435416434	-0.803161042	0.810264281	-0.428313195	-1.238577476	0.346876125	0.80821564	0.13988317
sp|P13647|K2C5_HUMAN	1	37	69	30	-0.10554	-0.211995163	0.059407302	-0.106456504	0.164945962	0.271402466	0.795500974	0.685801049	0.279217594
sp|P61163|ACTZ_HUMAN	4	29	55	24	-0.0891	0.112858945	0.255451787	0.20195511	0.344547953	0.142592843	0.128477198	0.017828011	0.4010125
sp|Q9HBI1|PARVB_HUMAN	8	40	76	33	0.012548	-0.180728307	0.001085328	-0.193276367	-0.011462732	0.181813634	0.491657972	0.998265392	0.575497304
sp|Q9Y6N7|ROBO1_HUMAN	1	40	76	33	0.027007	0.048615866	0.019474461	0.021609094	-0.00753231	-0.029141405	0.819303259	0.983398486	0.727727803
sp|P34059|GALNS_HUMAN	4	40	76	33	0.069049	-0.030370743	0.127291302	-0.099419952	0.058242094	0.157662045	0.16862705	0.652103027	0.021321147
sp|P12081|SYHC_HUMAN	2	15	28	11	0.18278	0.096971317	0.09830656	-0.085808659	-0.084473416	0.001335243	0.730965869	0.820479446	0.999938193
sp|O15061|SYNEM_HUMAN	15	4	6	3	0.11486	0.098117404	1.038768902	-0.016742623	0.923908875	0.940651498	0.999562981	0.419962086	0.356632627
sp|P17050|NAGAB_HUMAN	8	40	76	33	0.227421	0.179452416	0.107944006	-0.047968487	-0.119476897	-0.07150841	0.523767882	0.066586234	0.285434128
sp|Q9NR12|PDLI7_HUMAN	12	40	76	33	0.071441	-0.073804319	0.349661095	-0.145245129	0.278220286	0.423465415	0.4922195	0.169561739	0.006345442
sp|Q96CN7|ISOC1_HUMAN	166	40	76	33	-0.126	-0.158352177	0.013111569	-0.032349318	0.139114428	0.171463746	0.874917764	0.18685109	0.041071731
sp|Q9H4G4|GAPR1_HUMAN	15	40	76	33	0.102094	0.064076594	0.007635722	-0.038017018	-0.09445789	-0.056440872	0.661878747	0.176672908	0.451424978
sp|P52790|HXK3_HUMAN	15	40	76	33	-0.4556	-0.386865701	0.096672221	0.068737094	0.552275016	0.483537922	0.735740315	5.11E-06	6.70E-06
sp|P30613|KPYR_HUMAN	5	40	76	33	-0.14506	-0.015939458	0.239062987	0.129116086	0.384118531	0.255002445	0.216312468	0.000164586	0.006352511
sp|P00451|FA8_HUMAN	94	40	76	33	-0.10071	0.037506493	0.438319966	0.138211567	0.539025039	0.400813472	0.041745594	1.84E-12	1.81E-09
sp|Q86UD1|OAF_HUMAN	10	40	76	33	0.157855	0.212153447	0.472405869	0.054298047	0.31455047	0.260252422	0.565441276	7.23E-06	2.92E-05
sp|Q9NR99|MXRA5_HUMAN	9	40	76	33	0.007784	-0.004555788	0.281592709	-0.012340274	0.273808222	0.286148497	0.974199715	0.000279381	1.55E-05
sp|Q9NNW7|TRXR2_HUMAN	17	4	7	3	-0.11502	-0.068510339	1.098196762	0.046512424	1.213219524	1.166707101	0.984448962	0.010470813	0.007053599
sp|Q92824|PCSK5_HUMAN	11	19	34	14	-0.1695	-0.148259847	0.472046855	0.02124072	0.641547423	0.620306703	0.986712491	0.000859439	0.000341569
sp|P23470|PTPRG_HUMAN	2	40	76	33	0.151802	0.047583604	0.094406068	-0.104218204	-0.057395741	0.046822464	0.028758629	0.465625048	0.523039195
sp|P16402|H13_HUMAN	1	11	21	9	-0.59699	-0.465027823	0.566445158	0.13195977	1.163432752	1.031472982	0.912898352	0.013824211	0.013803874
sp|Q14247|SRC8_HUMAN	9	40	76	33	-0.0623	-0.225813759	0.035404563	-0.163510993	0.097707328	0.261218322	0.451478642	0.821046558	0.171378545
sp|P78504|JAG1_HUMAN	7	40	76	33	0.025911	0.063286311	0.102937244	0.03737559	0.077026523	0.039650933	0.557894441	0.184451936	0.561747245
sp|Q15019|SEPT2_HUMAN	144	40	76	33	-0.01205	-0.096925379	0.277008097	-0.084874428	0.289059048	0.373933476	0.752533198	0.107604308	0.009724705
sp|P22748|CAH4_HUMAN	31	32	62	27	-0.13582	-0.158850451	0.105083001	-0.023026386	0.240907066	0.263933452	0.970020505	0.105397585	0.032680304
sp|Q16394|EXT1_HUMAN	10	40	76	33	0.151433	0.074477438	0.13448841	-0.076955743	-0.016944772	0.060010972	0.08777317	0.919960609	0.268690014
sp|P02533|K1C14_HUMAN	2	36	70	30	-0.01512	-0.053497984	-0.028845403	-0.038375014	-0.013722432	0.024652581	0.953226795	0.995790714	0.982682995
sp|Q8WZA1|PMGT1_HUMAN	13	40	76	33	0.150586	0.124991643	-0.112569852	-0.025594286	-0.263155782	-0.237561496	0.716160296	1.57E-09	8.31E-10
sp|P09960|LKHA4_HUMAN	16	40	76	33	-0.22026	-0.025233771	0.430040908	0.195030226	0.650304905	0.455274678	0.007030021	9.49E-14	1.09E-09
sp|O75509|TNR21_HUMAN	17	40	76	33	0.033807	0.006450347	0.179379338	-0.027357007	0.145571984	0.172928992	0.876006406	0.080280189	0.011771372
sp|P34913|HYES_HUMAN	2	29	55	24	-0.23947	-0.06964499	0.052859595	0.169824653	0.292329238	0.122504585	0.393625923	0.151562032	0.650647366
sp|O15335|CHAD_HUMAN	2	40	76	33	0.289343	0.251055217	-0.174470591	-0.038287816	-0.463813624	-0.425525808	0.863171631	1.95E-06	8.50E-07
sp|O15143|ARC1B_HUMAN	5	40	76	33	-0.21289	-0.230643968	0.095333155	-0.017754857	0.308222265	0.325977122	0.992096472	0.197505772	0.101008412
sp|O43665|RGS10_HUMAN	3	40	76	33	-0.17396	-0.204438005	0.083050841	-0.030481082	0.257007764	0.287488846	0.96927526	0.221568282	0.092746585
sp|P02730|B3AT_HUMAN	8	40	76	33	-1.17185	-0.979120225	-0.388328298	0.19272909	0.783521016	0.590791926	0.456663082	0.000249613	0.002184674
sp|P58215|LOXL3_HUMAN	5	40	76	33	-0.27574	0.001089983	-0.12735828	0.276832833	0.14838457	-0.128448263	0.012312933	0.405163368	0.422380142

sp|P05771|KPCB_HUMAN	9	40	76	33	-0.33718	-0.186352856	-0.025191144	0.150827121	0.311988833	0.161161712	0.543918821	0.169339282	0.543122572
sp|Q13561|DCTN2_HUMAN	1	33	63	27	-0.22981	-0.134230934	0.30926801	0.095578523	0.539077467	0.443498944	0.69807514	0.000716321	0.001830984
sp|Q9BZR6|RTN4R_HUMAN	12	36	68	30	0.085379	0.074627217	0.254402853	-0.010751899	0.169023738	0.179775637	0.989031034	0.156357818	0.070862743
sp|P07585|PGS2_HUMAN	2	40	76	33	-0.03701	-0.006095973	0.219752173	0.030917684	0.256765831	0.225848147	0.910611037	0.01401282	0.014932328
sp|P62993|GRB2_HUMAN	159	40	76	33	-0.17686	-0.28047464	0.192277725	-0.103612139	0.369140225	0.472752364	0.675709746	0.035804772	0.00120512
sp|Q9NQ38|ISK5_HUMAN	7	40	76	33	0.114116	0.018100474	0.186350223	-0.09601547	0.072234279	0.168249748	0.230267932	0.560520885	0.021005146
sp|Q5VW32|BROX_HUMAN	6	18	35	16	-0.01424	-0.12915479	0.205633296	-0.114916978	0.219871109	0.334788087	0.646764939	0.325600056	0.03911416
sp|P20929|NEBU_HUMAN	5	11	20	8	0.032741	-0.152616468	0.339768481	-0.18535774	0.307027209	0.492384949	0.68514487	0.511295314	0.130248855
sp|Q06830|PRDX1_HUMAN	15	40	76	33	-0.0059	0.221103686	0.51550997	0.227005693	0.521411977	0.294406284	0.01941964	1.91E-06	0.003281959
sp|Q9H251|CAD23_HUMAN	2	40	76	33	0.084604	0.104236019	-0.190857433	0.019632173	-0.275461278	-0.295093452	0.893394754	1.41E-06	6.87E-09
sp|P01036|CYTS_HUMAN	27	33	61	27	-0.05515	-0.250166058	0.019867454	-0.195012163	0.075021349	0.270033511	0.503645841	0.931532786	0.31887211
sp|Q10472|GALT1_HUMAN	32	40	76	33	0.081366	0.10447713	0.142015582	0.023110967	0.060649418	0.037538452	0.731879127	0.231026151	0.486805826
sp|P00568|KAD1_HUMAN	1	40	76	33	-0.24962	-0.041415425	0.277244545	0.208204505	0.526864475	0.318659969	0.104381665	8.95E-05	0.010659548
sp|O00592|PODXL_HUMAN	17	40	76	33	0.158028	0.149865826	0.051220736	-0.008162334	-0.106807424	-0.09864509	0.97570063	0.059470302	0.047072892
sp|P01880|IGHD_HUMAN	8	40	76	33	-0.33563	-0.144439631	-0.320638842	0.19118721	0.014987998	-0.176199211	0.350293375	0.995512282	0.456375359
sp|Q6UX73|CP089_HUMAN	5	29	55	25	0.040021	0.092594386	0.138977814	0.052572959	0.098956387	0.046383428	0.707594552	0.422910343	0.783461001
sp|P51149|RAB7A_HUMAN	6	40	76	33	-0.19631	-0.23634675	0.045128726	-0.040034575	0.241440902	0.281475477	0.93888984	0.210648764	0.069734014
sp|P42229|STA5A_HUMAN	22	21	42	17	-0.12341	-0.137611224	0.38679079	-0.014197596	0.510204418	0.524402015	0.994199529	0.009390031	0.002031621
sp|Q99832|TCPH_HUMAN	6	29	56	24	0.239755	0.217889496	0.545260015	-0.021865384	0.305505135	0.327370519	0.972417266	0.027779812	0.005736574
sp|P69891|HBG1_HUMAN	4	40	76	33	-1.34798	-1.29786924	-0.259552757	0.050107232	1.088423715	1.038316483	0.970149181	0.000120656	3.28E-05
sp|P04062|GLCM_HUMAN	189	40	76	33	0.132762	0.158286774	0.23984081	0.02552443	0.107078465	0.081554035	0.704881647	0.016809101	0.047469402
sp|A6NI73|LIRA5_HUMAN	72	29	55	24	-0.43988	-0.307286352	0.171978985	0.132595998	0.611861335	0.479265337	0.472126088	5.21E-05	0.000377084
sp|O00154|BACH_HUMAN	11	12	20	8	-0.3169	-0.232956491	0.091116285	0.083945444	0.40801822	0.324072776	0.945986065	0.440478942	0.538169281
sp|P60842|IF4A1_HUMAN	96	40	76	33	-0.16454	-0.134090281	0.286363142	0.030445206	0.45089863	0.420453423	0.966508031	0.00742058	0.004520629
sp|P51692|STA5B_HUMAN	41	4	7	3	-0.32657	-0.053245196	0.658991502	0.273325847	0.985562544	0.712236698	0.74101557	0.11268254	0.224221622
sp|P51161|FABP6_HUMAN	192	40	76	33	0.005392	-0.083600226	0.151815706	-0.088991835	0.146424097	0.235415932	0.653039206	0.452547952	0.077285119
sp|Q9H1E3|NUCKS_HUMAN	15	4	6	3	-0.24323	0.290643712	1.909053721	0.533874303	2.152284312	1.618410009	0.853427779	0.205767346	0.33333906
sp|Q9H0R4|HDHD2_HUMAN	11	29	55	25	-0.38148	-0.105344769	0.152149096	0.276139358	0.533633223	0.257493865	0.125811237	0.005209323	0.193835042
sp|Q9NP79|VTA1_HUMAN	2	22	41	18	0.081402	-0.071609832	0.156723741	-0.153011832	0.075321742	0.228333573	0.513948751	0.893539983	0.277531466
sp|P98066|TSG6_HUMAN	1	40	76	33	-0.07679	-0.057004292	0.050763318	0.019789927	0.127557538	0.10776761	0.93668083	0.158778131	0.187433446
sp|Q06481|APLP2_HUMAN	24	40	76	33	-0.33416	-0.061016751	0.099758932	0.273145956	0.433921638	0.160775683	0.004598687	0.000117266	0.18283836
sp|P21399|ACOC_HUMAN	8	40	76	33	-0.16954	-0.097330072	0.108525329	0.072208503	0.278063903	0.205855401	0.615517287	0.008629648	0.034703102
sp|Q504Y2|PKDCC_HUMAN	43	40	76	33	0.046595	-0.056143631	-0.003646847	-0.10273816	-0.050241375	0.052496785	0.114941411	0.695047312	0.603728589
sp|P62906|RL10A_HUMAN	28	23	41	17	-0.11861	-0.050057588	0.297363194	0.06854939	0.415970172	0.347420782	0.872163021	0.041655696	0.064255814
sp|P01236|PRL_HUMAN	21	24	49	22	-0.28144	-0.127720008	0.190111353	0.153716534	0.471547895	0.317831361	0.440501836	0.005700967	0.041076729
sp|P25788|PSA3_HUMAN	22	40	76	33	-0.44956	-0.217854065	0.400699658	0.231706004	0.850259727	0.618553723	0.14138152	1.18E-07	1.37E-05
sp|O14737|PDCD5_HUMAN	14	13	27	12	-0.67007	-0.410843468	0.049206567	0.259224938	0.719274973	0.460050035	0.811576092	0.32691289	0.539882023
sp|O00194|RB27B_HUMAN	16	40	76	33	0.035361	0.109384775	0.276326329	0.074023752	0.240965306	0.166941553	0.751672594	0.128903438	0.283205613
sp|Q8WW52|F151A_HUMAN	5	30	56	24	-0.26128	0.023936667	-0.030377714	0.28521222	0.230897839	-0.054314381	0.245775113	0.530412262	0.956423078
sp|P01130|LDLR_HUMAN	113	40	76	33	-0.10144	-0.03031294	0.270434734	0.071130592	0.371878267	0.300747675	0.620678075	0.000243824	0.000903357
sp|P60981|DEST_HUMAN	22	40	76	33	0.034237	-0.169883879	0.092787272	-0.204121183	0.058549967	0.262671151	0.353825615	0.942143045	0.222422411
sp|Q9Y281|COF2_HUMAN	27	7	13	6	0.413198	0.770429476	1.040904547	0.357231734	0.627706805	0.270475071	0.622939396	0.363732187	0.780782256
sp|Q99650|OSMR_HUMAN	4	40	76	33	0.155494	0.113459315	0.181370753	-0.04203447	0.025876967	0.067911437	0.671105031	0.900668911	0.402901524
sp|Q9H361|PABP3_HUMAN	30	40	76	33	-0.172	-0.118554807	0.304786794	0.05344761	0.47678921	0.4233416	0.816375349	4.09E-05	3.97E-05
sp|Q99941|ATF6B_HUMAN	24	40	76	33	0.036678	0.036639231	0.027548085	-3.86E-05	-0.009129765	-0.009091146	0.999999119	0.966604916	0.95805386
sp|Q702N8|XIRP1_HUMAN	5	4	6	3	-0.06484	-0.014239519	0.824595702	0.050603479	0.8894387	0.838835221	0.991002856	0.188108967	0.17839664
sp|Q8WVQ1|CANT1_HUMAN	1	40	76	33	0.021111	0.196580853	0.276370962	0.17546991	0.255260019	0.079790109	3.20E-05	4.74E-07	0.13049872
sp|Q8WUM4|PDC6I_HUMAN	119	40	76	33	-0.11292	-0.028997675	0.199589287	0.083919819	0.312506781	0.228586962	0.403988546	0.000311005	0.003595854
sp|P42126|ECI1_HUMAN	1	40	76	33	-0.16136	0.045357055	0.142611229	0.206713168	0.303967342	0.097254174	0.045055493	0.0104873	0.538920349
sp|Q9UKV8|AGO2_HUMAN	3	37	69	30	-0.15356	-0.071916049	0.167408894	0.081640277	0.32096522	0.239324943	0.580544953	0.00417107	0.020054647
sp|Q12906|ILF3_HUMAN	147	40	76	33	-0.27543	-0.131706217	0.163708261	0.143719813	0.439134292	0.295414478	0.256768275	0.000278494	0.007699806
sp|Q12913|PTPRJ_HUMAN	7	40	76	33	0.263511	0.193336655	-0.034453251	-0.070174143	-0.297964049	-0.227789906	0.036296842	5.06E-14	1.05E-11
sp|O94933|SLIK3_HUMAN	1	40	76	33	0.104755	0.109955594	-0.229708794	0.005200909	-0.33446348	-0.339664389	0.999030186	0.067773085	0.030098758
sp|P28827|PTPRM_HUMAN	5	40	76	33	0.113045	0.089021111	0.066582702	-0.024024026	-0.046462434	-0.022438409	0.889662804	0.739981692	0.914323395
sp|Q04917|1433F_HUMAN	2	40	76	33	-0.08393	-0.152575511	0.317657712	-0.068645264	0.401587959	0.470233224	0.868729955	0.040032702	0.004132006
sp|Q4VXU2|PAP1L_HUMAN	21	36	69	30	-0.35828	-0.301770973	0.075693842	0.056513177	0.433977992	0.377464816	0.841446751	0.001403103	0.001723266
sp|P27348|1433T_HUMAN	13	40	76	33	-0.25805	-0.149347771	0.251477453	0.108705229	0.509530453	0.400825224	0.60241251	0.000758496	0.003226708
sp|P31946|1433B_HUMAN	10	40	76	33	-0.17466	-0.233681362	0.30341794	-0.059023725	0.478075577	0.537099302	0.896554367	0.008969775	0.000624615
sp|Q9NQS3|NECT3_HUMAN	13	40	76	33	-0.00575	-0.024263938	0.096108957	-0.018517425	0.10185547	0.120372896	0.909693118	0.144023068	0.033613385
sp|Q9UKY7|CDV3_HUMAN	16	32	62	28	-0.06272	-0.119283203	0.421728055	-0.056559337	0.484451921	0.541011258	0.890145631	0.003486455	0.000150078
sp|P08637|FCG3A_HUMAN	2	37	69	30	-0.31379	-0.07243856	0.164899075	0.241350914	0.478688549	0.237337635	0.060340471	0.000709589	0.093622031
sp|P61916|NPC2_HUMAN	4	40	76	33	-0.04654	0.007275255	0.385785443	0.053814251	0.432324439	0.378510188	0.61749578	1.24E-08	1.83E-08
sp|Q86YT9|JAML_HUMAN	2	40	76	33	-0.17935	-0.113011228	0.189219759	0.06633686	0.368567847	0.302230987	0.614164364	7.48E-05	0.000267875
sp|P63010|AP2B1_HUMAN	3	40	76	33	-0.15332	-0.200031143	0.369853177	-0.046710742	0.523173578	0.56988432	0.881696626	5.03E-05	5.78E-07
sp|O94769|ECM2_HUMAN	12	40	76	33	0.072605	0.056516112	0.153399867	-0.01608887	0.080794886	0.096883755	0.873247579	0.099745501	0.015924693
sp|P49588|SYAC_HUMAN	35	40	76	33	-0.11701	-0.076581344	0.282269598	0.04043189	0.399282832	0.358850942	0.928963633	0.008860265	0.007815522
sp|P07306|ASGR1_HUMAN	8	29	55	25	-0.38389	-0.379165397	0.280273726	0.004722072	0.664161195	0.659439123	0.999352805	0.000283283	4.20E-05
sp|Q00722|PLCB2_HUMAN	13	4	7	3	0.198677	0.091203945	0.337457819	-0.107473133	0.138780741	0.246253874	0.930154924	0.921971865	0.735909222
sp|Q9BYJ0|FGFP2_HUMAN	2	40	76	33	-0.15178	-0.006298747	0.06846106	0.145478391	0.220238199	0.074759807	0.033478806	0.005132404	0.445308049
sp|P17405|ASM_HUMAN	9	37	69	30	0.003549	0.132861663	0.448828496	0.129312427	0.44527926	0.315966833	0.336606715	0.000265468	0.00457549
sp|Q9NUQ9|FA49B_HUMAN	10	40	76	33	-0.20585	-0.160420243	0.322889653	0.045427507	0.528737403	0.483309896	0.825184285	1.80E-07	7.59E-08
sp|P11277|SPTB1_HUMAN	5	11	21	9	0.327362	-0.011628958	0.448732151	-0.33899078	0.12137033	0.460361109	0.255007834	0.882751261	0.116701274
sp|P06737|PYGL_HUMAN	3	40	76	33	-0.14567	-0.008880306	0.401445825	0.136787396	0.547113527	0.410326131	0.355123052	2.96E-05	0.000472703
sp|Q13576|IQGA2_HUMAN	127	36	70	30	-0.07906	-0.129148782	0.242835028	-0.050092961	0.321890849	0.37198381	0.91612143	0.088420589	0.016852037
sp|P14780|MMP9_HUMAN	9	40	76	33	-0.55379	-0.118001263	0.34919934	0.43578706	0.902987663	0.467200603	0.001683035	3.45E-08	0.00159318
sp|P39059|COFA1_HUMAN	14	40	76	33	0.116499	0.130281771	0.280055419	0.013783118	0.163556767	0.149773649	0.9467242	0.00639133	0.004632723
sp|O75976|CBPD_HUMAN	128	40	76	33	0.034366	0.068904846	0.154830664	0.034538916	0.120464734	0.085925818	0.662438482	0.034995723	0.111214633
sp|Q12905|ILF2_HUMAN	10	40	76	33	-0.14349	0.112838553	0.486245596	0.256330211	0.629737254	0.373407043	0.042988447	5.86E-06	0.003295312
sp|O14602|IF1AY_HUMAN	2	37	69	29	-0.14951	-0.088995234	0.278267986	0.060517409	0.427780629	0.36726322	0.797823546	0.000846562	0.00138506
sp|P05026|AT1B1_HUMAN	31	40	76	33	0.047828	0.052312889	0.083643651	0.004485004	0.035815767	0.031330762	0.989692692	0.635257857	0.642835961
sp|Q06141|REG3A_HUMAN	1	40	76	33	-0.70058	-0.73335799	-0.094173879	-0.032778569	0.606405542	0.639184111	0.976106477	0.004496317	0.000559057
sp|Q9BQE3|TBA1C_HUMAN	1	4	7	3	0.108225	0.258429718	0.02684863	0.150204826	-0.081376263	-0.231581088	0.780828958	0.951384191	0.622079923
sp|P13612|ITA4_HUMAN	44	7	13	6	-0.0575	0.078249918	0.341809585	0.135745641	0.399305308	0.263559667	0.347659723	0.005036263	0.039301962
sp|P13639|EF2_HUMAN	4	40	76	33	-0.73982	-0.402636025	0.146990096	0.337186436	0.886812557	0.549626121	0.009523211	3.54E-09	3.39E-05
sp|P05166|PCCB_HUMAN	17	4	7	3	0.03017	0.189029052	1.330520947	0.158858725	1.30035062	1.141491895	0.926852711	0.069914571	0.078738006
sp|P61981|1433G_HUMAN	99	40	76	33	-0.10204	-0.147222514	0.368370248	-0.045181508	0.470411255	0.515592762	0.925428238	0.00415119	0.000282604
sp|O76003|GLRX3_HUMAN	15	40	76	33	-0.37048	-0.210607346	0.149120069	0.15987033	0.519597746	0.359727415	0.310543764	0.000346651	0.006740651
sp|A6NMY6|AXA2L_HUMAN	10	33	62	26	-0.26099	-0.229940557	0.073789178	0.031054249	0.334783984	0.303729736	0.953350764	0.027532765	0.024257295
sp|Q9P1F3|ABRAL_HUMAN	5	37	69	29	-0.76101	-0.344132621	0.186823075	0.416879224	0.94783492	0.530955696	0.130960612	0.001176296	0.062480738
sp|O95967|FBLN4_HUMAN	16	40	76	33	-0.15367	-0.123780498	0.186061683	0.029889638	0.339731819	0.309842181	0.833132141	6.61E-07	3.16E-07
sp|P05090|APOD_HUMAN	10	40	76	33	0.230711	0.016963375	0.208200954	-0.213747278	-0.022509699	0.191237579	0.000393602	0.937197773	0.00359657
sp|Q4KMG0|CDON_HUMAN	10	40	76	33	-0.00623	0.052039139	-0.063597604	0.058270398	-0.057366346	-0.115636743	0.504772834	0.632373227	0.097922496
sp|Q16643|DREB_HUMAN	9	40	76	33	-0.07542	0.018983494	0.463975501	0.09440846	0.539400467	0.444992007	0.762688281	0.003122394	0.006523477
sp|P49767|VEGFC_HUMAN	9	40	76	33	0.000121	0.255451509	0.285525049	0.255330892	0.285404432	0.03007354	0.002935846	0.006317928	0.927450821
sp|P23467|PTPRB_HUMAN	5	40	76	33	0.116048	0.118398265	0.024267706	0.002349943	-0.091780616	-0.094130559	0.996929968	0.043629351	0.015774495
sp|Q12841|FSTL1_HUMAN	2	40	76	33	0.056713	0.042239629	0.2509916	-0.014473466	0.194278505	0.208751971	0.952156833	0.003182751	0.000261504
sp|P80294|MT1H_HUMAN	2	36	69	30	-1.27888	-1.084787199	-0.157828232	0.194091791	1.121050758	0.926958968	0.49152635	6.38E-07	3.20E-06
sp|P07438|MT1B_HUMAN	2	21	41	17	-1.02943	-0.671455005	0.47443796	0.357976872	1.503869836	1.145892965	0.340750031	1.74E-05	0.000210898
sp|O75874|IDHC_HUMAN	31	40	76	33	-0.2716	0.072158912	0.360794406	0.343754165	0.632389658	0.288635494	0.000441819	5.80E-08	0.007352951
sp|Q9BXJ4|C1QT3_HUMAN	26	40	76	33	0.563733	0.393978552	0.077391785	-0.169754199	-0.486340966	-0.316586767	0.057555598	5.02E-07	0.000256112
sp|P29279|CCN2_HUMAN	24	40	76	33	-0.18331	-0.12562091	0.269438617	0.057684548	0.452744075	0.395059527	0.741717114	1.12E-05	1.55E-05
sp|P19957|ELAF_HUMAN	8	40	76	33	-0.28215	-0.202931119	0.221190476	0.079218624	0.503340218	0.424121595	0.700767096	0.000113447	0.00025625
sp|P03973|SLPI_HUMAN	4	40	76	33	-0.14936	-0.048391704	0.342911647	0.100969378	0.49227273	0.391303351	0.168918799	4.08E-11	2.32E-09
sp|Q9BX93|PG12B_HUMAN	8	40	76	33	0.047884	0.057815551	0.223263619	0.009932047	0.175380116	0.165448069	0.981646045	0.021697476	0.013342405
sp|Q8TEU8|WFKN2_HUMAN	6	40	76	33	0.170618	0.079797849	-0.145553403	-0.090820299	-0.316171551	-0.225351252	0.346178123	0.000258748	0.004158566

sp|P04054|PA21B_HUMAN	9	40	76	33	-0.19658	-0.004269493	-0.031707468	0.19231546	0.164877484	-0.027437975	0.152742636	0.382080351	0.966338048
sp|Q14508|WFDC2_HUMAN	13	40	76	33	-1.3826	-1.302509458	-0.325046331	0.080093057	1.057556183	0.977463127	0.878619298	1.16E-06	4.03E-07
sp|P01859|IGHG2_HUMAN	7	40	76	33	-0.18204	-0.120685319	0.013136108	0.061350846	0.195172273	0.133821428	0.77736841	0.177054574	0.352322295
sp|P11717|MPRI_HUMAN	16	40	76	33	0.071738	0.067760421	0.201935167	-0.003977367	0.130197379	0.134174746	0.992109277	0.003946662	0.000642182
sp|P30086|PEBP1_HUMAN	1	40	76	33	-0.14204	-0.000800814	0.404649338	0.141241717	0.546691869	0.405450152	0.177511797	1.54E-07	1.12E-05
sp|P05161|ISG15_HUMAN	8	40	76	33	-0.56885	-0.022637958	0.150286693	0.54620845	0.7191331	0.172924651	1.86E-06	1.91E-07	0.272480933
sp|Q04760|LGUL_HUMAN	25	40	76	33	-0.07746	0.041099664	0.282784825	0.118561573	0.360246735	0.241685162	0.194435693	6.45E-05	0.003236541
sp|P98155|VLDLR_HUMAN	36	40	76	33	-0.07914	-0.050531433	0.027894646	0.028612677	0.107038756	0.078426079	0.929541267	0.496186526	0.618876358
sp|P16581|LYAM2_HUMAN	2	40	76	33	-0.10858	-0.080787822	0.251369343	0.027791504	0.359948669	0.332157165	0.925301128	0.000253921	0.00013405
sp|Q96GP6|SREC2_HUMAN	157	40	76	33	-0.00656	-0.092745407	0.290013195	-0.086183344	0.296575258	0.382758602	0.497994775	0.004390475	1.79E-05
sp|P17252|KPCA_HUMAN	1	10	21	9	0.000992	0.124239838	0.236062625	0.123247973	0.23507076	0.111822787	0.77887976	0.533521453	0.825587007
sp|P07477|TRY1_HUMAN	1	40	76	33	0.118633	0.106414072	0.148743315	-0.012218598	0.030110644	0.042329243	0.979139732	0.915514357	0.801190766
sp|Q14314|FGL2_HUMAN	10	40	76	33	-0.21237	-0.073781698	0.098118569	0.138592875	0.310493142	0.171900267	0.054781052	7.93E-05	0.020563333
sp|Q9UK23|NAGPA_HUMAN	1	40	76	33	0.191227	0.168826488	0.043171273	-0.022400583	-0.148055798	-0.125655215	0.737426085	0.000210901	0.000407396
sp|O95428|PPN_HUMAN	1	40	76	33	0.019309	0.039002354	0.205617777	0.019693434	0.186308857	0.166615422	0.929605063	0.013376537	0.012433545
sp|P78552|I13R1_HUMAN	8	40	76	33	0.006806	0.002666849	0.072811791	-0.004138784	0.066006157	0.070144941	0.994664466	0.394690203	0.264388075
sp|Q86TH1|ATL2_HUMAN	17	40	76	33	-0.05033	0.077220703	0.416597349	0.127546489	0.466923135	0.339376647	0.201518959	1.74E-06	9.71E-05
sp|Q9ULV4|COR1C_HUMAN	16	40	76	33	-0.14697	-0.149568157	0.086590542	-0.002596184	0.233562515	0.236158699	0.999855337	0.448864027	0.353645123
sp|Q9BR76|COR1B_HUMAN	9	40	76	33	-0.14703	-0.201921878	0.15063118	-0.054890274	0.297662784	0.352553058	0.896404511	0.114021507	0.022110506
sp|Q8IW52|SLIK4_HUMAN	7	25	48	21	0.344418	0.177491572	0.207318503	-0.166926428	-0.137099496	0.029826932	0.101347087	0.335865416	0.935093509
sp|P06731|CEAM5_HUMAN	1	4	6	3	-0.13024	0.441305672	0.744486561	0.571546563	0.874727452	0.303180889	0.706735642	0.567017644	0.919730531
sp|P07203|GPX1_HUMAN	3	32	63	27	-0.13805	-0.125591183	0.184064708	0.012462706	0.322118597	0.309655891	0.993611779	0.057566514	0.03391693
sp|Q8NHW5|RLA0L_HUMAN	2	40	76	33	-0.35629	-0.166352771	0.465882703	0.189937532	0.822173006	0.632235474	0.163201539	2.33E-09	1.83E-07
sp|Q13867|BLMH_HUMAN	1	40	76	33	-0.06557	-0.019860967	0.250828891	0.045713853	0.316403711	0.270689858	0.737326053	9.89E-05	0.000177804
sp|Q9NYL9|TMOD3_HUMAN	9	17	35	15	-0.36651	-0.07500991	0.416681336	0.291501252	0.783192498	0.491691246	0.385827749	0.01137754	0.08916676
sp|P51858|HDGF_HUMAN	10	32	62	28	-0.07412	0.05397265	0.468570942	0.128092628	0.542690921	0.414598292	0.68929475	0.011111759	0.032245995
sp|Q9UL46|PSME2_HUMAN	35	40	76	33	-0.16594	-0.017931937	0.332673701	0.14801158	0.498617218	0.350605637	0.139426001	1.02E-06	0.000116574
sp|P78509|RELN_HUMAN	14	40	76	33	0.19313	0.200121807	0.349912537	0.006991464	0.156782193	0.14979073	0.986920414	0.0126889	0.006481555
sp|P50053|KHK_HUMAN	1	8	14	6	0.0401	0.049079681	0.343576742	0.008979626	0.303476688	0.294497062	0.998598013	0.356575316	0.306758713
sp|Q13228|SBP1_HUMAN	5	40	76	33	0.201723	0.393090055	0.640658961	0.191367422	0.438936329	0.247568907	0.014366143	7.79E-07	0.002196868
sp|Q92496|FHR4_HUMAN	8	40	76	33	-0.04066	-0.059648774	0.004969077	-0.018986138	0.045631713	0.064617851	0.955858583	0.835543585	0.633113242
sp|Q7LFX5|CHSTF_HUMAN	5	40	76	33	0.041682	0.050993152	0.279428874	0.009310718	0.237746439	0.228435721	0.980141925	0.000247004	6.52E-05
sp|P61160|ARP2_HUMAN	7	40	76	33	-0.02665	-0.083206882	0.171809641	-0.056552686	0.198463837	0.255016523	0.834737422	0.220145138	0.043837557
sp|P48426|PI42A_HUMAN	7	40	76	33	-0.08066	-0.023082753	0.302345532	0.057579692	0.383007977	0.325428285	0.886128011	0.028410888	0.03760742
sp|Q5VY43|PEAR1_HUMAN	2	40	76	33	0.156371	0.124578936	0.078164841	-0.031792164	-0.078206259	-0.046414095	0.625334154	0.145114502	0.416966845
sp|P52823|STC1_HUMAN	18	6	14	7	0.023067	-0.259113836	0.578819627	-0.282181246	0.555752218	0.837933464	0.594773018	0.226912962	0.013849447
sp|Q04446|GLGB_HUMAN	2	40	76	33	-0.08099	-0.068361392	0.121923719	0.012629141	0.202914252	0.190285111	0.970697991	0.006527498	0.003700174
sp|O95897|NOE2_HUMAN	2	40	76	33	0.083777	0.091578939	0.090752328	0.007801519	0.006974908	-0.000826611	0.991848691	0.995496037	0.999919322
sp|Q15435|PP1R7_HUMAN	18	40	76	33	-0.22515	-0.143617446	0.124434805	0.081530668	0.349582919	0.268052251	0.406340274	3.01E-05	0.000346911
sp|P09958|FURIN_HUMAN	25	10	20	10	0.098563	0.220581031	0.541388348	0.122018406	0.442825723	0.320807317	0.617555325	0.014407403	0.046175067
sp|Q9UBW8|CSN7A_HUMAN	3	4	6	3	0.039803	0.168491914	0.001582195	0.1286893	-0.038220419	-0.166909719	0.390020543	0.936988546	0.279784202
sp|P11413|G6PD_HUMAN	2	40	76	33	-0.34941	-0.274410765	0.217794693	0.074998588	0.567204046	0.492205458	0.864069885	0.004250763	0.005281128
sp|P10645|CMGA_HUMAN	9	40	76	33	-0.02011	-0.185809101	0.262882237	-0.165699942	0.282991396	0.448691338	0.162160068	0.027459018	2.16E-05
sp|P35030|TRY3_HUMAN	2	40	76	33	0.108814	-0.059306606	0.076135193	-0.168120213	-0.032678414	0.135441799	0.009697086	0.88108392	0.067614984
sp|P21266|GSTM3_HUMAN	23	40	76	33	-0.1396	0.005811232	0.359859991	0.145414988	0.499463747	0.354048759	0.171013867	2.43E-06	0.000184995
sp|P48060|GLIP1_HUMAN	4	33	62	28	0.298762	0.344817879	0.283040479	0.046055998	-0.015721402	-0.061777399	0.875223805	0.989120799	0.806902987
sp|P08238|HS90B_HUMAN	2	40	76	33	-0.0372	0.009111358	0.426132695	0.046308935	0.463330272	0.417021337	0.889140279	0.000535356	0.000431186
sp|Q99466|NOTC4_HUMAN	5	40	76	33	0.013242	-0.005224119	-0.006303051	-0.018466509	-0.019545441	-0.001078931	0.926964061	0.943053327	0.999772539
sp|O60704|TPST2_HUMAN	20	4	7	3	0.098164	0.119162914	0.305059781	0.020998507	0.206895374	0.185896867	0.967453064	0.162226394	0.16501523
sp|Q9NTU7|CBLN4_HUMAN	4	40	76	33	0.215563	0.131832302	-0.383469298	-0.083730267	-0.599031867	-0.5153016	0.4029073	6.82E-12	2.38E-11
sp|P23435|CBLN1_HUMAN	6	40	76	33	0.265362	0.009369555	-0.314494551	-0.255991988	-0.579856095	-0.323864106	0.002904233	9.44E-09	0.000322634
sp|Q8IUK8|CBLN2_HUMAN	3	37	69	30	0.497742	0.324586265	0.00424122	-0.17315618	-0.493501225	-0.320345045	0.251920853	0.000719161	0.018656742
sp|Q9NP84|TNR12_HUMAN	26	40	76	33	-0.88015	-0.878124569	0.12707055	0.002025204	1.007220322	1.005195119	0.999913954	2.35E-06	1.13E-07
sp|P10599|THIO_HUMAN	4	40	76	33	-0.16707	-0.010094679	0.482406575	0.156973614	0.649474868	0.492501254	0.18671813	3.48E-08	2.21E-06
sp|P11142|HSP7C_HUMAN	2	40	76	33	-0.06812	-0.026920031	0.375715055	0.04119542	0.443830506	0.402635086	0.912479495	0.001058897	0.000782208
sp|Q05655|KPCD_HUMAN	38	15	28	11	-0.18259	-0.323322737	0.160827632	-0.140733774	0.343416595	0.484150369	0.709169	0.272513823	0.04573299
sp|P48506|GSH1_HUMAN	1	40	76	33	-0.39166	-0.071624713	0.284937752	0.320036665	0.67659913	0.356562465	0.000110469	2.04E-11	5.22E-05
sp|O95185|UNC5C_HUMAN	20	30	55	23	-0.0253	-0.013648566	0.255259492	0.01164901	0.280557067	0.268908057	0.987932685	0.011592489	0.006329618
sp|P14207|FOLR2_HUMAN	3	40	76	33	-0.14034	-0.060280505	0.159666946	0.080057186	0.300004638	0.219947451	0.378310842	0.000162664	0.00220803
sp|Q9NPH3|IL1AP_HUMAN	1	40	76	33	0.141183	0.170276921	-0.13460036	0.02909383	-0.275783451	-0.304877281	0.785491061	1.83E-06	3.46E-09
sp|O60667|FAIM3_HUMAN	27	40	76	33	0.007692	0.115997188	0.151320444	0.108305102	0.143628358	0.035323256	0.170434374	0.117791097	0.845296926
sp|Q9BRN9|TM2D3_HUMAN	1	13	27	13	-0.10204	-0.014182027	-0.064550148	0.087853352	0.037485232	-0.050368121	0.314282249	0.852268793	0.678746844
sp|P11362|FGFR1_HUMAN	10	40	76	33	0.204572	0.149975654	0.017493467	-0.054596508	-0.187078695	-0.132482186	0.302452031	0.00012668	0.002751575
sp|P05106|ITB3_HUMAN	60	40	76	33	-0.57087	-0.289532118	-0.24270006	0.281335465	0.328167522	0.046832057	0.042055937	0.050764182	0.923466709
sp|Q96TA1|NIBA2_HUMAN	3	40	76	33	0.124623	0.10460916	0.113989295	-0.020013404	-0.010633269	0.009380135	0.874468149	0.974182225	0.974431233
sp|Q9ULI3|HEG1_HUMAN	41	40	76	33	0.192811	0.145056861	0.183472614	-0.047754042	-0.00933829	0.038415753	0.236132972	0.962083549	0.438041992
sp|P54652|HSP72_HUMAN	11	11	20	9	-0.18266	-1.026036042	-0.213692994	-0.84337749	-0.031034442	0.812343048	0.184660264	0.998320377	0.250651586
sp|Q14CN2|CLCA4_HUMAN	19	11	21	9	0.167327	-0.289746537	-0.285476955	-0.457073996	-0.452804413	0.004269582	0.072659067	0.163939274	0.999783905
sp|P13284|GILT_HUMAN	5	19	35	14	-0.35422	-0.298965468	0.22537581	0.055255336	0.579596614	0.524341278	0.873698535	0.000237948	0.000212968
sp|O14917|PCD17_HUMAN	6	36	69	30	-0.19116	-0.137870729	0.197284821	0.053288995	0.388444546	0.335155551	0.681485072	3.97E-06	6.85E-06
sp|O75051|PLXA2_HUMAN	45	40	76	33	0.013781	-0.021197908	-0.001979774	-0.034978985	-0.015760851	0.019218134	0.686187981	0.948438676	0.90474109
sp|P13501|CCL5_HUMAN	2	40	76	33	-0.09394	-0.057730983	-0.176542136	0.036209817	-0.082601336	-0.118811153	0.958484506	0.858931737	0.67080477
sp|Q9P126|CLC1B_HUMAN	7	10	21	10	-0.02646	-0.156446936	0.670817902	-0.129982195	0.697282643	0.827264838	0.843447188	0.037200316	0.002971447
sp|P14324|FPPS_HUMAN	13	40	76	33	-0.0812	-0.121247011	0.168695898	-0.040043043	0.249899866	0.289942909	0.891185394	0.049602631	0.006465405
sp|Q9H2E6|SEM6A_HUMAN	14	40	76	33	0.03536	0.056740375	0.060394173	0.02138076	0.025034558	0.003653798	0.841869984	0.849724922	0.995588309
sp|P11586|C1TC_HUMAN	8	26	49	21	-0.19821	-0.098032252	0.213622266	0.10018184	0.411836358	0.311654518	0.484601895	0.000496905	0.003484185
sp|Q13201|MMRN1_HUMAN	6	40	76	33	-0.33048	0.089761726	0.28252018	0.420241135	0.612999588	0.192758453	0.000349508	1.20E-05	0.208846464
sp|O75095|MEGF6_HUMAN	2	29	55	23	-0.00734	-0.002969365	0.559274744	0.00436935	0.56661346	0.562244109	0.999211522	0.000309653	5.29E-05
sp|O00548|DLL1_HUMAN	30	40	76	33	-0.0603	-0.026280845	0.291794654	0.034019808	0.352095307	0.318075499	0.876769987	0.000135348	9.87E-05
sp|Q03154|ACY1_HUMAN	76	40	76	33	-0.43603	-0.103209463	0.192779926	0.33282332	0.62881271	0.29598939	0.00740854	1.15E-05	0.03156321
sp|P15153|RAC2_HUMAN	2	32	62	28	-0.4223	-0.356901831	0.126993246	0.065395029	0.549290106	0.483895076	0.815168652	0.000100967	9.89E-05
sp|Q9Y274|SIA10_HUMAN	36	40	76	33	0.067329	0.071362207	-0.052349599	0.004033264	-0.119678542	-0.123711806	0.991673358	0.007959377	0.001551986
sp|P07686|HEXB_HUMAN	22	40	76	33	0.052021	0.060846448	0.302417097	0.008825487	0.250396136	0.241570649	0.985465508	0.000532041	0.000147412
sp|O43866|CD5L_HUMAN	152	40	76	33	-0.15356	-0.056821836	0.415708213	0.096741855	0.569271905	0.47253005	0.471939981	1.68E-07	9.38E-07
sp|P00995|ISK1_HUMAN	17	40	76	33	-0.24445	-0.206174043	0.341394806	0.038278283	0.585847131	0.547568848	0.945154096	0.000227463	9.60E-05
sp|P01591|IGJ_HUMAN	1	40	76	33	0.16767	0.112705135	0.067138897	-0.054965344	-0.100531582	-0.045566238	0.198218154	0.025781583	0.374168738
sp|Q5KU26|COL12_HUMAN	57	40	76	33	-0.35396	-0.373904568	0.002651595	-0.019940723	0.35661544	0.376556163	0.952775396	6.11E-05	1.63E-06
sp|Q13564|ULA1_HUMAN	35	16	35	16	-0.254	-0.105924111	0.317897993	0.148072339	0.571894442	0.423822104	0.434115791	0.00035904	0.002077018
sp|Q5VU97|CAHD1_HUMAN	2	37	69	30	0.110529	0.182523255	0.243184113	0.071994222	0.13265508	0.060660859	0.239947627	0.038132876	0.412686456
sp|P21802|FGFR2_HUMAN	6	40	76	33	0.039804	0.037562806	0.115527555	-0.002241309	0.07572344	0.077964749	0.99890738	0.426046847	0.317481164
sp|Q58EX2|SDK2_HUMAN	1	40	76	33	0.195973	0.216623581	0.050558112	0.020650526	-0.145414942	-0.166065468	0.884366736	0.017648681	0.00144781
sp|Q92626|PXDN_HUMAN	1	40	76	33	-0.20099	-0.057131534	0.225196867	0.143859227	0.426187628	0.282328401	0.035424081	1.97E-08	2.63E-05
sp|Q13630|FCL_HUMAN	1	40	76	33	-0.26699	-0.160413888	0.114827281	0.10657343	0.381814599	0.275241169	0.353202195	0.000192294	0.003004806
sp|P53621|COPA_HUMAN	5	14	27	11	-0.07893	0.022602995	0.538906959	0.101532869	0.617836833	0.516303964	0.844540889	0.021762821	0.032575704
sp|P13645|K1C10_HUMAN	8	40	76	33	0.263668	0.056933835	-0.101109936	-0.206733844	-0.364777615	-0.158043771	0.380088511	0.128154071	0.607235943
sp|Q04695|K1C17_HUMAN	113	11	21	9	0.033091	-0.062554612	-0.203528975	-0.095645487	-0.23661985	-0.140974363	0.945875777	0.792725582	0.900018392
sp|P01210|PENK_HUMAN	31	8	14	6	-0.1476	-0.115291744	-0.055822795	0.032304851	0.0917738	0.059468949	0.989201786	0.942814961	0.970128003
sp|O75563|SKAP2_HUMAN	41	36	69	31	0.031184	0.022491202	0.234163194	-0.008692722	0.20297927	0.211671992	0.996378492	0.253730255	0.148972916
sp|Q9Y266|NUDC_HUMAN	15	40	76	33	-0.35116	-0.232452349	0.331386433	0.11870619	0.682544972	0.563838782	0.532637949	2.80E-06	1.30E-05
sp|P22894|MMP8_HUMAN	3	28	55	24	-0.55902	-0.313844809	0.310740816	0.24517539	0.869761014	0.624585625	0.226736646	1.03E-05	0.000340072
sp|P11021|BIP_HUMAN	26	40	76	33	0.155221	0.201180766	0.174080132	0.045959931	0.018859297	-0.027100634	0.365513991	0.888661684	0.733797093
sp|O60462|NRP2_HUMAN	12	40	76	33	0.016484	0.058944305	0.254246944	0.042460054	0.237762693	0.195302639	0.50738901	2.17E-06	1.16E-05
sp|Q92896|GSLG1_HUMAN	2	40	76	33	-0.10753	0.044477988	0.191197298	0.152005156	0.298724466	0.14671931	0.011531461	1.42E-05	0.025245487
sp|Q05707|COEA1_HUMAN	5	37	69	29	-0.02665	0.005219744	0.050427386	0.031872992	0.077080634	0.045207642	0.885426383	0.61974929	0.812748692
sp|Q13790|APOF_HUMAN	1	40	76	33	-0.20939	0.190182297	0.343354898	0.399571707	0.552744309	0.153172601	1.87E-06	4.72E-08	0.150524632

sp|Q14697|GANAB_HUMAN	31	40	76	33	-0.06303	0.031931133	0.379093931	0.094959618	0.442122417	0.347162799	0.204910387	1.99E-09	8.95E-08
sp|P20908|CO5A1_HUMAN	6	40	76	33	-0.241	-0.195779948	0.575448015	0.045222163	0.816450126	0.771227963	0.906316967	8.19E-09	9.55E-10
sp|O00629|IMA3_HUMAN	2	4	7	3	0.050546	0.020761915	0.36609751	-0.029784291	0.315551303	0.345335595	0.991784092	0.554447665	0.429871972
sp|P20042|IF2B_HUMAN	132	40	76	33	-0.12475	-0.026172971	0.326903781	0.098577161	0.451653913	0.353076752	0.606560404	0.001118326	0.004707319
sp|P09104|ENOG_HUMAN	4	40	76	33	-0.02157	-0.049409402	-0.03433117	-0.027841671	-0.012763439	0.015078232	0.940223269	0.991097063	0.984245196
sp|P08254|MMP3_HUMAN	6	40	76	33	0.03444	-0.068066899	0.056720865	-0.10250669	0.022281074	0.124787764	0.445172038	0.97374753	0.349822996
sp|Q96Q06|PLIN4_HUMAN	139	4	6	3	0.071308	0.111021747	1.036226729	0.039714117	0.9649191	0.925204983	0.996620663	0.286352801	0.264499558
sp|Q6UWY5|OLFL1_HUMAN	3	40	76	33	0.069336	0.066637488	0.111651741	-0.002698147	0.042316105	0.045014252	0.9970264	0.604884357	0.48568858
sp|Q10567|AP1B1_HUMAN	5	40	76	33	-0.10173	-0.138793332	0.333598051	-0.037062377	0.435329005	0.472391383	0.948153775	0.008027196	0.000846999
sp|P35754|GLRX1_HUMAN	29	40	76	33	-0.85434	-0.568959001	0.115368385	0.285384954	0.96971234	0.684327386	0.062062301	5.10E-09	2.84E-06
sp|Q99471|PFD5_HUMAN	20	22	42	17	-0.16234	0.085572314	0.228120697	0.247912205	0.390460588	0.142548383	0.108491935	0.027879796	0.531597781
sp|Q00169|PIPNA_HUMAN	5	7	14	7	0.003877	0.075812004	0.072705557	0.071934826	0.068828379	-0.003106448	0.933853038	0.954054731	0.999871998
sp|Q14974|IMB1_HUMAN	1	40	76	33	-0.22259	-0.234879564	0.18178691	-0.012286204	0.40438027	0.416666475	0.994610042	0.020645937	0.0056552
sp|Q9Y5Y6|ST14_HUMAN	2	40	76	33	-0.37644	-0.341136124	0.17296556	0.035306402	0.549408086	0.514101684	0.958287162	0.001284823	0.000631532
sp|Q14696|MESD_HUMAN	2	37	69	29	-0.06169	-0.020988538	0.339485515	0.040703441	0.401177494	0.360474053	0.897290205	0.001331967	0.001221305
sp|P27797|CALR_HUMAN	4	40	76	33	-0.08299	-0.028629574	0.531759992	0.054358416	0.614747982	0.560389566	0.797468226	3.92E-08	1.67E-08
sp|Q9UIW2|PLXA1_HUMAN	16	40	76	33	0.034166	0.014677663	0.111657278	-0.01948821	0.077491405	0.096979615	0.81754039	0.116129192	0.014957522
sp|P54819|KAD2_HUMAN	28	37	69	30	-0.01177	-0.06262794	0.280539144	-0.050861164	0.29230592	0.343167084	0.855164962	0.032447022	0.002983666
sp|Q6IBS0|TWF2_HUMAN	4	40	76	33	0.066394	-0.002538292	0.374283949	-0.068932617	0.307889624	0.37682224	0.821058005	0.07099324	0.007245035
sp|P06213|INSR_HUMAN	5	21	42	17	0.127372	0.144345289	0.036236103	0.016973334	-0.091135851	-0.108109186	0.987794498	0.789238597	0.65204256
sp|P09972|ALDOC_HUMAN	36	40	76	33	0.047322	0.040988708	-0.032713493	-0.006332792	-0.080034993	-0.073702201	0.986597257	0.231229804	0.206335549
sp|Q6UXI9|NPNT_HUMAN	23	40	76	33	-0.08504	-0.040867506	0.068042243	0.044170637	0.153080387	0.108909749	0.79375771	0.152419416	0.295226788
sp|Q15370|ELOB_HUMAN	5	40	76	33	0.289546	0.302913263	0.720167398	0.01336681	0.430620944	0.417254134	0.988152526	0.000375925	9.15E-05
sp|Q96NZ9|PRAP1_HUMAN	7	40	76	33	-0.166	-0.171767688	0.314076726	-0.005771404	0.480073011	0.485844415	0.997581045	2.94E-05	1.74E-06
sp|Q00013|EM55_HUMAN	10	40	76	33	-0.37381	-0.265813922	0.104912113	0.107993105	0.47871914	0.370726035	0.674285103	0.006143907	0.019622255
sp|P55287|CAD11_HUMAN	5	40	76	33	0.134456	0.118424877	0.387918417	-0.016030999	0.253462541	0.26949354	0.962871336	0.002169704	0.000180847
sp|P63279|UBC9_HUMAN	15	23	41	18	-0.15026	-0.142150031	0.224439791	0.00811324	0.374703062	0.366589822	0.997402914	0.02770691	0.014845485
sp|Q96RT1|ERBIN_HUMAN	10	19	34	14	-0.83919	-0.464221635	-0.833783935	0.374968587	0.005406287	-0.3695623	0.575343133	0.999923184	0.645421856
sp|Q8NCL4|GALT6_HUMAN	3	40	76	33	0.383465	0.323950626	0.398261781	-0.059514321	0.014796833	0.074311154	0.398295065	0.961142003	0.284890083
sp|Q9Y316|MEMO1_HUMAN	8	8	13	6	0.263275	-0.281233504	0.147225246	-0.544508713	-0.116049963	0.42845875	0.213613787	0.949347389	0.440842242
sp|Q8TAG5|VTM2A_HUMAN	1	40	76	33	0.034413	-0.076670928	-0.139057089	-0.111084084	-0.173470245	-0.06238616	0.141456982	0.038874724	0.577146139
sp|P22303|ACES_HUMAN	5	36	69	30	0.181483	0.13645027	0.057506904	-0.045032493	-0.123975858	-0.078943366	0.767666072	0.254387049	0.489446777
sp|P05121|PAI1_HUMAN	4	40	76	33	-0.34254	0.032165671	0.208799663	0.374702746	0.551336738	0.176633992	0.000492989	1.63E-05	0.206513042
sp|P16157|ANK1_HUMAN	21	33	62	26	-0.40746	-0.090552314	0.510919122	0.316911709	0.918383145	0.601471437	0.082311619	3.21E-06	0.00071413
sp|Q16719|KYNU_HUMAN	15	29	55	25	-0.2727	-0.144326669	0.178135937	0.128375784	0.450838391	0.322462607	0.684056006	0.041077193	0.120067129
sp|Q9NS00|C1GLT_HUMAN	1	7	14	5	0.104182	0.070233551	0.055519616	-0.033948352	-0.048662287	-0.014713935	0.936750388	0.919585065	0.990331266
sp|O00499|BIN1_HUMAN	8	22	41	18	-0.76478	-0.839207021	-0.193810591	-0.074431451	0.570964978	0.645396429	0.9316069	0.063441009	0.013038884
sp|Q01638|ILRL1_HUMAN	9	40	76	33	-0.25226	-0.238360902	0.463369246	0.013894505	0.715624652	0.701730147	0.994668347	0.000129558	2.10E-05
sp|P50552|VASP_HUMAN	3	40	76	33	-0.34894	-0.529260501	-0.172265513	-0.180318952	0.176676036	0.356994988	0.38168952	0.527209179	0.039268283
sp|P47756|CAPZB_HUMAN	7	40	76	33	-0.22185	-0.213229803	0.209877236	0.008625025	0.431732063	0.423107038	0.99695683	0.006705656	0.002347707
sp|P31749|AKT1_HUMAN	2	15	28	11	0.013476	0.093650182	0.110230819	0.080174138	0.096754775	0.016580637	0.882655425	0.888580583	0.995680645
sp|Q5JSH3|WDR44_HUMAN	9	40	76	33	-0.13793	-0.114977248	0.136803502	0.022957553	0.274738303	0.25178075	0.971000454	0.059366811	0.049181338
sp|P20774|MIME_HUMAN	1	40	76	33	0.26511	0.172931036	0.331909455	-0.092178518	0.066799902	0.158978419	0.207782472	0.562503555	0.018267705
sp|O14980|XPO1_HUMAN	4	32	63	27	-0.00735	0.140192734	0.574536294	0.14754508	0.581888639	0.434343559	0.322664046	1.89E-05	0.000315168
sp|P12883|MYH7_HUMAN	2	40	76	33	-0.10036	-0.305550988	0.097775136	-0.205191722	0.198134402	0.403326124	0.125136361	0.259939741	0.001193061
sp|Q9BQB4|SOST_HUMAN	1	18	34	14	0.019923	-0.170949623	0.389974329	-0.190873115	0.370050837	0.560923951	0.328531866	0.066302209	0.00074088
sp|O95084|PRS23_HUMAN	4	37	69	30	0.063264	0.065847744	0.044914839	0.002583413	-0.018349491	-0.020932904	0.998609215	0.952874761	0.923802413
sp|Q02108|GCYA1_HUMAN	5	34	62	26	-0.14175	0.077058133	0.257472199	0.218810516	0.399224582	0.180414066	0.078378686	0.004102018	0.231578329
sp|Q13332|PTPRS_HUMAN	13	40	76	33	0.161577	0.128591396	-0.071360158	-0.032985478	-0.232937032	-0.199951554	0.680653536	7.17E-06	1.41E-05
sp|P23284|PPIB_HUMAN	1	40	76	33	-0.21479	-0.04540357	0.151120439	0.169389103	0.365913112	0.196524009	0.124557841	0.001624481	0.086094585
sp|Q96HC4|PDLI5_HUMAN	16	22	41	17	-0.41719	-0.518964243	0.335764645	-0.101776176	0.752952712	0.854728888	0.832574241	0.002248174	8.65E-05
sp|P48643|TCPE_HUMAN	9	36	69	30	0.143227	0.229696727	0.327382668	0.086470023	0.184155964	0.097685941	0.748034679	0.404765251	0.720849914
sp|P31937|3HIDH_HUMAN	10	29	55	24	-0.28717	0.006289767	0.269111612	0.293460492	0.556282337	0.262821845	0.054863088	0.001044659	0.126042263
sp|Q15126|PMVK_HUMAN	46	21	41	18	-0.2736	-0.176520699	0.209726008	0.097080694	0.483327401	0.386246707	0.913469416	0.216883726	0.282179343
sp|Q6ZRP7|QSOX2_HUMAN	5	40	76	33	0.008693	0.013838157	0.02487588	0.005145274	0.016182997	0.011037723	0.997055788	0.980079347	0.988158388
sp|P0DP23|CALM1_HUMAN	126	40	76	33	-0.23353	-0.212735078	0.176535234	0.020792331	0.410062642	0.389270312	0.988812733	0.053484239	0.035301887
sp|P30041|PRDX6_HUMAN	4	40	76	33	-0.39156	-0.06183631	0.332256157	0.32972173	0.723814197	0.394092467	0.006045019	1.93E-07	0.001779029
sp|O75356|ENTP5_HUMAN	6	40	76	33	0.069634	0.076130332	0.09886606	0.00649655	0.029232277	0.022735727	0.993390361	0.911596731	0.931218575
sp|Q13177|PAK2_HUMAN	7	36	69	30	-0.1328	-0.137638969	0.136008899	-0.004840294	0.268807574	0.273647868	0.997971443	0.01595919	0.004489604
sp|O43852|CALU_HUMAN	272	40	76	33	-0.26332	0.050085396	0.088980914	0.313401223	0.352296742	0.038895518	0.004350935	0.008465441	0.925260428
sp|P09382|LEG1_HUMAN	1	40	76	33	0.033168	0.115787414	0.43411586	0.08261947	0.400947916	0.318328446	0.277581617	1.75E-08	4.06E-07
sp|O60883|G37L1_HUMAN	5	30	55	25	-0.09879	-0.239844654	-0.10394466	-0.141053629	-0.005153635	0.135899994	0.662068311	0.999611244	0.712292509
sp|Q8WZ75|ROBO4_HUMAN	2	40	76	33	0.114322	0.089982902	0.149743429	-0.024339386	0.035421141	0.059760527	0.875594934	0.823649691	0.497111319
sp|Q8NBF2|NHLC2_HUMAN	16	40	76	33	-0.26775	-0.363102033	-0.074786617	-0.095352167	0.192963249	0.288315417	0.698910088	0.365926123	0.060626571
sp|Q12765|SCRN1_HUMAN	1	19	34	15	-0.15275	-0.026176545	0.281412276	0.126576788	0.434165609	0.307588822	0.71659433	0.075539458	0.194193403
sp|Q9NZN3|EHD3_HUMAN	4	40	76	33	-0.14924	-0.243983974	-0.081911274	-0.094747143	0.067325557	0.1620727	0.731762665	0.896696262	0.450149216
sp|P68104|EF1A1_HUMAN	9	36	69	30	-0.41077	-0.29815505	0.215685382	0.112610318	0.62645075	0.513840432	0.632280755	0.000127922	0.000410919
sp|Q15303|ERBB4_HUMAN	42	36	69	30	0.226608	0.123980221	0.010520811	-0.102627782	-0.216087192	-0.11345941	0.132531951	0.002628109	0.113122899
sp|Q9UDY2|ZO2_HUMAN	1	29	55	23	0.095324	-0.079647291	0.219293224	-0.174971302	0.123969214	0.298940516	0.611489525	0.845758395	0.296860559
sp|Q16658|FSCN1_HUMAN	5	40	76	33	-0.09182	0.07040312	0.165614285	0.162223269	0.257434434	0.095211166	0.006122632	0.0001905	0.202548617
sp|P22455|FGFR4_HUMAN	4	40	76	33	0.173338	0.040807685	-0.09964607	-0.132530399	-0.272984154	-0.140453755	0.040658873	0.000139926	0.042450835
sp|Q9UJW2|TINAG_HUMAN	7	36	69	30	0.18841	0.070593426	-0.1392192	-0.117816318	-0.327628944	-0.209812626	0.208670002	0.000393238	0.014057348
sp|O15240|VGF_HUMAN	10	40	76	33	0.217822	0.122076911	0.015577737	-0.095745421	-0.202244595	-0.106499174	0.391909993	0.059152162	0.361792417
sp|P42574|CASP3_HUMAN	1	40	76	33	-0.35487	-0.182987134	0.083972226	0.171882621	0.43884198	0.266959359	0.505208384	0.049894784	0.238194925
sp|P22607|FGFR3_HUMAN	4	33	62	27	-0.03317	-0.037052019	0.04215367	-0.003881118	0.07532457	0.079205688	0.996036154	0.361016927	0.241723874
sp|P37802|TAGL2_HUMAN	3	40	76	33	0.037021	-0.025179568	0.322011276	-0.062200517	0.284990327	0.347190844	0.918952371	0.298283348	0.104380318
sp|Q92747|ARC1A_HUMAN	19	17	35	16	-0.12193	-0.051695981	0.386109847	0.070236991	0.508042819	0.437805828	0.843050419	0.003061762	0.003238313
sp|Q96LZ3|CANB2_HUMAN	3	21	42	19	-0.00982	-0.080187578	0.236609364	-0.070369774	0.246427168	0.316796942	0.731043657	0.071679854	0.004245598
sp|P31949|S10AB_HUMAN	23	40	76	33	-0.78064	-0.489194716	0.215785408	0.291443399	0.996423523	0.704980124	0.073858895	1.22E-08	4.94E-06
sp|Q9NPR2|SEM4B_HUMAN	14	40	76	33	0.045841	0.11928455	0.244309402	0.073443728	0.198468581	0.125024853	0.198258645	0.000462834	0.018000831
sp|Q8IWY4|SCUB1_HUMAN	11	29	55	24	-0.18078	-0.13079434	0.262291678	0.049989563	0.443075581	0.393086018	0.90611271	0.006570009	0.006524861
sp|Q96MU8|KREM1_HUMAN	16	40	76	33	0.120595	0.176289928	0.136421354	0.055694798	0.015826224	-0.039868574	0.35940011	0.944025961	0.629306956
sp|Q92854|SEM4D_HUMAN	11	40	76	33	-0.13695	0.063450579	0.07437847	0.200396284	0.211324175	0.010927891	5.03E-05	0.000432339	0.971918578
sp|Q9Y570|PPME1_HUMAN	4	4	7	3	0.119982	0.105053345	0.352378333	-0.014928999	0.232395989	0.247324988	0.995338278	0.49044995	0.381141435
sp|Q9H6X2|ANTR1_HUMAN	18	40	76	33	0.023907	-0.058072385	0.07689033	-0.081979524	0.052983191	0.134962715	0.328211293	0.723400988	0.073523117
sp|O75832|PSD10_HUMAN	8	30	55	23	0.238293	0.313810074	0.474011444	0.075516775	0.235718145	0.160201371	0.787647793	0.215836633	0.410758054
sp|P52907|CAZA1_HUMAN	2	40	76	33	-0.22003	-0.187112547	0.188290086	0.032922404	0.408325037	0.375402633	0.95191474	0.006928237	0.00484834
sp|O75368|SH3L1_HUMAN	2	40	76	33	-0.19714	-0.16777484	0.271903852	0.029366649	0.469045341	0.439678692	0.964136169	0.002365617	0.001209492
sp|Q13200|PSMD2_HUMAN	5	36	69	30	-0.51712	-0.323543221	0.147779601	0.193578593	0.664901414	0.471322822	0.215560156	1.22E-05	0.000530548
sp|P36969|GPX4_HUMAN	2	40	76	33	0.35453	0.284237736	0.386504808	-0.070292192	0.03197488	0.102267071	0.696929139	0.949593434	0.512309533
sp|Q9H7Y0|DIK2B_HUMAN	32	40	76	33	0.132642	0.110853121	0.057388984	-0.021788414	-0.075252551	-0.053464137	0.905344544	0.443859856	0.592560311
sp|P14384|CBPM_HUMAN	13	40	76	33	0.023882	-0.015620769	0.097784273	-0.039502462	0.07390258	0.113405042	0.48225057	0.175077327	0.006413585
sp|P00387|NB5R3_HUMAN	16	37	69	30	-0.14001	-0.068346989	0.190478421	0.071661876	0.330487286	0.258825411	0.704786302	0.007662701	0.022070462
sp|P07858|CATB_HUMAN	9	40	76	33	-0.07811	-0.156310742	0.365521175	-0.078201192	0.443630725	0.521831916	0.564470671	1.09E-05	6.36E-09
sp|Q9NZK5|ADA2_HUMAN	13	40	76	33	0.094761	0.100107791	0.459232018	0.005346997	0.364471224	0.359124227	0.996528829	4.14E-05	4.88E-06
sp|Q9NT99|LRC4B_HUMAN	1	40	76	33	0.215465	0.121782958	-0.142216475	-0.093682183	-0.357681615	-0.263999433	0.188675773	3.65E-07	2.35E-05
sp|P19440|GGT1_HUMAN	6	40	76	33	-0.15225	-0.083059062	0.189835026	0.069185981	0.342080069	0.272894089	0.644260573	0.00096312	0.003370874
sp|P47755|CAZA2_HUMAN	110	40	76	33	-0.10398	-0.149310225	0.057949546	-0.04532842	0.161931351	0.207259771	0.900989168	0.402427757	0.152850082
sp|P16083|NQO2_HUMAN	7	40	76	33	-0.37861	-0.353824073	0.066344597	0.024783823	0.444952492	0.420168669	0.981012577	0.016785268	0.009917409
sp|Q5TFE4|NT5D1_HUMAN	6	3	7	4	-0.00443	-0.043422583	0.156704125	-0.038992182	0.161134526	0.200126708	0.97006895	0.664608777	0.409432905
sp|Q9UKX5|ITA11_HUMAN	12	25	49	21	0.331864	0.145703925	-0.081867248	-0.186160445	-0.413731619	-0.227571173	0.056291359	0.00012274	0.023050658
sp|Q92882|OSTF1_HUMAN	1	40	76	33	0.028412	0.007858416	0.307039138	-0.020553556	0.278627166	0.299180721	0.980693894	0.089770953	0.030272617
sp|P19652|A1AG2_HUMAN	11	40	76	33	-0.7884	-0.842035044	-0.329500929	-0.053637398	0.458896717	0.512534115	0.941639666	0.052518948	0.010051293
sp|P61978|HNRPK_HUMAN	12	40	76	33	-0.35291	-0.199921782	0.424145992	0.152986076	0.77705385	0.624067774	0.466557865	5.24E-06	3.87E-05
sp|O95497|VNN1_HUMAN	13	40	76	33	0.152957	-0.112997126	-0.114251305	-0.265954117	-0.267208296	-0.001254179	0.066554263	0.14910339	0.999945568

sp|O14656|TOR1A_HUMAN	8	4	7	3	0.088368	0.142624131	0.395967007	0.054255802	0.307598678	0.253342876	0.974736981	0.589879113	0.642591134
sp|P40925|MDHC_HUMAN	4	40	76	33	0.11526	0.17570081	0.338027203	0.06044124	0.222767633	0.162326393	0.594856111	0.009413207	0.040800607
sp|O75347|TBCA_HUMAN	13	40	76	33	-0.24048	-0.141014845	0.424380991	0.099469947	0.664865783	0.565395836	0.681165127	2.25E-05	4.94E-05
sp|P48681|NEST_HUMAN	11	7	13	5	-0.72611	-0.840250483	1.158487457	-0.114144301	1.88459364	1.998737941	0.97170759	0.016711404	0.004769422
sp|Q15555|MARE2_HUMAN	12	40	76	33	-0.16318	-0.354016367	-0.098259468	-0.190839482	0.064917417	0.255756899	0.436238055	0.935407141	0.272083649
sp|P12277|KCRB_HUMAN	1	32	62	28	-0.05305	-0.242735247	-0.334289547	-0.189683068	-0.281237369	-0.0915543	0.354092189	0.20113142	0.799916485
sp|Q9NY97|B3GN2_HUMAN	7	40	76	33	0.173281	0.13387899	0.065271779	-0.039402187	-0.108009398	-0.068607211	0.188843266	0.000300668	0.013319661
sp|Q9UHL4|DPP2_HUMAN	6	32	62	27	-0.04003	-0.039168729	0.149459467	0.00086266	0.189490856	0.188628196	0.999961327	0.279536632	0.19877525
sp|Q9UIV8|SPB13_HUMAN	44	7	14	5	-0.00527	0.050683496	-0.051052447	0.055955554	-0.045780389	-0.101735942	0.934574963	0.972037498	0.838887673
sp|Q9BRK5|CAB45_HUMAN	13	40	76	33	-0.23021	-0.165188008	0.220271897	0.065020128	0.450480033	0.385459905	0.602793186	4.31E-07	1.06E-06
sp|Q8WWU7|ITLN2_HUMAN	7	40	76	33	0.085793	-0.079515904	0.019470517	-0.165308907	-0.066322485	0.098986422	0.254234778	0.857210921	0.647000962
sp|P50395|GDIB_HUMAN	9	40	76	33	0.083629	0.152282603	0.446143736	0.068654004	0.362515137	0.293861133	0.679959961	0.000962888	0.002828701
sp|Q8IW75|SPA12_HUMAN	108	18	35	14	-0.02007	0.225622328	-0.245482418	0.245689838	-0.225414909	-0.471104746	0.612297042	0.759790877	0.225776804
sp|Q10471|GALT2_HUMAN	6	40	76	33	-0.07204	-0.022247773	0.167477768	0.049794166	0.239519707	0.189725541	0.518546625	6.77E-05	0.000411851
sp|Q14C87|T132D_HUMAN	4	8	14	6	0.127904	0.273569283	-0.76850829	0.145665311	-0.896412263	-1.042077573	0.938542653	0.219359093	0.08949218
sp|Q6UVK1|CSPG4_HUMAN	3	40	76	33	0.125091	0.029400593	0.291367378	-0.095690097	0.166276688	0.261966785	0.121311224	0.013595737	3.48E-06
sp|Q16531|DDB1_HUMAN	1	40	76	33	-0.25379	-0.183749524	0.260174805	0.070038984	0.513963312	0.443924328	0.787685922	0.000277363	0.000408441
sp|Q7Z7M8|B3GN8_HUMAN	40	40	76	33	0.154531	0.085712374	-0.022811796	-0.068818472	-0.177342642	-0.10852417	0.22120066	0.001400299	0.039325346
sp|Q9Y5C1|ANGL3_HUMAN	10	40	76	33	0.018562	0.044960455	0.247354158	0.026398358	0.228792062	0.202393703	0.880162557	0.001992272	0.002042262
sp|P45378|TNNT3_HUMAN	2	11	20	9	-0.80302	-1.035245392	0.565286662	-0.232228386	1.368303668	1.600532054	0.862989337	0.039058204	0.005336952
sp|Q9NZU0|FLRT3_HUMAN	2	21	42	19	0.090399	0.189111253	0.418346926	0.098712487	0.327948159	0.229235673	0.679075053	0.053901193	0.14919511
sp|P14735|IDE_HUMAN	2	32	62	27	-0.1234	0.017363795	0.08959927	0.14076653	0.213002005	0.072235475	0.139278898	0.045495935	0.624311738
sp|Q96BJ3|AIDA_HUMAN	2	4	7	3	0.204489	0.170740902	0.349132953	-0.033748347	0.144643705	0.178392051	0.929122758	0.429807339	0.227876981
sp|P08397|HEM3_HUMAN	2	40	76	33	-0.30301	-0.005561344	0.35639975	0.29744763	0.659408725	0.361961094	0.006734263	2.01E-07	0.00164051
sp|Q9UNM6|PSD13_HUMAN	2	4	7	3	0.307914	0.500701072	0.350281905	0.192786638	0.042367471	-0.150419168	0.771360515	0.991388416	0.876355737
sp|P08887|IL6RA_HUMAN	32	40	76	33	0.036764	0.061304133	-0.008197424	0.024540393	-0.044961165	-0.069501557	0.912105151	0.808317014	0.525144738
sp|P53618|COPB_HUMAN	2	7	14	6	-0.12209	0.111871257	0.635599416	0.233958438	0.757686597	0.523728159	0.591209947	0.035062275	0.111328366
sp|Q5ZPR3|CD276_HUMAN	15	40	76	33	-0.06203	-0.026642474	0.298198138	0.035383252	0.360223864	0.324840612	0.785846448	3.11E-07	1.97E-07
sp|Q99715|COCA1_HUMAN	10	40	76	33	0.067394	0.03306853	0.040324122	-0.03432526	-0.027069669	0.007255592	0.685311462	0.84999192	0.985228689
sp|Q6ICL3|TNG2_HUMAN	22	40	76	33	0.622236	0.72615182	1.008805319	0.103916081	0.38656958	0.282653499	0.59646605	0.008868061	0.038307752
sp|Q08257|QOR_HUMAN	2	40	76	33	-0.09703	-0.01343668	0.077948683	0.083590971	0.174976334	0.091385363	0.494173678	0.122450482	0.477408832
sp|Q9NQ76|MEPE_HUMAN	2	40	76	33	-0.13459	0.024660451	0.162047111	0.159255052	0.296641711	0.137386659	0.079183168	0.00281671	0.18788044
sp|P39687|AN32A_HUMAN	4	29	55	25	-0.33859	-0.210593079	0.391054201	0.128000182	0.729647462	0.60164728	0.610289847	4.22E-05	0.000137682
sp|Q13813|SPTN1_HUMAN	1	29	55	25	-0.56171	-0.315832639	0.231244287	0.245880683	0.792957608	0.547076926	0.225537267	5.15E-05	0.001870797
sp|Q14393|GAS6_HUMAN	15	40	76	33	0.011766	0.14643383	0.27028648	0.13466758	0.25852023	0.12385265	0.030140113	0.000206546	0.072515451
sp|P68133|ACTS_HUMAN	2	40	76	33	0.004768	0.035225495	0.044454468	0.03045757	0.039686544	0.009228973	0.8999168	0.883811758	0.991526448
sp|Q562R1|ACTBL_HUMAN	22	40	76	33	-0.24186	-0.402994982	0.019959262	-0.16113061	0.261823635	0.422954245	0.530422243	0.316989414	0.024343473
sp|P02144|MYG_HUMAN	6	40	76	33	-0.86123	-0.977784507	-0.397969153	-0.116559278	0.463256076	0.579815354	0.708047016	0.026346093	0.000900014
sp|Q10588|BST1_HUMAN	1	40	76	33	0.103542	0.082387226	-0.137681086	-0.021155179	-0.241223491	-0.220068312	0.922770178	0.001182402	0.000814392
sp|Q08174|PCDH1_HUMAN	3	40	76	33	-0.06347	-0.042754483	0.324703189	0.020714445	0.388172117	0.367457672	0.922387645	5.39E-08	7.11E-09
sp|P78356|PI42B_HUMAN	2	40	76	33	-0.15835	-0.033506055	0.271845528	0.124841304	0.430192886	0.305351583	0.500036728	0.004463341	0.029164169
sp|Q6NW40|RGMB_HUMAN	7	40	76	33	-0.03175	-0.095770974	0.067552462	-0.064025874	0.099297562	0.163323435	0.615429985	0.448022994	0.066562764
sp|Q15274|NADC_HUMAN	6	7	14	6	-0.30538	0.282633174	0.259917317	0.588014327	0.56529847	-0.022715856	0.052676461	0.139456721	0.995484284
sp|Q13637|RAB32_HUMAN	6	4	7	3	-0.58172	-0.279721263	0.225052878	0.301998788	0.806772929	0.504774141	0.613205536	0.132243802	0.344404575
sp|Q15121|PEA15_HUMAN	3	18	34	15	0.192503	0.20238187	0.473443642	0.009878851	0.280940624	0.271061772	0.996274983	0.132939297	0.093168223
sp|P22314|UBA1_HUMAN	1	40	76	33	-0.13881	-0.106269457	0.172415453	0.032543583	0.311228493	0.27868491	0.927873034	0.010970862	0.010051635
sp|P13611|CSPG2_HUMAN	2	40	76	33	-0.11294	-0.013628699	0.333961399	0.099308431	0.44689853	0.347590098	0.280837545	1.81E-07	4.60E-06
sp|P29508|SPB3_HUMAN	2	18	34	15	-0.85642	-0.977297911	-1.393020142	-0.120873306	-0.536595537	-0.415722231	0.951733182	0.511904389	0.59878759
sp|P30153|2AAA_HUMAN	15	40	76	33	-0.28246	-0.127310512	0.350180929	0.155150838	0.632642278	0.477491441	0.436066401	0.000150755	0.001477566
sp|Q15166|PON3_HUMAN	3	40	76	33	0.221849	0.158545197	-0.289475651	-0.06330357	-0.511324417	-0.448020848	0.533623547	9.56E-11	1.50E-10
sp|Q7Z5N4|SDK1_HUMAN	10	40	76	33	0.052193	-0.017375044	0.04414293	-0.069568379	-0.008050406	0.061517973	0.16804111	0.98335031	0.29183371
sp|Q7Z7G0|TARSH_HUMAN	111	40	76	33	0.082764	0.070378893	0.082058077	-0.012385181	-0.000705998	0.011679183	0.97040185	0.999932619	0.976814062
sp|P98153|IDD_HUMAN	5	21	41	19	-0.20981	-0.069243772	0.495943637	0.140562501	0.70574991	0.565187409	0.598138207	0.000267679	0.000913235
sp|O95998|I18BP_HUMAN	26	40	76	33	-0.2223	-0.116711495	0.369545819	0.105592046	0.591849359	0.486257314	0.403846793	4.46E-08	3.72E-07
sp|O43529|CHSTA_HUMAN	5	40	76	33	0.114736	0.061161674	-0.076865765	-0.053573916	-0.191601355	-0.138027439	0.318327623	8.94E-05	0.001779141
sp|P49591|SYSC_HUMAN	8	40	76	33	0.461254	0.480357555	0.678091038	0.019103223	0.216836706	0.197733483	0.990656901	0.437257016	0.416907306
sp|Q9NRN5|OLFL3_HUMAN	18	40	76	33	0.041896	0.085085987	0.093491771	0.043189825	0.051595609	0.008405784	0.317942128	0.32350369	0.962174304
sp|Q9UJU6|DBNL_HUMAN	1	40	76	33	-0.13376	-0.10261703	0.170079545	0.031138667	0.303835241	0.272696574	0.958802642	0.06801756	0.063710795
sp|P32321|DCTD_HUMAN	5	10	21	9	0.021348	-0.017716041	0.279993703	-0.039064158	0.258645585	0.297709743	0.968557105	0.386051367	0.193645136
sp|O95260|ATE1_HUMAN	19	11	21	9	-0.0489	-0.188716721	0.003136427	-0.139819503	0.052033644	0.191853147	0.799259023	0.978816916	0.693089016
sp|Q03167|TGBR3_HUMAN	6	40	76	33	0.13397	0.085115738	0.164584042	-0.048854269	0.030614035	0.079468304	0.293424451	0.715081336	0.06067422
sp|Q96H15|TIMD4_HUMAN	3	40	76	33	0.00012	0.050823102	0.255888066	0.05070299	0.255767954	0.205064964	0.808162504	0.027055409	0.051203217
sp|O00602|FCN1_HUMAN	8	40	76	33	-0.07251	-0.052782035	0.148802349	0.019731037	0.221315421	0.201584384	0.977430287	0.143429064	0.129015031
sp|Q14162|SREC_HUMAN	2	36	69	30	0.022962	0.115053948	-0.093354541	0.092092063	-0.116316425	-0.208408488	0.444360302	0.408936999	0.02839927
sp|P52306|GDS1_HUMAN	19	28	55	25	0.183925	0.109164614	0.420095027	-0.074760304	0.236170108	0.310930412	0.821378969	0.252567265	0.047955638
sp|P60660|MYL6_HUMAN	11	40	76	33	-0.49011	-0.154119011	0.309039331	0.335991627	0.79914997	0.463158342	0.003506296	3.36E-09	0.000108719
sp|P20700|LMNB1_HUMAN	1	40	76	33	-0.24998	0.014514748	0.320668412	0.264497117	0.570650782	0.306153665	0.008493666	7.83E-07	0.00382776
sp|Q9Y608|LRRF2_HUMAN	9	11	21	9	0.341048	-0.097706222	0.139212294	-0.43875428	-0.201835764	0.236918516	0.137666258	0.738801338	0.590214368
sp|Q14240|IF4A2_HUMAN	3	40	76	33	-0.19599	-0.256649647	0.118739488	-0.060662889	0.314726246	0.375389135	0.864485007	0.071735611	0.009346751
sp|P19022|CADH2_HUMAN	30	40	76	33	0.135251	0.138440502	0.455316661	0.003189092	0.320065251	0.316876159	0.998064863	6.25E-06	4.53E-07
sp|Q8TDY8|IGDC4_HUMAN	2	40	76	33	0.10024	0.070848833	-0.22335083	-0.029391172	-0.323590835	-0.294199663	0.855410109	8.49E-06	4.92E-06
sp|O60361|NDK8_HUMAN	4	40	76	33	-0.29049	-0.121598829	0.202617747	0.168894987	0.493111563	0.324216577	0.255789662	0.000530797	0.013823594
sp|O95633|FSTL3_HUMAN	13	40	76	33	-0.19532	-0.214993708	0.246275081	-0.019677155	0.441591635	0.461268789	0.974477455	0.000255357	1.39E-05
sp|Q92876|KLK6_HUMAN	4	40	76	33	0.012115	-0.069559526	-0.136258849	-0.081674626	-0.148373949	-0.066699323	0.329570451	0.082796604	0.520443191
sp|P35916|VGFR3_HUMAN	71	40	76	33	0.086589	0.148081343	0.102202239	0.061492807	0.015613702	-0.045879105	0.375571351	0.956955019	0.618072313
sp|O76074|PDE5A_HUMAN	3	40	76	33	-0.20392	-0.013519189	0.201538094	0.190403068	0.405460352	0.215057284	0.162287645	0.00415635	0.13104673
sp|P16234|PGFRA_HUMAN	73	22	42	18	-0.03378	-0.051101527	0.275482748	-0.017324231	0.309260045	0.326584276	0.976838729	0.00869848	0.001434182
sp|P51452|DUS3_HUMAN	2	40	76	33	-0.29543	-0.166255518	0.017336205	0.129172	0.312763724	0.183591723	0.515870378	0.07257142	0.311087443
sp|Q9HCL0|PCD18_HUMAN	2	40	76	33	0.124124	0.126901179	0.129932797	0.002777013	0.005808631	0.003031619	0.996690789	0.990044359	0.996537665
sp|Q96AP7|ESAM_HUMAN	4	40	76	33	-0.08311	-0.025615623	0.190387064	0.057493062	0.273495749	0.216002687	0.486010702	3.49E-05	0.000250125
sp|O60844|ZG16_HUMAN	16	40	76	33	0.022533	0.008262264	0.030817065	-0.014271211	0.008283589	0.0225548	0.965450494	0.991857514	0.925822472
sp|P10644|KAP0_HUMAN	16	40	76	33	-0.49778	-0.349885652	-0.201443696	0.14789567	0.296337626	0.148441956	0.347422522	0.056479544	0.39208412
sp|P56199|ITA1_HUMAN	4	40	76	33	0.157498	0.01144993	-0.068757974	-0.146048542	-0.226256446	-0.080207904	1.96E-05	4.08E-08	0.045453356
sp|P13489|RINI_HUMAN	1	40	76	33	-0.14872	0.060031465	0.26606571	0.208752208	0.414786453	0.206034245	0.000801753	2.09E-08	0.0021248
sp|O43491|E41L2_HUMAN	1	11	20	8	0.026131	0.171719273	0.472508771	0.145588477	0.446377976	0.300789498	0.670508189	0.099420997	0.263500977
sp|P01834|IGKC_HUMAN	13	40	76	33	-0.1687	-0.054892413	0.146166285	0.113805563	0.314864261	0.201058698	0.320885985	0.00324515	0.047188438
sp|P13688|CEAM1_HUMAN	7	40	76	33	0.036614	0.052511496	0.021972487	0.015897929	-0.01464108	-0.030539009	0.90020086	0.94030159	0.711936106
sp|Q9BQS7|HEPH_HUMAN	4	40	76	33	0.031479	0.020668392	0.008717484	-0.010810367	-0.022761275	-0.011950908	0.972518947	0.918344541	0.970542847
sp|Q8N126|CADM3_HUMAN	10	32	62	28	0.307966	0.125594217	0.406525397	-0.182371574	0.098559606	0.28093118	0.04708479	0.52209359	0.001696211
sp|Q9UBV8|PEF1_HUMAN	19	36	69	30	0.127863	0.117696908	0.31024529	-0.010165911	0.182382472	0.192548383	0.989410934	0.099311026	0.038571271
sp|A6NIZ1|RP1BL_HUMAN	30	40	76	33	-0.36145	-0.212704666	0.059888049	0.148750013	0.421342728	0.272592715	0.395307904	0.007211533	0.06809792
sp|O15145|ARPC3_HUMAN	7	40	76	33	-0.12035	-0.190632882	0.258049586	-0.070278863	0.378403605	0.448682468	0.858608795	0.051764843	0.005622086
sp|P27482|CALL3_HUMAN	10	32	62	26	-0.11652	-0.009802256	0.045300155	0.106720659	0.16182307	0.055102411	0.910014548	0.863074791	0.978399783
sp|Q14126|DSG2_HUMAN	2	40	76	33	0.204375	0.103729348	0.039773277	-0.100645303	-0.164601374	-0.063956071	0.08498793	0.011575942	0.411262552
sp|Q13421|MSLN_HUMAN	5	40	76	33	-0.12244	-0.23253913	0.42693469	-0.110099922	0.549373898	0.65947382	0.375167854	3.80E-07	1.51E-11
sp|Q7KZF4|SND1_HUMAN	1	40	76	33	-0.18924	-0.375333111	0.045947273	-0.186094166	0.235186218	0.421280384	0.297628707	0.263461032	0.005328666
sp|Q8IUX7|AEBP1_HUMAN	1	40	76	33	0.04153	0.024696108	0.134091923	-0.016834093	0.092561721	0.109395814	0.952161216	0.363433524	0.167879001
sp|Q9BT09|CNPY3_HUMAN	17	21	42	19	-0.28852	-0.145399939	0.266024258	0.143117974	0.554542171	0.411424197	0.528742264	0.00196216	0.009897621
sp|P22413|ENPP1_HUMAN	30	40	76	33	0.057423	0.078061397	0.128737701	0.020638785	0.071315088	0.050676303	0.798333422	0.161311657	0.307221911
sp|P51665|PSMD7_HUMAN	1	23	42	17	-0.43375	-0.038193587	0.278569106	0.395554768	0.712317461	0.316762693	0.02125533	0.000438647	0.126261239
sp|O60664|PLIN3_HUMAN	39	40	76	33	0.064237	0.032217188	0.509741218	-0.032019619	0.44550441	0.477524029	0.913049853	1.80E-05	2.12E-07
sp|Q9Y376|CAB39_HUMAN	11	40	76	32	-0.10346	-0.132407602	0.244913317	-0.028951842	0.348369078	0.37732092	0.970240492	0.056155937	0.014681723
sp|O95678|K2C75_HUMAN	5	40	76	33	-0.56484	-0.739072292	-0.728318561	-0.174229307	-0.163475576	0.010753731	0.697921937	0.803489359	0.998793178
sp|O43790|KRT86_HUMAN	16	8	13	6	-0.31126	0.413582215	-0.394629535	0.724844667	-0.083367083	-0.80821175	0.403353867	0.99137249	0.392752833
sp|Q9UKM7|MA1B1_HUMAN	7	34	62	27	-0.00242	0.052613401	-0.02542575	0.055036684	-0.023002468	-0.078039152	0.624424272	0.944912188	0.4458689

sp|Q96KP4|CNDP2_HUMAN	8	40	76	33	-0.22969	-0.138809183	0.218756825	0.090878401	0.448444409	0.357566008	0.659310351	0.001393374	0.004599584
sp|P08069|IGF1R_HUMAN	1	7	14	6	0.285919	0.061705322	-0.104236424	-0.224213936	-0.390155682	-0.165941746	0.425550539	0.178873269	0.650849089
sp|P12109|CO6A1_HUMAN	6	40	76	33	0.061964	0.114923749	0.268038152	0.052959621	0.206074024	0.153114403	0.533778577	0.00203208	0.011908725
sp|Q15181|IPYR_HUMAN	2	8	13	6	-0.14418	-0.160851385	0.152778967	-0.016674415	0.296955937	0.313630352	0.993751702	0.273314467	0.182570367
sp|P06280|AGAL_HUMAN	3	40	76	33	-0.03053	0.004813408	0.260779127	0.035341819	0.291307539	0.255965719	0.751590395	6.43E-06	7.78E-06
sp|P51114|FXR1_HUMAN	55	4	6	3	-0.03556	-0.055119396	0.111939283	-0.019557437	0.147501242	0.167058679	0.999835579	0.993345938	0.990061708
sp|P01871|IGHM_HUMAN	19	40	76	33	-0.20809	0.030150366	0.01682015	0.238239804	0.224909587	-0.013330216	0.05685049	0.168127293	0.991911667
sp|P04745|AMY1_HUMAN	1	40	76	33	0.138923	-1.88E-05	-0.228560639	-0.138942207	-0.367484058	-0.228541852	0.228280158	0.001156028	0.032101831
sp|Q13275|SEM3F_HUMAN	21	40	76	33	0.103232	0.087115814	-0.07226834	-0.016116233	-0.175500387	-0.159384155	0.855359701	1.06E-05	6.37E-06
sp|P55157|MTP_HUMAN	45	36	69	30	-0.014	-0.113998281	-0.04727904	-0.099999373	-0.033280132	0.066719241	0.375901952	0.927064475	0.678722097
sp|Q15185|TEBP_HUMAN	3	40	76	33	-0.17215	-0.137377268	0.23496243	0.034774246	0.407113944	0.372339698	0.944293123	0.005830252	0.004257446
sp|Q6P988|NOTUM_HUMAN	1	36	69	30	0.038547	0.113288839	0.128192851	0.07474221	0.089646223	0.014904013	0.585602184	0.587142639	0.981260731
sp|P62136|PP1A_HUMAN	29	40	76	33	-0.24966	-0.125144348	0.238888386	0.124513442	0.488546176	0.364032734	0.296959056	8.62E-06	0.000207437
sp|Q16543|CDC37_HUMAN	2	37	69	29	-0.48387	-0.485325199	0.045551271	-0.001458647	0.529417823	0.53087647	0.999931951	0.00339362	0.000843598
sp|Q14554|PDIA5_HUMAN	2	40	76	33	0.074756	0.069945296	0.160942702	-0.004810238	0.086187169	0.090997407	0.999044386	0.809531403	0.741231859
sp|Q14956|GPNMB_HUMAN	4	40	76	33	0.096983	0.063303223	0.140967704	-0.033679633	0.043984847	0.077664481	0.714332904	0.673251353	0.212130708
sp|Q6ZMJ2|SCAR5_HUMAN	1	40	76	33	0.078434	0.073818597	0.338054146	-0.004615333	0.259620217	0.26423555	0.996745607	0.001290519	0.000182454
sp|P21757|MSRE_HUMAN	6	36	70	30	-0.21243	-0.092222846	0.468274661	0.12020725	0.680704756	0.560497507	0.513368814	2.33E-06	1.07E-05
sp|P50238|CRIP1_HUMAN	4	37	69	30	-0.33527	-0.117259064	0.36369664	0.218015742	0.698971446	0.480955704	0.035731606	1.99E-09	2.77E-06
sp|P08217|CEL2A_HUMAN	22	32	62	27	-0.00298	-0.006345959	0.156465579	-0.003363438	0.1594481	0.162811538	0.999537813	0.489421744	0.38516639
sp|P61769|B2MG_HUMAN	3	40	76	33	-0.1413	-0.094636684	0.484946965	0.046662305	0.626245955	0.57958365	0.872500639	3.93E-07	1.23E-07
sp|Q9NZ53|PDXL2_HUMAN	1	8	14	5	-0.02612	0.115828788	0.010711159	0.141946443	0.036828814	-0.105117629	0.369747082	0.958593602	0.666521044
sp|Q00872|MYPC1_HUMAN	3	11	19	9	-0.71091	-0.856932509	0.238694321	-0.146026795	0.949600035	1.09562683	0.937685842	0.160731444	0.054907314
sp|P07195|LDHB_HUMAN	1	40	76	33	0.077285	0.047021021	0.280201036	-0.030264407	0.202915608	0.233180015	0.868744478	0.015215863	0.001056903
sp|Q15691|MARE1_HUMAN	7	40	76	33	-0.12902	-0.277771848	0.068094137	-0.148748549	0.197117436	0.345865985	0.446811404	0.377421342	0.024453249
sp|P12110|CO6A2_HUMAN	10	40	76	33	-0.03479	-0.021198849	0.293710243	0.01359111	0.328500202	0.314909092	0.970115084	1.69E-05	3.18E-06
sp|P61158|ARP3_HUMAN	10	40	76	33	-0.16197	-0.218599064	0.137933558	-0.056624822	0.299907799	0.356532622	0.889483199	0.108912997	0.019864827
sp|P05089|ARGI1_HUMAN	3	29	56	25	-0.38958	-0.087021405	0.163262082	0.302555511	0.552838999	0.250283488	0.116642936	0.007665498	0.260790608
sp|Q96PD2|DCBD2_HUMAN	6	40	76	33	-0.02166	-0.014235685	0.188815224	0.00742869	0.210479599	0.203050909	0.979324589	2.91E-05	5.14E-06
sp|P10321|HLAC_HUMAN	1	40	76	33	-0.14716	-0.017533823	0.085248092	0.129623883	0.232405798	0.102781915	0.351951029	0.101639094	0.560294668
sp|P17693|HLAG_HUMAN	9	36	69	30	-0.1734	0.114994978	0.157807793	0.288391417	0.331204232	0.042812815	0.014047847	0.020114867	0.916662639
sp|Q9NS98|SEM3G_HUMAN	5	40	76	33	0.040029	0.002287706	-0.05527108	-0.037740875	-0.095299661	-0.057558786	0.553435584	0.078083144	0.301075819
sp|P15121|ALDR_HUMAN	4	40	76	33	-0.02286	-0.01534818	0.385379253	0.00750781	0.408235244	0.400727433	0.996151146	0.000670056	0.000145749
sp|Q99538|LGMN_HUMAN	2	36	69	30	-0.1791	-0.093305135	0.030269891	0.085795672	0.209370698	0.123575026	0.425543546	0.032687315	0.211334534
sp|Q16774|KGUA_HUMAN	21	4	7	3	0.198408	0.248641264	0.038798939	0.050233671	-0.159608654	-0.209842324	0.932173192	0.631275314	0.394273881
sp|O95881|TXD12_HUMAN	2	18	35	14	-0.29215	-0.114381231	0.354825583	0.177768452	0.646975266	0.469206814	0.640085434	0.025241553	0.081063813
sp|P19883|FST_HUMAN	7	18	34	14	0.106521	0.068844881	0.425945702	-0.037675947	0.319424874	0.357100822	0.9570214	0.131080703	0.043691577
sp|Q16775|GLO2_HUMAN	89	37	69	30	-0.08396	-0.050387976	0.168723805	0.033573555	0.252685336	0.219111781	0.894527404	0.015706469	0.019248164
sp|P40967|PMEL_HUMAN	5	40	76	33	0.040215	0.032679788	-0.258077848	-0.007535021	-0.298292657	-0.290757636	0.992034051	0.000341051	7.37E-05
sp|P08138|TNR16_HUMAN	3	28	55	24	-0.20965	-0.3027074	0.51063215	-0.093056964	0.720282586	0.81333955	0.804667487	0.000277312	2.80E-06
sp|Q9NRV9|HEBP1_HUMAN	18	22	41	19	-0.45032	-0.109412515	0.427862065	0.340904357	0.878178937	0.53727458	0.112873168	9.78E-05	0.008927888
sp|P07910|HNRPC_HUMAN	4	40	75	32	-0.98933	-0.586838085	0.246231869	0.402490012	1.235559966	0.833069955	0.096541044	1.37E-06	0.000294286
sp|O43505|B4GA1_HUMAN	7	40	76	33	0.182003	0.149764317	-0.004435588	-0.032238345	-0.186438251	-0.154199905	0.46482784	2.05E-07	1.22E-06
sp|P04350|TBB4A_HUMAN	3	40	76	33	-0.28811	-0.085002444	0.24397106	0.203104718	0.532078222	0.328973503	0.201801628	0.000769344	0.027020005
sp|P19105|ML12A_HUMAN	3	40	76	33	-0.53211	-0.175274517	0.327712707	0.356830647	0.859817871	0.502987224	0.002410817	6.56E-10	4.02E-05
sp|P10916|MLRV_HUMAN	2	7	13	6	-0.96547	-1.27577837	-0.140130893	-0.310311055	0.825336422	1.135647478	0.895375274	0.580565428	0.282540895
sp|Q02045|MYL5_HUMAN	1	4	6	2	-0.38909	-0.418351805	2.417389276	-0.029264981	2.8064761	2.835741082	0.999464394	0.119376447	0.093552122
sp|Q96A32|MLRS_HUMAN	2	40	76	33	-0.34127	-0.484536014	-0.397720874	-0.143264267	-0.056449128	0.086815139	0.145625425	0.810452826	0.532748119
sp|Q8NC51|PAIRB_HUMAN	5	11	20	9	-0.04239	-0.079127113	0.723601283	-0.036737128	0.765991267	0.802728395	0.988639025	0.04306762	0.015094349
sp|P36222|CH3L1_HUMAN	8	40	76	33	-0.17093	-0.254403153	0.784653112	-0.083474729	0.955581536	1.039056265	0.84676875	1.74E-06	5.61E-09
sp|Q96C86|DCPS_HUMAN	7	33	62	27	-0.20252	0.012383461	0.320400936	0.214904958	0.522922433	0.308017475	0.075965551	6.05E-05	0.010881893
sp|P07988|PSPB_HUMAN	22	40	76	33	-0.47014	-0.319693324	1.125678494	0.150450673	1.595822491	1.445371819	0.538445244	3.92E-14	3.87E-14
sp|Q9P0L0|VAPA_HUMAN	25	32	63	28	-0.14743	-0.088737327	0.323365454	0.058689131	0.470791911	0.41210278	0.845331025	0.000887112	0.000918859
sp|O75131|CPNE3_HUMAN	2	32	63	27	-0.16274	-0.032107967	0.421159082	0.130630098	0.583897147	0.453267049	0.521248895	0.000265955	0.001467471
sp|Q8IZ83|A16A1_HUMAN	7	40	76	33	-0.51388	-0.025717117	0.378303426	0.488165804	0.892186347	0.404020542	2.12E-07	6.87E-14	6.04E-05
sp|Q15056|IF4H_HUMAN	1	14	28	12	-0.24649	-0.243835957	0.13977001	0.002657522	0.386263489	0.383605967	0.999941426	0.431732819	0.342617177
sp|Q96P70|IPO9_HUMAN	2	22	41	18	0.287471	0.284573063	0.39187543	-0.002898113	0.104404254	0.107302367	0.999527024	0.656021986	0.570462865
sp|Q8WXD2|SCG3_HUMAN	3	40	76	33	0.002514	-0.110773688	-0.132451976	-0.113287424	-0.134965713	-0.021678288	0.033083906	0.035419945	0.892779025
sp|Q9NSC7|SIA7A_HUMAN	56	40	76	33	-0.02484	-0.07628798	-0.088990172	-0.05144706	-0.064149252	-0.012702192	0.745610752	0.729909169	0.984365618
sp|Q9HBR0|S38AA_HUMAN	5	40	76	33	0.116567	0.125271117	0.277118233	0.00870449	0.160551607	0.151847117	0.985156755	0.033744017	0.02149495
sp|E9PAV3|NACAM_HUMAN	13	11	21	10	-0.1475	-0.236885983	0.449053046	-0.08938958	0.596549449	0.685939028	0.900042172	0.044401323	0.00651159
sp|Q01973|ROR1_HUMAN	12	40	76	33	0.073323	-0.059976579	0.088424742	-0.133299585	0.015101736	0.148401321	0.025995845	0.966995133	0.019075546
sp|P18850|ATF6A_HUMAN	1	40	76	33	0.094232	0.056048176	-0.05072649	-0.038183401	-0.144958067	-0.106774666	0.559376227	0.00410819	0.021160094
sp|P27105|STOM_HUMAN	2	40	76	33	-1.91668	-1.578343645	-1.116753805	0.338334633	0.799924473	0.46158984	0.05724129	3.45E-05	0.010114789
sp|Q9BYZ8|REG4_HUMAN	3	33	63	27	-0.00254	-0.054221327	0.057423138	-0.051679585	0.05996488	0.111644465	0.594639507	0.618712714	0.125187083
sp|Q13308|PTK7_HUMAN	5	40	76	33	-0.23527	-0.209301045	0.105816068	0.025965399	0.341082512	0.315117113	0.893633543	6.55E-06	2.60E-06
sp|P78371|TCPB_HUMAN	9	36	70	30	0.091233	0.073254374	0.448830219	-0.0179783	0.357597545	0.375575846	0.990700516	0.084158854	0.031236327
sp|Q01082|SPTB2_HUMAN	15	36	68	30	0.193872	0.308558679	0.521431806	0.114686758	0.327559885	0.212873127	0.811978141	0.310895498	0.53178239
sp|Q8N4A0|GALT4_HUMAN	12	18	35	16	0.071235	0.079379365	0.034101614	0.00814437	-0.037133381	-0.045277751	0.991520354	0.881731149	0.785019767
sp|Q6UXH1|CREL2_HUMAN	2	40	76	33	-0.23183	-0.141414741	0.41130974	0.090410547	0.643135028	0.552724481	0.583440742	8.92E-08	2.12E-07
sp|O15204|ADEC1_HUMAN	3	40	76	33	-0.08493	0.042535848	0.021432253	0.127465042	0.106361448	-0.021103594	0.049753172	0.231156994	0.928243433
sp|P19237|TNNI1_HUMAN	1	4	6	3	0.092164	0.081769679	1.416218122	-0.010394099	1.324054344	1.334448444	0.999909314	0.38647283	0.33027147
sp|Q9NQC3|RTN4_HUMAN	1	7	14	6	-0.82595	-0.231590628	0.559954097	0.594363446	1.385908172	0.791544725	0.253980157	0.011450194	0.120751717
sp|Q92956|TNR14_HUMAN	24	36	69	30	-0.38588	-0.265533911	0.227777978	0.120345136	0.613657025	0.493311889	0.571987473	0.000104147	0.000459445
sp|Q9Y251|HPSE_HUMAN	4	40	76	33	-0.24703	-0.171095118	0.216799873	0.075939749	0.463834741	0.387894992	0.831739113	0.01073367	0.017342961
sp|Q9C0C9|UBE2O_HUMAN	6	21	42	19	-0.48491	-0.196613484	0.18681422	0.288294954	0.671722658	0.383427704	0.11331865	0.000444085	0.029532102
sp|P82987|ATL3_HUMAN	5	37	69	30	0.043084	0.03604677	0.297524406	-0.00703693	0.254440705	0.261477636	0.995259605	0.016823103	0.004648189
sp|P78417|GSTO1_HUMAN	2	40	76	33	-0.16819	-0.055491529	0.398024503	0.112698792	0.566214824	0.453516032	0.298494486	1.49E-08	2.81E-07
sp|Q58FF6|H90B4_HUMAN	8	40	76	33	-0.09403	-0.110335329	0.271801544	-0.016308535	0.365828338	0.382136873	0.992217272	0.07145385	0.026593591
sp|P23229|ITA6_HUMAN	1	40	76	33	-0.17008	0.064780556	-0.041385241	0.234857951	0.128692154	-0.106165797	0.000250971	0.160378988	0.204139805
sp|P22626|ROA2_HUMAN	2	33	62	27	-0.29832	0.005801421	0.529062623	0.304121338	0.82738254	0.523261202	0.393655295	0.010477352	0.093564313
sp|Q9BS26|ERP44_HUMAN	7	40	76	33	0.109996	0.097092172	0.079550304	-0.012903568	-0.030445436	-0.017541868	0.960999921	0.858456255	0.937505796
sp|Q9UP52|TFR2_HUMAN	1	40	76	33	-0.12758	-0.296385855	-0.173759175	-0.168805094	-0.046178414	0.12262668	0.360545353	0.948171987	0.621641398
sp|Q9BZD6|TMG4_HUMAN	2	8	14	6	0.144332	0.188924986	0.053338706	0.044592718	-0.090993562	-0.13558628	0.889722717	0.722767945	0.422179871
sp|P13010|XRCC5_HUMAN	2	14	27	12	-0.63524	-0.462883449	0.463749779	0.172353682	1.09898691	0.926633228	0.84367761	0.012468985	0.01759554
sp|P28845|DHI1_HUMAN	4	40	76	33	0.038297	0.086287847	0.086566086	0.04799096	0.048269199	0.000278239	0.65834263	0.746635688	0.999987608
sp|P28072|PSB6_HUMAN	3	40	76	33	-0.11912	0.008246942	0.468511088	0.12737143	0.587635576	0.460264146	0.275715275	7.33E-08	1.87E-06
sp|Q9NS62|THSD1_HUMAN	19	40	76	33	0.141189	0.133797918	-0.06826934	-0.00739151	-0.209458768	-0.202067258	0.989808184	0.00464321	0.00182725
sp|Q6JBY9|CPZIP_HUMAN	4	24	48	21	-0.14596	0.069579453	0.611494518	0.215535305	0.75745037	0.541915064	0.285666616	6.60E-05	0.001243103
sp|Q6UWB1|I27RA_HUMAN	6	26	48	21	-0.28213	-0.262645597	-0.122983081	0.019482094	0.15914461	0.139662515	0.972696578	0.286551311	0.297860439
sp|P09681|GIP_HUMAN	11	7	14	6	-0.07744	-0.145250558	0.32228986	-0.067812927	0.399727491	0.467540418	0.952417757	0.327374874	0.147426251
sp|P58335|ANTR2_HUMAN	5	40	76	33	0.153833	-0.007171464	-0.055278395	-0.161004511	-0.209111442	-0.048106931	0.010626505	0.005234741	0.689464363
sp|Q9BXS4|TMM59_HUMAN	5	7	14	7	-0.22837	-0.048258065	0.356518962	0.180113138	0.584890165	0.404777027	0.465868653	0.006717758	0.032450446
sp|Q58FF8|H90B2_HUMAN	22	21	41	17	-0.23441	-0.377620772	0.502730232	-0.143211766	0.737139239	0.880351004	0.78533852	0.017193761	0.000856455
sp|Q9H479|FN3K_HUMAN	1	40	76	33	-0.30479	-0.149940058	0.110761437	0.154854579	0.415556074	0.260701495	0.402578156	0.012734108	0.107203735
sp|Q7LGC8|CHST3_HUMAN	6	40	76	33	0.142589	0.101524931	0.074595398	-0.041063948	-0.06799348	-0.026929533	0.358733723	0.146432272	0.677249244
sp|Q9UMS6|SYNP2_HUMAN	6	4	6	3	0.070832	0.157863916	1.022687643	0.087031581	0.951855308	0.864823726	0.984845154	0.314683029	0.326913269
sp|Q08345|DDR1_HUMAN	1	40	76	33	-0.02788	-0.042936385	0.080422842	-0.015057791	0.108301436	0.123359227	0.92252317	0.06095754	0.010691857
sp|P80404|GABT_HUMAN	4	33	62	27	-0.707	-0.535257846	-0.147132076	0.171747154	0.559872924	0.38812577	0.70190126	0.079927858	0.211003896
sp|P43034|LIS1_HUMAN	1	40	76	33	-0.15827	-0.176400725	0.164182425	-0.018131521	0.322451628	0.34058315	0.984711488	0.03876068	0.010522496
sp|Q13126|MTAP_HUMAN	7	40	76	33	-0.05922	0.011731498	0.229102443	0.070950766	0.28832171	0.217370944	0.530061548	0.001116882	0.006721581
sp|Q14165|MLEC_HUMAN	4	40	76	33	-0.11526	-0.137253954	0.150930162	-0.021992606	0.26619151	0.288184116	0.94323856	0.003764041	0.00029575
sp|Q9NTK5|OLA1_HUMAN	1	40	76	33	-0.27379	-0.129032908	0.213293717	0.144760722	0.487087347	0.342326625	0.293146799	0.000137884	0.003166347
sp|P00352|AL1A1_HUMAN	11	40	76	33	-0.36371	-0.058949526	0.348630076	0.304758087	0.712337689	0.407579602	0.010276798	1.67E-07	0.000893401
sp|Q8IZA0|K319L_HUMAN	17	40	76	33	0.017313	0.064007174	0.236128393	0.046694147	0.218815366	0.172121219	0.53864319	0.000174048	0.000980966

sp|O15212|PFD6_HUMAN	7	15	27	11	-0.06699	0.03833721	0.236498748	0.105329934	0.303491473	0.198161539	0.68570348	0.137488222	0.344791021
sp|Q9Y315|DEOC_HUMAN	5	20	42	19	-0.12485	-0.04611837	0.289204707	0.078726721	0.414049797	0.335323076	0.6320913	0.000310634	0.00073994
sp|P54687|BCAT1_HUMAN	2	4	7	2	-0.2772	0.264303649	0.26273122	0.5414996	0.53992717	-0.001572429	0.710250746	0.834254402	0.999998172
sp|P45974|UBP5_HUMAN	1	40	76	33	-0.33605	-0.18681597	0.146963602	0.149235087	0.483014659	0.333779572	0.237738684	6.85E-05	0.002418295
sp|Q13797|ITA9_HUMAN	5	40	76	33	0.136166	0.132441362	0.134442231	-0.003724347	-0.001723479	0.002000868	0.998380862	0.999760593	0.999589442
sp|O60240|PLIN1_HUMAN	2	22	42	17	0.042589	0.228680289	0.273357289	0.186091392	0.230768393	0.044677	0.333308609	0.325686965	0.947420162
sp|P21980|TGM2_HUMAN	39	29	56	24	-0.45219	-0.130048732	0.119388233	0.322142091	0.571579056	0.249436964	0.028649961	0.0006518	0.147674285
sp|P27930|IL1R2_HUMAN	36	40	76	33	0.060974	0.051165983	0.073007567	-0.009808178	0.012033406	0.021841585	0.989715084	0.989320563	0.956002761
sp|Q8NBJ4|GOLM1_HUMAN	17	40	76	33	-0.15074	0.014918011	0.493037598	0.165658391	0.643777977	0.478119587	0.239954826	1.70E-06	6.54E-05
sp|P09497|CLCB_HUMAN	1	12	20	9	0.228592	0.099497171	0.472928255	-0.12909524	0.244335845	0.373431085	0.790182677	0.564068353	0.208790904
sp|Q13287|NMI_HUMAN	62	14	28	11	0.044521	0.196193332	0.364301984	0.151672292	0.319780944	0.168108653	0.520057385	0.155083726	0.507013298
sp|Q9H0U4|RAB1B_HUMAN	14	40	76	33	-0.2034	-0.211262644	0.330147985	-0.007866449	0.53354418	0.541410629	0.997503996	0.000632995	7.76E-05
sp|Q9H173|SIL1_HUMAN	6	40	76	33	-0.40544	-0.34347171	0.163651291	0.061968537	0.569091538	0.507123001	0.827289975	4.47E-05	4.06E-05
sp|Q96FW1|OTUB1_HUMAN	12	40	76	33	-0.23508	-0.179648592	-0.010190368	0.055435916	0.22489414	0.169458224	0.826146351	0.119432287	0.213407208
sp|Q9Y2T3|GUAD_HUMAN	6	40	76	33	0.00446	0.043389193	0.196049296	0.038928879	0.191588983	0.152660104	0.84349237	0.062779302	0.105570983
sp|P12882|MYH1_HUMAN	16	26	48	22	-0.00323	-0.025159004	0.025419898	-0.02193098	0.028647922	0.050578902	0.987132463	0.984506713	0.940282905
sp|Q8N1Q1|CAH13_HUMAN	19	36	69	31	-0.07284	-0.169053384	0.084119058	-0.096209658	0.156962785	0.253172443	0.780313021	0.628925254	0.216351567
sp|A6NMZ7|CO6A6_HUMAN	80	15	28	13	0.176156	0.123527063	0.252718359	-0.052628462	0.076562834	0.129191296	0.921612842	0.884207402	0.641828317
sp|P38571|LICH_HUMAN	5	36	69	30	-0.04576	0.031391707	0.297574318	0.077153876	0.343336488	0.266182611	0.497825079	0.000155561	0.001043274
sp|P58546|MTPN_HUMAN	10	40	76	33	-0.20172	-0.068257301	0.130465041	0.133459433	0.332181774	0.198722342	0.507223541	0.058599352	0.269131276
sp|O60506|HNRPQ_HUMAN	113	30	55	24	-0.25623	-0.252453972	0.240241591	0.003773531	0.496469095	0.492695563	0.999458059	0.002551562	0.000706624
sp|Q9BZQ8|NIBA1_HUMAN	22	14	28	11	-0.32157	-0.187242569	0.151883883	0.134327624	0.473454076	0.339126452	0.695444002	0.060205658	0.151228852
sp|P11215|ITAM_HUMAN	3	14	28	13	0.00194	-0.089575649	0.478807924	-0.091515591	0.476867982	0.568383573	0.779555169	0.01182027	0.000445721
sp|Q9NZL9|MAT2B_HUMAN	2	37	69	30	-0.08915	0.139694605	0.432072963	0.228844794	0.521223151	0.292378358	0.029282793	9.08E-06	0.007230343
sp|P11940|PABP1_HUMAN	9	26	49	20	0.117483	0.122978417	0.34773759	0.005495079	0.230254251	0.224759173	0.997329779	0.050208556	0.028639369
sp|P16885|PLCG2_HUMAN	4	7	14	6	-0.56219	-0.466608725	0.672622371	0.09558466	1.234815756	1.139231096	0.959713325	0.018968128	0.013349851
sp|O00506|STK25_HUMAN	9	10	21	9	-0.07104	-0.027220683	0.716880196	0.043818885	0.787919764	0.744100879	0.986181109	0.056172001	0.034570397
sp|P17655|CAN2_HUMAN	4	40	76	33	-0.14048	-0.008432287	0.197218374	0.132044122	0.337694783	0.205650661	0.015999723	5.87E-08	0.000214288
sp|Q8NHL6|LIRB1_HUMAN	15	40	76	33	0.06448	0.015449345	0.097548003	-0.049030801	0.033067857	0.082098658	0.697364208	0.892773464	0.413799287
sp|Q6PI73|LIRA6_HUMAN	1	40	76	33	-0.21016	-0.012801267	0.070622828	0.197360437	0.280784531	0.083424095	0.020516847	0.004749746	0.532301756
sp|Q16822|PCKGM_HUMAN	1	40	76	33	-0.28061	0.035003968	0.086559509	0.31560959	0.36716513	0.05155554	0.008215445	0.011137525	0.88864976
sp|Q9HCN6|GPVI_HUMAN	5	40	76	33	-0.20616	0.013315994	0.162575343	0.219477351	0.3687367	0.149259349	0.027704752	0.001148342	0.2258375
sp|Q14914|PTGR1_HUMAN	5	40	76	33	-0.25433	-0.104683861	-0.046007175	0.149643804	0.208320489	0.058676686	0.218651167	0.132358237	0.812133199
sp|P18827|SDC1_HUMAN	2	29	55	24	-0.77524	-0.617425243	0.328042011	0.157816571	1.103283826	0.945467255	0.664038843	6.22E-06	1.25E-05
sp|Q6PCE3|PGM2L_HUMAN	5	7	14	6	-0.53203	-0.260304991	0.332223047	0.271723666	0.864251705	0.592528039	0.544622025	0.024927755	0.0911423
sp|P36551|HEM6_HUMAN	1	37	68	30	-0.15748	-0.072625518	0.105806492	0.084859069	0.263291079	0.17843201	0.483616959	0.009733353	0.065308766
sp|P20827|EFNA1_HUMAN	1	40	76	33	-0.46422	-0.35973953	0.089314798	0.104482685	0.553537013	0.449054328	0.528376376	1.43E-05	7.61E-05
sp|P62987|RL40_HUMAN	7	40	76	33	-0.37093	-0.180121859	0.339445315	0.190810642	0.710377817	0.519567175	0.188625499	6.97E-07	4.48E-05
sp|Q9NY33|DPP3_HUMAN	2	40	76	33	-0.13073	-0.106054348	0.246793573	0.024680406	0.377528327	0.352847921	0.939157503	9.60E-05	3.73E-05
sp|Q9H4D0|CSTN2_HUMAN	29	14	27	12	0.164509	0.077606954	0.388671145	-0.086902058	0.224162133	0.311064191	0.764247141	0.293612078	0.054191639
sp|Q58FG0|HS905_HUMAN	2	40	76	33	-0.34698	-0.255075604	0.259979437	0.091902635	0.606957675	0.515055041	0.760011966	0.000467363	0.000853049
sp|Q29983|MICA_HUMAN	6	16	27	12	-0.02831	-0.013195373	0.294741956	0.015113397	0.323050726	0.30793733	0.992235194	0.099691846	0.080021791
sp|P11117|PPAL_HUMAN	212	21	42	18	0.095352	0.017774304	0.115192991	-0.077577883	0.019840804	0.097418687	0.556266811	0.973547608	0.436469374
sp|Q9UKZ9|PCOC2_HUMAN	11	40	76	33	0.14236	0.112247693	-0.067271069	-0.030111843	-0.209630604	-0.179518762	0.714518584	3.71E-05	6.94E-05
sp|P05204|HMGN2_HUMAN	8	36	69	30	-1.13318	-0.874484969	0.23830951	0.258696238	1.371490717	1.112794478	0.43007925	6.19E-07	4.74E-06
sp|Q3LXA3|TKFC_HUMAN	2	40	76	33	-0.15621	0.005442595	0.207736946	0.161652136	0.363946487	0.202294351	0.135871688	0.001276245	0.06561461
sp|Q99497|PARK7_HUMAN	8	40	76	33	-0.10487	-0.040654802	0.329448998	0.064218542	0.434322343	0.3701038	0.724127248	8.96E-05	0.000172728
sp|P08476|INHBA_HUMAN	3	30	55	23	-0.09003	0.006718777	0.186828205	0.096753087	0.276862516	0.180109428	0.501575848	0.026093062	0.140242773
sp|P36269|GGT5_HUMAN	1	40	76	33	0.248686	0.197747369	0.119067763	-0.050938795	-0.129618401	-0.078679606	0.434456809	0.026816475	0.177309409
sp|O15372|EIF3H_HUMAN	1	4	7	3	-0.72543	-0.424642871	0.407629848	0.300791489	1.133064208	0.832272719	0.83516151	0.220314703	0.351182789
sp|Q13443|ADAM9_HUMAN	31	36	69	30	-0.21437	-0.072437413	0.247630683	0.141932469	0.462000566	0.320068097	0.133948561	1.95E-06	0.000215379
sp|P01589|IL2RA_HUMAN	4	4	7	2	0.047202	0.603220202	0.00093951	0.556017979	-0.046262712	-0.602280692	0.711781608	0.998723322	0.781766729
sp|Q14112|NID2_HUMAN	1	40	76	33	-0.14025	-0.006054395	0.147044232	0.134196711	0.287295338	0.153098626	0.064932563	0.000275286	0.044482945
sp|P17900|SAP3_HUMAN	10	40	76	33	-0.03985	-0.029225198	0.540912108	0.010629433	0.580766738	0.570137306	0.992247275	8.17E-07	5.12E-08
sp|Q16143|SYUB_HUMAN	1	40	76	33	-0.16094	-0.194672933	0.257595297	-0.033736974	0.418531256	0.45226823	0.958325293	0.01324135	0.001831903
sp|P16152|CBR1_HUMAN	17	40	76	33	-0.16649	-0.006089472	0.30163986	0.160397215	0.468126547	0.307729332	0.137537775	2.21E-05	0.002134637
sp|Q9H0P0|5NT3A_HUMAN	3	26	48	20	-0.01183	-0.021736644	0.078940508	-0.009902196	0.090774956	0.100677152	0.995816478	0.790304703	0.697083575
sp|Q13361|MFAP5_HUMAN	10	40	76	33	0.061832	-0.014185041	0.259995948	-0.076016771	0.198164218	0.274180989	0.306852004	0.00493265	5.32E-06
sp|P43490|NAMPT_HUMAN	1	40	76	33	-0.27993	-0.128119909	0.264683327	0.15180954	0.544612776	0.392803236	0.293802555	4.61E-05	0.001104764
sp|P13521|SCG2_HUMAN	3	29	55	25	0.29165	0.286154492	0.237394042	-0.005495587	-0.054256038	-0.048760451	0.997718583	0.854631175	0.850092698
sp|P15170|ERF3A_HUMAN	38	29	56	24	-0.41856	-0.295217729	0.248516933	0.123340411	0.667075073	0.543734662	0.72864694	0.002672764	0.006170037
sp|Q92187|SIA8D_HUMAN	7	40	76	33	-0.01779	0.019952169	0.011954198	0.03774637	0.029748399	-0.007997971	0.715377032	0.866027912	0.986838941
sp|Q15843|NEDD8_HUMAN	27	8	14	6	0.110791	-0.007254823	0.355697638	-0.118046219	0.244906242	0.362952461	0.620453883	0.263872917	0.037372726
sp|Q15257|PTPA_HUMAN	2	40	76	33	-0.12014	-0.087742218	0.311412058	0.032394119	0.431548394	0.399154275	0.911846038	3.62E-05	1.59E-05
sp|P55263|ADK_HUMAN	2	37	69	30	-0.2524	-0.107955162	0.180984753	0.144445062	0.433384977	0.288939915	0.207129656	0.000121252	0.005215717
sp|Q99983|OMD_HUMAN	3	40	76	33	0.122497	0.054527186	-0.079528516	-0.06796954	-0.202025242	-0.134055701	0.600385906	0.048348756	0.179005155
sp|P29218|IMPA1_HUMAN	7	36	69	30	0.048856	-0.060507109	0.275579458	-0.109362853	0.226723713	0.336086566	0.369218155	0.055021834	0.00043572
sp|P22392|NDKB_HUMAN	6	11	21	9	-0.28559	0.012821661	0.619286665	0.298409723	0.904874727	0.606465004	0.415363935	0.007390846	0.051134402
sp|Q9BWD1|THIC_HUMAN	8	40	76	33	-0.17356	-0.05915392	0.140415767	0.11440767	0.313977357	0.199569687	0.361909184	0.00629467	0.069323573
sp|P48357|LEPR_HUMAN	5	40	76	33	0.077705	0.035055828	0.039575992	-0.042648676	-0.038128512	0.004520164	0.668352013	0.800403792	0.996016994
sp|P13473|LAMP2_HUMAN	7	40	76	33	0.058572	0.086522898	-0.076353248	0.027950927	-0.134925219	-0.162876146	0.58912692	0.000369632	9.32E-07
sp|Q9H461|FZD8_HUMAN	11	19	34	14	0.285653	0.157824718	0.39371214	-0.127828143	0.108059279	0.235887422	0.533256574	0.741517587	0.181586247
sp|Q6GMV3|PTRD1_HUMAN	1	8	14	6	0.053722	0.113645032	0.062924378	0.059923198	0.009202544	-0.050720654	0.887569413	0.998097581	0.931791055
sp|Q86X29|LSR_HUMAN	5	40	76	33	-0.09246	-0.070812257	0.221934267	0.02164874	0.314395265	0.292746525	0.930316295	6.99E-05	2.84E-05
sp|Q9Y678|COPG1_HUMAN	2	27	48	20	-0.38421	-0.10696642	0.161979906	0.277242176	0.546188502	0.268946326	0.133964509	0.006912686	0.211046378
sp|O14672|ADA10_HUMAN	30	40	76	33	-0.28191	-0.166475693	0.211937206	0.115435169	0.493848068	0.378412899	0.321592221	2.73E-06	5.38E-05
sp|Q6P4E1|CASC4_HUMAN	2	40	76	33	-0.02049	0.105389899	0.276337888	0.125884335	0.296832324	0.170947989	0.081449571	0.000119827	0.018328549
sp|P67775|PP2AA_HUMAN	23	40	76	33	-0.48402	-0.27397666	0.095216625	0.210038783	0.579232069	0.369193286	0.241588422	0.000870052	0.023241318
sp|Q9H4X1|RGCC_HUMAN	7	20	34	15	-0.23293	-0.17365589	-0.275105581	0.059273196	-0.042176495	-0.101449691	0.964308024	0.987546819	0.915840204
sp|Q9UMX5|NENF_HUMAN	1	40	76	33	0.007757	-0.085368441	0.126345122	-0.093125649	0.118587914	0.211713563	0.217922092	0.182399477	0.001397556
sp|P48788|TNNI2_HUMAN	19	11	20	9	-0.77774	-1.008798709	0.202529215	-0.23106231	0.980265614	1.211327924	0.847703389	0.140577169	0.028026453
sp|P05060|SCG1_HUMAN	3	40	76	33	-0.04139	-0.118718884	0.11196887	-0.077325079	0.153362675	0.230687754	0.576556652	0.227628176	0.01581889
sp|P02794|FRIH_HUMAN	18	40	76	33	-0.34192	-0.206735573	0.372769274	0.135186306	0.714691153	0.579504847	0.565672597	4.48E-05	0.000204305
sp|Q6UXK5|LRRN1_HUMAN	24	40	76	33	0.214052	0.115936588	-0.289501231	-0.098115178	-0.503552997	-0.405437819	0.179014333	9.95E-12	4.36E-10
sp|P43405|KSYK_HUMAN	19	14	28	11	-0.03273	0.029447956	0.556078129	0.062176066	0.58880624	0.526630174	0.946289894	0.047651725	0.044316664
sp|Q06187|BTK_HUMAN	9	40	76	33	0.018916	-0.050504621	0.072699601	-0.069420559	0.053783664	0.123204222	0.755408537	0.890143596	0.462251933
sp|Q01469|FABP5_HUMAN	3	40	76	33	-0.23402	-0.078529375	0.353050453	0.15549078	0.587070608	0.431579828	0.409615045	0.000283934	0.003192126
sp|P04271|S100B_HUMAN	1	8	14	5	0.27778	0.18394617	-0.15902054	-0.093833392	-0.436800102	-0.34296671	0.624361428	0.006719094	0.020451402
sp|O95817|BAG3_HUMAN	20	11	20	9	0.237214	0.122414771	0.53064989	-0.11479944	0.293435679	0.408235119	0.872838028	0.542953413	0.235871039
sp|Q9BUL8|PDC10_HUMAN	14	36	69	30	-0.36102	-0.208985734	0.044217477	0.152031365	0.405234576	0.253203211	0.626566837	0.105199586	0.32063634
sp|P59998|ARPC4_HUMAN	1	40	76	33	-0.08407	-0.108455217	0.143423311	-0.024385115	0.227493412	0.251878528	0.969988098	0.165959454	0.062446159
sp|O75914|PAK3_HUMAN	2	29	55	23	-0.0593	-0.037446033	0.309513134	0.021852482	0.368811649	0.346959167	0.97098134	0.00503794	0.002803392
sp|Q96C90|PP14B_HUMAN	152	4	6	3	0.035912	0.115297509	1.06768294	0.079385414	1.031770845	0.952385431	0.993204345	0.467699436	0.469662863
sp|P48960|CD97_HUMAN	15	40	76	33	-0.00249	-0.03061782	0.092649679	-0.0281291	0.0951384	0.123267499	0.806561711	0.188084887	0.0301155
sp|Q9HC38|GLOD4_HUMAN	1	40	76	33	-0.10151	-0.058010749	0.327107318	0.043499389	0.428617456	0.385118067	0.836835811	2.13E-05	1.63E-05
sp|Q99674|CGRE1_HUMAN	2	40	76	33	-0.14679	-0.262241197	0.224538655	-0.115446439	0.371333413	0.486779852	0.555456795	0.017425112	0.000206486
sp|P25815|S100P_HUMAN	61	40	76	33	-0.7255	-0.582685042	0.090479064	0.142819113	0.815983219	0.673164106	0.663564396	0.000199187	0.000579267
sp|O60749|SNX2_HUMAN	107	14	28	12	-0.02175	0.022392839	0.355400151	0.044144746	0.377152058	0.333007311	0.95451503	0.106996138	0.103975698
sp|O00754|MA2B1_HUMAN	1	40	76	33	0.151673	0.184243714	0.440759612	0.032570987	0.289086884	0.256515898	0.877356506	0.001285189	0.001270048
sp|Q9NQ25|SLAF7_HUMAN	6	14	27	13	0.037432	0.098562772	0.150567301	0.061131132	0.113135662	0.05200453	0.808459656	0.589478216	0.86356626
sp|P28676|GRAN_HUMAN	14	7	13	6	0.380309	0.061499725	0.810382322	-0.31880933	0.430073267	0.748882597	0.729044005	0.665916373	0.225897306
sp|O95831|AIFM1_HUMAN	2	4	7	3	-0.1501	0.105246315	0.175336971	0.25534432	0.325434975	0.070090656	0.637932213	0.612720346	0.971326887
sp|P63104|1433Z_HUMAN	1	40	76	33	-0.04385	-0.243076568	0.129411075	-0.199228505	0.173259138	0.372487643	0.289338554	0.521426893	0.024463335
sp|P48723|HSP13_HUMAN	4	40	76	33	0.02316	-0.000497305	0.196377024	-0.023657438	0.173216891	0.196874329	0.921120827	0.052372043	0.008558818
sp|P00492|HPRT_HUMAN	6	40	76	33	-0.26965	-0.0860166	0.238223793	0.183633931	0.507874324	0.324240392	0.039000567	2.23E-07	0.000215375

sp|Q86TY3|ARMD4_HUMAN	19	40	76	33	0.124548	-0.005767869	-0.198542523	-0.130316146	-0.3230908	-0.192774654	0.037870584	3.03E-06	0.002209315
sp|Q9NR34|MA1C1_HUMAN	14	40	76	33	-0.01629	-0.001690063	0.196540649	0.014600104	0.212830816	0.198230712	0.937149872	0.000161609	7.02E-05
sp|P13686|PPA5_HUMAN	253	40	76	33	-0.09247	-0.024840512	0.223040994	0.067626142	0.315507648	0.247881505	0.499679033	7.12E-05	0.000482996
sp|Q9NQ30|ESM1_HUMAN	6	4	7	3	0.190104	-0.007052533	0.181154736	-0.197156425	-0.008949156	0.188207269	0.458967925	0.998836184	0.551051049
sp|Q86SG5|S1A7A_HUMAN	8	40	76	33	-1.77038	-1.891262406	-2.177428167	-0.120882038	-0.407047799	-0.286165761	0.886307718	0.392165383	0.553844482
sp|P22304|IDS_HUMAN	16	40	76	33	0.293056	0.202264556	0.113690652	-0.090791858	-0.179365762	-0.088573904	0.137303143	0.005642401	0.189246175
sp|Q92598|HS105_HUMAN	1	25	48	20	-0.35481	-0.045961505	0.425614652	0.308843515	0.780419672	0.471576157	0.100799441	0.000122016	0.011634551
sp|P16989|YBOX3_HUMAN	13	4	6	3	0.155497	0.145127887	0.825182739	-0.01036951	0.669685342	0.680054852	0.99972131	0.464885534	0.403449686
sp|P63208|SKP1_HUMAN	3	40	76	33	-0.38232	-0.169453745	0.517504935	0.212864618	0.899823298	0.686958681	0.163299288	5.19E-09	4.20E-07
sp|P52799|EFNB2_HUMAN	13	40	76	33	-0.11429	-0.122487046	0.226896706	-0.008197786	0.341185967	0.349383753	0.993535211	0.000740578	8.09E-05
sp|O00410|IPO5_HUMAN	4	28	56	24	-0.39668	-0.297189211	0.350088885	0.099495023	0.746773119	0.647278096	0.818910628	0.000799526	0.000932013
sp|P17174|AATC_HUMAN	11	40	76	33	-0.04939	-0.012906125	0.169724646	0.036479355	0.219110125	0.18263077	0.888458142	0.057232304	0.079078162
sp|Q8WY91|THAP4_HUMAN	49	4	6	3	-0.34236	-0.273675816	0.535740797	0.068679695	0.878096308	0.809416613	0.987613224	0.279947032	0.282689163
sp|P55000|SLUR1_HUMAN	4	30	55	25	0.206895	0.105836861	0.183223552	-0.101057811	-0.023671121	0.077386691	0.406151031	0.965484299	0.624707067
sp|P07451|CAH3_HUMAN	3	40	76	33	-1.24722	-1.204989977	-0.634785177	0.04222852	0.61243332	0.5702048	0.933862384	0.000113911	4.83E-05
sp|P20036|DPA1_HUMAN	3	40	76	33	-0.09792	-0.206275714	-0.204285752	-0.108356715	-0.106366753	0.001989962	0.441690625	0.579918973	0.999755942
sp|Q8IWL1|SFPA2_HUMAN	226	40	76	33	-0.12242	-0.059404939	0.301442432	0.063012338	0.423859709	0.360847371	0.525892431	3.42E-08	1.11E-07
sp|Q01433|AMPD2_HUMAN	1	7	14	6	-0.08752	0.104942843	0.821032153	0.192466651	0.908555961	0.71608931	0.774154199	0.032891274	0.058852944
sp|P58400|NRX1B_HUMAN	16	29	56	24	0.264152	0.207784677	0.051786643	-0.05636764	-0.212365675	-0.155998034	0.699196651	0.034823498	0.095571925
sp|Q9Y2J2|E41L3_HUMAN	16	10	21	9	0.031057	-0.132578386	0.057755799	-0.163635807	0.026698378	0.190334184	0.436267798	0.98428963	0.354510782
sp|P02763|A1AG1_HUMAN	1	40	76	33	-0.98163	-0.875308321	-0.200417449	0.106323157	0.78121403	0.674890873	0.826567621	0.001299057	0.001780612
sp|Q9NRA1|PDGFC_HUMAN	5	40	76	33	-0.00253	0.034922339	0.154930686	0.037451819	0.157460167	0.120008348	0.658485149	0.007686183	0.026182636
sp|O00231|PSD11_HUMAN	14	22	42	18	-0.20446	-0.10288312	0.208829449	0.101576574	0.413289143	0.311712568	0.741095053	0.039071497	0.092531012
sp|P08779|K1C16_HUMAN	2	17	35	16	0.055556	0.019821135	-0.08210174	-0.035734496	-0.137657371	-0.101922875	0.988745438	0.886269389	0.915551309
sp|Q9UKK9|NUDT5_HUMAN	10	40	76	33	-0.07552	-0.038357631	0.333326706	0.03716682	0.408851157	0.371684337	0.882377531	7.33E-05	4.67E-05
sp|Q9UJ68|MSRA_HUMAN	38	32	63	27	0.038727	0.024294817	0.271793038	-0.014432637	0.233065584	0.247498221	0.988287201	0.126432932	0.050913403
sp|Q05209|PTN12_HUMAN	1	29	55	24	-0.04877	0.03083437	0.264912067	0.079605491	0.313683188	0.234077697	0.885934367	0.277850184	0.401792763
sp|Q9BRT3|MIEN1_HUMAN	4	25	48	21	-0.26966	-0.310532607	0.376324174	-0.040874436	0.645982346	0.686856782	0.966082591	0.003971509	0.000427043
sp|Q93074|MED12_HUMAN	4	4	6	3	0.030767	-0.251086183	0.223481135	-0.281853559	0.192713758	0.474567318	0.424149315	0.738077853	0.161135094
sp|O14618|CCS_HUMAN	5	34	62	26	-0.20127	-0.025498045	0.284961105	0.17577583	0.48623498	0.31045915	0.305821141	0.003131861	0.048966346
sp|Q8NFP4|MDGA1_HUMAN	3	22	42	18	0.134589	0.07183909	-0.085002327	-0.062749731	-0.219591147	-0.156841416	0.433145214	0.001617477	0.01339044
sp|P05451|REG1A_HUMAN	1	40	76	33	-0.2005	-0.145045922	0.246134396	0.055458504	0.446638821	0.391180317	0.913124411	0.020056649	0.021945672
sp|Q13510|ASAH1_HUMAN	22	40	76	33	-0.08155	-0.092691619	0.159318742	-0.011146514	0.240863846	0.25201036	0.97449934	0.000450852	2.86E-05
sp|Q9UJC5|SH3L2_HUMAN	3	40	76	33	-0.22248	-0.25159108	-0.206354313	-0.029106693	0.016130074	0.045236767	0.981113168	0.995967185	0.960378843
sp|Q99972|MYOC_HUMAN	6	40	76	33	0.105383	0.097102472	-0.007268605	-0.008280929	-0.112652005	-0.104371077	0.989271157	0.257223906	0.227368199
sp|Q9BXD5|NPL_HUMAN	12	32	62	27	-0.27801	-0.177642435	0.323754667	0.100363146	0.601760248	0.501397102	0.632817209	3.69E-05	0.000100875
sp|O75695|XRP2_HUMAN	29	14	27	12	-0.05946	-0.093580327	0.303396568	-0.034117018	0.362859877	0.396976895	0.951283567	0.026334781	0.00463503
sp|O60636|TSN2_HUMAN	4	14	28	13	-0.0044	-0.156276047	0.287132203	-0.151875976	0.291532274	0.44340825	0.450528707	0.127314214	0.003108004
sp|P61758|PFD3_HUMAN	6	22	42	18	-0.35171	-0.099890016	0.343132309	0.251824953	0.694847278	0.443022326	0.56593135	0.057089101	0.220022385
sp|P30040|ERP29_HUMAN	1	40	76	33	-0.11821	-0.100145883	0.165006203	0.018065733	0.283217819	0.265152086	0.983638238	0.065920764	0.04863192
sp|Q8N257|H2B3B_HUMAN	5	40	76	33	-0.44526	-0.400679674	0.24314063	0.044579686	0.68839999	0.643820304	0.961266093	0.0022208	0.001161375
sp|P62807|H2B1C_HUMAN	12	25	48	21	-0.653	-0.548596655	0.330371625	0.104400963	0.983369243	0.87896828	0.903958698	0.003228626	0.002863285
sp|Q15631|TSN_HUMAN	34	40	76	33	-0.31428	-0.137594122	0.292287266	0.176685897	0.606567285	0.429881388	0.126999504	3.44E-07	4.84E-05
sp|O60234|GMFG_HUMAN	18	40	76	33	-0.33829	-0.181359876	0.198924791	0.156933765	0.537218432	0.380284667	0.444635269	0.002018318	0.017566721
sp|O95433|AHSA1_HUMAN	12	8	13	6	-0.11479	0.016461502	0.294433064	0.131251119	0.409222682	0.277971562	0.786290772	0.217534907	0.419558338
sp|P17612|KAPCA_HUMAN	14	11	21	9	0.023313	-0.179147898	0.568421404	-0.202460967	0.545108335	0.747569303	0.669130067	0.148334114	0.014169793
sp|P22223|CADH3_HUMAN	1	28	55	24	-0.10201	-0.181275105	0.097835515	-0.079267133	0.199843487	0.27911062	0.78577806	0.347951116	0.07364099
sp|O14745|NHRF1_HUMAN	8	40	76	33	-0.11085	-0.175088326	0.143720006	-0.064235637	0.254572695	0.318808332	0.771922721	0.064983491	0.00491175
sp|P50897|PPT1_HUMAN	5	29	55	24	0.065309	0.077763118	0.151085651	0.012453787	0.085776319	0.073322533	0.981892225	0.551604354	0.574979592
sp|Q8WZA0|LZIC_HUMAN	2	36	69	30	-0.11691	-0.039380231	0.243776107	0.07753039	0.360686728	0.283156338	0.660920275	0.002899382	0.009473699
sp|Q15323|K1H1_HUMAN	9	8	13	6	-0.20276	0.412831452	-0.197189786	0.615595952	0.005574713	-0.610021238	0.375467352	0.999941831	0.44760636
sp|P60983|GMFB_HUMAN	97	36	69	30	-0.05131	0.098933408	0.412989298	0.150240831	0.464296721	0.31405589	0.407053435	0.003556099	0.03414401
sp|Q8TD46|MO2R1_HUMAN	20	16	27	12	-0.318	-0.173887882	0.099269688	0.144109747	0.417267317	0.27315757	0.673946863	0.114427192	0.315985704
sp|Q9NQZ7|ENTP7_HUMAN	80	19	34	14	0.041955	0.154485455	0.330671269	0.112530846	0.28871666	0.176185814	0.666204968	0.178436878	0.447630605
sp|P50135|HNMT_HUMAN	12	4	7	3	-0.38845	-0.066150653	-0.188912636	0.322296821	0.199534839	-0.122761982	0.09553984	0.490677924	0.710269246
sp|Q9Y2Q3|GSTK1_HUMAN	7	28	55	24	-0.10035	-0.299535639	0.271397876	-0.199188031	0.371745483	0.570933514	0.4008797	0.112961596	0.001819114
sp|Q9Y2S2|CRYL1_HUMAN	32	31	55	23	-0.27115	-0.014369648	0.202324578	0.256782261	0.473476487	0.216694227	0.048285262	0.001407157	0.16631359
sp|P54317|LIPR2_HUMAN	44	15	28	11	-0.04866	0.02014941	0.001689584	0.068813549	0.050353722	-0.018459826	0.834773001	0.938941431	0.989505266
sp|Q9BVA1|TBB2B_HUMAN	11	40	76	33	-0.39174	-0.097067531	0.221001242	0.294676487	0.612745259	0.318068772	0.045679223	0.00016368	0.042655075
sp|P31150|GDIA_HUMAN	15	40	76	33	0.026653	-0.047156709	0.180585831	-0.073809291	0.15393325	0.227742541	0.637304311	0.262013185	0.026169762
sp|Q641Q3|METRL_HUMAN	25	40	76	33	-0.00706	0.020886869	0.131194921	0.027948923	0.138256975	0.110308052	0.799641941	0.026163879	0.051234194
sp|P17987|TCPA_HUMAN	24	37	69	29	-0.18748	-0.112032053	0.287165958	0.07545047	0.474648481	0.399198011	0.715211986	0.000267037	0.000627841
sp|P15090|FABP4_HUMAN	1	40	76	33	-0.35404	-0.309634966	0.263891042	0.044403378	0.617929386	0.573526008	0.917022554	2.88E-05	1.16E-05
sp|P31997|CEAM8_HUMAN	2	32	62	27	0.092119	0.230126794	0.308698112	0.138008118	0.216579435	0.078571317	0.201105109	0.066885518	0.625165031
sp|Q13217|DNJC3_HUMAN	1	40	76	33	-0.16827	-0.063310643	0.14618093	0.104959644	0.314451217	0.209491573	0.127932805	8.98E-06	0.001052189
sp|Q9NS71|GKN1_HUMAN	6	40	76	33	-0.10099	-0.093985856	0.156270261	0.007001731	0.257257848	0.250256117	0.995609953	0.019559681	0.009082273
sp|Q9NS28|RGS18_HUMAN	4	19	34	15	-0.0082	0.056604787	0.181208104	0.064803613	0.18940693	0.124603317	0.94528088	0.719739402	0.837577664
sp|Q9NX62|IMPA3_HUMAN	2	40	76	33	-0.02308	-0.070596892	0.178260436	-0.047517458	0.20133987	0.248857328	0.530619095	0.000649222	1.38E-06
sp|Q16832|DDR2_HUMAN	57	37	69	30	0.187256	0.080085241	-0.225713574	-0.107171095	-0.41296991	-0.305798815	0.063436457	8.79E-11	4.38E-08
sp|O75558|STX11_HUMAN	4	8	14	6	0.177835	-0.200094679	-0.295861136	-0.377929955	-0.473696412	-0.095766457	0.361495869	0.341685261	0.945313624
sp|Q14574|DSC3_HUMAN	3	40	76	33	0.10057	0.090483673	0.12584647	-0.010086647	0.025276151	0.035362797	0.963564444	0.851631556	0.670996222
sp|P0DPI2|GAL3A_HUMAN	7	14	27	12	-0.09999	0.186162949	0.877248266	0.28615288	0.977238197	0.691085317	0.351755255	0.000632638	0.006717942
sp|P06454|PTMA_HUMAN	7	40	76	33	-0.74247	-0.420720906	0.326347633	0.321751134	1.068819674	0.747068539	0.093607186	1.24E-07	3.11E-05
sp|Q96PX8|SLIK1_HUMAN	5	40	76	33	0.192498	0.03164121	-0.054730116	-0.160856293	-0.247227619	-0.086371326	0.006000066	0.000302555	0.260391175
sp|Q16881|TRXR1_HUMAN	8	40	76	33	-0.08475	0.046621911	0.335324271	0.131369545	0.420071905	0.28870236	0.128546985	2.17E-06	0.000277557
sp|Q9NU53|GINM1_HUMAN	2	29	55	25	-0.11114	-0.046089277	0.144345258	0.065054576	0.25548911	0.190434535	0.745483489	0.045561553	0.108455572
sp|Q9C0C4|SEM4C_HUMAN	7	40	76	33	0.06489	0.059302324	0.093283401	-0.005587239	0.028393838	0.033981077	0.986153168	0.780482916	0.637166358
sp|P26992|CNTFR_HUMAN	52	40	76	33	0.14903	0.125975439	0.008608679	-0.023054071	-0.140420831	-0.11736676	0.864735067	0.027618125	0.040632496
sp|P00505|AATM_HUMAN	2	4	7	3	0.033082	-0.204697867	-0.138950978	-0.237779536	-0.172032647	0.065746889	0.64607559	0.853704233	0.971753764
sp|P36941|TNR3_HUMAN	8	27	48	20	-0.03322	-0.036661266	0.450860652	-0.003445663	0.484076255	0.487521918	0.999438885	0.001233267	0.000279657
sp|P20138|CD33_HUMAN	27	40	76	33	0.091373	0.113742477	0.111952968	0.022369749	0.02058024	-0.001789509	0.958967463	0.975823883	0.999764512
sp|Q7Z794|K2C1B_HUMAN	14	40	76	33	-0.13065	-0.396146987	-0.495939341	-0.265500581	-0.365292936	-0.099792354	0.203439242	0.126240819	0.818367695
sp|Q9BS40|LXN_HUMAN	5	30	55	23	-0.01948	0.090793148	0.229763952	0.110270063	0.249240867	0.138970804	0.133264358	0.001469903	0.070484642
sp|O60476|MA1A2_HUMAN	1	36	69	30	0.051709	0.012619603	0.142743724	-0.039088944	0.091035176	0.130124121	0.791981986	0.419513199	0.107160925
sp|Q9UBC2|EP15R_HUMAN	25	17	35	14	-0.48678	-0.338100414	0.546947258	0.148681196	1.033728868	0.885047672	0.776250602	0.000754338	0.001005993
sp|Q9Y624|JAM1_HUMAN	2	40	76	33	-0.46828	-0.351241175	0.309466319	0.117037572	0.777745066	0.660707494	0.533092895	6.73E-08	2.22E-07
sp|Q9UBQ0|VPS29_HUMAN	1	33	63	26	-0.31122	-0.23892293	0.239140766	0.072301796	0.550365491	0.478063696	0.810545789	0.000548225	0.000750306
sp|Q9NPF2|CHSTB_HUMAN	27	11	21	9	-0.36228	-0.080900286	0.274660832	0.281381671	0.636942789	0.355561118	0.144437935	0.002442364	0.071380078
sp|P28070|PSB4_HUMAN	4	40	76	33	-0.25872	-0.107753868	0.442695474	0.150966473	0.701415815	0.550449342	0.301098688	1.65E-07	3.49E-06
sp|P61020|RAB5B_HUMAN	48	26	48	21	0.005085	0.046379583	0.293780106	0.041294607	0.288695131	0.247400524	0.932058722	0.100931504	0.119663151
sp|Q9NRB3|CHSTC_HUMAN	2	40	76	33	-0.13575	-0.079775868	-0.015884195	0.055969246	0.11986092	0.063891673	0.362825851	0.043356083	0.314053835
sp|Q16401|PSMD5_HUMAN	2	18	35	15	-0.33324	-0.18821322	0.346748072	0.145029315	0.679990607	0.534961292	0.633220542	0.00201577	0.006490977
sp|P50570|DYN2_HUMAN	7	15	28	12	0.197786	-0.009994068	0.512913542	-0.207780452	0.315127158	0.522907611	0.611994074	0.464858404	0.078003504
sp|P20472|PRVA_HUMAN	27	15	28	11	0.028368	-0.102851438	0.032917531	-0.131219408	0.00454956	0.135768969	0.831610897	0.999855367	0.852400494
sp|O95782|AP2A1_HUMAN	11	15	27	11	0.375981	0.272632536	0.28593216	-0.1033482	-0.090048576	0.013299624	0.730709075	0.854410477	0.995766406
sp|Q9BRF8|CPPED_HUMAN	6	4	7	3	0.407514	0.072416762	0.3639609	-0.335097116	-0.043552978	0.291544138	0.476918814	0.991004017	0.622258686
sp|O43847|NRDC_HUMAN	3	4	7	3	-0.10921	0.077535583	0.74930486	0.186746171	0.858515448	0.671769277	0.824453183	0.105641793	0.170659169
sp|O94919|ENDD1_HUMAN	4	40	76	33	-0.12233	0.005604214	0.235905479	0.127935807	0.358237071	0.230301264	0.153539538	8.12E-05	0.00575811
sp|Q14644|RASA3_HUMAN	14	37	69	30	0.039907	-0.148071164	-0.009799711	-0.187977724	-0.04970627	0.138271454	0.329667459	0.947420688	0.591741841
sp|Q14103|HNRPD_HUMAN	1	30	55	23	-0.34951	-0.096790414	0.304622161	0.252720229	0.654132803	0.401412574	0.186778518	0.000872406	0.031555388
sp|Q9UN19|DAPP1_HUMAN	3	22	41	17	-0.03428	-0.123313025	0.118520629	-0.089028371	0.152805283	0.241833654	0.817698918	0.673129075	0.293696446
sp|Q00577|PURA_HUMAN	1	4	7	3	0.318005	-0.05330921	0.314914994	-0.371314593	-0.00309039	0.368224203	0.653033192	0.999979293	0.705870982
sp|P00480|OTC_HUMAN	17	40	76	33	-0.62398	-0.427577134	-0.136296615	0.196398331	0.48767885	0.291280519	0.354261354	0.013971362	0.137475087
sp|P24752|THIL_HUMAN	5	4	7	3	-0.04723	-0.175161228	-0.205228972	-0.127934634	-0.158002378	-0.030067744	0.833713937	0.829667226	0.991609243
sp|P62495|ERF1_HUMAN	3	32	62	28	-0.15658	-0.170235715	0.160626831	-0.013654857	0.317207688	0.330862546	0.991193141	0.038825628	0.011114371

sp|P01903|DRA_HUMAN	4	40	76	33	0.032938	0.081040614	0.160757882	0.04810246	0.127819728	0.079717268	0.737265458	0.230653051	0.481111024
sp|Q9H4A9|DPEP2_HUMAN	6	40	76	33	0.09588	0.145783177	-0.041640792	0.049903576	-0.137520393	-0.187423969	0.443636802	0.01630653	9.50E-05
sp|O95025|SEM3D_HUMAN	5	8	14	6	-0.28087	-0.312329713	-0.288585088	-0.0314619	-0.007717275	0.023744625	0.957261913	0.998228426	0.979663815
sp|Q7L576|CYFP1_HUMAN	4	37	69	30	-0.35028	-0.119942453	0.156487067	0.23033445	0.50676397	0.27642952	0.218369158	0.007558786	0.150367874
sp|P00167|CYB5_HUMAN	23	30	55	24	-0.07092	0.100064685	0.324278331	0.170984188	0.395197835	0.224213647	0.13776416	0.001066715	0.055055648
sp|P26639|SYTC_HUMAN	1	40	76	33	-0.06252	-0.094349723	0.244908558	-0.031827873	0.307430408	0.339258281	0.946425324	0.032634116	0.005463051
sp|P30085|KCY_HUMAN	1	40	76	33	-0.29152	-0.141241513	0.127777461	0.150274716	0.419293689	0.269018973	0.290264234	0.001811473	0.033256459
sp|Q9NP98|MYOZ1_HUMAN	12	4	6	3	0.004958	0.010692812	1.586671638	0.005735218	1.581714043	1.575978825	0.999947928	0.107761144	0.081832946
sp|Q16772|GSTA3_HUMAN	3	36	69	30	-0.36183	-0.044941834	0.176669291	0.316885622	0.538496747	0.221611125	0.145382554	0.022942019	0.430081645
sp|Q9UIA9|XPO7_HUMAN	8	19	35	14	-0.17237	-0.031900101	0.31989531	0.140472171	0.492267582	0.351795411	0.546849705	0.011032261	0.052843887
sp|P02008|HBAZ_HUMAN	1	12	21	9	-0.00516	-0.15428431	0.653029089	-0.149126561	0.658186837	0.807313398	0.804665198	0.070405955	0.009884215
sp|Q92743|HTRA1_HUMAN	11	40	76	33	-0.23217	-0.145512572	0.337879101	0.086660745	0.570052418	0.483391673	0.434253485	9.69E-10	4.44E-09
sp|Q6B0K9|HBM_HUMAN	8	4	7	3	-0.40272	-0.008090311	0.606140441	0.394634111	1.008864862	0.614230751	0.621083832	0.159473245	0.401481465
sp|Q9UGT4|SUSD2_HUMAN	7	40	76	33	0.081278	0.003640831	0.057746134	-0.077637221	-0.023531918	0.054105303	0.321853466	0.929902155	0.614635933
sp|P15531|NDKA_HUMAN	42	40	76	33	-0.33588	-0.105492124	0.165339494	0.230392181	0.501223799	0.270831618	0.018963615	6.10E-06	0.008460693
sp|P07814|SYEP_HUMAN	3	37	69	30	-0.3997	-0.164149395	0.267859191	0.235550269	0.667558855	0.432008586	0.071741955	2.05E-06	0.000659917
sp|P42224|STAT1_HUMAN	39	18	34	15	-0.54305	-0.223130075	0.242940656	0.319924791	0.785995522	0.46607073	0.227878284	0.003261471	0.066477687
sp|Q5JS37|NHLC3_HUMAN	10	33	62	27	-0.08304	-0.025850085	0.172017985	0.057191655	0.255059725	0.19786807	0.600036576	0.001459504	0.006342873
sp|P67870|CSK2B_HUMAN	10	23	41	18	0.058679	-0.009287538	0.103138239	-0.067966945	0.044458831	0.112425776	0.608346739	0.863653295	0.319094209
sp|P19367|HXK1_HUMAN	80	33	62	27	0.088627	-0.422535215	-0.136585828	-0.511162585	-0.225213198	0.285949387	8.25E-05	0.251927516	0.062744005
sp|P62826|RAN_HUMAN	21	40	76	33	-0.297	-0.071188584	0.288181641	0.225809511	0.585179737	0.359370225	0.02940403	4.00E-07	0.000530778
sp|P01857|IGHG1_HUMAN	2	40	76	33	-0.4312	-0.21572312	0.223048232	0.215473856	0.654245209	0.438771352	0.273795693	0.000439581	0.01044863
sp|Q96S96|PEBP4_HUMAN	1	40	76	33	0.127081	0.209943017	0.276355338	0.082861699	0.14927402	0.066412321	0.450391533	0.170679857	0.636658889
sp|Q8TAX7|MUC7_HUMAN	2	11	21	9	0.015322	-0.165687424	-0.171298826	-0.181009427	-0.186620829	-0.005611402	0.384869789	0.495922008	0.999176004
sp|Q92542|NICA_HUMAN	3	15	27	12	0.021522	0.026244841	0.126217834	0.004723223	0.104696217	0.099972993	0.998672114	0.639758103	0.602415694
sp|Q9UBS4|DJB11_HUMAN	13	23	41	17	-0.14516	-0.076520817	0.098988255	0.06864194	0.244151011	0.175509071	0.755025099	0.102095878	0.23013643
sp|P98172|EFNB1_HUMAN	2	40	76	33	-0.28156	-0.138339178	0.327424692	0.143217326	0.608981196	0.46576387	0.261867052	3.99E-07	1.24E-05
sp|P41218|MNDA_HUMAN	1	14	28	12	-0.46228	-0.447059714	0.514861471	0.015219545	0.97714073	0.961921185	0.998453653	0.017920809	0.007020261
sp|P28062|PSB8_HUMAN	5	40	76	33	-0.39403	-0.239334468	0.273672313	0.15469756	0.667704341	0.513006781	0.292010193	8.18E-07	1.98E-05
sp|Q15818|NPTX1_HUMAN	21	36	69	31	0.190353	0.135726554	0.065250113	-0.054626766	-0.125103208	-0.070476442	0.842588024	0.53301142	0.772971672
sp|P31944|CASPE_HUMAN	1	30	56	24	-0.29526	-0.283982978	-0.552497572	0.011280201	-0.257234393	-0.268514594	0.99844969	0.578832799	0.473004689
sp|Q99784|NOE1_HUMAN	26	40	76	33	0.177181	0.152502415	0.113748594	-0.024678471	-0.063432293	-0.038753821	0.735047761	0.249762111	0.514820136
sp|P17538|CTRB1_HUMAN	33	40	76	33	-0.0701	-0.022771653	0.062959961	0.0473281	0.133059713	0.085731614	0.765590044	0.237218991	0.465127684
sp|P00326|ADH1G_HUMAN	10	30	55	23	-0.6153	-0.26542586	0.073738383	0.349871886	0.68903613	0.339164243	0.144761377	0.007881176	0.217514799
sp|Q9P2T1|GMPR2_HUMAN	3	40	76	33	-0.08769	-0.066912386	0.281172952	0.020781021	0.368866359	0.348085338	0.984859307	0.040445107	0.026788774
sp|P55083|MFAP4_HUMAN	8	37	69	30	0.007503	-0.04250214	0.263539282	-0.050005435	0.256035988	0.306041422	0.82873403	0.037870349	0.003182575
sp|P02462|CO4A1_HUMAN	1	36	69	30	-0.05744	-0.048157983	0.190623327	0.009286888	0.248068198	0.23878131	0.99549375	0.113591109	0.07698687
sp|A6NGU5|GGT3_HUMAN	3	40	76	33	-0.26162	-0.205557798	0.150958776	0.056058179	0.412574752	0.356516574	0.847254422	0.002890931	0.003811102
sp|P14778|IL1R1_HUMAN	3	40	76	33	0.000684	0.056083913	-0.003616071	0.055399805	-0.004300179	-0.059699985	0.357511775	0.995686498	0.350464111
sp|Q9GZP4|PITH1_HUMAN	3	40	76	33	-0.29993	-0.108672522	0.270153336	0.191256853	0.570082711	0.378825858	0.09776038	2.50E-06	0.00049873
sp|Q8IX30|SCUB3_HUMAN	1	37	69	30	0.001259	-0.169032603	0.147625731	-0.170291375	0.146366959	0.316658334	0.067743333	0.249615222	0.00046663
sp|Q9ULC4|MCTS1_HUMAN	1	26	48	20	-0.22348	0.054931252	0.419521599	0.27841284	0.643003188	0.364590347	0.243280642	0.008120327	0.133781405
sp|P14222|PERF_HUMAN	8	40	76	33	0.091129	0.105622314	0.058832556	0.014493369	-0.032296389	-0.046789757	0.941138248	0.812596422	0.575673515
sp|Q495W5|FUT11_HUMAN	2	40	76	33	0.108765	0.086488866	0.138954473	-0.022275827	0.03018978	0.052465607	0.863583823	0.830445182	0.491624175
sp|Q9UJA9|ENPP5_HUMAN	1	16	27	11	0.176317	-0.007929412	-0.105852776	-0.184246362	-0.282169726	-0.097923364	0.02915102	0.005625011	0.43720768
sp|Q9Y644|RFNG_HUMAN	16	15	28	13	0.159421	0.129199002	0.151982507	-0.030222233	-0.007438728	0.022783504	0.921348444	0.996461479	0.958530727
sp|Q92485|ASM3B_HUMAN	16	12	20	8	-0.03864	-0.0625871	0.188787148	-0.023946077	0.227428171	0.251374248	0.968131201	0.170043955	0.080616448
sp|P41439|FOLR3_HUMAN	57	40	76	33	-0.32058	-0.075712633	0.147568776	0.244870686	0.468152095	0.223281409	0.032665611	0.000265268	0.080405976
sp|P55209|NP1L1_HUMAN	1	40	76	33	-0.255	-0.319879806	-0.102840044	-0.06488267	0.152157092	0.217039763	0.923251092	0.739122803	0.459004066
sp|Q13555|KCC2G_HUMAN	17	37	69	30	0.014003	0.094399197	-0.083040352	0.080395908	-0.09704364	-0.177439549	0.236327209	0.235578602	0.002968289
sp|P50281|MMP14_HUMAN	11	14	27	12	-0.20374	0.097454623	0.788683657	0.301192763	0.992421797	0.691229034	0.166622672	1.66E-05	0.000580507
sp|O00264|PGRC1_HUMAN	67	40	76	33	-0.03511	-0.007208331	0.240999601	0.027904541	0.276112473	0.248207932	0.881225137	0.000370234	0.000300816
sp|P62256|UBE2H_HUMAN	52	4	7	2	-0.0076	-0.056069565	-0.372923779	-0.04847069	-0.365324904	-0.316854214	0.982023822	0.599046316	0.635997002
sp|Q5VVQ6|OTU1_HUMAN	153	37	69	30	-0.02808	0.029818186	0.2020785	0.057895415	0.230155729	0.172260314	0.736433241	0.039955976	0.100311919
sp|Q9NR19|ACSA_HUMAN	2	14	28	12	0.061823	0.145390544	0.494910268	0.083567671	0.433087394	0.349519723	0.9023794	0.159763774	0.209554588
sp|Q13283|G3BP1_HUMAN	7	18	34	15	-0.24801	-0.116212096	0.210492719	0.131793292	0.458498106	0.326704814	0.678626045	0.045227368	0.129964915
sp|Q7Z5L0|VMO1_HUMAN	12	40	76	33	-0.48779	-0.346312225	0.302235796	0.141479445	0.790027466	0.648548021	0.389751659	2.79E-08	2.51E-07
sp|P54760|EPHB4_HUMAN	7	40	76	33	0.020349	0.043549568	0.263517066	0.023201049	0.243168548	0.219967498	0.906044711	0.000933773	0.000713406
sp|P05997|CO5A2_HUMAN	2	40	76	33	0.037691	0.058499135	0.289055753	0.020807701	0.251364319	0.230556618	0.942025891	0.003420499	0.002343335
sp|Q15008|PSMD6_HUMAN	619	15	28	11	-0.06252	-0.023407954	0.247308746	0.039112439	0.309829139	0.2707167	0.956671171	0.176269652	0.191607521
sp|O75503|CLN5_HUMAN	11	40	76	33	0.043991	-0.017057598	0.148423176	-0.061048272	0.104432502	0.165480774	0.56850297	0.321922065	0.02922191
sp|P16444|DPEP1_HUMAN	5	37	69	30	0.139027	0.064790629	-0.004655915	-0.074236567	-0.143683111	-0.069446544	0.567073475	0.235192677	0.64945087
sp|Q9UI15|TAGL3_HUMAN	7	40	76	33	-0.0829	-0.135715719	0.027849623	-0.052819844	0.110745497	0.163565342	0.734849682	0.39520895	0.079336418
sp|Q86X76|NIT1_HUMAN	28	25	49	21	-0.37041	-0.073087753	0.342479941	0.297319183	0.712886876	0.415567694	0.071578166	7.41E-05	0.011581595
sp|P12931|SRC_HUMAN	62	40	76	33	-0.07476	-0.035906568	0.045051929	0.038854162	0.11981266	0.080958497	0.927276868	0.610690518	0.750395579
sp|O14894|T4S5_HUMAN	31	4	6	2	-2.1392	-1.44299171	2.694655742	0.696203907	4.833851359	4.137647452	0.824130384	0.030940855	0.048284016
sp|P51606|RENBP_HUMAN	12	18	35	16	-0.17698	-0.037077856	0.042047227	0.139903728	0.21902881	0.079125082	0.557821874	0.363750515	0.840444034
sp|P25774|CATS_HUMAN	5	40	76	33	-0.10333	-0.047667696	0.128174033	0.055663806	0.231505534	0.175841728	0.475070825	0.000262648	0.002085542
sp|P32320|CDD_HUMAN	19	36	69	30	0.11084	0.015629004	0.165220549	-0.095210976	0.054380569	0.149591545	0.240514	0.722118239	0.047193724
sp|Q8TDF6|GRP4_HUMAN	1	25	48	22	-0.40481	-0.677191303	-0.155136895	-0.272380683	0.249673724	0.522054408	0.424684728	0.597608399	0.060390887
sp|Q96CG8|CTHR1_HUMAN	16	32	62	27	-0.30181	-0.208142301	0.246107618	0.093670966	0.547920885	0.454249919	0.586841248	1.36E-05	4.45E-05
sp|Q8NFL0|B3GN7_HUMAN	4	40	76	33	-0.02187	-0.014173325	0.064567211	0.007694633	0.086435169	0.078740536	0.97169524	0.087391374	0.076509283
sp|Q9H1R3|MYLK2_HUMAN	1	4	6	3	-0.17246	-0.219235197	0.972555048	-0.046777278	1.145012968	1.191790246	0.995107815	0.174881463	0.120514641
sp|Q9H3U1|UN45A_HUMAN	4	29	56	24	-0.73465	-0.434990619	0.036316796	0.299664234	0.770971649	0.471307415	0.362817815	0.012088678	0.113930304
sp|P07355|ANXA2_HUMAN	2	17	35	15	-0.07833	0.168711042	0.318798201	0.24704006	0.397127219	0.150087159	0.314229511	0.129002403	0.671706483
sp|P40763|STAT3_HUMAN	13	14	28	12	-0.01819	0.047415804	0.129219358	0.065608137	0.147411691	0.081803554	0.801622273	0.466253763	0.734368483
sp|P08311|CATG_HUMAN	4	40	76	33	-0.61053	-0.505461915	0.057359062	0.105064436	0.667885413	0.562820977	0.624078996	7.65E-06	2.16E-05
sp|Q7RTY9|PRS41_HUMAN	3	40	76	33	0.06036	0.057634755	0.152716568	-0.002725124	0.092356688	0.095081812	0.999234921	0.547348417	0.444408017
sp|Q9BQR3|PRS27_HUMAN	61	4	7	3	-0.09488	-0.026759395	-0.179417772	0.068124751	-0.084533626	-0.152658376	0.78777819	0.781020603	0.396578781
sp|Q9H3G5|CPVL_HUMAN	15	40	76	33	0.056576	-0.032582574	-0.082632422	-0.089158645	-0.139208493	-0.050049848	0.323241247	0.151877898	0.729664094
sp|P42773|CDN2C_HUMAN	6	15	27	11	0.022155	0.162193723	0.384696832	0.14003905	0.36254216	0.222503109	0.273706802	0.005447949	0.076360838
sp|Q15375|EPHA7_HUMAN	47	40	76	33	-0.01111	0.019853158	0.182256575	0.030961321	0.193364738	0.162403417	0.875802584	0.031814418	0.044799293
sp|P01876|IGHA1_HUMAN	2	40	76	33	-0.43794	-0.376192359	0.223296853	0.061747113	0.661236325	0.599489211	0.88564708	0.000148826	0.000102487
sp|P54710|ATNG_HUMAN	2	4	6	3	-0.29558	-0.129104609	0.013977829	0.166471712	0.30955415	0.143082439	0.858521572	0.691909194	0.909844206
sp|Q16186|ADRM1_HUMAN	35	11	20	9	-0.0378	-0.155216405	0.603078117	-0.117412997	0.640881526	0.758294523	0.78590973	0.012239329	0.000815503
sp|P50991|TCPD_HUMAN	28	30	55	25	-0.26603	-0.211915712	0.078792343	0.054118046	0.344826101	0.290708055	0.901793767	0.058132516	0.077457711
sp|Q99542|MMP19_HUMAN	2	40	76	33	-0.34677	-0.273336252	0.196054784	0.073429018	0.542820055	0.469391036	0.485959896	1.96E-10	4.92E-10
sp|Q15223|NECT1_HUMAN	6	40	76	33	0.11228	0.128504585	-0.049449923	0.01622428	-0.161730227	-0.177954508	0.913955494	0.002972115	0.000163162
sp|Q3T906|GNPTA_HUMAN	2	4	7	3	0.144514	0.201437318	-0.177453336	0.056923356	-0.321967298	-0.378890655	0.787209321	0.025528085	0.005173508
sp|O14798|TR10C_HUMAN	1	40	76	33	-0.11044	-0.175894711	0.321816665	-0.065457333	0.432254042	0.497711375	0.825754441	0.004260005	0.000134777
sp|P27701|CD82_HUMAN	10	29	55	24	-0.38176	-0.141851361	0.372561538	0.239905844	0.754318744	0.514412899	0.133255916	5.19E-06	0.000499796
sp|Q14061|COX17_HUMAN	9	7	13	7	-0.32402	-0.29588121	0.593901935	0.028140254	0.917923399	0.889783145	0.997238392	0.127522045	0.084698843
sp|P31947|1433S_HUMAN	14	7	14	6	-0.98284	-0.815716758	-0.454135171	0.167125488	0.528707075	0.361581586	0.592734372	0.040640684	0.12826348
sp|P09429|HMGB1_HUMAN	1	14	28	12	-0.47853	-0.331578184	0.61092487	0.146949607	1.08945266	0.942503053	0.859705883	0.005943258	0.006730612
sp|Q02790|FKBP4_HUMAN	1	22	41	17	-0.34895	-0.221588886	0.137548868	0.127363418	0.486501172	0.359137754	0.662477777	0.02226784	0.070813737
sp|P04156|PRIO_HUMAN	10	40	76	33	-0.14898	-0.193623945	0.211614635	-0.044641752	0.360596828	0.40523858	0.821682368	0.000284474	3.36E-06
sp|Q8TAC1|RFESD_HUMAN	5	4	7	3	-0.23068	0.490508985	0.185926449	0.721191401	0.416608864	-0.304582536	0.229601569	0.692059509	0.783566162
sp|P21291|CSRP1_HUMAN	12	40	76	33	-0.21184	-0.235518009	-0.000997138	-0.02367327	0.2108476	0.234520871	0.984781158	0.435129161	0.271589766
sp|P04746|AMYP_HUMAN	1	40	76	33	-0.00471	0.030860542	0.016209672	0.035568713	0.020917843	-0.014650871	0.941116386	0.985614936	0.99099549
sp|P05107|ITB2_HUMAN	9	40	76	33	-0.10672	-0.018046674	0.107745021	0.088674903	0.214466598	0.125791695	0.094217886	0.000130819	0.016565576
sp|P52849|NDST2_HUMAN	3	12	20	9	0.058896	0.12117663	0.175257786	0.062281048	0.116362204	0.054081156	0.762575016	0.526470375	0.843949889
sp|P50851|LRBA_HUMAN	3	4	7	3	-0.26951	-0.030608003	0.674677814	0.238906536	0.944192353	0.705285817	0.676525719	0.043527638	0.097816647
sp|P14868|SYDC_HUMAN	4	40	76	33	-0.37456	-0.277898388	0.059468622	0.096666584	0.434033594	0.33736701	0.632036521	0.002403155	0.009118843
sp|Q9H3R1|NDST4_HUMAN	9	19	34	15	-0.28799	0.014444225	-0.150349268	0.302432797	0.137639304	-0.164793493	0.002739912	0.39748484	0.197816381
sp|Q6UXH9|PAMR1_HUMAN	1	40	76	33	-0.00027	-0.016141911	-0.006994618	-0.01587588	-0.006728587	0.009147293	0.90921999	0.98826382	0.972622927

sp|Q9H2X0|CHRD_HUMAN	1	8	13	6	0.182855	0.085112697	-0.038705507	-0.097742005	-0.221560209	-0.123818205	0.658885002	0.242314743	0.576039218
sp|P01861|IGHG4_HUMAN	18	40	76	33	-0.33895	-0.141077692	-0.098058106	0.197872395	0.240891981	0.043019587	0.105971624	0.100846328	0.909116626
sp|Q9UK05|GDF2_HUMAN	12	37	69	29	-0.01669	-0.015234448	0.103586624	0.001450623	0.120271695	0.118821072	0.999509997	0.108815415	0.066907094
sp|P61604|CH10_HUMAN	1	33	62	28	-0.14643	-0.003085354	0.443787702	0.143345481	0.590218536	0.446873056	0.547058852	0.001228041	0.006823874
sp|Q9GZM7|TINAL_HUMAN	16	29	55	24	-0.20839	-0.101380621	0.017524449	0.107005289	0.225910359	0.11890507	0.438349493	0.083122545	0.408487715
sp|Q9Y235|ABEC2_HUMAN	3	4	6	3	0.242025	0.007803717	1.895791247	-0.234221647	1.653765883	1.887987531	0.963732484	0.311301933	0.186558221
sp|O60449|LY75_HUMAN	8	40	76	33	-0.02348	0.037700989	-0.041825469	0.061181441	-0.018345017	-0.079526458	0.525739084	0.960652524	0.386481259
sp|P01893|HLAH_HUMAN	90	22	41	19	-0.24261	-0.173590239	0.152786297	0.069018128	0.395394664	0.326376536	0.854238411	0.030566166	0.047463448
sp|Q9H7M9|VISTA_HUMAN	6	15	27	11	-0.33166	-0.115404578	0.05805084	0.216254246	0.389709665	0.173455418	0.222997285	0.04554505	0.451255098
sp|Q06124|PTN11_HUMAN	1	40	76	33	-0.37647	-0.011416875	0.346261433	0.365050437	0.722728746	0.357678309	0.00273989	4.02E-07	0.006631412
sp|P36959|GMPR1_HUMAN	4	31	55	23	0.028318	0.027789471	0.286400627	-0.000528422	0.258082734	0.258611156	0.999993354	0.352960804	0.277937848
sp|Q14242|SELPL_HUMAN	11	28	56	25	0.148259	0.021884195	0.241575491	-0.126374608	0.093316688	0.219691296	0.504884629	0.767108915	0.152199791
sp|P30520|PURA2_HUMAN	1	28	56	24	-0.24482	-0.114437384	0.310701804	0.130386215	0.555525402	0.425139188	0.50875674	0.000425156	0.002389361
sp|Q9BU40|CRDL1_HUMAN	12	36	69	30	-0.0169	-0.058748148	0.207767129	-0.041846156	0.224669121	0.266515277	0.726195483	0.002487707	3.29E-05
sp|Q14982|OPCM_HUMAN	2	40	76	33	0.123098	-0.032612387	-0.058512219	-0.155709964	-0.181609796	-0.025899832	0.028500907	0.035206729	0.914296645
sp|O60888|CUTA_HUMAN	4	40	76	33	0.16433	0.264993916	0.027209957	0.100663627	-0.137120332	-0.237783959	0.170071818	0.1047041	0.000288784
sp|P13693|TCTP_HUMAN	6	40	76	33	-0.06581	-0.053523713	0.26422203	0.012286383	0.330032126	0.317745743	0.989859795	0.007999429	0.003519508
sp|Q8N3J6|CADM2_HUMAN	1	32	62	28	0.051778	-0.104393131	-0.131568075	-0.156171168	-0.183346113	-0.027174945	0.056605723	0.060649286	0.921111379
sp|O95450|ATS2_HUMAN	11	19	34	13	-0.70765	-0.580662711	0.832171499	0.12698542	1.539819629	1.41283421	0.869422204	2.34E-05	1.86E-05
sp|Q06418|TYRO3_HUMAN	9	40	76	33	0.083125	0.017367041	0.001555692	-0.065757619	-0.081568968	-0.015811349	0.261010383	0.24055139	0.933223897
sp|P36888|FLT3_HUMAN	1	31	55	23	0.175336	0.272050175	-0.044271096	0.09671467	-0.219606602	-0.316321271	0.465406365	0.076887391	0.001944089
sp|O60568|PLOD3_HUMAN	37	40	76	33	-0.08285	0.032384678	0.271720659	0.11523962	0.354575601	0.239335981	0.130314053	5.60E-06	0.000659728
sp|Q9P289|STK26_HUMAN	3	40	76	33	-0.09143	-0.129272507	0.169489178	-0.037840097	0.260921588	0.298761685	0.963041474	0.295228617	0.132860817
sp|P46109|CRKL_HUMAN	24	40	76	33	0.027208	-0.010515511	0.268209234	-0.037723226	0.24100152	0.278724745	0.911358465	0.078283512	0.014105917
sp|Q9UJ14|GGT7_HUMAN	2	40	76	33	-0.07914	-0.249036817	-0.438043758	-0.169895247	-0.358902188	-0.189006942	0.073883616	0.000483211	0.059333443
sp|O00233|PSMD9_HUMAN	2	32	62	27	-0.21098	-0.090593385	0.238470529	0.120390315	0.449454229	0.329063914	0.373195948	0.000163397	0.002081029
sp|Q9Y6Y9|LY96_HUMAN	15	33	62	27	-0.23817	-0.117661983	0.343416051	0.120509494	0.581587529	0.461078034	0.167827015	1.12E-10	5.79E-09
sp|Q8IYT4|KATL2_HUMAN	2	26	48	21	-0.40884	-0.407012088	-0.147413072	0.001824908	0.261423924	0.259599016	0.99996663	0.625954463	0.559912078
sp|P46926|GNPI1_HUMAN	22	28	56	24	-0.03629	0.051006322	0.274352523	0.087301207	0.310647408	0.223346201	0.536991503	0.005848324	0.0294107
sp|P21810|PGS1_HUMAN	1	25	49	22	-0.20547	-0.088656015	0.279986376	0.116816479	0.485458869	0.36864239	0.454663307	0.000178247	0.001315371
sp|Q86Z14|KLOTB_HUMAN	8	36	69	31	-0.02803	0.048422217	0.045223113	0.076451837	0.073252733	-0.003199104	0.649272544	0.756038452	0.999313097
sp|Q08209|PP2BA_HUMAN	5	8	14	6	-0.17508	0.25556345	-0.16362823	0.430645044	0.011453364	-0.41919168	0.052972307	0.998407428	0.094733524
sp|Q8NCW5|NNRE_HUMAN	1	40	76	33	0.014373	0.086724741	0.331567667	0.07235222	0.317195147	0.244842926	0.429161794	3.59E-05	0.000361145
sp|O95394|AGM1_HUMAN	28	32	62	28	-0.54778	-0.204942061	0.322578634	0.342834157	0.870354852	0.527520695	0.008239257	6.43E-09	5.42E-05
sp|P14550|AK1A1_HUMAN	4	40	76	33	-0.03364	0.036474016	0.386992757	0.070115287	0.420634028	0.350518741	0.567224357	3.56E-06	1.34E-05
sp|Q6UX06|OLFM4_HUMAN	13	25	48	21	-0.24045	-0.174527579	0.230457424	0.065924885	0.470909888	0.404985003	0.889475587	0.019727171	0.024064377
sp|Q8IX05|CD302_HUMAN	15	4	7	3	0.043217	-0.044726091	0.815035297	-0.087943161	0.771818228	0.859761388	0.979288917	0.371963041	0.23724257
sp|O60512|B4GT3_HUMAN	5	11	21	9	0.112409	0.29740452	0.490235625	0.18499541	0.377826514	0.192831105	0.591445058	0.23216581	0.607502815
sp|Q2TAA2|IAH1_HUMAN	3	29	55	24	-0.2358	-0.169052178	0.135837335	0.066745355	0.371634869	0.304889514	0.796551599	0.009978186	0.018737849
sp|Q13045|FLII_HUMAN	6	29	55	23	-0.04968	-0.161125844	0.211896459	-0.111448424	0.261573879	0.373022303	0.769819509	0.38123858	0.087862519
sp|P24844|MYL9_HUMAN	161	10	21	9	-0.37316	-0.086718659	0.728294922	0.286446334	1.101459915	0.815013581	0.483456032	0.001792131	0.00804351
sp|Q9GZP0|PDGFD_HUMAN	3	36	69	30	-0.1472	0.115682105	0.362801189	0.2628833	0.510002383	0.247119083	0.026355029	0.000128686	0.057051443
sp|Q15782|CH3L2_HUMAN	14	14	28	13	0.148082	0.115876526	-0.035976594	-0.032205096	-0.184058216	-0.15185312	0.951627586	0.319652662	0.358729182
sp|P26006|ITA3_HUMAN	3	25	48	22	0.063785	-0.027806788	0.125544934	-0.091592105	0.061759617	0.153351722	0.50182045	0.798753061	0.174343071
sp|Q9NR71|ASAH2_HUMAN	4	40	76	33	-0.03685	-0.06695104	-0.306867687	-0.030104086	-0.270020733	-0.239916647	0.960518065	0.112351584	0.111261433
sp|Q8N2Q7|NLGN1_HUMAN	12	11	21	10	0.159709	0.043791797	0.018372785	-0.115916763	-0.141335776	-0.025419012	0.475958789	0.449534537	0.966366315
sp|Q92686|NEUG_HUMAN	2	40	76	33	-0.35608	-0.20345141	0.118201517	0.152632522	0.474285449	0.321652926	0.616731563	0.043612888	0.156068709
sp|P04626|ERBB2_HUMAN	3	40	76	33	0.166701	0.04311158	-0.092623519	-0.123589182	-0.259324281	-0.135735098	0.025863961	3.01E-05	0.021013667
sp|P10124|SRGN_HUMAN	3	40	76	33	-0.26274	0.078045807	0.124099979	0.340781897	0.386836068	0.046054171	0.00484298	0.008520002	0.913760914
sp|P28066|PSA5_HUMAN	2	40	76	33	-0.1923	0.005811276	0.547263422	0.198114162	0.739566308	0.541452146	0.143710559	8.16E-08	9.19E-06
sp|P50579|MAP2_HUMAN	61	8	13	6	0.324526	0.256840937	0.947388096	-0.067684787	0.622862372	0.690547159	0.982243167	0.366429439	0.235103245
sp|P06132|DCUP_HUMAN	5	40	76	33	-0.20517	-0.107286474	0.215745765	0.097882211	0.42091445	0.323032239	0.551208602	0.000810631	0.004417019
sp|P35813|PPM1A_HUMAN	1	40	76	33	-0.11144	-0.141866174	0.120499451	-0.030428141	0.231937483	0.262365624	0.922555779	0.043711825	0.006723818
sp|Q13616|CUL1_HUMAN	4	37	69	30	-0.17642	-0.096776994	0.191334752	0.07964018	0.367751926	0.288111746	0.524031985	0.000166045	0.001040921
sp|O43570|CAH12_HUMAN	2	4	7	3	-0.3037	-0.228098991	0.779589368	0.075604857	1.083293216	1.007688359	0.989153748	0.2650995	0.247175047
sp|P01266|THYG_HUMAN	7	29	55	24	0.358235	0.471453017	0.340072791	0.113217568	-0.018162657	-0.131380225	0.851819514	0.997143517	0.82698666
sp|O15067|PUR4_HUMAN	18	29	55	24	-0.22361	-0.036431833	0.465392684	0.187182719	0.689007237	0.501824518	0.267788196	1.74E-05	0.000457835
sp|Q9UQ52|CNTN6_HUMAN	1	18	35	15	0.204035	0.120331428	0.035233841	-0.083703504	-0.168801091	-0.085097588	0.261921533	0.027492254	0.293516238
sp|O15117|FYB1_HUMAN	1	33	62	27	-0.12514	-0.100649507	0.122384711	0.024489813	0.247524031	0.223034218	0.978633496	0.224401551	0.215254224
sp|P68036|UB2L3_HUMAN	6	40	76	33	-0.07117	0.130223237	0.426648097	0.201395764	0.497820625	0.296424861	0.105868755	0.000139999	0.015181779
sp|P12830|CADH1_HUMAN	14	40	76	33	-0.03229	-0.026784696	0.277443259	0.005505087	0.309733042	0.304227955	0.996158874	0.000420296	8.26E-05
sp|P32926|DSG3_HUMAN	5	8	14	6	0.068683	0.035822753	-0.018120873	-0.032860078	-0.086803704	-0.053943626	0.979193925	0.906219524	0.954380243
sp|P13861|KAP2_HUMAN	1	11	20	9	-0.08651	-0.059958663	0.495125969	0.026552931	0.581637563	0.555084632	0.986064973	0.015995798	0.009572349
sp|Q05315|LEG10_HUMAN	1	4	6	3	0.372435	0.222275542	0.223598758	-0.150159235	-0.14883602	0.001323215	0.922625785	0.944920251	0.999994745
sp|Q0ZGT2|NEXN_HUMAN	30	33	62	27	-0.32762	-0.332695008	-0.013904212	-0.005073094	0.313717702	0.318790797	0.999529794	0.294699021	0.203742827
sp|Q14203|DCTN1_HUMAN	24	11	21	9	-0.14221	0.166154282	0.668519745	0.30836383	0.810729292	0.502365463	0.244620809	0.002903672	0.045071938
sp|P35611|ADDA_HUMAN	14	4	7	3	-0.72214	-1.12190512	-0.758646192	-0.399763296	-0.036504368	0.363258928	0.889066329	0.999332496	0.922761621
sp|Q8IUK5|PLDX1_HUMAN	12	40	76	33	0.108717	0.06885278	-0.066541023	-0.039864461	-0.175258264	-0.135393803	0.463058787	8.04E-05	0.000673259
sp|Q16820|MEP1B_HUMAN	2	40	76	33	-0.0459	-0.054007058	-0.203514096	-0.008102569	-0.157609608	-0.149507039	0.99793505	0.584746029	0.5412468
sp|O60279|SUSD5_HUMAN	1	40	76	33	-0.10143	-0.238873002	0.062674858	-0.137446364	0.164101496	0.30154786	0.026856804	0.028445199	9.25E-07
sp|Q16799|RTN1_HUMAN	4	4	7	3	-0.02168	0.043119517	0.625568593	0.064799385	0.647248461	0.582449076	0.97712285	0.255204312	0.257678809
sp|O00232|PSD12_HUMAN	80	14	28	12	-0.12468	-0.036505771	0.582089491	0.088177622	0.706772883	0.618595262	0.81385769	0.00044972	0.000462118
sp|P41240|CSK_HUMAN	2	40	76	33	-0.01294	-0.186290873	-0.09160977	-0.173347315	-0.078666211	0.094681103	0.223075739	0.805659679	0.671958838
sp|P54315|LIPR1_HUMAN	2	33	62	27	-0.10534	-0.135951751	-0.05977855	-0.030607828	0.045565373	0.076173201	0.97964006	0.969060018	0.894812414
sp|P28332|ADH6_HUMAN	2	16	27	11	-0.90311	-0.354525393	0.286371204	0.54858163	1.189478227	0.640896597	0.115295064	0.002408308	0.101564478
sp|Q9NYQ6|CELR1_HUMAN	19	18	34	15	-0.13659	-0.093917846	-0.215411126	0.042676316	-0.078816965	-0.121493281	0.854631621	0.690094783	0.331114961
sp|P05120|PAI2_HUMAN	1	29	55	24	-0.19388	-0.127112589	0.059751664	0.066768509	0.253632762	0.186864253	0.76497861	0.074792756	0.163778126
sp|Q5VTT5|MYOM3_HUMAN	11	29	55	24	0.081978	0.006319462	-0.037236663	-0.075658903	-0.119215029	-0.043556126	0.699683911	0.542729105	0.900770764
sp|Q9Y275|TN13B_HUMAN	8	40	76	33	-0.30633	-0.209066726	-0.093058088	0.097265363	0.213274002	0.116008638	0.347091224	0.032532751	0.267669309
sp|P30048|PRDX3_HUMAN	8	11	21	9	-0.03329	-0.025042596	0.191990004	0.008251078	0.225283678	0.2170326	0.996463644	0.179180119	0.133583593
sp|P04921|GLPC_HUMAN	12	3	7	4	-0.24474	-0.266212563	0.124731234	-0.021475412	0.369468385	0.390943797	0.996410127	0.447293964	0.278772261
sp|Q9Y4G6|TLN2_HUMAN	101	26	48	21	-0.14294	-0.176675	-0.016721784	-0.033730261	0.126222955	0.159953216	0.980014445	0.823465048	0.676309993
sp|O00757|F16P2_HUMAN	5	40	76	33	-0.1148	0.033058078	0.286048726	0.147854549	0.400845198	0.252990649	0.263480178	0.001617659	0.034815286
sp|Q9P121|NTRI_HUMAN	3	40	76	33	0.21461	0.102479298	-0.073276308	-0.112130715	-0.28788632	-0.175755605	0.014066348	3.26E-08	0.00014992
sp|Q8NFT8|DNER_HUMAN	3	40	76	33	0.236844	0.073399444	-0.255630233	-0.163444206	-0.492473884	-0.329029678	0.007712233	8.72E-12	1.54E-07
sp|Q9ULC0|MUCEN_HUMAN	2	37	69	30	-0.09772	-0.086262422	0.005451596	0.011458792	0.10317281	0.091714018	0.990855389	0.600865114	0.601685888
sp|P50895|BCAM_HUMAN	11	40	76	33	0.013681	0.023430703	0.209895876	0.009749974	0.196215147	0.186465173	0.977843841	0.00274851	0.001203388
sp|P31151|S10A7_HUMAN	2	37	69	30	-1.68059	-1.992991441	-2.257660232	-0.312400589	-0.57706938	-0.264668791	0.620946546	0.3294054	0.742652801
sp|P49746|TSP3_HUMAN	9	40	76	33	0.001888	0.212014652	0.17824857	0.210126297	0.176360216	-0.033766082	0.038897881	0.200887458	0.926734376
sp|P30566|PUR8_HUMAN	2	40	76	33	-0.6354	0.108032407	0.36597618	0.74343696	1.001380734	0.257943774	1.79E-11	1.59E-13	0.042221022
sp|P14621|ACYP2_HUMAN	2	18	34	15	-0.28399	-0.287815046	0.202076011	-0.003820646	0.48607041	0.489891056	0.999576307	0.012480003	0.003916236
sp|P19438|TNR1A_HUMAN	29	37	69	30	-0.23864	-0.323303096	0.091646067	-0.084660661	0.330288502	0.414949163	0.909676781	0.37485538	0.144578511
sp|Q99536|VAT1_HUMAN	2	40	76	33	-0.08111	-0.062827343	0.186661836	0.018280792	0.267769971	0.249489179	0.945724309	0.000474292	0.000225723
sp|P49327|FAS_HUMAN	3	22	41	18	-0.29062	0.224961969	0.706437435	0.515584292	0.997059758	0.481475466	0.011660962	2.81E-05	0.031852475
sp|P42702|LIFR_HUMAN	2	32	62	27	0.085746	0.144455717	0.142746761	0.058709685	0.05700073	-0.001708955	0.401368937	0.549179135	0.999303178
sp|A2VDF0|FUCM_HUMAN	4	25	48	22	-0.38446	-0.044865193	0.159846219	0.339591973	0.544303386	0.204711413	0.117190348	0.021752001	0.482000481
sp|P35998|PRS7_HUMAN	3	10	21	10	-0.49071	-0.109556582	0.156985397	0.381150142	0.647692121	0.266541979	0.123340634	0.015171584	0.347854313
sp|P48444|COPD_HUMAN	2	18	35	15	-0.06113	-0.074530274	0.733771976	-0.013404913	0.794897337	0.80830225	0.998281179	0.020881342	0.006572625
sp|Q6QNK2|AGRD1_HUMAN	1	29	55	25	0.130587	0.090988347	0.363966674	-0.039599121	0.233379206	0.272978327	0.798342164	0.005574721	0.000165078
sp|Q96BY9|SARAF_HUMAN	1	18	34	16	0.138896	0.061245739	0.212716605	-0.077650699	0.073820167	0.151470866	0.742152004	0.823362451	0.355500927
sp|P26885|FKBP2_HUMAN	1	36	69	30	-0.14415	-0.152888245	0.269605419	-0.008734915	0.413758749	0.422493664	0.996984395	0.011542569	0.002858338
sp|Q9UN36|NDRG2_HUMAN	1	14	27	12	-0.39963	-0.256772321	0.205171264	0.142857818	0.604801402	0.461943585	0.607540694	0.003859785	0.013665853
sp|O60547|GMDS_HUMAN	14	12	20	9	-0.15569	-0.13890428	-0.049966111	0.016785553	0.105723722	0.088938169	0.986920439	0.701550224	0.738442332
sp|P01137|TGFB1_HUMAN	3	40	76	33	-0.24918	0.047217375	0.154764372	0.296392413	0.40393941	0.107546997	0.001341859	0.000239049	0.444616017
sp|P40926|MDHM_HUMAN	24	37	69	29	-0.12191	-0.030462015	0.162068541	0.091448691	0.283979247	0.192530556	0.570871679	0.029284481	0.126048419

sp|P24298|ALAT1_HUMAN	2	40	76	33	-0.22069	0.004922728	0.086301778	0.225617688	0.306996739	0.08137905	0.065187415	0.03135812	0.726250917
sp|O75475|PSIP1_HUMAN	1	20	41	18	-0.36977	0.15969219	1.310937882	0.529457366	1.680703057	1.151245692	0.401405811	0.002568678	0.021807454
sp|P43234|CATO_HUMAN	7	36	69	30	0.058253	0.17579594	0.304351003	0.117542675	0.246097737	0.128555062	0.161195767	0.004853083	0.145532943
sp|Q9Y5S9|RBM8A_HUMAN	7	7	14	7	-0.13961	0.092546253	0.266089993	0.232158979	0.405702719	0.17354374	0.268736457	0.059857773	0.471089086
sp|Q9H8S9|MOB1A_HUMAN	2	40	76	33	0.162716	0.183810835	0.401354727	0.021094676	0.238638568	0.217543892	0.978260069	0.149169542	0.134021369
sp|Q96RP7|G3ST4_HUMAN	1	21	42	18	0.075034	0.068708069	0.16173594	-0.006326043	0.086701828	0.093027871	0.995086049	0.530510405	0.389121467
sp|Q6UW63|PLGT2_HUMAN	1	4	7	3	-0.01309	-0.121271697	0.044090953	-0.108186421	0.057176229	0.16536265	0.585407887	0.900351052	0.372386902
sp|Q9P1W8|SIRPG_HUMAN	3	25	48	22	-0.60404	-0.291472979	-0.144479675	0.312568993	0.459562297	0.146993304	0.45905775	0.303934566	0.852599602
sp|O76061|STC2_HUMAN	1	40	76	33	0.052432	0.12979858	0.218512991	0.077366484	0.166080895	0.088714411	0.178626757	0.005076615	0.137645584
sp|P36575|ARRC_HUMAN	5	21	42	19	0.128884	-0.006582434	0.21057501	-0.135466822	0.081690622	0.217157444	0.420393285	0.796996348	0.129861383
sp|Q16539|MK14_HUMAN	2	40	76	33	-0.06273	-0.126872169	0.116823948	-0.064141961	0.179554156	0.243696117	0.649846074	0.101720095	0.005503787
sp|P08134|RHOC_HUMAN	1	37	69	30	0.232162	0.23787826	0.513052361	0.005715872	0.280889973	0.2751741	0.998883996	0.162449887	0.111671811
sp|O14558|HSPB6_HUMAN	4	4	6	3	0.280811	0.292720133	1.45721134	0.011909172	1.176400378	1.164491207	0.999825301	0.337711319	0.294394821
sp|Q8IUZ5|AT2L2_HUMAN	7	40	76	33	0.046069	0.101838891	0.296409074	0.055769452	0.250339635	0.194570183	0.686961749	0.006877941	0.020858059
sp|Q9Y263|PLAP_HUMAN	3	29	55	24	0.115917	0.262442458	0.458112678	0.146525727	0.342195947	0.19567022	0.422097406	0.042537091	0.260569908
sp|Q9H993|ARMT1_HUMAN	5	30	55	23	-0.01697	0.175451939	0.410839732	0.192422943	0.427810735	0.235387793	0.110557224	0.001025951	0.064938726
sp|P62333|PRS10_HUMAN	2	21	42	18	-0.45219	-0.157604876	0.184560324	0.29458413	0.636749329	0.3421652	0.054890582	0.000187279	0.030476958
sp|Q13162|PRDX4_HUMAN	2	36	69	30	-0.36982	-0.152910207	0.307768221	0.216905159	0.677583587	0.460678428	0.073164336	1.83E-07	6.21E-05
sp|Q8NFY4|SEM6D_HUMAN	23	40	76	33	0.005236	-0.11288574	-0.242259232	-0.118122173	-0.247495666	-0.129373493	0.001092202	8.26E-09	0.000777655
sp|Q8IZP0|ABI1_HUMAN	1	39	76	33	0.059553	0.220400332	0.447801579	0.160847449	0.388248696	0.227401247	0.372992773	0.020902998	0.174526294
sp|Q9BQT9|CSTN3_HUMAN	2	36	69	30	0.00709	0.007990251	0.079781241	0.000900044	0.072691034	0.07179099	0.999849225	0.509103578	0.431782308
sp|P18065|IBP2_HUMAN	5	40	76	33	0.020491	-0.004612951	0.602380258	-0.0251042	0.581889008	0.606993208	0.964800005	7.19E-06	1.32E-07
sp|P31153|METK2_HUMAN	6	40	76	33	-0.23302	-0.054802912	0.247172094	0.178215554	0.48019056	0.301975006	0.05404848	1.74E-06	0.00085766
sp|Q9H1B5|XYLT2_HUMAN	1	40	76	33	-0.28457	-0.067928831	0.040873564	0.216645509	0.325447904	0.108802395	0.075910189	0.019091199	0.558243382
sp|Q08495|DEMA_HUMAN	1	28	55	24	-0.25911	-0.389182932	-0.025443825	-0.130077615	0.233661492	0.363739107	0.681486065	0.424685009	0.072694975
sp|Q13976|KGP1_HUMAN	6	6	14	7	0.239043	-0.234895648	0.081841211	-0.473938188	-0.157201329	0.316736859	0.535218745	0.94714487	0.730043669
sp|Q14032|BAAT_HUMAN	1	11	20	9	-0.22944	-0.12664067	0.482436537	0.102797186	0.711874392	0.609077207	0.914105041	0.062939614	0.077683643
sp|Q9H741|CL049_HUMAN	1	4	7	3	0.231817	0.294387988	0.391859144	0.062570929	0.160042085	0.097471156	0.725969804	0.276633423	0.536478805
sp|Q8WWX9|SELM_HUMAN	1	4	6	3	0.137166	-0.012428934	0.429091007	-0.149594983	0.291924959	0.441519942	0.775549317	0.515700373	0.202205777
sp|Q9UBR1|BUP1_HUMAN	7	33	62	27	0.028697	0.216703407	0.288982576	0.188006818	0.260285987	0.072279169	0.223994957	0.139991455	0.821850931
sp|Q96C23|GALM_HUMAN	2	10	21	9	-0.24404	-0.023044637	0.179660018	0.22099985	0.423704505	0.202704655	0.421047918	0.117944011	0.506285385
sp|Q9Y240|CLC11_HUMAN	30	40	76	33	-0.04901	0.00114192	0.246613364	0.05015039	0.295621834	0.245471444	0.694326861	0.000304609	0.000772365
sp|P28161|GSTM2_HUMAN	3	40	76	33	-0.11142	-0.174229337	-0.008741912	-0.062811477	0.102675947	0.165487425	0.73391634	0.566205338	0.156465959
sp|Q03013|GSTM4_HUMAN	2	14	28	13	-0.80234	-0.235094026	-0.055229274	0.567250182	0.747114934	0.179864752	0.436964733	0.356167347	0.922600972
sp|Q99969|RARR2_HUMAN	2	40	76	33	-0.0255	0.111585571	0.293267382	0.137082893	0.318764704	0.181681812	0.006545282	4.76E-08	0.00051647
sp|Q14210|LY6D_HUMAN	12	40	76	33	-0.10494	-0.184241268	0.140118478	-0.07929921	0.245060536	0.324359747	0.68312555	0.085691426	0.004882964
sp|Q9HCK5|AGO4_HUMAN	1	4	7	3	0.013416	0.132972748	0.109029767	0.119557179	0.095614199	-0.02394298	0.67686355	0.842254627	0.986701054
sp|P22307|NLTP_HUMAN	13	21	41	19	0.058689	0.058751366	0.338942892	6.28E-05	0.280254296	0.280191526	0.999999861	0.145275331	0.083157561
sp|P04216|THY1_HUMAN	7	40	76	33	-0.06641	-0.053586845	0.241981435	0.012825381	0.308393661	0.29556828	0.983992745	0.002349876	0.00090208
sp|P30405|PPIF_HUMAN	3	7	14	6	-0.02023	0.15220586	0.158261015	0.172438463	0.178493618	0.006055155	0.873401716	0.904323994	0.999848863
sp|Q08752|PPID_HUMAN	1	7	14	6	0.241332	0.146491644	0.310160034	-0.09484064	0.06882775	0.163668389	0.913722631	0.967552893	0.786484533
sp|P24855|DNAS1_HUMAN	4	22	42	17	-0.04126	-0.151651225	-0.235034751	-0.110393821	-0.193777347	-0.083383526	0.68562808	0.464206049	0.834367366
sp|Q14232|EI2BA_HUMAN	18	4	7	3	-0.11417	-0.063965437	0.37605825	0.050204428	0.490228115	0.440023687	0.972827306	0.216644991	0.220445207
sp|Q8TF64|GIPC3_HUMAN	1	4	7	3	0.114215	0.163210152	-0.012509141	0.048994757	-0.126724535	-0.175719293	0.944643204	0.777372198	0.562700422
sp|Q9UMY4|SNX12_HUMAN	7	40	76	33	0.093435	0.034494576	0.398700906	-0.058940181	0.305266149	0.364206329	0.75925359	0.007728124	0.000202171
sp|P32942|ICAM3_HUMAN	2	40	76	33	0.076718	0.187750998	0.123710186	0.111033104	0.046992291	-0.064040812	0.049291722	0.682259464	0.407124358
sp|Q5JPE7|NOMO2_HUMAN	41	18	35	16	0.202384	0.172434703	-0.08258028	-0.029948927	-0.28496391	-0.255014983	0.896445649	0.001857207	0.001498576
sp|P11684|UTER_HUMAN	13	40	76	33	-0.32314	-0.244311999	0.258118634	0.078826976	0.581257609	0.502430633	0.728041175	2.14E-05	3.47E-05
sp|Q8N128|F177A_HUMAN	1	22	41	17	0.05478	-0.055019418	0.257151708	-0.109799905	0.202371221	0.312171126	0.551483995	0.26252905	0.021756227
sp|Q13557|KCC2D_HUMAN	7	40	76	33	-0.11113	0.028483588	-0.13666652	0.139611298	-0.025538811	-0.165150108	0.058531428	0.934765463	0.031279611
sp|Q13554|KCC2B_HUMAN	3	29	55	24	-0.02179	-0.02062228	-0.272560382	0.001168306	-0.250769796	-0.251938102	0.999939503	0.152556571	0.090861178
sp|Q00266|METK1_HUMAN	3	4	7	3	-0.54155	-0.208530535	1.546266278	0.33302057	2.087817383	1.754796813	0.628211511	0.001399691	0.00240147
sp|Q8NCC3|PAG15_HUMAN	8	40	76	33	0.020723	0.030489969	0.103636272	0.009767341	0.082913644	0.073146303	0.976616436	0.312767776	0.31625804
sp|P62140|PP1B_HUMAN	11	34	62	26	-0.04018	-0.066069787	0.369521162	-0.025892127	0.409698822	0.435590949	0.949148079	0.000336524	1.86E-05
sp|Q8NEU8|DP13B_HUMAN	6	18	34	14	0.008665	-0.055424129	0.354647124	-0.064089246	0.345982006	0.410071252	0.929856056	0.251061303	0.090993079
sp|P54727|RD23B_HUMAN	54	40	76	33	-0.11863	-0.169852183	0.264022466	-0.051221444	0.382653205	0.433874649	0.845620458	0.002288085	6.63E-05
sp|Q9BY32|ITPA_HUMAN	1	7	14	6	-0.13468	-0.053870734	0.241586439	0.080811876	0.376269049	0.295457173	0.883365566	0.177443143	0.244954259
sp|P16871|IL7RA_HUMAN	6	40	76	33	0.257077	0.20904513	0.044830723	-0.048032122	-0.212246529	-0.164214407	0.751868159	0.024521016	0.057883562
sp|Q5JZY3|EPHAA_HUMAN	3	7	14	6	-0.05839	-0.1263343	-0.101797404	-0.067943656	-0.04340676	0.024536897	0.849343901	0.954671519	0.980891373
sp|P18510|IL1RA_HUMAN	3	10	20	10	-0.96212	-0.590016426	0.410720289	0.372105924	1.372842639	1.000736715	0.619171874	0.012986194	0.041216726
sp|Q92905|CSN5_HUMAN	1	15	28	12	-0.53973	-0.22454186	0.371997115	0.315189697	0.911728671	0.596538975	0.163843758	0.000147421	0.005718692
sp|P09326|CD48_HUMAN	33	40	76	33	-0.05144	0.038894289	0.066907789	0.090332191	0.11834569	0.0280135	0.32678769	0.266674945	0.90894467
sp|Q15746|MYLK_HUMAN	6	40	76	33	0.044814	-0.001335587	0.045720089	-0.046149244	0.000906433	0.047055677	0.861924891	0.999960387	0.873147656
sp|P55212|CASP6_HUMAN	6	21	42	18	-0.10829	-0.184950066	0.184156958	-0.076657957	0.292449067	0.369107024	0.898135644	0.344597677	0.114564301
sp|P24666|PPAC_HUMAN	9	40	76	33	-0.14626	-0.062666592	0.176557563	0.083597359	0.322821514	0.239224155	0.647129446	0.013530163	0.047594614
sp|Q14651|PLSI_HUMAN	4	40	76	33	-0.19499	0.084921938	0.138101606	0.279916301	0.33309597	0.053179668	0.018127029	0.019805381	0.876078516
sp|Q08334|I10R2_HUMAN	29	3	7	4	-0.11845	0.003958392	0.048734221	0.122407915	0.167183744	0.044775829	0.803703591	0.719465567	0.964576858
sp|Q09328|MGT5A_HUMAN	6	40	76	33	0.090994	0.056937572	-0.026622114	-0.034056071	-0.117615758	-0.083559686	0.6661006	0.038914357	0.121300359
sp|Q9H756|LRC19_HUMAN	1	37	69	30	0.000597	0.131432575	-0.412282379	0.130835499	-0.412879455	-0.543714954	0.5592967	0.021490572	0.000320224
sp|Q12866|MERTK_HUMAN	42	40	76	33	0.017169	0.149230479	0.226365432	0.132061642	0.209196595	0.077134953	0.027382018	0.002291368	0.330974591
sp|Q05639|EF1A2_HUMAN	8	40	76	33	-0.47845	-0.330251769	0.255957199	0.148193366	0.734402333	0.586208967	0.34744325	1.64E-07	2.35E-06
sp|Q9BYG0|B3GN5_HUMAN	4	19	34	14	-0.32097	-0.241410722	0.124327445	0.079560468	0.445298634	0.365738167	0.847386389	0.039413002	0.066499528
sp|P10746|HEM4_HUMAN	6	4	7	2	-0.46576	-0.717232829	-0.624152141	-0.251471653	-0.158390965	0.093080688	0.694739523	0.924966653	0.968914475
sp|Q96AT9|RPE_HUMAN	5	7	14	7	-0.5335	-0.289584358	-0.679924273	0.243917698	-0.146422216	-0.390339915	0.761115365	0.928278378	0.503378954
sp|P30046|DOPD_HUMAN	21	40	76	33	-0.51555	-0.296782808	0.572224768	0.218763501	1.087771077	0.869007576	0.311061972	3.50E-08	6.23E-07
sp|Q01581|HMCS1_HUMAN	3	25	48	21	-0.96699	-0.655247835	-0.428349135	0.311739371	0.538638071	0.226898699	0.290410799	0.080812427	0.555596201
sp|Q9ULB1|NRX1A_HUMAN	7	40	76	33	0.111935	0.003970341	-0.225000329	-0.107964469	-0.336935138	-0.22897067	0.04851259	1.91E-08	1.56E-05
sp|Q04637|IF4G1_HUMAN	14	8	13	6	-0.41136	-0.401110431	0.487204315	0.010253551	0.898568297	0.888314746	0.999385047	0.056884694	0.037267532
sp|P46108|CRK_HUMAN	32	25	48	21	0.18915	0.042766189	0.42055676	-0.146383907	0.231406664	0.377790571	0.465338175	0.26805647	0.013532232
sp|P49862|KLK7_HUMAN	33	25	49	22	0.33991	0.249337277	0.171364301	-0.090572865	-0.168545842	-0.077972977	0.509296055	0.196114182	0.631233383
sp|Q6UXI7|VITRN_HUMAN	2	10	21	9	-0.18451	-0.121479602	0.186608944	0.063026491	0.371115036	0.308088546	0.886362984	0.067183865	0.082814388
sp|O94779|CNTN5_HUMAN	11	15	28	12	0.256265	0.060389235	0.06963881	-0.195875422	-0.186625846	0.009249575	0.092761029	0.222453925	0.995195883
sp|P05387|RLA2_HUMAN	9	40	76	33	-0.51176	-0.300078273	0.342532646	0.211684079	0.854294998	0.642610919	0.108589236	7.23E-10	1.33E-07
sp|P41271|NBL1_HUMAN	62	40	76	33	-0.25321	-0.293323665	0.315679085	-0.040114337	0.568888413	0.60900275	0.91582354	1.72E-05	2.07E-07
sp|P53634|CATC_HUMAN	10	40	76	33	-0.04166	-0.025680037	0.203927473	0.015976834	0.245584343	0.229607509	0.96310324	0.003089472	0.00167663
sp|Q6UWH4|GAK1B_HUMAN	6	18	35	16	0.12446	0.062335141	0.247762612	-0.062124986	0.123302484	0.18542747	0.884102062	0.70869242	0.368973144
sp|P13598|ICAM2_HUMAN	1	40	76	33	0.207718	0.2459264	0.154515813	0.038208381	-0.053202206	-0.091410588	0.691879312	0.611338153	0.161561647
sp|Q03113|GNA12_HUMAN	24	14	25	12	-0.229	-0.095763666	0.684597481	0.133238579	0.913599726	0.780361146	0.833597017	0.004422141	0.006655257
sp|P54725|RD23A_HUMAN	1	40	76	33	-0.18612	-0.176086007	0.212578844	0.010029121	0.398693972	0.388664851	0.990443097	7.27E-05	1.19E-05
sp|Q9BSL1|UBAC1_HUMAN	2	7	14	5	-0.15775	-0.084919162	0.405523809	0.072832021	0.563274993	0.490442971	0.929547502	0.087255328	0.095750692
sp|Q6UY14|ATL4_HUMAN	13	40	76	33	0.227612	0.061229267	-0.089861343	-0.16638232	-0.31747293	-0.15109061	0.00203212	5.31E-07	0.010458177
sp|P0C862|C1T9A_HUMAN	17	33	62	27	0.060508	-0.011901315	-0.184935671	-0.07240887	-0.245443227	-0.173034356	0.819461872	0.211880292	0.373980241
sp|Q6UXD5|SE6L2_HUMAN	2	40	76	33	0.13201	0.117393929	0.251277306	-0.014616152	0.119267225	0.133883377	0.973033569	0.289432562	0.139057785
sp|Q96IU4|ABHEB_HUMAN	89	40	76	33	-0.13228	0.01823028	0.285662952	0.1505097	0.417942372	0.267432672	0.152322529	9.04E-05	0.006399181
sp|Q9NY65|TBA8_HUMAN	2	21	42	19	-0.61458	-0.208256822	0.270850234	0.406322912	0.885429969	0.479107056	0.275884972	0.015604093	0.189600923
sp|Q3ZCW2|LEGL_HUMAN	6	40	76	33	-0.07968	-0.181339757	-0.100329896	-0.10166296	-0.020653099	0.081009861	0.688769595	0.989398099	0.812024653
sp|Q15819|UB2V2_HUMAN	15	4	7	3	-0.06725	-0.011514422	0.147403399	0.055733884	0.214651705	0.158917821	0.841941379	0.22100241	0.346713051
sp|Q13404|UB2V1_HUMAN	3	40	76	33	-0.33855	-0.133766486	0.212548313	0.20478727	0.551102069	0.346314799	0.12299045	5.98E-05	0.006069067
sp|Q13094|LCP2_HUMAN	11	37	69	29	-0.08597	-0.215903134	0.107864772	-0.129931394	0.193836512	0.323767906	0.558182473	0.417669833	0.050383173
sp|P50591|TNF10_HUMAN	2	18	35	16	0.114234	0.179352545	0.121391404	0.065118234	0.007157094	-0.05796114	0.439723062	0.992842638	0.546738453
sp|P13805|TNNT1_HUMAN	2	18	34	16	-1.89163	-2.07535678	-1.122237023	-0.183724476	0.769395281	0.953119757	0.892505706	0.246500645	0.067647076
sp|P61086|UBE2K_HUMAN	2	32	62	28	-0.21892	-0.120211866	0.266283547	0.098707604	0.485203016	0.386495412	0.607193741	0.000395329	0.001478961
sp|Q06828|FMOD_HUMAN	4	40	76	33	0.073155	0.04354437	-0.104260785	-0.029610533	-0.177415688	-0.147805155	0.845601322	0.018450151	0.02894859
sp|Q9BX67|JAM3_HUMAN	10	4	6	3	0.035853	-0.015052604	0.533918496	-0.05090529	0.49806581	0.5489711	0.966067504	0.145445553	0.077980191
sp|Q8TBC4|UBA3_HUMAN	10	12	21	9	-0.28815	-0.149385782	0.106337559	0.138767553	0.394490894	0.25572334	0.851363204	0.424036135	0.639524151

sp|P61019|RAB2A_HUMAN	1	33	62	27	0.019608	0.072924186	0.384679108	0.053315753	0.365070676	0.311754922	0.793115745	0.000977531	0.001601728
sp|P60022|DEFB1_HUMAN	1	36	69	30	-0.17874	-0.128414335	0.147492153	0.050323019	0.326229507	0.275906488	0.837069037	0.00739005	0.011057369
sp|Q9H082|RB33B_HUMAN	3	6	14	7	-1.11648	-0.85459409	-0.770721971	0.261884352	0.345756471	0.083872119	0.841236267	0.793588627	0.980354202
sp|O00584|RNT2_HUMAN	13	40	76	33	0.206238	0.112552655	0.30685174	-0.093685184	0.100613902	0.194299086	0.317776542	0.400693844	0.015054919
sp|Q9HAB8|PPCS_HUMAN	2	17	35	15	0.115327	0.132406285	0.332605124	0.017078795	0.217277634	0.200198838	0.988313232	0.274597125	0.236541979
sp|P12956|XRCC6_HUMAN	6	21	42	18	-0.03628	-0.042465921	0.506041172	-0.006188219	0.542318874	0.548507093	0.99922254	0.020638745	0.006320244
sp|A8MVW5|HECA2_HUMAN	4	30	55	23	0.180464	0.055322393	-0.073926125	-0.125141492	-0.254390011	-0.129248518	0.120263061	0.003644132	0.150589502
sp|Q96C24|SYTL4_HUMAN	11	4	7	3	0.26423	-0.0239036	-0.30699022	-0.288133534	-0.571220154	-0.28308662	0.584855454	0.268151418	0.649539013
sp|Q7Z5L7|PODN_HUMAN	24	36	69	30	-0.04608	-0.022314751	0.081605094	0.023767282	0.127687127	0.103919845	0.883608319	0.090014082	0.129245312
sp|Q02750|MP2K1_HUMAN	3	4	7	3	-0.05741	-0.080553087	0.107022439	-0.023142678	0.164432849	0.187575526	0.990718411	0.734840788	0.616958977
sp|Q9HB71|CYBP_HUMAN	5	17	35	15	-0.07436	-0.188984275	0.396690923	-0.114622849	0.471052349	0.585675198	0.803353196	0.084934454	0.008188888
sp|O15123|ANGP2_HUMAN	36	11	21	9	-0.08855	-0.107174049	0.239798187	-0.018620648	0.328351588	0.346972236	0.989900671	0.130576893	0.059291642
sp|Q14116|IL18_HUMAN	1	24	48	21	-0.19019	-0.084680349	0.319089748	0.105506844	0.509276941	0.403770097	0.649104403	0.001561858	0.004612852
sp|P40197|GPV_HUMAN	88	40	76	33	-0.12092	0.182341081	0.099982444	0.303260058	0.220901421	-0.082358637	1.52E-05	0.013190008	0.452081994
sp|Q8TEM1|PO210_HUMAN	18	16	27	11	0.125305	0.122133614	0.102611276	-0.00317106	-0.022693398	-0.019522338	0.999350846	0.978663479	0.981043305
sp|P07478|TRY2_HUMAN	14	40	76	33	0.033772	0.079990457	0.485737038	0.046218556	0.451965137	0.405746581	0.92371425	0.006884496	0.006099624
sp|O15400|STX7_HUMAN	32	22	41	18	-0.11516	-0.07652956	0.689638574	0.038626967	0.8047951	0.766168133	0.954468716	8.78E-06	2.15E-06
sp|Q6UWL2|SUSD1_HUMAN	11	25	49	21	-0.05788	0.005975734	-0.095981036	0.063857806	-0.038098964	-0.10195677	0.749785798	0.931557502	0.522868651
sp|P53990|IST1_HUMAN	2	18	35	16	-0.42209	-0.424178305	0.056443268	-0.002091336	0.478530236	0.480621572	0.999957781	0.216499942	0.13752602
sp|P48507|GSH0_HUMAN	23	40	76	33	-0.32794	-0.071681768	0.277009143	0.256254467	0.604945378	0.348690911	0.006162451	2.51E-08	0.000321512
sp|O95336|6PGL_HUMAN	14	40	76	33	-0.00835	0.036475215	0.587248793	0.044823441	0.595597019	0.550773578	0.892285662	4.40E-06	1.66E-06
sp|O94898|LRIG2_HUMAN	6	33	62	27	0.246463	0.081682514	0.085861561	-0.164780326	-0.160601279	0.004179047	0.095230856	0.211212474	0.998641984
sp|P63241|IF5A1_HUMAN	1	40	76	33	-0.28743	-0.125906846	0.285397961	0.16152809	0.572832897	0.411304807	0.352227627	0.000221006	0.003454
sp|P54136|SYRC_HUMAN	1	18	35	15	-0.08075	-0.177935288	0.245620155	-0.097187235	0.326368208	0.423555443	0.711332335	0.079221968	0.00544486
sp|P06730|IF4E_HUMAN	37	40	76	33	-0.11078	-0.074417263	0.285913791	0.036363024	0.396694078	0.360331054	0.931208649	0.003948767	0.003040647
sp|P08514|ITA2B_HUMAN	2	36	70	30	-0.38825	-0.086720263	0.118107098	0.301527378	0.506354739	0.204827362	0.012781966	0.000291881	0.160961442
sp|Q99685|MGLL_HUMAN	5	33	62	27	0.050806	0.080304309	0.069195754	0.029497823	0.018389268	-0.011108555	0.961694655	0.98958432	0.995172036
sp|P61601|NCALD_HUMAN	21	20	41	19	-0.1067	-0.042800498	0.240854205	0.063901344	0.347556048	0.283654703	0.882542461	0.076379061	0.10092793
sp|Q9Y2X8|UB2D4_HUMAN	23	11	20	9	0.068946	0.073220981	0.057426951	0.004275301	-0.011518729	-0.01579403	0.998814929	0.99401514	0.985951676
sp|P61106|RAB14_HUMAN	3	36	69	31	-0.13784	-0.154510354	0.272844759	-0.016675226	0.410679887	0.427355113	0.98409974	0.001681048	0.000169948
sp|Q9UI42|CBPA4_HUMAN	10	10	21	10	0.003572	0.055684171	-0.193024346	0.05211221	-0.196596307	-0.248708516	0.813406793	0.128500984	0.015389262
sp|P80188|NGAL_HUMAN	10	40	76	33	-0.20375	-0.040148718	0.490077091	0.163603093	0.693828901	0.530225808	0.287002959	1.06E-06	2.70E-05
sp|O75822|EIF3J_HUMAN	44	4	6	3	-0.31883	-0.166680457	0.36939182	0.152151882	0.68822416	0.536072277	0.965156708	0.610246812	0.701336858
sp|Q8N114|SHSA5_HUMAN	1	7	14	6	-0.65669	-0.515026662	0.568106758	0.141665852	1.224799272	1.08313342	0.933617823	0.045374665	0.043378191
sp|P63302|SELW_HUMAN	64	4	6	3	0.253349	0.095221251	1.59307659	-0.158127991	1.339727347	1.497855338	0.958594133	0.165683034	0.086948616
sp|P09619|PGFRB_HUMAN	36	40	76	33	0.093555	0.009195013	-0.061536077	-0.084359611	-0.155090701	-0.070731089	0.390207173	0.114556571	0.558189531
sp|P31431|SDC4_HUMAN	6	40	76	33	-0.34206	0.143470201	0.051915991	0.485531409	0.393977199	-0.09155421	2.77E-10	1.70E-05	0.434829348
sp|P02792|FRIL_HUMAN	1	40	76	33	-0.47744	-0.187989291	0.759909989	0.289454376	1.237353656	0.94789928	0.183751482	1.10E-08	6.95E-07
sp|P30711|GSTT1_HUMAN	103	4	7	3	0.719449	0.454278197	-0.091642988	-0.265170503	-0.811091687	-0.545921184	0.448818232	0.023353916	0.091212975
sp|O43451|MGA_HUMAN	9	34	62	26	-0.16281	-0.115046812	0.136135037	0.047764375	0.298946224	0.251181849	0.902370989	0.072846971	0.09949115
sp|P14649|MYL6B_HUMAN	1	40	76	33	-0.49415	-0.256057406	0.404548643	0.23809548	0.898701529	0.660606049	0.150633012	8.51E-08	8.70E-06
sp|O00442|RTCA_HUMAN	2	11	21	9	-0.10933	0.058270925	0.210837306	0.167599304	0.320165685	0.152566382	0.648940117	0.345885375	0.730633526
sp|Q92530|PSMF1_HUMAN	4	22	41	17	-0.19804	-0.005779436	0.375591419	0.192264431	0.573635287	0.381370856	0.251202629	0.000572302	0.012960691
sp|Q9H159|CAD19_HUMAN	6	40	76	33	0.077794	0.027653648	0.054696367	-0.050139988	-0.023097269	0.027042718	0.42923181	0.882684893	0.804564424
sp|Q16762|THTR_HUMAN	8	8	13	6	-0.25624	-0.003620026	0.570440111	0.252617371	0.826677508	0.574060137	0.520541546	0.01618121	0.077300325
sp|Q13185|CBX3_HUMAN	5	7	14	7	-0.39835	-0.417419065	0.408159322	-0.019073955	0.806504431	0.825578387	0.998083915	0.098173097	0.043781748
sp|P35247|SFTPD_HUMAN	6	40	76	33	-0.31402	-0.264474921	0.329871435	0.049542636	0.643888992	0.594346356	0.9060551	3.07E-05	1.39E-05
sp|P11166|GTR1_HUMAN	7	15	28	11	-0.85686	-0.705924257	-0.153694161	0.150933403	0.703163499	0.552230097	0.649575009	0.004425338	0.013962843
sp|Q01546|K22O_HUMAN	2	36	69	30	0.016083	-0.462559727	-0.651165557	-0.478642751	-0.667248582	-0.188605831	0.122260625	0.060613029	0.745026802
sp|Q96FJ2|DYL2_HUMAN	8	37	69	30	-0.25059	-0.10826318	0.220801161	0.142331274	0.471395614	0.329064341	0.409053013	0.001729989	0.018155834
sp|Q9UBY9|HSPB7_HUMAN	8	4	6	3	0.033524	0.011014477	1.356688638	-0.022509805	1.323164357	1.345674161	0.999398575	0.27407148	0.217900277
sp|O75608|LYPA1_HUMAN	3	40	76	33	-0.11701	-0.264543906	-0.006371891	-0.147534211	0.110637804	0.258172015	0.31195158	0.634181303	0.046388505
sp|P07741|APT_HUMAN	26	40	76	33	-0.19666	-0.197675619	0.147635992	-0.001020255	0.344291356	0.345311611	0.999950975	0.024566257	0.009117289
sp|P04792|HSPB1_HUMAN	8	40	76	33	-0.08222	-0.237206141	0.317489116	-0.154988113	0.399707144	0.554695258	0.482014462	0.038306758	0.00047214
sp|P26842|CD27_HUMAN	4	32	62	27	-0.63438	-0.633441341	-0.159866804	0.000941815	0.474516351	0.473574537	0.9999736	0.012147186	0.003817384
sp|Q96P44|COLA1_HUMAN	4	14	28	12	0.08612	0.010009479	-0.070485659	-0.076110663	-0.1566058	-0.080495137	0.593646261	0.224464284	0.591607502
sp|P13942|COBA2_HUMAN	2	40	76	33	0.224592	0.009564559	-0.602821423	-0.215027343	-0.827413326	-0.612385983	0.107757159	3.55E-09	6.94E-07
sp|P68032|ACTC_HUMAN	4	40	76	33	-0.14879	-0.34040623	-0.009222043	-0.191620067	0.13956412	0.331184187	0.234988838	0.585547743	0.02445493
sp|A5A3E0|POTEF_HUMAN	10	24	48	22	0.144908	-0.160965965	0.248516256	-0.305874238	0.103607983	0.409482221	0.191182716	0.870000672	0.063821471
sp|P0CG38|POTEI_HUMAN	12	4	6	2	0.114757	-0.349970452	0.573646559	-0.464727365	0.458889646	0.923617011	0.322887148	0.52291406	0.091246671
sp|P0CG39|POTEJ_HUMAN	12	25	48	21	-0.05971	-0.261220455	0.112579538	-0.2015146	0.172285393	0.373799993	0.405046477	0.630241586	0.067714715
sp|P48052|CBPA2_HUMAN	2	31	60	27	0.139744	0.00305196	0.157786068	-0.136692493	0.018041615	0.154734108	0.27936954	0.984193275	0.22654723
sp|Q9Y4Y9|LSM5_HUMAN	38	4	6	3	0.485221	0.536160582	0.362727377	0.050939651	-0.122493555	-0.173433206	0.958573974	0.841657462	0.674440598
sp|Q96GG9|DCNL1_HUMAN	2	18	35	15	-0.1495	0.019660009	0.252091315	0.169164237	0.401595543	0.232431306	0.300631907	0.012395327	0.138766618
sp|Q86TP1|PRUN1_HUMAN	1	22	42	18	-0.04702	0.116560312	0.18708262	0.163579798	0.234102106	0.070522308	0.42701117	0.304683811	0.869654527
sp|Q8WVM8|SCFD1_HUMAN	3	28	55	24	-0.27868	-0.21037199	0.192852579	0.06830753	0.4715321	0.403224569	0.913560091	0.055504513	0.064630172
sp|Q9Y625|GPC6_HUMAN	27	17	34	16	-0.15594	-0.241972878	0.111020535	-0.086029943	0.266963471	0.352993414	0.825535934	0.268818911	0.052933797
sp|Q9UPY8|MARE3_HUMAN	3	36	69	30	-0.21845	-0.461186476	-0.161375999	-0.242731992	0.057078486	0.299810477	0.365513606	0.961826963	0.258770313
sp|Q13444|ADA15_HUMAN	1	18	34	16	-0.14122	-0.038018722	0.447201885	0.103199138	0.588419745	0.485220607	0.698049337	0.000625632	0.001441639
sp|Q9Y2Z0|SGT1_HUMAN	5	7	14	6	0.139109	0.051207262	0.434030583	-0.087901376	0.294921945	0.382823321	0.906035478	0.474017462	0.207179601
sp|P51888|PRELP_HUMAN	1	29	55	24	0.132474	0.042295349	0.428497856	-0.090178911	0.296023596	0.386202507	0.724776922	0.096715032	0.007474531
sp|O00423|EMAL1_HUMAN	8	4	7	3	0.110214	0.185484964	-0.263450385	0.075270944	-0.373664405	-0.448935349	0.964915045	0.569220985	0.383294902
sp|Q96E39|RMXL1_HUMAN	12	11	20	9	-0.2201	-0.11654231	0.816882137	0.103556616	1.036981063	0.933424447	0.952337257	0.044710273	0.042731451
sp|Q7Z3B1|NEGR1_HUMAN	37	40	76	33	0.195911	0.12168238	0.028324213	-0.074228245	-0.167586412	-0.093358167	0.098730159	0.000443353	0.041291924
sp|Q9UDX3|S14L4_HUMAN	5	14	27	13	-0.16775	0.171987146	0.452144014	0.339739093	0.619895961	0.280156869	0.099378268	0.005238371	0.218289207
sp|O76054|S14L2_HUMAN	1	19	34	15	-0.3111	-0.020253563	0.392581715	0.290842348	0.703677626	0.412835278	0.153452554	0.001033185	0.04292983
sp|Q9ULZ3|ASC_HUMAN	7	33	62	27	-0.58693	-0.482659836	0.358573003	0.104266921	0.94549976	0.841232839	0.754077902	1.05E-06	1.01E-06
sp|Q53FA7|QORX_HUMAN	8	21	42	18	-0.23207	-0.061325511	0.385618392	0.170745384	0.617689287	0.446943903	0.277106839	4.06E-05	0.000747473
sp|Q96DA0|ZG16B_HUMAN	5	37	69	30	0.050131	0.058119855	0.059856736	0.007989004	0.009725886	0.001736881	0.993723108	0.993601271	0.999741637
sp|Q9HA64|KT3K_HUMAN	4	40	76	33	-0.3587	-0.161640986	0.226422797	0.197063718	0.5851275	0.388063783	0.130261246	1.19E-05	0.001321087
sp|P06734|FCER2_HUMAN	5	11	20	9	-0.15119	-0.017998588	0.336371115	0.133195981	0.487565685	0.354369703	0.735549475	0.069357518	0.162879846
sp|P07205|PGK2_HUMAN	4	40	76	33	-0.13936	-0.046314046	0.232705642	0.093043313	0.372063001	0.279019688	0.547149904	0.001870096	0.010346122
sp|P18085|ARF4_HUMAN	15	36	69	30	0.041601	-0.073411203	0.382705663	-0.115012289	0.341104577	0.456116866	0.616032312	0.056695508	0.001798377
sp|Q9Y3I1|FBX7_HUMAN	3	32	62	28	-0.181	0.082081187	0.415897957	0.263085884	0.596902655	0.333816771	0.088991616	0.000262076	0.029778405
sp|Q92995|UBP13_HUMAN	4	4	7	3	0.261128	0.134330761	0.058687077	-0.126797128	-0.202440812	-0.075643684	0.54539984	0.367287099	0.830812507
sp|P51659|DHB4_HUMAN	4	4	7	2	0.232439	-0.003208462	0.259795991	-0.23564739	0.027357063	0.263004453	0.499575989	0.994745603	0.58440963
sp|Q5VUB5|F1711_HUMAN	2	26	48	20	0.493913	0.383716309	0.463779559	-0.110196768	-0.030133518	0.080063249	0.815838278	0.98982106	0.913846547
sp|P47972|NPTX2_HUMAN	19	40	76	33	0.056789	-0.035648349	0.077788894	-0.092437587	0.020999656	0.113437243	0.164429125	0.936620016	0.093205398
sp|P05413|FABPH_HUMAN	2	40	76	33	-1.57037	-1.636926905	-0.793708097	-0.066558922	0.776659885	0.843218807	0.920934692	0.000745189	2.81E-05
sp|Q86UN2|R4RL1_HUMAN	1	15	28	12	0.0882	0.125987118	0.181235514	0.037786909	0.093035305	0.055248396	0.859033363	0.536930833	0.756894248
sp|O14775|GNB5_HUMAN	14	8	14	6	-0.04999	-0.062163007	-0.013057206	-0.012177779	0.036928022	0.049105801	0.997563825	0.98501644	0.967851157
sp|P09486|SPRC_HUMAN	1	40	76	33	-0.17129	0.18471035	0.168622142	0.35599766	0.339909452	-0.016088208	0.001653772	0.016246151	0.98781971
sp|P08263|GSTA1_HUMAN	4	21	41	17	-0.12246	0.177641527	-0.038494414	0.300097727	0.083961785	-0.216135941	0.133240584	0.895629085	0.397902783
sp|P41236|IPP2_HUMAN	27	7	13	6	-0.03042	0.018712949	0.779929881	0.049131345	0.810348277	0.761216932	0.989235816	0.148193419	0.120115497
sp|Q9BYZ2|LDH6B_HUMAN	1	30	55	23	-0.20423	0.032129896	0.280122304	0.236358212	0.484350619	0.247992408	0.146646949	0.00559662	0.17047974
sp|P62873|GBB1_HUMAN	5	40	76	33	0.023729	8.69E-05	0.16445001	-0.023642217	0.140720889	0.164363106	0.906267422	0.095414307	0.018125568
sp|P17980|PRS6A_HUMAN	1	31	55	23	-0.52097	-0.324776314	0.057656496	0.196197348	0.578630159	0.38243281	0.277399315	0.00098905	0.021158922
sp|Q9H7Z3|NRDE2_HUMAN	3	7	14	6	0.060592	-0.033236783	0.574172316	-0.093829107	0.513579992	0.607409099	0.960937109	0.450126564	0.243849547
sp|P20936|RASA1_HUMAN	6	7	14	6	-0.35671	-0.18390223	0.669040828	0.172810135	1.025753193	0.852943058	0.848186436	0.031680754	0.042976986
sp|P28074|PSB5_HUMAN	12	40	76	33	-0.13863	-0.026236759	0.432775993	0.112390114	0.571402865	0.459012752	0.459338379	4.09E-06	3.12E-05
sp|O95834|EMAL2_HUMAN	1	40	76	33	-0.17635	-0.244777127	0.012451023	-0.068423636	0.188804514	0.25722815	0.842507554	0.409256585	0.124429991
sp|P14174|MIF_HUMAN	11	40	76	33	-0.3683	-0.164121271	0.248835633	0.204176795	0.617133699	0.412956904	0.174437806	3.93E-05	0.002457087
sp|A6NI72|NCF1B_HUMAN	2	25	47	20	-0.96373	-0.689474092	0.176348076	0.274258575	1.140080742	0.865822168	0.495670405	0.000560187	0.003701556
sp|Q8TD30|ALAT2_HUMAN	14	40	76	33	0.062037	0.168219612	0.091877799	0.106182124	0.029840311	-0.076341813	0.36702606	0.946321658	0.632841421
sp|Q16853|AOC3_HUMAN	9	40	76	33	0.196174	0.134597487	0.10864817	-0.061576557	-0.087525875	-0.025949318	0.314185082	0.200606021	0.833266975

sp|Q15286|RAB35_HUMAN	1	18	34	16	-0.13916	-0.048499787	0.293964115	0.090660944	0.433124846	0.342463902	0.853604491	0.083154985	0.133314969
sp|Q86TD4|SRCA_HUMAN	31	23	41	17	0.090936	0.062987447	-0.007204807	-0.027948759	-0.098141013	-0.070192254	0.921975741	0.517803234	0.659959601
sp|Q92930|RAB8B_HUMAN	2	18	35	14	-0.40662	-0.233565653	0.394880247	0.173054853	0.801500754	0.6284459	0.628163428	0.002600044	0.008631546
sp|P29992|GNA11_HUMAN	4	4	7	3	-0.09034	0.325645524	-0.090909245	0.415981093	-0.000573675	-0.416554769	0.38389427	0.999998655	0.447575741
sp|Q9BRR6|ADPGK_HUMAN	39	4	7	3	-0.07251	0.078658462	-0.077428256	0.151167272	-0.004919446	-0.156086718	0.575672048	0.999584814	0.613425926
sp|Q9GZN8|CT027_HUMAN	19	30	55	24	-0.38382	-0.249851045	0.11016999	0.133968505	0.493989539	0.360021034	0.595018695	0.010047835	0.044159714
sp|Q9UQC9|CLCA2_HUMAN	1	22	42	17	0.342175	0.107727461	0.016925687	-0.234447161	-0.325248935	-0.090801773	0.010556393	0.003306762	0.543274864
sp|Q9UKU9|ANGL2_HUMAN	1	40	76	33	-0.021	0.00148832	0.265042294	0.022491907	0.286045881	0.263553974	0.894538756	1.42E-05	6.31E-06
sp|O14561|ACPM_HUMAN	9	4	6	3	0.053716	0.094742797	1.231969003	0.041027229	1.178253435	1.137226206	0.998172428	0.378117747	0.350479246
sp|Q8NBZ7|UXS1_HUMAN	11	4	6	3	-0.01299	-0.082723904	-0.50026263	-0.069730726	-0.487269452	-0.417538726	0.807481502	0.010114496	0.015837482
sp|Q01344|IL5RA_HUMAN	8	4	7	3	-0.37256	-0.138157526	-0.491612411	0.234399838	-0.119055047	-0.353454884	0.372767843	0.830910884	0.178634431
sp|Q15459|SF3A1_HUMAN	70	4	6	3	-0.03816	0.274541136	0.753525381	0.312705929	0.791690174	0.478984245	0.859842288	0.519170796	0.747563458
sp|O15389|SIGL5_HUMAN	4	40	76	33	-0.59687	-0.218961074	-0.340318677	0.377905018	0.256547415	-0.121357603	0.198738375	0.594662342	0.861927042
sp|P07738|PMGE_HUMAN	6	40	76	33	-0.34092	-0.17039902	0.377781465	0.170523135	0.71870362	0.548180485	0.273930762	7.81E-07	2.21E-05
sp|P37173|TGFR2_HUMAN	11	40	76	33	-0.08023	-0.073690148	0.216442209	0.006542242	0.2966746	0.290132357	0.994899865	0.00114296	0.000292095
sp|Q9Y2V2|CHSP1_HUMAN	2	30	55	23	-0.51584	-0.211309047	0.25995396	0.304532792	0.775795799	0.471263007	0.066960672	2.32E-05	0.005311498
sp|Q10589|BST2_HUMAN	7	26	48	20	-0.63504	-0.165338103	0.377803533	0.469701465	1.0128431	0.543141636	0.044833921	0.000132863	0.031498638
sp|P08861|CEL3B_HUMAN	9	36	69	30	-0.23754	-0.230471201	0.136846922	0.007073541	0.374391664	0.367318123	0.998401912	0.049939514	0.025741482
sp|Q9NNX6|CD209_HUMAN	1	11	20	9	-0.06518	-0.05744733	0.354361634	0.007729319	0.419538283	0.411808963	0.998122118	0.031112185	0.016397054
sp|Q9NT22|EMIL3_HUMAN	3	36	69	30	0.193502	0.037307391	-0.336515258	-0.156194562	-0.530017211	-0.373822649	0.082520867	3.49E-08	1.00E-05
sp|P29692|EF1D_HUMAN	1	29	55	25	-0.0604	-0.048808395	0.26958106	0.011592194	0.329981649	0.318389455	0.996451218	0.137454367	0.095005338
sp|Q14964|RB39A_HUMAN	7	6	14	7	-0.68491	-0.298670244	0.286921122	0.386244379	0.971835745	0.585591366	0.390001131	0.018600331	0.104033003
sp|Q96N76|HUTU_HUMAN	20	30	55	24	-0.0866	0.009628172	0.330226053	0.096226372	0.416824253	0.32059788	0.596619192	0.002044889	0.009301689
sp|P37235|HPCL1_HUMAN	3	37	69	30	-0.18622	-0.091397873	0.175578585	0.094825358	0.361801816	0.266976458	0.693117576	0.02890108	0.085082284
sp|Q16661|GUC2B_HUMAN	7	40	76	33	0.020956	-0.029808753	0.182459616	-0.050764285	0.161504083	0.212268369	0.778088784	0.178130063	0.024337373
sp|O95865|DDAH2_HUMAN	4	40	76	33	0.063922	0.006279683	0.294570315	-0.057642321	0.230648311	0.288290632	0.656092513	0.011493539	0.000195882
sp|P05787|K2C8_HUMAN	1	26	48	22	-0.46767	-0.414624151	0.286428484	0.05304627	0.754098905	0.701052635	0.955364735	0.002491131	0.001483803
sp|Q15904|VAS1_HUMAN	23	40	76	33	-0.17864	-0.173884257	0.319730926	0.004752342	0.498367525	0.493615183	0.998157688	4.09E-06	2.69E-07
sp|P11171|41_HUMAN	1	4	7	3	0.240321	0.153907004	1.010893928	-0.086413808	0.770573115	0.856986924	0.975397779	0.303655536	0.179893569
sp|P98088|MUC5A_HUMAN	2	14	27	13	0.439153	0.028635008	0.392929441	-0.410517681	-0.046223249	0.364294432	0.19968474	0.984616808	0.295644333
sp|A0A087WSY4|HV432_HUMAN	4	10	20	10	0.253084	0.426128387	0.247490202	0.173044473	-0.005593712	-0.178638185	0.566196697	0.999546395	0.545805039
sp|P16870|CBPE_HUMAN	1	26	48	21	0.187372	0.114615157	0.044441712	-0.07275648	-0.142929924	-0.070173444	0.517109163	0.177964889	0.587180788
sp|Q9Y333|LSM2_HUMAN	1	4	7	3	-0.0273	-0.121016424	-0.314292636	-0.093712166	-0.286988379	-0.193276213	0.541131894	0.047439441	0.149518982
sp|Q9Y5X9|LIPE_HUMAN	4	40	76	33	0.038051	0.089028048	0.187108885	0.050976707	0.149057544	0.098080836	0.603161061	0.054547749	0.197120888
sp|Q9H074|PAIP1_HUMAN	2	7	14	6	0.00794	0.040751685	0.042811494	0.03281198	0.034871789	0.002059809	0.972774904	0.978641435	0.999901982
sp|P12104|FABPI_HUMAN	1	14	28	13	-0.11999	-0.078464368	0.245261618	0.041523463	0.365249449	0.323725987	0.978881561	0.312943704	0.30092847
sp|Q9P0V9|SEP10_HUMAN	3	7	14	6	0.193961	-0.109119668	0.598734959	-0.303080414	0.404774214	0.707854627	0.695962885	0.640267823	0.187251835
sp|O00148|DX39A_HUMAN	5	12	21	9	-0.81573	-0.326188301	0.156138888	0.489537491	0.971864679	0.482327189	0.09595356	0.003526441	0.14930763
sp|P28906|CD34_HUMAN	3	40	76	33	-0.09972	-0.111530639	0.034551482	-0.011810671	0.13427145	0.146082122	0.98187378	0.201070056	0.091055712
sp|P54922|ADPRH_HUMAN	2	4	7	3	0.122534	0.099215275	0.284983314	-0.023318572	0.162449467	0.185768038	0.983122496	0.588806934	0.438401028
sp|O43583|DENR_HUMAN	4	24	48	22	-0.18226	0.015505176	0.314480627	0.197765666	0.496741117	0.298975451	0.202058244	0.001193694	0.034753179
sp|Q6XQN6|PNCB_HUMAN	1	40	76	33	-0.35458	-0.168040609	0.137722324	0.186536074	0.492299006	0.305762933	0.065782284	6.28E-06	0.002026157
sp|P25398|RS12_HUMAN	7	4	7	3	-0.25928	-0.096883918	0.267503284	0.162397376	0.526784578	0.364387202	0.716901936	0.134855744	0.282743816
sp|P20340|RAB6A_HUMAN	9	37	69	30	-0.17152	-0.148948565	0.331051771	0.022571911	0.502572247	0.480000336	0.971055831	0.000111964	3.21E-05
sp|P06858|LIPL_HUMAN	8	40	76	33	0.050351	0.032164392	-0.157889718	-0.018186337	-0.208240447	-0.19005411	0.965277951	0.045219621	0.037787495
sp|P55060|XPO2_HUMAN	21	7	14	6	0.148309	0.103369985	0.282151354	-0.044939176	0.133842193	0.178781369	0.957985449	0.770307953	0.550962821
sp|P50452|SPB8_HUMAN	1	37	69	30	-0.35134	-0.211629672	0.293067358	0.139707708	0.644404738	0.50469703	0.600726575	0.000950159	0.004208762
sp|P21583|SCF_HUMAN	3	21	41	17	0.756751	0.542652916	0.927765788	-0.21409769	0.171015182	0.385112872	0.617544576	0.811378973	0.264388696
sp|P24534|EF1B_HUMAN	4	40	76	33	-0.47684	-0.316703467	0.109197656	0.160135498	0.58603662	0.425901123	0.470320933	0.001396815	0.011022668
sp|Q13232|NDK3_HUMAN	30	40	76	33	0.121649	0.082513522	-0.038095376	-0.039135572	-0.15974447	-0.120608898	0.479721193	0.000384058	0.002975653
sp|P02689|MYP2_HUMAN	10	40	76	33	-0.2832	-0.232588896	0.485465039	0.050610691	0.768664626	0.718053935	0.930221584	3.04E-05	1.07E-05
sp|Q0Z7S8|FABP9_HUMAN	2	11	20	9	-0.29734	-0.234922547	0.96848306	0.062417607	1.265823213	1.203405607	0.980472441	0.007667031	0.004397898
sp|P62834|RAP1A_HUMAN	6	40	76	33	-0.23503	-0.164734832	0.045817668	0.070296526	0.280849027	0.210552501	0.727259153	0.033478392	0.086040197
sp|P63244|RACK1_HUMAN	2	4	7	3	-0.42716	-0.069932186	0.354885039	0.357230297	0.782047523	0.424817225	0.531489907	0.162505556	0.481686809
sp|Q9BSE5|SPEB_HUMAN	6	7	14	6	-0.2777	0.17275587	0.769636249	0.450457794	1.047338173	0.596880379	0.695707411	0.272346859	0.566677109
sp|P78536|ADA17_HUMAN	1	40	76	33	-0.01003	0.076760173	0.223541431	0.086785347	0.233566605	0.146781258	0.182707965	0.000340867	0.015557653
sp|P07949|RET_HUMAN	24	37	69	30	0.017881	0.185285239	-0.073156426	0.167404024	-0.091037641	-0.258441666	0.023899623	0.456287403	0.000590968
sp|P35052|GPC1_HUMAN	27	40	76	33	-0.05469	-0.072020495	0.191410657	-0.017328459	0.246102693	0.263431152	0.957070784	0.003150625	0.000273271
sp|P19256|LFA3_HUMAN	3	40	76	33	0.051751	-0.013974755	-0.182564458	-0.065725301	-0.234315004	-0.168589703	0.185353916	1.77E-06	0.000116408
sp|Q4G148|GXLT1_HUMAN	1	40	76	33	0.153968	0.153438936	0.174100761	-0.000529448	0.020132377	0.020661825	0.999952171	0.953425802	0.938087543
sp|Q7L7X3|TAOK1_HUMAN	4	7	14	6	0.330722	0.482525294	0.922729034	0.151803305	0.592007045	0.44020374	0.905686451	0.367594342	0.48268623
sp|P07437|TBB5_HUMAN	5	40	76	33	-0.29108	-0.095547128	0.155762854	0.195537682	0.446847664	0.251309982	0.136962406	0.00108436	0.057413859
sp|Q14194|DPYL1_HUMAN	8	36	69	30	0.059386	0.009300495	0.248542834	-0.050085167	0.189157172	0.239242339	0.757668432	0.069553715	0.005007829
sp|P41159|LEP_HUMAN	5	40	76	33	-0.17024	-0.190483817	-0.136163532	-0.020242587	0.034077699	0.054320285	0.985811921	0.972448161	0.913683889
sp|Q99729|ROAA_HUMAN	9	7	13	6	-0.26929	-0.089471488	0.761459927	0.179817496	1.03074891	0.850931414	0.932459934	0.218225942	0.264370881
sp|Q92692|NECT2_HUMAN	1	40	76	33	-0.3775	-0.256240326	0.422788697	0.12126168	0.800290703	0.679029024	0.465314268	3.87E-09	1.59E-08
sp|Q15349|KS6A2_HUMAN	1	4	7	2	-0.24002	-0.095661429	-0.148665144	0.144355214	0.0913515	-0.053003714	0.959086596	0.991245407	0.996550435
sp|P30990|NEUT_HUMAN	23	16	28	11	0.216119	0.134795533	-0.10793923	-0.0813232	-0.324057964	-0.242734763	0.730560519	0.049750996	0.124567466
sp|P69892|HBG2_HUMAN	4	10	21	9	-0.03591	-0.321804362	0.547515882	-0.285890189	0.583430055	0.869320244	0.641082737	0.282989	0.030777294
sp|P49721|PSB2_HUMAN	5	40	76	33	-0.26105	-0.085252753	0.416291052	0.175792333	0.677336139	0.501543806	0.179320642	1.90E-07	1.35E-05
sp|P63167|DYL1_HUMAN	1	7	14	6	0.000134	0.100355283	0.539235048	0.10022136	0.539101125	0.438879765	0.865678704	0.07554962	0.104461066
sp|Q9Y3C8|UFC1_HUMAN	1	40	76	33	-0.3215	-0.142202205	0.209631636	0.179298937	0.531132777	0.351833841	0.197230869	0.000108131	0.005049725
sp|Q7KYR7|BT2A1_HUMAN	26	40	76	33	-0.08401	-0.093906542	0.158487864	-0.009896825	0.242497581	0.252394406	0.988648864	0.010953044	0.002186981
sp|P27695|APEX1_HUMAN	1	7	13	6	-0.65697	-0.419946713	0.383244529	0.237023471	1.040214714	0.803191242	0.887951492	0.218702641	0.310075364
sp|Q9NTX5|ECHD1_HUMAN	11	4	7	3	0.308702	0.408033924	0.346383274	0.099331716	0.037681066	-0.061650651	0.798189981	0.977972269	0.929889603
sp|Q08431|MFGM_HUMAN	1	7	14	7	-0.24572	-0.113203412	-0.146344466	0.132512848	0.099371793	-0.033141055	0.389102148	0.665208637	0.940459155
sp|P35556|FBN2_HUMAN	78	40	76	33	0.025249	-0.018175966	0.038270603	-0.04342541	0.013021159	0.056446569	0.544285757	0.962745567	0.406744085
sp|P49720|PSB3_HUMAN	19	40	76	33	-0.27391	-0.122998947	0.400433838	0.150909705	0.67434249	0.523432784	0.2876818	2.85E-07	6.93E-06
sp|Q8TB96|TIP_HUMAN	7	15	27	13	0.069334	-0.001122261	0.148042897	-0.070456006	0.078709152	0.149165158	0.636961472	0.665672376	0.167939078
sp|Q9H6Z4|RANB3_HUMAN	23	4	6	3	-0.18479	0.29288685	1.118012647	0.477675652	1.302801449	0.825125797	0.723558856	0.220011264	0.46410962
sp|Q9Y262|EIF3L_HUMAN	9	10	21	10	-0.40518	-0.235522063	0.547781218	0.169658617	0.952961898	0.783303281	0.807203322	0.012312099	0.017157788
sp|Q96B86|RGMA_HUMAN	14	40	76	33	0.134338	0.021306337	-0.213794426	-0.113031926	-0.348132688	-0.235100763	0.044728217	1.88E-08	1.75E-05
sp|O76011|KRT34_HUMAN	3	8	13	6	-0.29216	0.346976165	-0.547139593	0.639132894	-0.254982864	-0.894115758	0.42397004	0.906733409	0.256572682
sp|Q96P63|SPB12_HUMAN	15	19	35	15	0.231569	0.047626916	-0.27018631	-0.183941616	-0.501754842	-0.317813226	0.075312942	1.36E-05	0.002103952
sp|P84077|ARF1_HUMAN	14	40	76	33	-0.20115	-0.106230054	0.199513265	0.094921514	0.400664833	0.305743319	0.750730176	0.032980551	0.078051754
sp|Q86T26|TM11B_HUMAN	4	29	55	23	-0.3654	-0.382149285	0.054706473	-0.016744831	0.420110927	0.436855758	0.994484213	0.102111676	0.04564331
sp|P31323|KAP3_HUMAN	3	10	21	10	-0.11062	0.212627002	0.243078375	0.323246817	0.353698191	0.030451373	0.366788348	0.410908996	0.990869075
sp|Q9H0V9|LMA2L_HUMAN	5	8	13	5	0.503701	0.41338021	0.587499009	-0.090320954	0.083797844	0.174118799	0.859698531	0.922084944	0.667156024
sp|P01160|ANF_HUMAN	6	31	55	23	-0.60238	-0.653148442	0.249907302	-0.0507649	0.852290844	0.903055744	0.940496058	3.89E-05	1.40E-06
sp|Q8TD06|AGR3_HUMAN	33	29	55	24	-0.02477	0.033489771	0.226870115	0.058257473	0.251637817	0.193380344	0.902615175	0.272219772	0.374617138
sp|P59665|DEF1_HUMAN	3	40	76	33	-0.41199	-0.344012535	0.402858165	0.067980001	0.814850702	0.746870701	0.857724716	1.52E-06	6.68E-07
sp|Q8NI22|MCFD2_HUMAN	1	18	35	15	-0.08023	0.049709991	0.332263227	0.129943516	0.412496752	0.282553235	0.36965344	0.001920108	0.019603804
sp|P60033|CD81_HUMAN	7	40	76	33	-0.10472	-0.029235849	0.2457372	0.075485748	0.350458797	0.274973049	0.594137905	0.000718767	0.003178639
sp|P31025|LCN1_HUMAN	2	29	55	24	-0.17422	-0.088193097	0.077537698	0.086027109	0.251757904	0.165730795	0.809220934	0.290299922	0.50310228
sp|Q9Y6E0|STK24_HUMAN	15	11	21	10	0.045196	0.025293859	0.061807279	-0.019902142	0.016611278	0.036513421	0.981497374	0.990601245	0.942781903
sp|A6NDG6|PGP_HUMAN	4	18	34	15	-0.12613	-0.027624509	0.388897386	0.098500954	0.515022849	0.416521895	0.707176473	0.00268112	0.006660829
sp|P01714|LV319_HUMAN	29	28	55	25	-0.27476	-0.136690891	0.287085965	0.138071937	0.561848794	0.423776856	0.490755151	0.000461707	0.002975049
sp|Q13618|CUL3_HUMAN	37	16	27	11	-0.13715	-0.10022022	0.018437008	0.036927764	0.155584993	0.118657228	0.977737639	0.772693782	0.835130214
sp|Q9BYF1|ACE2_HUMAN	4	28	56	24	-0.71816	-0.592788165	0.013163861	0.125371386	0.731323412	0.605952026	0.659776328	0.000148994	0.000353904
sp|Q92973|TNPO1_HUMAN	18	26	49	20	-0.38383	-0.16863342	0.345784941	0.215197488	0.729615849	0.514418361	0.606275387	0.025785339	0.097464176
sp|Q9BUD6|SPON2_HUMAN	47	40	76	33	-0.29664	-0.184519619	0.398906305	0.112118863	0.695544786	0.583425923	0.391211747	9.38E-10	6.17E-09
sp|Q15714|T22D1_HUMAN	10	4	6	3	0.149481	-0.015876467	0.276147139	-0.165357791	0.126665815	0.292023606	0.803067152	0.911060481	0.576695154
sp|O75923|DYSF_HUMAN	6	4	6	3	-0.15708	-0.154538406	0.31003581	0.002543754	0.467117971	0.464574216	0.999976875	0.590383804	0.547034045
sp|Q9UEW3|MARCO_HUMAN	11	40	76	33	-0.10529	0.01188891	0.333476871	0.117181933	0.438769895	0.321587962	0.233652547	3.24E-06	0.000131958
sp|P04233|HG2A_HUMAN	2	11	20	9	-0.04798	-0.098357709	0.609930424	-0.050373386	0.657914747	0.708288133	0.963579528	0.019920308	0.004374594

sp|P28908|TNR8_HUMAN	1	28	55	24	-1.40294	-1.280843284	-1.033095939	0.122097474	0.369844819	0.247747345	0.810926794	0.26724214	0.462449593
sp|Q96EE4|CC126_HUMAN	144	40	76	33	0.136424	0.098313797	-0.090093372	-0.038109921	-0.22651709	-0.188407169	0.515207228	6.73E-07	3.12E-06
sp|A8K7I4|CLCA1_HUMAN	1	6	14	7	-0.63532	-0.531050159	0.974348601	0.104271821	1.609670582	1.505398761	0.978343166	0.032364525	0.015222171
sp|P60953|CDC42_HUMAN	2	15	27	12	-0.18245	-0.049059437	0.301947681	0.133389121	0.484396239	0.351007118	0.553164422	0.007544128	0.036320511
sp|Q96J42|TXD15_HUMAN	1	40	76	33	-0.15576	0.018460151	0.126452743	0.174218947	0.282211539	0.107992592	0.004245218	7.36E-05	0.148120644
sp|Q13501|SQSTM_HUMAN	2	4	6	3	0.070055	-0.037992803	0.911238278	-0.108047348	0.841183732	0.94923108	0.988553433	0.622053197	0.501870458
sp|Q9NPH0|PPA6_HUMAN	1	16	27	11	0.330865	0.204190784	0.407567076	-0.126674481	0.07670181	0.203376291	0.367727761	0.784853505	0.140631133
sp|O43157|PLXB1_HUMAN	38	40	76	33	0.03774	0.015772358	0.080998096	-0.021967908	0.04325783	0.065225738	0.710792297	0.403398111	0.075697922
sp|Q15651|HMGN3_HUMAN	11	32	62	27	-1.6746	-1.0868435	-0.210477739	0.58775848	1.46412424	0.876365761	0.036171068	2.59E-06	0.001744711
sp|Q9BXJ0|C1QT5_HUMAN	1	36	69	30	0.080929	0.158336885	-0.038312601	0.077407983	-0.119241503	-0.196649486	0.230541195	0.092183865	0.00040061
sp|P01040|CYTA_HUMAN	10	36	69	30	-0.46683	-0.491230635	0.103229925	-0.024401802	0.570058758	0.594460561	0.98831096	0.014471541	0.00305941
sp|Q9BUN1|MENT_HUMAN	4	40	76	33	0.120761	0.088740262	0.191085811	-0.032020993	0.070324556	0.102345549	0.74522464	0.378463408	0.076134035
sp|P52943|CRIP2_HUMAN	5	4	7	3	0.524771	0.371857787	0.580871854	-0.152912727	0.05610134	0.209014067	0.859773166	0.986218737	0.7936535
sp|Q56UQ5|TPT1L_HUMAN	4	36	69	30	-0.25663	-0.058015356	0.220930261	0.198611154	0.477556771	0.278945617	0.262819642	0.005928939	0.099785969
sp|Q14141|SEPT6_HUMAN	2	40	76	33	-0.34321	-0.288948985	0.053707734	0.054258038	0.396914757	0.342656719	0.929424734	0.072018598	0.082218338
sp|Q8IYD1|ERF3B_HUMAN	1	26	48	21	-0.0981	-0.014115959	0.392806748	0.083986606	0.490909313	0.406922707	0.793191441	0.006177283	0.011850612
sp|Q8IYS5|OSCAR_HUMAN	3	40	76	33	-0.04516	0.027223103	0.116197968	0.072388011	0.161362876	0.088974865	0.482610028	0.08601559	0.381377437
sp|P01718|LV327_HUMAN	12	4	6	3	-0.14266	-0.064339321	0.415846864	0.078323356	0.558509541	0.480186185	0.960393426	0.276365179	0.323664087
sp|Q9GZP8|IMUP_HUMAN	1	40	76	33	-0.18146	-0.264193446	-0.353706646	-0.082733285	-0.172246485	-0.0895132	0.879252825	0.681263651	0.876119999
sp|Q16663|CCL15_HUMAN	1	40	76	33	-0.10087	-0.178758274	0.232576473	-0.07789277	0.333441976	0.411334746	0.480499674	0.000188968	1.68E-07
sp|P02810|PRPC_HUMAN	2	28	55	25	-0.44879	-0.594497344	0.053387662	-0.145709331	0.502175676	0.647885007	0.757032993	0.101088922	0.008171616
sp|P15151|PVR_HUMAN	8	40	76	33	-0.00798	0.02325285	0.101496564	0.031229861	0.109473575	0.078243714	0.737117325	0.079942039	0.190687745
sp|P28482|MK01_HUMAN	1	15	28	12	-0.07669	-0.125897201	-0.121519094	-0.049208242	-0.044830134	0.004378107	0.956076926	0.974864812	0.999693953
sp|Q9H9Q2|CSN7B_HUMAN	7	19	34	15	-0.29338	-0.099228455	0.286818651	0.194152366	0.580199472	0.386047106	0.455494413	0.011081588	0.076810214
sp|Q8NHJ6|LIRB4_HUMAN	1	7	14	6	-0.65539	-0.768523358	0.17477274	-0.113130907	0.830165191	0.943296098	0.963945705	0.274645095	0.123589692
sp|Q9HAT2|SIAE_HUMAN	2	40	76	33	-0.15295	-0.170256283	0.185343697	-0.017305889	0.338294091	0.35559998	0.963213198	0.00011899	4.40E-06
sp|P15813|CD1D_HUMAN	12	18	35	15	0.139167	0.092063481	-0.091578348	-0.047103763	-0.230745592	-0.183641829	0.90570533	0.203969336	0.272681936
sp|P49901|MCSP_HUMAN	1	4	6	3	0.311945	0.242975725	0.105745752	-0.068969103	-0.206199076	-0.137229973	0.906280521	0.55091132	0.728126075
sp|Q9UFE4|CCD39_HUMAN	2	29	55	24	0.716525	0.290763536	-0.065459297	-0.425761314	-0.781984147	-0.356222833	0.163217562	0.016476283	0.324094603
sp|Q14012|KCC1A_HUMAN	1	21	42	19	0.015884	-0.048406691	0.258961231	-0.064291128	0.243076794	0.307367922	0.897797438	0.339387256	0.108153751
sp|P05114|HMGN1_HUMAN	5	32	62	27	-0.70507	-0.55342206	0.074229123	0.151650215	0.779301398	0.627651183	0.60687747	0.000235346	0.000858074
sp|Q96I15|SCLY_HUMAN	1	22	41	17	-0.15616	0.056761868	0.230662711	0.212921998	0.386822841	0.173900843	0.262973121	0.056222007	0.469944193
sp|O60268|K0513_HUMAN	5	8	14	6	-0.07693	0.08879441	-0.01610933	0.165727132	0.060823392	-0.10490374	0.718953644	0.970125104	0.895713804
sp|Q9Y3B3|TMED7_HUMAN	6	22	41	18	-0.08389	-0.318362588	0.088689747	-0.234475064	0.17257727	0.407052334	0.172824828	0.511978428	0.011956379
sp|Q8NBK3|SUMF1_HUMAN	15	20	34	14	-0.07795	0.075899907	0.55646583	0.15384786	0.634413784	0.480565923	0.312000451	1.97E-05	0.000372067
sp|Q5D862|FILA2_HUMAN	4	11	21	9	-0.16787	0.20971719	-0.330389769	0.377582782	-0.162524178	-0.54010696	0.07212482	0.699248625	0.011724782
sp|Q8IUI8|CRLF3_HUMAN	3	37	69	29	-0.26255	-0.235425799	0.240359578	0.027127739	0.502913117	0.475785377	0.982629869	0.020369663	0.012838848
sp|Q9UKJ1|PILRA_HUMAN	5	40	76	33	-0.37394	-0.253921807	0.426045751	0.120015129	0.799982687	0.679967558	0.459462758	2.09E-09	8.46E-09
sp|O43768|ENSA_HUMAN	2	22	41	18	-0.32206	-0.223877816	0.645821444	0.0981865	0.967885761	0.869699261	0.903439209	0.002063919	0.00184282
sp|P61586|RHOA_HUMAN	2	26	48	20	-0.09993	-0.088540054	-0.15726956	0.011392601	-0.057336906	-0.068729507	0.995813964	0.931323581	0.880235118
sp|P04279|SEMG1_HUMAN	7	6	14	7	-0.23925	-0.195205927	0.868645472	0.044043007	1.107894407	1.0638514	0.993547275	0.062384655	0.028359458
sp|Q5T1J5|CHCH9_HUMAN	8	4	6	3	-0.5975	0.03690491	0.348739294	0.634406826	0.94624121	0.311834384	0.338993969	0.197545014	0.788044813
sp|Q9NRX4|PHP14_HUMAN	1	40	76	33	-0.4211	-0.180946166	0.418703785	0.240149446	0.839799398	0.599649952	0.0461653	3.01E-10	2.87E-07
sp|Q9Y219|JAG2_HUMAN	1	32	62	27	0.033829	0.036752172	-0.018432236	0.002922717	-0.052261691	-0.055184408	0.998533805	0.723100936	0.629079833
sp|Q96NU7|HUTI_HUMAN	10	26	49	21	-0.23839	-0.102813886	0.293379751	0.13557454	0.531768178	0.396193637	0.584459933	0.005072267	0.022614492
sp|P15941|MUC1_HUMAN	4	40	76	33	-0.14284	-0.066244195	0.430883373	0.076596034	0.573723601	0.497127568	0.535071588	1.65E-09	3.60E-09
sp|P22694|KAPCB_HUMAN	1	37	69	29	-0.18444	-0.181224796	0.171642573	0.003210571	0.35607794	0.352867369	0.999661343	0.065376483	0.035377089
sp|Q9UNN5|FAF1_HUMAN	2	4	7	3	0.241218	0.3214835	0.01139401	0.080265061	-0.229824429	-0.31008949	0.94275131	0.727933492	0.504790556
sp|Q14246|AGRE1_HUMAN	7	14	28	12	0.014539	0.000212575	0.01168524	-0.014326317	-0.002853653	0.011472664	0.99509974	0.999865061	0.997168653
sp|Q16134|ETFD_HUMAN	17	4	7	3	0.4642	0.466940077	1.596062405	0.002739682	1.13186201	1.129122328	0.999979418	0.141414064	0.099907348
sp|P01037|CYTN_HUMAN	3	14	27	13	0.562539	0.306884798	0.148744331	-0.255654451	-0.413794919	-0.158140467	0.782852978	0.627209619	0.914404328
sp|O43915|VEGFD_HUMAN	6	36	69	30	-0.08733	-0.058279255	0.02208694	0.029055112	0.109421308	0.080366196	0.878460971	0.285044459	0.419411024
sp|Q9Y2Y8|PRG3_HUMAN	2	32	62	27	-0.01522	-0.002448586	0.098829087	0.012775708	0.114053381	0.101277673	0.981036038	0.351534512	0.346928229
sp|Q5DT21|ISK9_HUMAN	6	11	20	9	-0.12733	-0.058137703	-0.017672629	0.069197129	0.109662203	0.040465074	0.865555802	0.777178517	0.957605859
sp|O76009|KT33A_HUMAN	7	4	6	3	-0.19751	0.664105537	-0.080742209	0.861612305	0.116764559	-0.744847746	0.525675183	0.991022033	0.663341465
sp|Q9HCU0|CD248_HUMAN	18	40	76	33	-0.0002	-0.030364394	0.393737772	-0.03016076	0.393941406	0.424102166	0.877850474	1.39E-06	5.69E-09
sp|P11150|LIPC_HUMAN	3	40	76	33	0.140667	0.027104502	0.009627512	-0.113562413	-0.131039403	-0.01747699	0.210127469	0.238097765	0.967568088
sp|P17096|HMGA1_HUMAN	2	4	6	3	0.208939	0.310374722	0.800173869	0.101436	0.591235147	0.489799147	0.959255468	0.398541397	0.472348081
sp|Q27J81|INF2_HUMAN	6	14	28	12	-0.48449	-0.349250819	0.407247383	0.135241729	0.891739931	0.756498202	0.86823216	0.020302989	0.025592772
sp|Q01523|DEF5_HUMAN	81	4	6	3	1.322419	1.931226185	0.970586004	0.608806819	-0.351833362	-0.960640181	0.363942044	0.770223383	0.148950516
sp|Q6UXH0|ANGL8_HUMAN	4	40	76	33	0.144854	0.162025734	0.24073041	0.017171563	0.095876239	0.078704676	0.976110505	0.596090325	0.6414779
sp|Q93033|IGSF2_HUMAN	1	16	27	11	0.27692	0.274101443	0.041542808	-0.002818559	-0.235377194	-0.232558635	0.999740142	0.318293436	0.263417243
sp|Q7L5N1|CSN6_HUMAN	1	33	62	27	-0.24693	-0.043298241	0.405174976	0.203629618	0.652102836	0.448473217	0.235599008	8.74E-05	0.00296798
sp|Q5VWZ2|LYPL1_HUMAN	12	10	21	9	0.000923	-0.009496067	0.828541377	-0.010419229	0.827618215	0.838037444	0.998441255	0.003144051	0.000576599
sp|Q9UFP1|GAK1A_HUMAN	1	36	69	30	0.060747	0.024583149	-0.022958574	-0.036164346	-0.083706069	-0.047541723	0.88516774	0.637422252	0.830127223
sp|P22102|PUR2_HUMAN	15	9	21	10	-0.02196	-0.057476229	0.298785774	-0.035513557	0.320748445	0.356262002	0.961492556	0.105478956	0.022706868
sp|O43556|SGCE_HUMAN	77	19	34	14	-0.03658	0.066587234	0.104604446	0.103167255	0.141184468	0.038017212	0.536466446	0.463432639	0.932814726
sp|P11169|GTR3_HUMAN	10	22	42	18	-0.18121	0.120478806	0.241298974	0.301693187	0.422513355	0.120820168	0.114071678	0.055786467	0.731078642
sp|P16671|CD36_HUMAN	1	3	7	4	0.018616	-0.182291319	0.396505643	-0.200907461	0.377889502	0.578796962	0.827899208	0.589806132	0.192278588
sp|Q9H3T3|SEM6B_HUMAN	1	36	69	30	-0.10144	-0.073973332	0.157478042	0.027462377	0.258913751	0.231451374	0.896781405	0.001904135	0.001682217
sp|P00813|ADA_HUMAN	1	40	76	33	-0.03209	-0.0016598	0.016012958	0.030427073	0.048099831	0.017672757	0.804313624	0.687388877	0.937436269
sp|Q66PJ3|AR6P4_HUMAN	12	4	7	3	0.353841	0.406870892	0.905601396	0.053029426	0.551759931	0.498730504	0.977289972	0.232769063	0.232517846
sp|Q8IWK6|AGRA3_HUMAN	4	40	76	33	0.023089	0.078499818	0.059893717	0.05541061	0.036804509	-0.018606101	0.450851123	0.783546166	0.923609606
sp|Q8NBJ7|SUMF2_HUMAN	3	23	41	18	-0.00172	0.007214217	0.044386345	0.00893751	0.046109638	0.037172128	0.987759326	0.799421461	0.834968933
sp|P42330|AK1C3_HUMAN	5	15	27	13	-0.11979	0.239701377	0.502882198	0.359492635	0.622673456	0.263180821	0.217371572	0.041420088	0.468783027
sp|Q9UNH7|SNX6_HUMAN	7	20	41	19	0.269985	0.026012325	0.311013719	-0.243972646	0.041028749	0.285001394	0.267306751	0.972740002	0.177790286
sp|Q16695|H31T_HUMAN	1	32	61	27	-2.00319	-1.847611612	-0.333600351	0.155576945	1.669588205	1.51401126	0.861697271	2.48E-05	1.53E-05
sp|Q8N339|MT1M_HUMAN	1	26	48	20	-1.86906	-1.522262895	0.019289087	0.346798611	1.888350593	1.541551983	0.420860187	6.15E-07	4.88E-06
sp|P16452|EPB42_HUMAN	4	4	7	3	0.154376	0.261702716	1.448530752	0.107327095	1.294155132	1.186828036	0.977473112	0.154853575	0.147683904
sp|P08865|RSSA_HUMAN	1	14	28	12	-0.32196	-0.10448897	0.342189282	0.217467649	0.6641459	0.446678251	0.592207	0.041588375	0.145857699
sp|Q99829|CPNE1_HUMAN	10	40	76	33	0.019518	0.100988057	0.252054775	0.081470345	0.232537062	0.151066718	0.616556456	0.070136994	0.235718417
sp|Q32MZ4|LRRF1_HUMAN	231	7	14	5	0.218915	0.387793847	0.464138054	0.168878721	0.245222928	0.076344207	0.88621575	0.853085346	0.980607336
sp|Q9NZU5|LMCD1_HUMAN	1	4	6	3	-0.0109	-0.083930733	0.50610888	-0.073033837	0.517005776	0.590039613	0.95480102	0.239496884	0.130863391
sp|Q00688|FKBP3_HUMAN	5	37	69	30	0.04841	0.024502217	0.302936109	-0.023907611	0.254526281	0.278433892	0.980897811	0.227831951	0.109064633
sp|Q96I99|SUCB2_HUMAN	5	4	7	3	0.186645	0.466749803	1.145929423	0.280105118	0.959284738	0.67917962	0.691949928	0.091947565	0.204622666
sp|P35613|BASI_HUMAN	1	4	7	3	-0.21324	-0.080536632	0.216049743	0.132698926	0.4292853	0.296586375	0.837645415	0.320475426	0.499249797
sp|Q9UHB6|LIMA1_HUMAN	15	7	14	6	-0.29354	-0.364197859	0.433963697	-0.070653956	0.727507601	0.798161557	0.940508295	0.022569093	0.004160637
sp|P51805|PLXA3_HUMAN	6	7	14	5	0.089233	0.058673558	0.068210142	-0.03055946	-0.021022875	0.009536585	0.934960927	0.980260969	0.994827666
sp|O60242|AGRB3_HUMAN	1	11	20	10	0.116204	0.006827586	0.098349242	-0.109376825	-0.017855169	0.091521656	0.333950561	0.977960494	0.482185672
sp|O75063|XYLK_HUMAN	23	14	27	13	0.159683	0.363456023	0.508327341	0.203773178	0.348644497	0.144871319	0.170509521	0.026606125	0.419334795
sp|P18627|LAG3_HUMAN	3	8	13	5	-0.08959	0.146024675	0.384942465	0.235615066	0.474532856	0.23891779	0.667054012	0.370771103	0.73711459
sp|Q08554|DSC1_HUMAN	1	40	76	33	0.178683	0.093975006	0.104448706	-0.084708132	-0.074234432	0.0104737	0.119620744	0.32082297	0.971282135
sp|Q9NZD4|AHSP_HUMAN	97	40	76	33	-0.78445	-0.469631613	-0.027729385	0.314821496	0.756723724	0.441902228	0.033828406	4.11E-06	0.003267188
sp|O00560|SDCB1_HUMAN	14	15	28	13	0.192166	0.23537447	0.17764485	0.043208513	-0.014521107	-0.05772962	0.905553037	0.992025991	0.851508862
sp|Q15517|CDSN_HUMAN	11	25	48	21	0.062495	0.078314015	0.094239421	0.015819105	0.031744511	0.015925406	0.960858255	0.894477532	0.964674255
sp|Q6P5S2|LEG1H_HUMAN	4	4	7	3	1.049719	0.207831474	0.023086388	-0.841887362	-1.026632448	-0.184745085	0.07208635	0.07186573	0.875062994
sp|P52565|GDIR1_HUMAN	15	40	76	33	-0.13905	-0.099685709	0.331630976	0.039364185	0.47068087	0.431316685	0.940778555	0.003393995	0.002348931
sp|Q16620|NTRK2_HUMAN	10	40	76	33	0.151119	0.086997221	-0.195379815	-0.064122047	-0.346499083	-0.282377035	0.330658513	6.06E-09	8.00E-08
sp|Q01970|PLCB3_HUMAN	12	26	48	21	0.023106	0.046770588	0.266898894	0.023664903	0.243793209	0.220128306	0.961827053	0.064832631	0.060667791
sp|P08236|BGLR_HUMAN	4	10	21	9	0.10676	-0.001302585	0.09326753	-0.108062609	-0.013492495	0.094570115	0.684473125	0.995827728	0.762669416
sp|P24592|IBP6_HUMAN	11	40	76	33	0.098201	0.048089234	0.299694611	-0.050111614	0.201493763	0.251605377	0.642006236	0.008821335	0.000122115
sp|P13747|HLAE_HUMAN	3	28	55	25	-0.15121	0.023898771	0.349666023	0.175112217	0.50087947	0.325767253	0.227810705	0.000355618	0.010483009
sp|P23588|IF4B_HUMAN	11	11	21	9	-0.50122	-0.167415813	0.604573523	0.333801575	1.10579091	0.771989336	0.597299358	0.029009762	0.102211172
sp|P15374|UCHL3_HUMAN	5	7	14	6	-0.12656	-0.014647135	0.549972533	0.111908969	0.676528637	0.564619668	0.861958283	0.038490693	0.050455444
sp|Q12794|HYAL1_HUMAN	10	19	34	15	-0.10666	-0.023543122	0.060762501	0.0831131	0.167418723	0.084305624	0.706135624	0.383047714	0.736419835

sp|P25325|THTM_HUMAN	13	40	76	33	-0.1187	-0.081945974	0.148530866	0.036758473	0.267235313	0.23047684	0.887620141	0.015469346	0.019171997
sp|Q9H299|SH3L3_HUMAN	4	40	76	33	-0.03527	-0.153845103	0.276733707	-0.118571652	0.312007158	0.43057881	0.692050032	0.176675105	0.016564093
sp|Q16555|DPYL2_HUMAN	17	40	76	33	-0.20666	-0.155245816	0.109090895	0.051411814	0.315748526	0.264336711	0.83819436	0.012306134	0.019449571
sp|P55809|SCOT1_HUMAN	4	4	6	3	0.045647	0.416955692	0.286668257	0.371308713	0.241021278	-0.130287435	0.335819998	0.701088408	0.883342788
sp|Q13609|DNSL3_HUMAN	1	16	27	11	-0.22162	-0.219136391	0.139085379	0.002483629	0.360705399	0.358221769	0.999888772	0.22977162	0.17751223
sp|P80748|LV321_HUMAN	1	4	7	3	-0.01278	-0.048879932	0.171272339	-0.036099994	0.184052278	0.220152272	0.948317902	0.423341452	0.240359199
sp|Q9BRA2|TXD17_HUMAN	16	40	76	33	-0.36837	-0.175098772	0.259481933	0.193269976	0.62785068	0.434580705	0.142926135	2.82E-06	0.000295688
sp|Q969H8|MYDGF_HUMAN	6	40	76	33	-0.28814	-0.247213392	0.33946372	0.040923803	0.627600914	0.586677112	0.921692863	7.46E-06	2.28E-06
sp|Q13347|EIF3I_HUMAN	5	4	7	3	-0.27312	-0.139066389	-0.37814624	0.134049688	-0.105030164	-0.239079852	0.901574651	0.957828816	0.765161405
sp|Q5BLP8|CD048_HUMAN	2	14	28	13	-0.00959	-0.018077273	-0.002498604	-0.008489364	0.007089305	0.015578669	0.997877283	0.998930306	0.993217023
sp|P51148|RAB5C_HUMAN	49	4	7	3	0.358012	0.05685159	0.311064206	-0.301160153	-0.046947537	0.254212616	0.482055136	0.987287373	0.643358772
sp|P48595|SPB10_HUMAN	9	10	20	10	-0.30398	-0.259496144	0.529644748	0.044484318	0.833625211	0.789140893	0.990843667	0.10437489	0.069501631
sp|Q00839|HNRPU_HUMAN	2	10	21	9	0.182851	0.4357232	1.179890237	0.252872414	0.997039451	0.744167037	0.76728715	0.069044871	0.132563123
sp|O14933|UB2L6_HUMAN	6	10	21	10	-0.14757	0.103092736	0.505602146	0.25066726	0.653176671	0.40250941	0.47545766	0.032201345	0.156640197
sp|P04632|CPNS1_HUMAN	31	40	76	33	0.10255	0.142488859	0.438305	0.039938791	0.335754932	0.295816141	0.823809468	0.000169087	0.000186594
sp|P26599|PTBP1_HUMAN	4	17	35	16	-0.25893	-0.111179936	0.374083776	0.147752001	0.633015713	0.485263712	0.561144311	0.001114185	0.004269742
sp|O75752|B3GL1_HUMAN	5	40	76	33	0.073452	0.011457971	-0.03545984	-0.061993535	-0.108911346	-0.046917811	0.226230619	0.044500216	0.470865714
sp|P61956|SUMO2_HUMAN	9	22	42	17	-0.15649	-0.157442471	0.565817875	-0.000947484	0.722312861	0.723260346	0.999977062	0.000405688	6.70E-05
sp|Q6EEV6|SUMO4_HUMAN	2	22	41	19	0.023354	-0.095200643	0.314207986	-0.118555139	0.29085349	0.409408629	0.712351124	0.239807025	0.030643445
sp|A4D0S4|LAMB4_HUMAN	12	32	63	28	0.009813	0.018592422	0.129994932	0.008779429	0.120181938	0.11140251	0.981292483	0.088965984	0.067879467
sp|Q8NFZ3|NLGNY_HUMAN	26	14	28	13	0.038224	0.095512178	0.020805526	0.057288509	-0.017418143	-0.074706652	0.806083311	0.985644653	0.706358378
sp|P10747|CD28_HUMAN	13	8	13	5	-0.15554	0.028721999	-0.111763353	0.184259833	0.043774481	-0.140485353	0.922280153	0.99715644	0.966214465
sp|P99999|CYC_HUMAN	2	40	76	33	-0.08774	-0.033583976	0.063751641	0.05416066	0.151496277	0.097335616	0.696332691	0.146311944	0.36088883
sp|Q96FV2|SCRN2_HUMAN	1	36	70	30	0.060396	0.0155055	0.121877653	-0.044890734	0.061481419	0.106372153	0.834933177	0.79232775	0.411626117
sp|P50225|ST1A1_HUMAN	3	33	62	27	-0.08085	-0.16570238	0.164073907	-0.08484838	0.244927907	0.329776287	0.849028988	0.393937662	0.121366193
sp|P46782|RS5_HUMAN	1	4	6	3	-0.46447	-0.355664474	0.152327912	0.108805015	0.616797402	0.507992387	0.955922757	0.390160488	0.467947553
sp|P15586|GNS_HUMAN	1	19	35	15	-0.00226	0.006826454	0.314651557	0.009084257	0.316909361	0.307825103	0.993853893	0.00928011	0.004281957
sp|P26022|PTX3_HUMAN	11	40	76	33	-0.58731	-0.433677554	0.056334212	0.153636509	0.643648275	0.490011765	0.367598847	1.67E-05	0.000245288
sp|O00161|SNP23_HUMAN	6	36	69	30	-0.31989	-0.236309712	0.016291629	0.083582534	0.336183876	0.252601341	0.750812344	0.04470294	0.104060255
sp|Q9NTN9|SEM4G_HUMAN	8	40	76	33	0.036519	0.049291555	-0.02181018	0.012772324	-0.058329411	-0.071101735	0.971199161	0.657842084	0.454425074
sp|P43487|RANG_HUMAN	4	40	76	33	-0.25099	-0.105716858	0.221041294	0.145277696	0.472035848	0.326758152	0.339299218	0.000615753	0.009757017
sp|P46940|IQGA1_HUMAN	2	22	41	18	0.200983	0.234579474	0.54423006	0.033596471	0.343247057	0.309650585	0.974086373	0.158990123	0.151177209
sp|P40939|ECHA_HUMAN	4	4	7	3	0.055732	0.024483338	1.454645463	-0.031249079	1.398913046	1.430162125	0.998845773	0.255119743	0.183865829
sp|Q86WC4|OSTM1_HUMAN	9	19	35	14	0.017595	0.034551344	-0.233799677	0.016956141	-0.25139488	-0.268351021	0.952801252	0.002035831	0.000221997
sp|Q9H3K6|BOLA2_HUMAN	5	33	62	28	-0.37312	-0.084623399	0.306301076	0.288494011	0.679418486	0.390924475	0.011626586	1.94E-07	0.000816341
sp|P04118|COL_HUMAN	1	12	20	9	-0.22249	-0.264784514	0.449669433	-0.042294953	0.672158994	0.714453947	0.985966118	0.101740271	0.047561324
sp|Q16849|PTPRN_HUMAN	2	7	13	6	0.190037	0.057385284	0.541828534	-0.13265183	0.351791421	0.48444325	0.895347461	0.58226446	0.283868077
sp|P09093|CEL3A_HUMAN	2	40	76	33	-0.23224	-0.148989679	-0.032729791	0.083250296	0.199510184	0.116259888	0.707932208	0.258150195	0.554386395
sp|P45877|PPIC_HUMAN	12	40	76	33	0.171326	0.123114417	0.501590265	-0.048211439	0.330264409	0.378475848	0.71025184	4.24E-05	1.15E-07
sp|Q96L96|ALPK3_HUMAN	4	4	6	3	-0.18244	-0.08912599	0.520849006	0.093318515	0.703293511	0.609974996	0.983724854	0.535567926	0.575677566
sp|Q13451|FKBP5_HUMAN	3	15	27	12	-0.20583	-0.379568045	0.316475863	-0.173735891	0.522308017	0.696043908	0.725544303	0.145059292	0.01713505
sp|P62633|CNBP_HUMAN	2	7	14	6	-0.89258	-0.629965635	0.7354263	0.262612625	1.62800456	1.365391935	0.745014779	0.00245628	0.00369313
sp|P56537|IF6_HUMAN	2	7	14	6	-0.3092	-0.006061445	0.308480582	0.303138611	0.617680638	0.314542028	0.203235386	0.016870046	0.212832011
sp|Q53RD9|FBLN7_HUMAN	6	40	76	33	-0.03434	-0.037057739	0.210527746	-0.002722476	0.244863009	0.247585485	0.998170158	8.96E-05	7.13E-06
sp|P30530|UFO_HUMAN	27	40	76	33	-0.00158	-0.049391831	0.057477275	-0.047810747	0.05905836	0.106869106	0.433099704	0.414548948	0.0281981
sp|Q9P2E9|RRBP1_HUMAN	7	18	34	16	-0.44139	-0.281903602	0.036041142	0.159482912	0.477427657	0.317944744	0.866790165	0.403094919	0.59367015
sp|P06576|ATPB_HUMAN	9	23	41	18	0.095552	0.065411266	0.148517364	-0.030140688	0.05296541	0.083106098	0.948449843	0.894138104	0.711791549
sp|P26010|ITB7_HUMAN	2	11	20	9	0.157607	0.108662831	0.134946247	-0.048943878	-0.022660462	0.026283416	0.790114518	0.965178777	0.942006862
sp|P62805|H4_HUMAN	2	40	76	33	-1.20159	-1.109526427	-0.055256677	0.092062822	1.146332572	1.05426975	0.896917338	2.73E-05	1.32E-05
sp|P48509|CD151_HUMAN	9	4	7	3	-0.24169	-0.178336558	0.726804751	0.063350376	0.968491684	0.905141308	0.993952626	0.41564359	0.392882277
sp|Q8TCD5|NT5C_HUMAN	20	24	41	17	0.047837	0.014953118	0.253818473	-0.032883958	0.205981397	0.238865355	0.9470729	0.253486037	0.110906884
sp|P12273|PIP_HUMAN	8	33	62	27	0.071268	0.011478608	0.024463351	-0.059789527	-0.046804784	0.012984742	0.629936069	0.822084651	0.981042571
sp|Q8WUA8|TSK_HUMAN	22	40	76	33	-0.18443	-0.064286748	0.209268951	0.120143539	0.393699238	0.273555699	0.478118084	0.005392949	0.037947434
sp|O95502|NPTXR_HUMAN	6	40	76	33	0.091742	-0.00949521	-0.296706231	-0.101237273	-0.388448294	-0.287211021	0.208207822	7.13E-07	3.73E-05
sp|P55957|BID_HUMAN	10	11	21	10	0.133593	0.060789611	0.425385172	-0.072803001	0.29179256	0.364595561	0.870170587	0.21128101	0.049413645
sp|Q9C005|DPY30_HUMAN	1	6	14	7	0.127547	0.207820997	1.034147794	0.080274192	0.906600989	0.826326797	0.960293955	0.033212007	0.018715778
sp|P06748|NPM_HUMAN	1	7	14	5	-0.46682	-0.075993851	0.754941002	0.39082472	1.221759573	0.830934853	0.710717805	0.144724843	0.309963645
sp|Q13724|MOGS_HUMAN	5	33	62	27	0.193169	0.193198039	0.154601638	2.86E-05	-0.038567834	-0.038596401	0.999999807	0.784723745	0.735456304
sp|P55286|CADH8_HUMAN	7	4	7	3	0.009908	0.01672207	0.10685321	0.00681405	0.096945191	0.09013114	0.997739794	0.74096598	0.728387743
sp|P55327|TPD52_HUMAN	3	7	13	6	0.226879	0.180204597	0.475680872	-0.046674415	0.248801861	0.295476276	0.97933458	0.661324544	0.48192555
sp|O43399|TPD54_HUMAN	12	8	13	6	-0.08002	-0.123453465	-0.315054974	-0.043431613	-0.235033122	-0.191601509	0.965030352	0.49657308	0.570862605
sp|P01906|DQA2_HUMAN	1	28	56	25	-0.21534	-0.060811587	0.051161036	0.154533359	0.266505981	0.111972623	0.535293722	0.271601402	0.737053522
sp|P48745|CCN3_HUMAN	104	40	76	33	-0.31851	-0.3465985	0.113357256	-0.028085513	0.431870243	0.459955756	0.941384333	0.000121513	3.37E-06
sp|Q96JQ0|PCD16_HUMAN	1	40	76	33	0.099528	0.096455524	0.115814269	-0.003072044	0.016286701	0.019358745	0.995342836	0.913525048	0.850037814
sp|Q6NUJ1|SAPL1_HUMAN	8	4	7	3	0.025841	0.237705459	-0.145265944	0.211864514	-0.171106888	-0.382971402	0.251795611	0.521867843	0.044001908
sp|P23327|SRCH_HUMAN	1	6	14	7	0.103588	0.074237012	0.236471302	-0.029351259	0.132883032	0.16223429	0.955140004	0.495493432	0.232205576
sp|Q02413|DSG1_HUMAN	23	6	14	7	0.082254	0.131520713	-0.411726117	0.049266639	-0.49398019	-0.543246829	0.990115099	0.47575413	0.281712985
sp|P61081|UBC12_HUMAN	5	32	63	27	-0.00518	-0.026759832	0.318752831	-0.021578881	0.323933782	0.345512663	0.970325021	0.011738273	0.001687367
sp|P31152|MK04_HUMAN	2	22	41	17	0.229558	0.146720013	0.448029266	-0.082837803	0.21847145	0.301309253	0.894514991	0.597020562	0.296667246
sp|Q9H2H8|PPIL3_HUMAN	28	4	7	2	0.023781	-0.056253511	-0.137549009	-0.080034419	-0.161329917	-0.081295498	0.939000176	0.875482851	0.960999777
sp|Q8NBI6|XXLT1_HUMAN	9	14	27	12	0.06153	0.04177761	0.126285049	-0.019752496	0.064754943	0.08450744	0.962696079	0.752259805	0.538805293
sp|O95727|CRTAM_HUMAN	3	26	48	20	-0.0051	-0.00309484	0.241972998	0.002007953	0.24707579	0.245067837	0.999720898	0.065731233	0.036289559
sp|Q6FHJ7|SFRP4_HUMAN	9	40	76	33	-0.06736	-0.020126938	0.007945783	0.047234292	0.075307014	0.028072721	0.712429277	0.552623904	0.899947038
sp|O75581|LRP6_HUMAN	6	14	28	11	0.046156	0.10331158	0.03151501	0.05715574	-0.01464083	-0.07179657	0.67948476	0.983258332	0.597882112
sp|P02511|CRYAB_HUMAN	1	4	6	3	-0.19844	-0.360067962	1.570813483	-0.161623371	1.769258074	1.930881445	0.976922	0.187163393	0.110901496
sp|P62837|UB2D2_HUMAN	3	40	76	33	-0.11074	-0.076301085	0.1905693	0.034441171	0.301311556	0.266870385	0.891613402	0.003275484	0.003307533
sp|Q96Q42|ALS2_HUMAN	3	3	7	4	-0.37803	0.105178848	-0.111967914	0.483205694	0.266058933	-0.217146762	0.804648386	0.946830089	0.947392049
sp|Q9UH65|SWP70_HUMAN	1	6	14	7	-0.08262	-0.037628249	0.339908531	0.04498737	0.42252415	0.37753678	0.967904371	0.132599072	0.100241797
sp|P61960|UFM1_HUMAN	5	37	69	30	-0.31045	-0.198561796	0.250098243	0.111883457	0.560543496	0.448660039	0.507741678	2.60E-05	0.000167826
sp|Q7Z4W1|DCXR_HUMAN	10	40	76	33	-0.29581	-0.096956087	-0.061085708	0.198849165	0.234719544	0.035870379	0.175290308	0.187273693	0.950614297
sp|Q9H0Q0|FA49A_HUMAN	3	18	34	14	-0.49563	-0.435776327	0.075228826	0.059852181	0.570857335	0.511005153	0.916001519	0.007692077	0.007388501
sp|Q9UPP5|K1107_HUMAN	2	4	6	3	-0.01408	0.579812264	-0.27697043	0.59389318	-0.262889513	-0.856782694	0.502016576	0.902483255	0.320089768
sp|Q5TDH0|DDI2_HUMAN	8	25	48	21	-0.46862	-0.133974311	0.069574703	0.334647297	0.538196312	0.203549014	0.060093602	0.007433615	0.386777284
sp|P34896|GLYC_HUMAN	11	19	34	15	-0.49017	-0.317128461	0.207009868	0.173039131	0.697177461	0.524138329	0.743549281	0.043537149	0.106771298
sp|P30039|PBLD_HUMAN	1	4	7	3	0.157223	0.53357735	0.396939925	0.376354319	0.239716894	-0.136637425	0.512539544	0.825970446	0.925953108
sp|O14638|ENPP3_HUMAN	1	32	62	27	0.127019	0.07617882	-0.065660834	-0.050840613	-0.192680267	-0.141839654	0.752778473	0.064121115	0.14504659
sp|O60760|HPGDS_HUMAN	2	12	21	8	-0.00723	0.046174789	-0.287884993	0.053399867	-0.280659915	-0.334059782	0.921309722	0.254427503	0.10257888
sp|O43639|NCK2_HUMAN	5	32	62	27	0.374056	0.250056716	0.436902129	-0.123999227	0.062846187	0.186845413	0.735824183	0.946633607	0.538843723
sp|Q9Y6C2|EMIL1_HUMAN	1	40	76	33	0.039886	0.146898762	0.45417331	0.107013055	0.414287603	0.307274548	0.336781511	3.40E-05	0.000612879
sp|O75351|VPS4B_HUMAN	4	15	28	11	-0.12039	-0.187194627	0.224253285	-0.066803553	0.344644359	0.411447911	0.910173255	0.207591584	0.066181659
sp|O60256|KPRB_HUMAN	8	4	7	3	-0.44054	0.250818489	-0.343192533	0.691358116	0.097347093	-0.594011023	0.459055523	0.988870479	0.614043883
sp|Q8NES3|LFNG_HUMAN	3	23	41	17	-0.07068	0.034300351	0.153895351	0.104980096	0.224575096	0.119595	0.484535912	0.116636279	0.464679341
sp|Q9UBS9|SUCO_HUMAN	16	9	21	10	0.079608	0.193099972	0.141356325	0.11349224	0.061748593	-0.051743647	0.702276403	0.923730166	0.923421763
sp|Q5JXA9|SIRB2_HUMAN	5	11	20	9	-0.03456	0.101465029	0.351925923	0.136021858	0.386482752	0.250460894	0.357188158	0.006024033	0.055963531
sp|Q9H0X4|F234A_HUMAN	1	40	76	33	0.209418	0.15007222	-0.034054824	-0.059346069	-0.243473113	-0.184127044	0.308196229	4.61E-06	0.000101642
sp|Q6FI13|H2A2A_HUMAN	1	32	62	27	-1.30937	-1.243575407	-0.050768021	0.065798638	1.258606024	1.192807386	0.950968977	1.32E-05	2.89E-06
sp|Q15208|STK38_HUMAN	1	7	14	6	0.140602	0.118174983	0.084828134	-0.0224274	-0.055774249	-0.033346849	0.975859819	0.901004256	0.952592582
sp|Q9H6B4|CLMP_HUMAN	1	40	76	33	-0.09102	-0.128001188	0.144975489	-0.036979273	0.235997404	0.272976677	0.922671538	0.109537629	0.024526499
sp|Q8N3V7|SYNPO_HUMAN	1	4	6	3	0.129747	0.075548605	0.955976104	-0.054198882	0.826228618	0.880427499	0.994762759	0.448698548	0.355060606
sp|Q9NP55|BPIA1_HUMAN	6	3	7	4	-0.41521	0.431153105	0.129515359	0.846367758	0.544730012	-0.301637746	0.138417124	0.470540496	0.700027318
sp|Q9NS15|LTBP3_HUMAN	2	32	62	27	-0.13865	-0.097973978	0.333965516	0.040680624	0.472620117	0.431939493	0.865956212	7.46E-06	3.49E-06
sp|Q9UI17|M2GD_HUMAN	5	12	20	9	-0.08962	0.030474131	0.467099783	0.120091405	0.556717057	0.436625652	0.746519583	0.020902312	0.052260494
sp|O00764|PDXK_HUMAN	5	4	7	3	0.108758	0.278559732	0.586797084	0.169801587	0.478038939	0.308237352	0.83748809	0.413007277	0.625734556
sp|A0AVT1|UBA6_HUMAN	1	8	14	6	-0.22015	-0.098325077	0.208336787	0.121828196	0.42849006	0.306661863	0.948639507	0.649224644	0.761130486
sp|Q6IEE7|T132E_HUMAN	2	7	13	6	0.105399	0.210312352	0.156912704	0.104912997	0.051513349	-0.053399648	0.592273445	0.912530638	0.882686073

sp|P05198|IF2A_HUMAN	7	22	41	18	-0.17859	-0.009167412	0.357931344	0.169423474	0.53652223	0.367098756	0.610717495	0.038110174	0.138938898
sp|P34949|MPI_HUMAN	1	4	7	3	-0.1131	-0.250472743	-0.040139379	-0.13737361	0.072959754	0.210333364	0.795267782	0.956673489	0.647658235
sp|Q8NFZ8|CADM4_HUMAN	11	36	69	30	0.04587	-0.051293499	0.23582418	-0.097163701	0.189953977	0.287117678	0.403949863	0.094624458	0.001387606
sp|O95841|ANGL1_HUMAN	11	10	21	10	0.050047	0.067156536	0.144482815	0.017109097	0.094435377	0.07732628	0.992817069	0.850996119	0.863611646
sp|P09529|INHBB_HUMAN	6	22	41	19	0.228148	0.288235175	0.480697629	0.060087652	0.252550106	0.192462454	0.788159586	0.056765832	0.116880227
sp|Q9NWD8|TM248_HUMAN	2	18	34	14	0.093721	0.073397247	0.06525598	-0.020323372	-0.028464639	-0.008141267	0.923183323	0.9004519	0.98923651
sp|Q5SRI9|MANEA_HUMAN	1	10	21	10	-0.02344	0.060897981	-0.024774389	0.084334404	-0.001337965	-0.08567237	0.629532422	0.999912816	0.620414583
sp|Q8N3F0|MTURN_HUMAN	17	12	21	9	0.230112	0.067780489	0.439453181	-0.162331556	0.209341135	0.371672691	0.77281437	0.749475063	0.337040492
sp|Q14166|TTL12_HUMAN	16	7	14	6	-0.01864	-0.123630846	0.276634385	-0.104992252	0.295272979	0.400265231	0.869633167	0.475232461	0.182543195
sp|Q9H2M3|BHMT2_HUMAN	7	40	76	33	-0.28342	-0.083205643	0.226764714	0.200212451	0.510182807	0.309970356	0.199546524	0.001056374	0.035712115
sp|O75791|GRAP2_HUMAN	7	29	56	24	0.013299	-0.0701582	-0.031560013	-0.083457442	-0.044859255	0.038598187	0.633018521	0.912793532	0.917203264
sp|Q9H0W9|CK054_HUMAN	10	12	21	9	-0.45078	-0.203385157	0.039945462	0.247397748	0.490728367	0.243330618	0.362375371	0.076585392	0.442668388
sp|O14773|TPP1_HUMAN	1	40	76	33	-0.01553	0.011994608	0.155537007	0.027521674	0.171064074	0.143542399	0.806218693	0.004326992	0.007427484
sp|Q96DR8|MUCL1_HUMAN	1	10	21	9	-0.02597	0.051085885	-0.182140609	0.077050886	-0.156175609	-0.233226495	0.898374089	0.736402774	0.410148222
sp|P51124|GRAM_HUMAN	3	34	62	26	0.174636	0.198324812	-0.01018267	0.023689281	-0.184818202	-0.208507482	0.887942425	0.010029589	0.000839865
sp|O15020|SPTN2_HUMAN	7	7	14	6	-0.25174	-0.162781932	0.224862229	0.088957414	0.476601575	0.387644161	0.811105041	0.028307776	0.043796745
sp|A0A075B6K4|LV310_HUMAN	4	11	20	9	-0.08497	-0.126924643	-0.081619596	-0.041957147	0.0033479	0.045305048	0.929758406	0.999675886	0.928424903
sp|P04899|GNAI2_HUMAN	8	11	20	9	0.116974	-0.024753246	0.373930954	-0.141727377	0.256956823	0.3986842	0.842143814	0.676223342	0.315555492
sp|P18577|RHCE_HUMAN	7	4	7	3	-0.46239	-0.38584723	1.357962172	0.076539258	1.820348661	1.743809403	0.994170348	0.155665005	0.128526785
sp|P56211|ARP19_HUMAN	8	8	14	6	-0.02687	-0.025071118	0.223746597	0.001794702	0.250612417	0.248817715	0.999890722	0.258738777	0.199151805
sp|P23378|GCSP_HUMAN	3	4	7	3	-0.0988	-0.000614304	0.897499587	0.0981826	0.996296491	0.89811389	0.97159635	0.182824796	0.184038727
sp|Q15661|TRYB1_HUMAN	1	40	76	33	0.077384	0.036895544	0.149862654	-0.040488951	0.072478159	0.11296711	0.729930974	0.499965281	0.121080221
sp|Q9HBW1|LRRC4_HUMAN	9	16	27	12	0.167504	0.143061674	-0.037881964	-0.024442351	-0.205385989	-0.180943638	0.913519863	0.018551857	0.023099864
sp|Q9Y3B8|ORN_HUMAN	6	27	48	21	-0.16453	-0.015308032	-0.082467707	0.149217567	0.082057892	-0.067159674	0.208353728	0.718831401	0.760554325
sp|Q9UNS2|CSN3_HUMAN	3	17	35	15	-0.08312	0.092227323	0.312502545	0.175350008	0.39562523	0.220275221	0.080430971	0.000317549	0.027959566
sp|O95166|GBRAP_HUMAN	1	18	34	14	-0.10481	-0.151076861	0.412593327	-0.046264049	0.517406139	0.563670188	0.942333579	0.010512596	0.001423311
sp|O95390|GDF11_HUMAN	7	3	7	4	0.138893	0.254659351	0.00448885	0.115766258	-0.134404242	-0.2501705	0.782540643	0.763995565	0.284125116
sp|Q9H0B8|CRLD2_HUMAN	2	4	6	3	0.232332	-0.048936811	0.346597416	-0.28126864	0.114265587	0.395534227	0.76842984	0.96868525	0.652674933
sp|P55008|AIF1_HUMAN	1	18	34	14	-0.13874	-0.045247589	0.333641765	0.093491764	0.472381118	0.378889354	0.533135151	0.00010779	0.000493542
sp|Q9BXK5|B2L13_HUMAN	22	4	6	3	-0.64224	-0.256232967	0.040339692	0.386010846	0.682583505	0.296572659	0.831538098	0.66852894	0.912438999
sp|Q9UGN4|CLM8_HUMAN	22	36	69	30	-0.25999	-0.174822538	0.249528421	0.085165547	0.509516506	0.424350959	0.657774971	8.06E-05	0.000216664
sp|P61923|COPZ1_HUMAN	24	4	7	3	-0.28791	-0.289889651	0.02701929	-0.001977988	0.314930953	0.316908941	0.999939923	0.391716132	0.319866397
sp|Q96AC1|FERM2_HUMAN	1	30	55	24	-0.36961	-0.674638485	-0.262551123	-0.305032586	0.107054776	0.412087362	0.378591853	0.920214659	0.219799773
sp|P28300|LYOX_HUMAN	8	40	76	33	-0.21037	-0.107971542	0.594466172	0.10240168	0.804839394	0.702437714	0.691939404	1.01E-06	1.48E-06
sp|P62942|FKB1A_HUMAN	18	40	76	33	-0.20611	-0.12056935	0.189967364	0.085535905	0.396072619	0.310536713	0.655812897	0.002731315	0.009341219
sp|O14556|G3PT_HUMAN	2	18	35	16	0.208371	0.175694263	0.07571847	-0.032676299	-0.132652093	-0.099975794	0.855773684	0.169663708	0.267816827
sp|Q9UBX5|FBLN5_HUMAN	3	40	76	33	-0.1267	-0.090482731	0.18401435	0.036221307	0.310718389	0.274497082	0.811367655	6.33E-05	6.73E-05
sp|P01889|HLAB_HUMAN	12	40	76	33	-0.02782	0.177500671	0.343392416	0.205325434	0.371217179	0.165891745	0.063541767	0.002436181	0.202180446
sp|Q9Y6U3|ADSV_HUMAN	1	17	34	16	0.387296	0.090303494	-0.368901848	-0.296992321	-0.756197663	-0.459205342	0.038855199	2.68E-06	0.00095501
sp|Q8TDZ2|MICA1_HUMAN	1	7	14	6	-0.21997	0.107797838	0.253949341	0.327767659	0.473919162	0.146151503	0.763994589	0.678742919	0.952504862
sp|Q5SQ64|LY66F_HUMAN	3	40	76	33	-0.34916	0.013312231	0.106334655	0.362467512	0.455489936	0.093022424	0.000848438	0.000470059	0.645843892
sp|Q8N2S1|LTBP4_HUMAN	1	40	76	33	-0.1049	-0.173331412	0.274499807	-0.06843111	0.379400109	0.447831219	0.651858003	0.000228339	7.37E-07
sp|P35475|IDUA_HUMAN	2	8	13	6	0.088847	0.249875279	0.088461261	0.161028119	-0.000385899	-0.161414018	0.654227122	0.99999828	0.701494023
sp|P20962|PTMS_HUMAN	2	7	13	6	-0.10876	0.073938374	0.456345973	0.18270038	0.56510798	0.382407599	0.664390427	0.081129228	0.216142058
sp|Q9Y5E6|PCDB3_HUMAN	9	7	14	6	-0.09221	0.019627374	0.152163971	0.111838064	0.244374661	0.132536597	0.491666062	0.111677638	0.410665639
sp|O00139|KIF2A_HUMAN	1	21	42	18	0.237935	0.367967108	0.537548469	0.130031993	0.299613354	0.169581362	0.783924028	0.412600567	0.689459355
sp|P01911|DRB_HUMAN	1	40	76	33	-0.18266	-0.104069429	-0.182752955	0.078590544	-9.30E-05	-0.078683526	0.88899585	0.999999886	0.901616572
sp|Q9H987|SYP2L_HUMAN	7	4	6	2	-0.39022	-0.596832695	2.477963797	-0.206616234	2.868180258	3.074796492	0.975920189	0.128665492	0.081547453
sp|Q9UHG2|PCS1N_HUMAN	20	17	35	15	-0.15796	-0.231000476	0.061692244	-0.073044623	0.219648097	0.29269272	0.886361383	0.472188468	0.178538294
sp|P55291|CAD15_HUMAN	4	29	55	24	-0.19867	-0.339616331	0.082185734	-0.140949549	0.280852517	0.421802066	0.596104536	0.245623641	0.020218823
sp|P0DP04|HV43D_HUMAN	2	7	14	6	0.173395	0.283119619	0.250774924	0.109724367	0.077379672	-0.032344695	0.764387044	0.91096051	0.978972024
sp|P0DP03|HVC05_HUMAN	8	14	28	13	-0.03494	-0.010094128	0.072755967	0.024844462	0.107694557	0.082850095	0.985451709	0.820340953	0.856825066
sp|Q13214|SEM3B_HUMAN	1	11	20	9	0.514553	0.307224402	0.3711916	-0.207328197	-0.143361	0.063967198	0.23885879	0.611629108	0.88325615
sp|Q16281|CNGA3_HUMAN	1	3	7	4	0.741788	0.084581371	0.059909623	-0.657206456	-0.681878205	-0.024671749	0.189613701	0.226113108	0.996669306
sp|Q14623|IHH_HUMAN	8	21	41	18	0.020469	-0.081641004	-0.037837203	-0.102109696	-0.058305895	0.043803801	0.478350436	0.844152656	0.883817783
sp|Q68CJ9|CR3L3_HUMAN	2	33	62	27	-0.07432	-0.057093329	0.055302678	0.017228903	0.12962491	0.112396007	0.981187051	0.479594651	0.496563681
sp|Q6W4X9|MUC6_HUMAN	5	4	6	3	-0.265	-0.020117823	1.682362428	0.244886032	1.947366283	1.702480251	0.937585886	0.10109789	0.123758606
sp|Q86T13|CLC14_HUMAN	3	40	76	33	-0.07922	-0.078881093	0.132504338	0.000343718	0.211729149	0.211385431	0.999974092	0.001732012	0.000354674
sp|Q96DG6|CMBL_HUMAN	8	26	48	22	0.010506	0.082076791	0.211400106	0.0715711	0.200894414	0.129323315	0.626494036	0.079877933	0.259667048
sp|Q8WVN6|SCTM1_HUMAN	5	36	69	30	0.000786	0.038543529	0.31798891	0.037757107	0.317202488	0.279445381	0.82862672	0.000223849	0.00023875
sp|Q16363|LAMA4_HUMAN	12	17	34	16	0.22044	0.304731179	0.472598911	0.084291428	0.25215916	0.167867732	0.745646616	0.156707837	0.332832462
sp|P49913|CAMP_HUMAN	8	40	76	33	-0.45545	-0.107857896	0.373705653	0.347590138	0.829153686	0.481563549	0.02256585	1.25E-06	0.00195513
sp|Q96K76|UBP47_HUMAN	34	4	7	3	0.043246	-0.25074724	0.343472528	-0.293993216	0.300226552	0.594219768	0.766054012	0.828137614	0.427787393
sp|Q8N423|LIRB2_HUMAN	2	40	76	33	-0.21849	-0.128814056	0.085558606	0.08968042	0.304053083	0.214372663	0.48973286	0.004524716	0.030798192
sp|Q9HD89|RETN_HUMAN	19	21	41	19	-0.48657	-0.310869865	0.069057466	0.17569724	0.555624571	0.379927331	0.664083427	0.059254352	0.173730961
sp|Q15366|PCBP2_HUMAN	10	30	55	23	-0.32152	-0.214997017	0.328747685	0.106522277	0.65026698	0.543744703	0.784825683	0.003525032	0.00700089
sp|Q8WUT4|LRRN4_HUMAN	18	40	76	33	-0.04481	0.056317406	0.019522361	0.10113146	0.064336415	-0.036795045	0.41489505	0.780896059	0.902042314
sp|P13646|K1C13_HUMAN	1	19	34	14	-0.03468	-0.089375096	0.042059056	-0.054694155	0.076739997	0.131434152	0.976321895	0.969288886	0.893694571
sp|Q86SJ2|AMGO2_HUMAN	24	22	42	17	0.093171	0.078893395	-0.08756238	-0.014277304	-0.180733078	-0.166455774	0.965753568	0.030089384	0.023841118
sp|P30047|GFRP_HUMAN	27	11	20	9	-0.10086	-0.030377099	-0.074474756	0.070484179	0.026386522	-0.044097657	0.510260501	0.935177844	0.791757867
sp|Q13753|LAMC2_HUMAN	8	32	62	27	-0.11971	-0.011441116	0.508115502	0.108267456	0.627824075	0.519556618	0.633948558	6.94E-05	0.000199452
sp|O75144|ICOSL_HUMAN	1	40	76	33	0.302181	0.218317797	0.011345192	-0.083863693	-0.290836298	-0.206972605	0.186539465	3.51E-06	0.000223957
sp|P07902|GALT_HUMAN	16	37	69	29	-0.06345	-0.145397386	0.122766206	-0.081952327	0.186211265	0.268163592	0.647311232	0.223659422	0.02229789
sp|Q8N0Y7|PGAM4_HUMAN	2	40	76	33	-0.11231	-0.035230577	0.339457469	0.077080957	0.451769003	0.374688046	0.653371193	9.66E-05	0.000282174
sp|Q13596|SNX1_HUMAN	12	13	27	12	-0.02794	0.017094045	0.226879433	0.045037915	0.254823303	0.209785388	0.915289199	0.145555546	0.174371644
sp|P05981|HEPS_HUMAN	14	40	76	33	-0.10087	-0.066331376	0.194620373	0.034541281	0.295493031	0.26095175	0.870754108	0.001432041	0.001500959
sp|Q96PB7|NOE3_HUMAN	3	8	14	6	0.142775	0.070061189	0.185651271	-0.072713546	0.042876536	0.115590082	0.568241653	0.873809947	0.317153837
sp|P0DJD7|PEPA4_HUMAN	3	40	76	33	0.064133	-0.018051938	0.348830505	-0.082185267	0.284697176	0.366882443	0.608487781	0.018907211	0.000315899
sp|Q12974|TP4A2_HUMAN	23	18	35	16	0.112216	0.18585786	0.220295002	0.073641779	0.108078921	0.034437142	0.781820902	0.686021016	0.951319356
sp|Q96LA6|FCRL1_HUMAN	1	3	7	4	-0.0078	0.035617124	-0.294845923	0.043417115	-0.287045932	-0.330463047	0.935644496	0.13920998	0.034373228
sp|P55884|EIF3B_HUMAN	3	7	14	6	-0.58886	-0.321018557	0.212797123	0.267836507	0.801652187	0.53381568	0.834416658	0.340456487	0.530534494
sp|Q9P2B2|FPRP_HUMAN	1	19	34	15	0.206736	0.225277014	0.323156847	0.018541345	0.116421178	0.097879833	0.98141846	0.604217822	0.642294753
sp|P56202|CATW_HUMAN	4	29	55	24	-0.17102	-0.156052158	-0.13657637	0.014964022	0.03443981	0.019475788	0.990994204	0.967412788	0.986606524
sp|P05165|PCCA_HUMAN	3	4	7	3	-0.27149	-0.098101584	0.952237323	0.173393113	1.22373202	1.050338908	0.889821274	0.051807733	0.064997189
sp|Q99952|PTN18_HUMAN	1	30	55	23	-0.1609	-0.152759798	-0.198225972	0.008141472	-0.037324702	-0.045466174	0.999265257	0.989694091	0.981035628
sp|Q86UN3|R4RL2_HUMAN	2	40	76	33	0.150976	0.047089144	0.08859854	-0.103886574	-0.062377178	0.041509396	0.079779539	0.526502948	0.695894366
sp|Q8IZP7|H6ST3_HUMAN	4	7	14	6	0.447771	0.072357117	-0.47073659	-0.375413913	-0.91850762	-0.543093707	0.073662291	0.000253234	0.011109203
sp|Q8TF66|LRC15_HUMAN	22	37	69	30	0.099407	0.012201304	-0.08268967	-0.087205934	-0.182096908	-0.094890975	0.675088973	0.310927743	0.667764094
sp|Q9NVG8|TBC13_HUMAN	2	7	14	6	0.114514	0.025281737	0.508617173	-0.089232226	0.394103209	0.483335435	0.914913349	0.318495752	0.117975569
sp|Q9BQ51|PD1L2_HUMAN	32	40	76	33	0.19442	0.195803711	0.174348375	0.001384115	-0.020071221	-0.021455336	0.999534547	0.934727821	0.906545027
sp|P04440|DPB1_HUMAN	32	37	69	30	-0.59456	-0.292558535	-0.139068491	0.30199886	0.455488904	0.153490044	0.208702758	0.088168419	0.700343543
sp|O00487|PSDE_HUMAN	40	11	21	8	-0.00898	0.096878931	0.152502619	0.105861404	0.161485091	0.055623688	0.653806743	0.532374854	0.909264143
sp|P38606|VATA_HUMAN	2	40	76	33	-0.31354	-0.279230833	0.04575507	0.034304466	0.359290369	0.324985903	0.950117047	0.024048198	0.020751916
sp|Q9HCM3|K1549_HUMAN	3	7	14	7	-0.0426	0.027579797	-0.183874593	0.070181342	-0.141273048	-0.21145439	0.640453461	0.27151477	0.029354936
sp|P13224|GP1BB_HUMAN	5	18	34	15	-0.06048	-0.038656628	0.118792671	0.021825825	0.179275123	0.157449298	0.9788376	0.373596366	0.380439714
sp|Q16842|SIA4B_HUMAN	34	26	48	22	-0.03477	-0.104582569	0.037371839	-0.069811781	0.072142626	0.141954408	0.703531013	0.766690316	0.277182674
sp|P54753|EPHB3_HUMAN	11	19	35	15	-0.06715	-0.112433046	0.124665441	-0.045279072	0.191819415	0.237098487	0.865711064	0.180840859	0.041417255
sp|Q96DN2|VWCE_HUMAN	45	40	76	33	-0.35382	-0.291919128	0.336531075	0.061896124	0.690346327	0.628450203	0.823630772	4.91E-07	2.44E-07
sp|O76076|WISP2_HUMAN	2	36	69	30	-0.0051	-0.031155202	0.155723946	-0.026059729	0.160819419	0.186879148	0.912312006	0.094730771	0.018416893
sp|Q9NZV1|CRIM1_HUMAN	9	22	41	19	-0.04542	-0.002686423	0.133902324	0.04272882	0.179317567	0.136588748	0.847470862	0.133507079	0.223064346
sp|Q0VD83|APOBR_HUMAN	5	28	55	25	-1.18151	-0.708136404	0.479938337	0.473368921	1.661443662	1.188074741	0.031152977	3.93E-11	3.40E-08
sp|P16144|ITB4_HUMAN	15	14	28	12	0.309701	0.182003873	0.115746655	-0.127696922	-0.193954141	-0.066257218	0.474814227	0.308022494	0.832875744
sp|Q6GTX8|LAIR1_HUMAN	3	17	35	16	-0.42721	-0.576775561	0.336258894	-0.149561987	0.763472468	0.913034455	0.799047988	0.019732461	0.000859702
sp|Q53H76|PLA1A_HUMAN	6	22	41	17	0.269572	0.189169201	0.317427094	-0.080402512	0.04785538	0.128257892	0.701943015	0.919102649	0.47196542
sp|Q9HC57|WFDC1_HUMAN	2	18	34	15	-0.43638	-0.290805399	0.72809109	0.145573815	1.164470304	1.018896489	0.684117777	1.71E-06	2.26E-06

sp|P01185|NEU2_HUMAN	3	14	28	13	0.10219	0.318899877	0.444288698	0.216709834	0.342098656	0.125388822	0.546350158	0.340896125	0.823380078
sp|Q75N90|FBN3_HUMAN	9	8	14	6	-0.10949	-0.086872667	-0.095657388	0.022620848	0.013836127	-0.008784721	0.964710993	0.990978159	0.995533772
sp|P21741|MK_HUMAN	7	8	14	6	-0.89474	-1.001933813	0.533441799	-0.10718975	1.428185862	1.535375612	0.972750953	0.054600703	0.019587262
sp|P30050|RL12_HUMAN	14	3	7	4	-0.42921	-0.267485471	0.349162239	0.161726591	0.778374301	0.61664771	0.831919844	0.066260178	0.076757062
sp|P0C7H8|KRA23_HUMAN	5	8	13	6	-0.29859	0.111376211	-1.20463398	0.409966725	-0.906043466	-1.316010191	0.876874053	0.645268068	0.341370033
sp|Q14008|CKAP5_HUMAN	8	4	7	3	0.008765	-0.337702256	0.250885385	-0.346467168	0.242120473	0.588587641	0.63573368	0.857848528	0.360289212
sp|Q08188|TGM3_HUMAN	15	21	42	19	-0.40565	-0.205091753	-0.508327211	0.200556767	-0.102678691	-0.303235458	0.721965391	0.940721994	0.500713677
sp|Q9NVD7|PARVA_HUMAN	1	40	76	33	-0.07466	-0.420977077	-0.196927477	-0.346319474	-0.122269874	0.2240496	0.109973518	0.823722476	0.439098269
sp|Q00973|B4GN1_HUMAN	3	20	34	14	-0.12468	-0.084988308	-0.098852632	0.039688616	0.025824292	-0.013864324	0.787664711	0.935844088	0.977230479
sp|Q15389|ANGP1_HUMAN	3	11	21	9	0.020675	0.191706938	-0.053012084	0.171032192	-0.073686831	-0.244719023	0.415502842	0.89189764	0.214756783
sp|P01877|IGHA2_HUMAN	1	11	21	10	-0.11885	-0.084375008	0.305774736	0.03447641	0.424626154	0.390149744	0.976921653	0.091063586	0.074239964
sp|Q9NRR1|CYTL1_HUMAN	5	8	13	5	0.418674	-0.020367669	-0.063226638	-0.439041407	-0.481900376	-0.042858969	0.008843904	0.024304233	0.959676052
sp|Q7L591|DOK3_HUMAN	2	11	21	9	-0.22208	-0.021767803	0.34590695	0.200308385	0.567983138	0.367674753	0.79304069	0.289375613	0.510288721
sp|Q13057|COASY_HUMAN	5	11	21	9	0.031699	0.03829523	0.431780175	0.006596295	0.40008124	0.393484945	0.999439844	0.257539708	0.191069509
sp|P18084|ITB5_HUMAN	7	40	76	33	0.029873	-0.103540711	0.143483514	-0.133413526	0.113610699	0.247024225	0.418372837	0.645320707	0.076030395
sp|P28065|PSB9_HUMAN	22	40	76	33	-0.40578	-0.179911869	0.430456715	0.225863713	0.836232297	0.610368584	0.154524464	1.77E-07	1.72E-05
sp|O75629|CREG1_HUMAN	14	32	62	27	0.20137	0.025422694	-0.284496096	-0.175947197	-0.485865987	-0.30991879	0.227621316	0.000663105	0.018818366
sp|Q8IW45|NNRD_HUMAN	7	4	7	3	0.02764	-0.043297448	0.23848494	-0.070937053	0.210845335	0.281782388	0.825147761	0.349111863	0.124819855
sp|Q9GZM5|YIPF3_HUMAN	8	32	62	28	-0.04632	-0.072143425	0.246923512	-0.02582706	0.293239877	0.319066938	0.970505526	0.070944653	0.018624408
sp|Q9C0K3|ARP3C_HUMAN	12	25	48	20	0.007735	-0.117330613	0.614319989	-0.125065553	0.606585049	0.731650602	0.79880086	0.033085654	0.002316153
sp|Q16819|MEP1A_HUMAN	11	21	41	18	-0.00023	-0.135070018	0.16915014	-0.13483615	0.169384008	0.304220158	0.47875164	0.444740314	0.039155678
sp|P10153|RNAS2_HUMAN	9	40	76	33	-0.00716	0.008709582	0.093885138	0.015864845	0.101040401	0.085175556	0.953388942	0.267674093	0.303202565
sp|O14579|COPE_HUMAN	1	8	14	6	-0.29112	-0.478905861	-0.247386427	-0.187783387	0.043736046	0.231519433	0.737116312	0.988775202	0.683032994
sp|Q13098|CSN1_HUMAN	3	8	14	6	0.011288	0.315832865	0.32584834	0.304545173	0.314560648	0.010015475	0.110064126	0.196565661	0.997831786
sp|P0DP57|SLUR2_HUMAN	14	28	55	24	0.071256	0.007373791	0.327796373	-0.0638826	0.256539982	0.320422582	0.741134257	0.039283283	0.001869457
sp|Q8IY63|AMOL1_HUMAN	3	29	56	23	-0.15126	-0.107659315	-0.013485694	0.043598272	0.137771892	0.09417362	0.880968038	0.431034268	0.605283094
sp|Q7Z304|MAMC2_HUMAN	2	11	20	9	-0.25373	-0.228505958	0.382529668	0.025228438	0.636264064	0.611035626	0.992946622	0.056475175	0.037549737
sp|Q9UGM3|DMBT1_HUMAN	3	36	69	30	-0.34827	-0.320656662	0.45327968	0.027617519	0.80155386	0.773936341	0.976577541	5.20E-06	6.72E-07
sp|P0DMQ5|INAM2_HUMAN	2	6	14	7	-0.13139	-0.155000746	0.359297022	-0.023608871	0.490688897	0.514297768	0.991629018	0.082743956	0.023909724
sp|P15509|CSF2R_HUMAN	7	25	49	22	0.02866	0.049745802	0.021785916	0.021086195	-0.006873692	-0.027959887	0.950071874	0.996157361	0.920759547
sp|Q8N729|NPW_HUMAN	9	23	41	18	0.225123	0.046234917	0.437939389	-0.178887964	0.212816509	0.391704473	0.18157218	0.190878395	0.001593747
sp|Q9H773|DCTP1_HUMAN	50	14	28	12	-0.4892	-0.231797196	0.244303486	0.257405116	0.733505798	0.476100682	0.309136772	0.002696141	0.032383158
sp|O00505|IMA4_HUMAN	15	15	28	12	0.058754	0.002069102	0.220010451	-0.056684887	0.161256462	0.217941348	0.925421457	0.653973922	0.38086773
sp|P01308|INS_HUMAN	9	4	7	3	-0.13146	0.029723776	-0.087373962	0.161180587	0.04408285	-0.117097738	0.750498489	0.985268937	0.880813054
sp|Q8WTU2|SRB4D_HUMAN	3	12	20	8	0.148187	0.16260475	-0.045313329	0.014417251	-0.193500828	-0.207918079	0.985972061	0.211637538	0.122610769
sp|Q68BL7|OLM2A_HUMAN	19	40	75	33	0.108881	0.032327065	0.411675007	-0.076553884	0.302794059	0.379347943	0.824338452	0.128231058	0.01822628
sp|P29965|CD40L_HUMAN	2	12	21	9	-0.01862	0.059349915	0.194016415	0.077965125	0.212631625	0.1346665	0.858914879	0.473076455	0.689420415
sp|P10636|TAU_HUMAN	4	4	6	3	0.514625	0.342990505	1.352312137	-0.171634349	0.837687282	1.009321632	0.973544964	0.64601028	0.487568275
sp|P43686|PRS6B_HUMAN	4	4	7	3	-0.18693	-0.137227641	0.536682916	0.049706316	0.723616874	0.673910558	0.939541651	0.005160876	0.004196803
sp|Q16674|MIA_HUMAN	32	14	28	12	-0.00024	0.041009159	0.100330488	0.04125088	0.10057221	0.059321329	0.854376915	0.527111952	0.746770853
sp|O15247|CLIC2_HUMAN	49	8	14	6	-0.02805	0.048542645	0.203458855	0.07659703	0.23151324	0.15491621	0.819521746	0.30944646	0.517791902
sp|Q9Y2G1|MYRF_HUMAN	2	40	76	33	-0.06723	-0.050383413	0.313705535	0.016845485	0.380934432	0.364088947	0.956302586	1.00E-06	1.39E-07
sp|O75309|CAD16_HUMAN	3	7	14	6	-0.11783	-0.184471969	0.663761347	-0.066645631	0.781587684	0.848233315	0.901348239	0.000798417	6.32E-05
sp|Q9Y336|SIGL9_HUMAN	29	30	56	24	-0.06331	0.117173478	0.214005741	0.180483546	0.277315809	0.096832263	0.01342945	0.001180809	0.329082712
sp|P62857|RS28_HUMAN	5	14	27	12	-0.22584	-0.166556928	0.942769999	0.059287894	1.168614821	1.109326928	0.980217487	0.007799382	0.003946731
sp|Q969M7|UBE2F_HUMAN	13	17	35	15	0.049818	0.062506652	0.232396893	0.01268859	0.182578832	0.169890241	0.993665233	0.406361003	0.358835944
sp|Q8WUW1|BRK1_HUMAN	90	17	35	16	-0.10985	0.045362463	0.229072748	0.15521105	0.338921336	0.183710285	0.291687178	0.018037315	0.193313195
sp|Q9UL54|TAOK2_HUMAN	1	8	14	6	-0.70089	-0.489286034	0.628287886	0.211600618	1.329174538	1.117573921	0.886845653	0.058994459	0.083028344
sp|Q9UHY1|NRBP_HUMAN	2	7	14	5	-0.27122	-0.239440698	0.457981725	0.031780283	0.729202706	0.697422423	0.993306666	0.134219709	0.101329368
sp|Q8N386|LRC25_HUMAN	6	4	7	3	-0.24099	-0.389319783	-0.57913634	-0.148326244	-0.3381428	-0.189816557	0.414639739	0.074273899	0.314191283
sp|Q9P2X0|DPM3_HUMAN	1	40	76	33	-0.13276	0.073911377	-0.049254789	0.206672807	0.08350664	-0.123166167	0.019765489	0.63246645	0.284367984
sp|Q92688|AN32B_HUMAN	1	7	14	6	-0.10537	-0.097321185	0.446414696	0.00805082	0.551786702	0.543735882	0.999303181	0.127182223	0.078417159
sp|Q9ULA0|DNPEP_HUMAN	1	10	20	10	-0.32503	0.025862798	0.352214135	0.350894316	0.677245653	0.326351337	0.214208238	0.018468949	0.261568881
sp|Q5XPI4|RN123_HUMAN	2	8	14	6	0.548053	0.71947609	0.818717173	0.171423211	0.270664294	0.099241083	0.811290488	0.70542241	0.943450793
sp|O00587|MFNG_HUMAN	2	23	41	17	0.053212	0.112763313	0.178892037	0.059551584	0.125680308	0.066128724	0.311124196	0.035786508	0.309101096
sp|Q9Y6N8|CAD10_HUMAN	2	36	69	30	0.054489	-0.006070471	0.142114733	-0.06055937	0.087625834	0.148185204	0.611401483	0.491284061	0.07850978
sp|Q6UWN8|ISK6_HUMAN	9	11	21	9	0.182248	0.126253636	0.106107853	-0.055994328	-0.076140112	-0.020145784	0.945499878	0.931441135	0.993679555
sp|Q8TB24|RIN3_HUMAN	1	7	14	5	-0.133	-0.062234385	0.603942375	0.070769073	0.736945833	0.666176761	0.962804958	0.099755728	0.093325764
sp|Q8WWA1|TMM40_HUMAN	3	4	7	3	0.637924	0.206091392	-0.195332979	-0.43183266	-0.833257031	-0.401424371	0.50384779	0.206823394	0.607975345
sp|P15924|DESP_HUMAN	4	7	13	5	-0.18266	0.333112734	0.008269933	0.515772792	0.190929991	-0.324842801	0.68076379	0.966212266	0.884577507
sp|O95989|NUDT3_HUMAN	49	11	21	10	0.134219	0.139526159	0.251998945	0.005306741	0.117779527	0.112472786	0.999069721	0.719324061	0.678511109
sp|P17661|DESM_HUMAN	5	4	6	3	-0.02009	0.056793736	0.821156991	0.076887981	0.841251236	0.764363255	0.986979081	0.36469423	0.377180795
sp|P04439|HLAA_HUMAN	3	40	76	33	-0.23279	-0.061325561	0.081552495	0.171468505	0.314346561	0.142878056	0.341005216	0.085510506	0.517498587
sp|Q30154|DRB5_HUMAN	3	14	27	13	0.046239	0.05920479	0.212494505	0.012965474	0.16625519	0.153289715	0.990995462	0.346154254	0.310055614
sp|O94766|B3GA3_HUMAN	3	36	69	30	-0.173	-0.091390263	0.263888169	0.081610416	0.436888848	0.355278433	0.509065363	6.73E-06	3.61E-05
sp|O94910|AGRL1_HUMAN	2	7	13	6	0.249384	0.13057617	0.534561983	-0.118807853	0.28517796	0.403985813	0.427458224	0.044223965	0.001252578
sp|P38570|ITAE_HUMAN	2	4	7	3	0.608814	0.309740997	0.466667582	-0.29907294	-0.142146356	0.156926584	0.226431662	0.775201349	0.68676068
sp|Q9H488|OFUT1_HUMAN	33	7	14	6	-0.04629	0.122493596	0.268314498	0.168782565	0.314603467	0.145820902	0.481321641	0.185718749	0.608635908
sp|O43598|DNPH1_HUMAN	16	23	41	18	-0.28224	-0.027755106	0.153395563	0.25448946	0.43564013	0.181150669	0.093919302	0.010207107	0.353591465
sp|Q9Y286|SIGL7_HUMAN	5	36	69	31	0.002241	-0.052094483	0.155509279	-0.054335725	0.153268036	0.207603761	0.706840717	0.148090213	0.012512743
sp|O75828|CBR3_HUMAN	21	30	55	24	-0.02169	0.071187286	0.218010685	0.092880597	0.239703995	0.146823399	0.315153683	0.006554849	0.08695288
sp|Q8TCA0|LRC20_HUMAN	6	4	6	3	-0.14387	0.086017865	0.692254532	0.229885803	0.83612247	0.606236667	0.965750984	0.726444637	0.819937967
sp|Q16378|PROL4_HUMAN	7	12	20	8	0.256967	0.24282339	0.202411758	-0.014143433	-0.054555064	-0.040411631	0.984510547	0.862397601	0.907686144
sp|Q5VYK3|ECM29_HUMAN	11	8	13	6	0.093941	0.067718645	-0.0473479	-0.026222525	-0.141289071	-0.115066545	0.983640325	0.721195703	0.770774207
sp|A0A075B6R9|KVD24_HUMAN	2	8	14	5	-0.01792	0.019342329	-0.103519171	0.037259485	-0.085602015	-0.1228615	0.954097427	0.861392921	0.694606923
sp|A0A075B6H9|LV469_HUMAN	1	22	41	19	-0.05403	-0.008457314	0.108775802	0.045575127	0.162808243	0.117233116	0.897622596	0.379978691	0.526050049
sp|P18669|PGAM1_HUMAN	1	40	76	33	-0.12824	-0.067445481	0.264727395	0.060797254	0.392970129	0.332172875	0.783711082	0.001376449	0.002423084
sp|Q96J84|KIRR1_HUMAN	4	4	6	3	0.257123	0.201734535	0.582340557	-0.055388446	0.325217576	0.380606022	0.837554206	0.042526164	0.012462302
sp|O95154|ARK73_HUMAN	16	22	41	19	-0.26361	-0.059707573	0.069897291	0.203899061	0.333503925	0.129604864	0.392446477	0.172376836	0.70748547
sp|Q8NHP1|ARK74_HUMAN	1	37	69	30	-0.32882	-0.165337218	0.050788907	0.163479334	0.379605459	0.216126125	0.441887135	0.051918123	0.291295351
sp|P01732|CD8A_HUMAN	22	26	48	21	0.036394	0.20390649	0.258552238	0.167512311	0.222158059	0.054645749	0.032751265	0.016533749	0.719261075
sp|Q9H4A3|WNK1_HUMAN	14	11	21	8	-0.01147	0.169531286	0.508619222	0.181003217	0.520091153	0.339087936	0.602443628	0.080271119	0.249369486
sp|Q8WUD1|RAB2B_HUMAN	3	10	21	10	0.089838	0.106660666	0.352471897	0.016822528	0.262633759	0.245811231	0.994551556	0.384816219	0.32383565
sp|Q9Y303|NAGA_HUMAN	4	12	20	8	0.171923	-0.055700922	-0.242330983	-0.227624201	-0.414254262	-0.186630061	0.149125107	0.022275008	0.367075012
sp|O95757|HS74L_HUMAN	8	40	76	33	-0.34309	-0.16469427	0.280388961	0.17839611	0.623479341	0.445083231	0.151136135	6.92E-07	6.90E-05
sp|P12838|DEF4_HUMAN	7	33	62	27	-0.22795	-0.213423045	-0.045854974	0.014526633	0.182094704	0.167568071	0.995509134	0.615822511	0.594664594
sp|Q96JK4|HIPL1_HUMAN	2	7	13	6	-0.24864	-0.188946698	0.315045977	0.059689681	0.563682356	0.503992676	0.928620613	0.020193535	0.019174506
sp|P02771|FETA_HUMAN	7	4	6	3	-0.22467	-0.278486642	0.193039868	-0.053816006	0.417710504	0.47152651	0.984715128	0.536965542	0.407504775
sp|Q14011|CIRBP_HUMAN	3	11	20	8	0.530509	0.413137385	1.225468837	-0.117371839	0.694959614	0.812331452	0.915828789	0.149654729	0.045766648
sp|A8K2U0|A2ML1_HUMAN	98	4	7	3	0.328635	-0.099442573	-0.348226109	-0.42807733	-0.676860866	-0.248783536	0.197016493	0.081618009	0.603620528
sp|Q9Y227|ENTP4_HUMAN	4	7	13	6	0.021926	0.091520607	0.0845179	0.069594324	0.062591617	-0.007002707	0.869674863	0.922722299	0.998716798
sp|O75390|CISY_HUMAN	7	15	27	12	-0.07758	0.177996888	0.468614585	0.255573386	0.546191083	0.290617697	0.162675748	0.00502917	0.133488443
sp|Q96QR8|PURB_HUMAN	1	3	7	4	-0.321	-0.157378155	0.141927313	0.163619872	0.462925341	0.299305468	0.701313553	0.138261692	0.269390741
sp|Q6ZVN8|RGMC_HUMAN	2	34	62	26	-0.23364	-0.103247388	0.121646429	0.130396917	0.355290733	0.224893817	0.220779721	0.00086025	0.02587274
sp|P17858|PFKAL_HUMAN	2	21	42	19	-0.25825	-0.280228638	0.235676262	-0.021974279	0.493930622	0.5159049	0.993231654	0.095112115	0.0363512
sp|Q9ULF5|S39AA_HUMAN	2	12	21	8	-0.04193	-0.039532181	-0.064631446	0.002400588	-0.022698677	-0.025099265	0.999690868	0.982783622	0.974704808
sp|P80217|IN35_HUMAN	71	29	55	24	-0.08244	0.116237331	0.3181817	0.198681663	0.400626031	0.201944368	0.050687257	0.000375187	0.065861742
sp|Q9BRK3|MXRA8_HUMAN	4	40	76	33	0.037457	0.002280589	0.084600685	-0.035176107	0.047143989	0.082320096	0.751508925	0.702022908	0.2571448
sp|P02458|CO2A1_HUMAN	8	40	76	33	-1.22172	-1.313490613	-1.155888087	-0.091771035	0.065831491	0.157602526	0.859152398	0.947473241	0.675645222
sp|P12532|KCRU_HUMAN	1	4	7	3	0.331502	0.219840086	-0.240904668	-0.111661491	-0.572406245	-0.460744754	0.916548812	0.255872421	0.329872891
sp|Q5IJ48|CRUM2_HUMAN	2	4	7	2	0.227397	0.206919345	0.02427279	-0.020477288	-0.203123843	-0.182646555	0.988166619	0.560994736	0.578649659
sp|Q13477|MADCA_HUMAN	2	40	76	33	-0.01343	0.019715659	0.074064814	0.033141091	0.087490246	0.054349155	0.876943018	0.533605407	0.73383588
sp|O75888|TNF13_HUMAN	6	36	69	30	-0.18231	-0.151132026	-0.011439902	0.031180639	0.170872762	0.139692124	0.954052788	0.380260508	0.437346216
sp|O15273|TELT_HUMAN	4	4	6	3	0.001106	-0.128932374	0.915607204	-0.13003852	0.914501058	1.044539578	0.959453634	0.277526146	0.159274967
sp|Q9Y5X1|SNX9_HUMAN	5	4	6	3	0.032335	0.072261249	0.548123456	0.039925931	0.515788138	0.475862207	0.987419645	0.268623795	0.270787137

sp|P02538|K2C6A_HUMAN	7	18	34	13	-1.79909	-1.411949932	-1.56589522	0.387135652	0.233190364	-0.153945288	0.788048681	0.94588715	0.970229784
sp|O95292|VAPB_HUMAN	9	10	20	9	-0.19236	-0.136439759	0.341335952	0.055917537	0.533693248	0.477775712	0.93984357	0.027566904	0.023467936
sp|Q6ISS4|LAIR2_HUMAN	5	10	21	9	-0.963	-0.869393207	0.442060792	0.093606522	1.405060521	1.311453999	0.956602934	0.002893884	0.001340948
sp|Q9P0G3|KLK14_HUMAN	1	11	21	8	0.082968	0.051885391	-0.190512981	-0.031082788	-0.27348116	-0.242398372	0.948769193	0.088293937	0.091831701
sp|Q5T749|KPRP_HUMAN	15	26	48	21	-0.53344	-0.563311131	-0.849578719	-0.029875399	-0.316142986	-0.286267588	0.995250609	0.694009706	0.686217489
sp|O14657|TOR1B_HUMAN	9	11	20	9	0.095921	0.10496391	0.255774877	0.009042776	0.159853743	0.150810967	0.994185268	0.294049353	0.256577063
sp|Q86YZ3|HORN_HUMAN	3	40	76	33	0.925392	0.393523936	0.553420531	-0.531868025	-0.37197143	0.159896595	0.024115742	0.275555505	0.736204318
sp|Q8WX77|IBPL1_HUMAN	3	4	6	3	0.443231	0.750375662	1.704797438	0.307144829	1.261566605	0.954421776	0.886796952	0.27805259	0.410231801
sp|P07311|ACYP1_HUMAN	7	18	35	16	-0.02005	0.154894713	0.167663444	0.174943427	0.187712159	0.012768731	0.180719197	0.243773144	0.991342908
sp|O43405|COCH_HUMAN	4	37	69	29	-0.02037	0.024068154	0.153297965	0.044436424	0.173666236	0.129229812	0.823815202	0.141024311	0.253798899
sp|Q12931|TRAP1_HUMAN	10	21	41	19	-0.2535	-0.110941224	0.173045009	0.142559074	0.426545307	0.283986233	0.74395934	0.156685194	0.338561599
sp|O00170|AIP_HUMAN	1	3	7	4	0.350459	0.339443142	0.533492939	-0.011015386	0.183034411	0.194049797	0.999389695	0.872990367	0.798698163
sp|O94788|AL1A2_HUMAN	21	4	6	3	-0.49523	-0.557538128	-0.241082395	-0.062310392	0.25414534	0.316455732	0.991551938	0.904971081	0.836001897
sp|P07204|TRBM_HUMAN	6	29	56	24	0.010542	-0.013119032	0.317638067	-0.023660578	0.307096521	0.330757099	0.944591148	0.002222654	0.00015398
sp|Q9Y2A9|B3GN3_HUMAN	7	4	6	3	0.292781	0.104528883	0.473019979	-0.188252606	0.180238491	0.368491096	0.131118983	0.241347526	0.008553605
sp|P09466|PAEP_HUMAN	14	20	35	15	0.185691	0.037240627	-0.436678275	-0.148450038	-0.622368939	-0.473918902	0.89756797	0.285911782	0.408482785
sp|Q9Y2B0|CNPY2_HUMAN	111	12	21	9	-0.15615	-0.20579737	0.078669956	-0.049644047	0.234823278	0.284467326	0.949431029	0.465064638	0.258559771
sp|P09327|VILI_HUMAN	3	23	42	17	0.219819	0.149380941	-0.193618355	-0.07043852	-0.413437816	-0.342999296	0.780059442	0.005531138	0.011344021
sp|Q66K79|CBPZ_HUMAN	5	4	7	3	-0.02658	0.222491844	-0.517699377	0.249067087	-0.491124135	-0.740191222	0.822702625	0.608676781	0.277968043
sp|Q6P9A2|GLT18_HUMAN	5	22	41	18	0.077897	0.10652073	0.363503102	0.028623718	0.28560609	0.256982372	0.96980252	0.129802396	0.124060165
sp|P60891|PRPS1_HUMAN	1	4	7	3	0.133493	0.18479391	0.191290117	0.05130111	0.057797318	0.006496207	0.923599548	0.934247844	0.998941276
sp|P68371|TBB4B_HUMAN	30	25	48	22	-0.23247	-0.126848032	0.374367388	0.105618198	0.606833619	0.501215421	0.776504327	0.004027198	0.007506991
sp|Q9BRP8|PYM1_HUMAN	11	11	20	8	0.038316	-0.019258894	0.293930619	-0.057574493	0.255615019	0.313189513	0.893188901	0.247796991	0.082447111
sp|P49589|SYCC_HUMAN	1	4	7	3	0.098454	0.147101513	0.472519507	0.048647079	0.374065073	0.325417994	0.913408151	0.062543002	0.073413033
sp|P59190|RAB15_HUMAN	15	4	7	3	-0.38738	-0.259253469	0.861663595	0.1281309	1.249047963	1.120917064	0.94368313	0.059214215	0.060994534
sp|P36507|MP2K2_HUMAN	17	15	27	12	0.025095	0.037333102	0.305482208	0.012237835	0.280386942	0.268149107	0.995365291	0.197279448	0.158720406
sp|Q9H8W4|PKHF2_HUMAN	5	13	28	13	-0.23358	-0.104134938	0.279351414	0.129442393	0.512928745	0.383486352	0.895898989	0.29202055	0.388267017
sp|O60218|AK1BA_HUMAN	4	4	7	3	-0.40919	-0.565739598	0.379165959	-0.156549755	0.788355802	0.944905557	0.940991129	0.385511994	0.206386523
sp|O75022|LIRB3_HUMAN	5	7	14	7	-0.1394	0.031407475	-0.015831297	0.170803003	0.123564231	-0.047238772	0.726205804	0.881041917	0.975512964
sp|Q99627|CSN8_HUMAN	10	3	7	4	0.185207	-0.109957825	0.202703075	-0.295164436	0.017496464	0.3126609	0.768898888	0.999227366	0.701665439
sp|Q9NPF0|CD320_HUMAN	10	25	49	22	-0.13695	-0.012671605	0.348183335	0.124279357	0.485134297	0.360854939	0.387636568	0.000109466	0.001163158
sp|O60245|PCDH7_HUMAN	2	12	21	8	0.111567	0.172781634	0.00776711	0.061214271	-0.103800253	-0.165014524	0.721710683	0.557196841	0.178440021
sp|Q8IUC8|GLT13_HUMAN	4	24	48	22	-0.15441	-0.084460956	-0.047364653	0.069946548	0.107042852	0.037096303	0.573221519	0.394626989	0.862020667
sp|A6NH11|GLTD2_HUMAN	11	18	34	15	0.036455	0.180591505	0.20450766	0.144136801	0.168052957	0.023916155	0.297645242	0.31768971	0.970258826
sp|O75354|ENTP6_HUMAN	2	11	21	10	0.010696	-0.053321292	-0.137667546	-0.064017025	-0.148363279	-0.084346254	0.689459447	0.245214549	0.547905086
sp|Q53FT3|HIKES_HUMAN	4	18	34	16	0.146219	0.066197172	0.083299418	-0.080021826	-0.062919579	0.017102246	0.727228164	0.867439862	0.986562368
sp|P62195|PRS8_HUMAN	1	16	27	11	-0.1859	-0.004579837	0.370851319	0.181316188	0.556747344	0.375431156	0.391433073	0.005519881	0.050641587
sp|O60259|KLK8_HUMAN	30	7	14	6	0.166203	-0.025980711	-0.120286863	-0.19218418	-0.286490332	-0.094306151	0.363656796	0.218655081	0.796724373
sp|P18564|ITB6_HUMAN	25	30	55	23	0.113204	0.056663273	-0.023332902	-0.056540873	-0.136537048	-0.079996175	0.603668083	0.144135712	0.431555934
sp|P08246|ELNE_HUMAN	2	36	69	30	-0.30093	-0.135344957	-0.09637545	0.165581673	0.20455118	0.038969507	0.401830155	0.382178603	0.955924715
sp|P55160|NCKPL_HUMAN	27	4	7	3	-0.40625	0.026384922	0.478759681	0.432635325	0.885010085	0.45237476	0.488799663	0.163299253	0.522156719
sp|Q5T2D2|TRML2_HUMAN	4	40	76	33	-0.12214	0.09088487	-0.033773448	0.21302934	0.088371023	-0.124658317	5.57E-05	0.282451125	0.043297404
sp|P04085|PDGFA_HUMAN	7	4	7	3	-0.19346	0.19118705	0.272359513	0.384648136	0.465820599	0.081172463	0.566240298	0.570008222	0.978219566
sp|Q96AB3|ISOC2_HUMAN	4	8	13	6	0.031563	0.148288459	0.343266516	0.116725717	0.311703774	0.194978057	0.923254057	0.677957326	0.832091607
sp|P38405|GNAL_HUMAN	3	10	21	10	-0.44318	-0.207799047	0.430252477	0.235385382	0.873436906	0.638051524	0.571137287	0.006852175	0.023760631
sp|P84074|HPCA_HUMAN	6	17	35	14	-0.10717	-0.109026611	0.266435807	-0.001861141	0.373601276	0.375462417	0.999864279	0.032324602	0.011922332
sp|P54296|MYOM2_HUMAN	8	37	69	30	0.08167	-0.019037153	-0.077416768	-0.100707464	-0.159087078	-0.058379614	0.557472977	0.36848091	0.8425909
sp|Q86Y38|XYLT1_HUMAN	8	7	14	5	0.237067	0.326367498	0.056016052	0.089300469	-0.181050977	-0.270351446	0.886350437	0.735507228	0.430258999
sp|Q96C19|EFHD2_HUMAN	2	8	14	6	0.085231	0.185185781	0.052237043	0.099954374	-0.032994363	-0.132948737	0.810048151	0.984528322	0.736256246
sp|P06870|KLK1_HUMAN	3	15	28	12	0.149206	-0.106708515	-0.063023956	-0.255914782	-0.212230224	0.043684558	0.258658637	0.524566773	0.96567052
sp|Q9NR16|C163B_HUMAN	1	4	6	3	-0.05901	0.032590401	0.6476174	0.091604558	0.706631558	0.615026999	0.952421581	0.177025406	0.21031667
sp|P57721|PCBP3_HUMAN	15	26	49	20	-0.34798	-0.274006569	0.169018161	0.073971825	0.516996555	0.44302473	0.929286749	0.099492203	0.118319601
sp|Q03405|UPAR_HUMAN	4	26	48	21	-0.32279	-0.235578572	0.161054179	0.087208485	0.483841237	0.396632752	0.721171933	0.001725457	0.004318885
sp|P62820|RAB1A_HUMAN	50	19	35	14	-0.10816	-0.032430715	0.148700958	0.075726149	0.256857821	0.181131673	0.792922214	0.182881289	0.346126328
sp|Q8IU80|TMPS6_HUMAN	11	40	76	33	0.168482	0.153926026	-0.037344765	-0.014555755	-0.205826546	-0.191270791	0.907342299	6.42E-06	2.23E-06
sp|Q9GZZ9|UBA5_HUMAN	3	4	7	3	-1.83769	-2.12764023	-0.366193375	-0.289948225	1.47149863	1.761446855	0.949158253	0.432101801	0.247795841
sp|O94973|AP2A2_HUMAN	10	15	27	11	-0.16326	-0.322078783	0.128553086	-0.158818835	0.291813034	0.450631869	0.793100496	0.59953826	0.23023313
sp|P61026|RAB10_HUMAN	1	26	48	22	-0.1584	-0.147659455	0.266290647	0.010738237	0.424688339	0.413950102	0.993907178	0.002049472	0.000654773
sp|P48735|IDHP_HUMAN	1	40	76	33	-0.34441	-0.03660713	0.289186347	0.307805515	0.633598993	0.325793477	0.006038217	1.02E-06	0.006540239
sp|Q9BYE2|TMPSD_HUMAN	14	40	76	33	0.221018	-0.058951166	-0.237921936	-0.279968853	-0.458939623	-0.178970771	4.30E-06	5.93E-10	0.008583336
sp|Q5SZK8|FREM2_HUMAN	8	8	13	5	0.199195	0.203875093	0.171607753	0.004680138	-0.027587202	-0.03226734	0.999075773	0.980254731	0.968505004
sp|Q96PE1|AGRA2_HUMAN	15	4	7	3	0.099983	-0.063299483	-0.471156732	-0.163282412	-0.571139661	-0.407857249	0.74145192	0.125820307	0.25011881
sp|P11217|PYGM_HUMAN	4	11	21	8	0.238001	-0.028375293	0.010503774	-0.26637634	-0.227497274	0.038879067	0.049615666	0.229128644	0.945309186
sp|Q14525|KT33B_HUMAN	39	4	7	3	-0.23903	0.182980782	-0.412042328	0.422005937	-0.173017173	-0.59502311	0.702137955	0.959591662	0.566574684
sp|Q9UHN6|CEIP2_HUMAN	2	3	7	4	0.138495	0.123169072	-0.020942311	-0.015326129	-0.159437513	-0.144111384	0.991133362	0.480050524	0.415649545
sp|Q13247|SRSF6_HUMAN	7	14	28	12	-0.27745	-0.166233651	0.536365645	0.111215346	0.813814642	0.702599296	0.834851825	0.002833585	0.003328984
sp|Q04759|KPCT_HUMAN	2	15	28	11	0.057223	-0.065489586	0.384263789	-0.122712673	0.327040702	0.449753375	0.845769548	0.466598719	0.173255568
sp|P41091|IF2G_HUMAN	4	7	14	6	0.195786	-0.050424235	0.613993665	-0.246210596	0.418207304	0.6644179	0.595785787	0.363761992	0.048591224
sp|Q5H9R7|PP6R3_HUMAN	9	7	14	6	0.047084	0.265251953	0.402450793	0.218167727	0.355366567	0.13719884	0.511404641	0.30056707	0.783953919
sp|P84157|MXRA7_HUMAN	11	14	27	13	-0.26422	-0.303549597	0.175072853	-0.039326037	0.439296414	0.478622451	0.967599879	0.059856009	0.014797652
sp|O75084|FZD7_HUMAN	1	7	13	6	-0.02871	-0.120302467	0.280909605	-0.091593089	0.309618982	0.401212072	0.782959485	0.158887645	0.027181447
sp|Q07507|DERM_HUMAN	2	7	14	6	0.274236	0.191859333	0.260982127	-0.082377155	-0.01325436	0.069122794	0.79731873	0.995907309	0.86582474
sp|O60496|DOK2_HUMAN	8	11	21	9	-0.52942	-0.055007285	0.48473374	0.474412271	1.014153296	0.539741025	0.508575387	0.130856514	0.466818416
sp|Q15762|CD226_HUMAN	13	33	62	28	0.037884	-0.052069827	0.033898936	-0.089953835	-0.003985072	0.085968763	0.45378094	0.998899411	0.523366849
sp|Q9H853|TBA4B_HUMAN	4	14	28	13	-0.12508	0.088602681	0.004884327	0.213681256	0.129962902	-0.083718354	0.585180471	0.865490822	0.923974832
sp|Q06278|AOXA_HUMAN	21	4	7	3	-0.30331	0.202802765	0.10633494	0.506109789	0.409641964	-0.096467826	0.337770108	0.602600847	0.964642818
sp|P04259|K2C6B_HUMAN	1	4	7	3	0.660859	-0.398713538	-0.637947034	-1.059572857	-1.298806353	-0.239233496	0.149115852	0.14630248	0.908986845
sp|P09564|CD7_HUMAN	1	4	6	3	0.030495	0.011498124	0.791422524	-0.018997283	0.760927117	0.7799244	0.998815491	0.302217656	0.239264689
sp|Q7Z7H5|TMED4_HUMAN	7	8	13	6	0.250772	0.024392227	0.50336949	-0.22637938	0.252597883	0.478977263	0.380882339	0.433037546	0.039660347
sp|P18054|LOX12_HUMAN	3	7	14	6	-0.24481	-0.104665786	0.343576333	0.140147335	0.588389454	0.448242119	0.868770486	0.200880167	0.291737412
sp|P08962|CD63_HUMAN	1	4	7	3	1.155806	1.069230794	0.843818172	-0.086574942	-0.311987564	-0.225412622	0.93698646	0.580602977	0.701823886
sp|Q7Z3S9|NT2NA_HUMAN	3	26	48	21	0.048453	-0.03815405	0.128627342	-0.086607298	0.080174094	0.166781392	0.726508232	0.827814186	0.362070147
sp|Q9H772|GREM2_HUMAN	20	18	35	16	-0.11092	-0.160594565	0.241142216	-0.049677493	0.352059288	0.401736781	0.919529604	0.057838734	0.009529611
sp|P42566|EPS15_HUMAN	4	12	21	8	-0.33466	-0.272852272	0.552152248	0.061805276	0.886809796	0.82500452	0.972200767	0.03669905	0.032116565
sp|O60518|RNBP6_HUMAN	2	4	7	2	-0.25657	-0.044563526	1.01782939	0.212002527	1.274395443	1.062392916	0.932113717	0.306483464	0.375355127
sp|Q9BZZ2|SN_HUMAN	2	32	62	27	-0.51866	-0.289385384	0.068241914	0.229270762	0.58689806	0.357627298	0.09861549	6.20E-05	0.007638417
sp|Q8TEA8|DTD1_HUMAN	2	25	49	20	-0.05741	-0.23164318	0.143626189	-0.174228751	0.201040617	0.375269368	0.574992431	0.609578219	0.116284938
sp|Q76M96|CCD80_HUMAN	5	21	42	19	-0.40747	-0.323162841	0.277186638	0.084306599	0.684656078	0.600349479	0.809062887	0.000165935	0.000155597
sp|P35558|PCKGC_HUMAN	14	7	14	5	0.18947	0.357118635	0.598719224	0.167648354	0.409248943	0.241600588	0.870590604	0.602209822	0.797500987
sp|P0DP01|HV108_HUMAN	2	7	14	6	-0.5333	-0.188576827	0.338371326	0.344727661	0.871675814	0.526948153	0.512252966	0.067395607	0.255986439
sp|Q07955|SRSF1_HUMAN	1	4	6	3	-0.23547	-0.06035606	-0.002036418	0.175115273	0.233434914	0.058319642	0.643418936	0.57516306	0.958390084
sp|P01127|PDGFB_HUMAN	3	7	14	6	-0.01336	-0.231791852	0.72971255	-0.218429082	0.74307532	0.961504402	0.699688187	0.075554696	0.00660365
sp|Q96FN4|CPNE2_HUMAN	2	10	21	9	0.111212	0.098976911	0.705559165	-0.012235239	0.594347016	0.606582254	0.997537763	0.026360085	0.007812473
sp|P68363|TBA1B_HUMAN	2	36	69	30	-0.63967	-0.168901978	0.068773079	0.470771403	0.70844646	0.237675057	0.015242129	0.001657748	0.376686577
sp|Q9Y613|FHOD1_HUMAN	5	4	7	3	0.098943	0.236042741	-0.386908521	0.137100127	-0.485851136	-0.622951263	0.941084443	0.610961991	0.386971026
sp|Q86V81|THOC4_HUMAN	1	4	6	3	-0.14692	0.257369884	0.628506688	0.404290349	0.775427152	0.371136803	0.696526055	0.407475906	0.773528213
sp|Q99598|TSNAX_HUMAN	1	4	7	3	0.482411	0.650097671	1.355874137	0.167686356	0.873462822	0.705776466	0.809047589	0.052061701	0.083762717
sp|P35318|ADML_HUMAN	1	40	76	33	-0.50141	-0.580594135	0.292292864	-0.07918314	0.793703859	0.872886999	0.84457393	2.56E-05	1.72E-07
sp|P13535|MYH8_HUMAN	9	4	7	3	0.104229	-0.019147401	0.003783924	-0.123376056	-0.100444731	0.022931325	0.518975483	0.738668128	0.980325351
sp|Q96EM0|T3HPD_HUMAN	2	10	21	10	-0.24417	0.160954343	0.435041112	0.405120256	0.679207025	0.274086769	0.182918288	0.034974275	0.449792276
sp|O43897|TLL1_HUMAN	3	40	76	33	-0.07546	0.039609497	-0.151091577	0.115073857	-0.075627218	-0.190701074	0.19495919	0.610700912	0.021201213
sp|P22004|BMP6_HUMAN	2	22	41	18	0.115789	-0.037876225	-0.155618439	-0.153664898	-0.271407112	-0.117742214	0.416267787	0.155661242	0.635896748
sp|Q8IWU5|SULF2_HUMAN	8	33	62	26	-0.08322	-0.191066059	0.319366714	-0.107844003	0.40258877	0.510432773	0.600916583	0.01039545	0.000148283
sp|P20142|PEPC_HUMAN	3	14	28	12	-0.00735	-0.081255752	0.188145792	-0.073908359	0.195493184	0.269401543	0.929579909	0.703712081	0.424329832
sp|Q9BX10|GTPB2_HUMAN	1	3	7	4	0.292547	0.070685181	0.364532803	-0.221862279	0.071985342	0.293847622	0.787925405	0.979303166	0.609884444

sp|Q5TFQ8|SIRBL_HUMAN	229	30	55	24	-0.34539	-0.069523328	-0.121868815	0.275870012	0.223524525	-0.052345487	0.340556606	0.612921608	0.966719751
sp|O75487|GPC4_HUMAN	16	4	7	3	-0.02067	0.017984564	-0.127974765	0.038652987	-0.107306342	-0.145959329	0.918753865	0.653328665	0.398603874
sp|P0C7U1|ASA2B_HUMAN	30	23	41	17	0.203415	0.092183289	-0.097155334	-0.111231709	-0.300570332	-0.189338623	0.440678971	0.022776266	0.149242511
sp|O94903|PLPHP_HUMAN	6	11	20	9	-0.14922	-0.12929562	0.28183041	0.019922219	0.431048249	0.41112603	0.992828966	0.111238885	0.083494157
sp|O95302|FKBP9_HUMAN	3	11	20	9	0.114261	0.150392806	0.246434448	0.036131487	0.132173129	0.096041643	0.950102247	0.624025094	0.730709176
sp|P20337|RAB3B_HUMAN	41	24	48	22	-0.19569	-0.083824729	0.23894058	0.111868968	0.434634277	0.322765309	0.419855306	0.000214764	0.001829913
sp|P12724|ECP_HUMAN	1	24	49	21	-0.05481	-0.070090477	0.141470896	-0.01527773	0.196283642	0.211561372	0.992219378	0.412794823	0.261813699
sp|Q8N1N4|K2C78_HUMAN	2	14	28	13	0.109004	-0.056593359	-0.364940975	-0.165597752	-0.473945369	-0.308347616	0.891156387	0.510188883	0.685406027
sp|A8MUU1|FB5L3_HUMAN	28	40	76	33	-0.52415	-0.373750618	0.091972651	0.150403505	0.616126774	0.465723268	0.523288523	0.000882698	0.005494206
sp|Q9C0H2|TTYH3_HUMAN	1	15	28	12	-1.09134	0.094287384	0.150328271	1.185623958	1.241664845	0.056040887	0.000100929	0.00074551	0.978480657
sp|O95866|G6B_HUMAN	2	33	62	27	-0.42435	0.137710678	0.059612075	0.562059654	0.483961052	-0.078098602	5.87E-05	0.005331295	0.832556361
sp|Q9BYX7|ACTBM_HUMAN	1	15	27	11	-0.01456	-0.191253411	0.055619203	-0.176690788	0.070181826	0.246872614	0.461665051	0.921649503	0.29810833
sp|Q9Y3Q8|T22D4_HUMAN	9	7	14	6	-0.69278	-0.112799324	0.78922918	0.579982511	1.482011015	0.902028504	0.163422999	0.001412357	0.026616062
sp|Q9UKR3|KLK13_HUMAN	12	7	14	6	-0.4191	-0.113066021	-0.41877019	0.306037611	0.000333442	-0.305704169	0.733542801	0.999999742	0.756787138
sp|P17066|HSP76_HUMAN	15	40	76	33	0.053013	0.087365127	0.125023723	0.034351831	0.072010427	0.037658596	0.726715521	0.382399175	0.714078862
sp|P35606|COPB2_HUMAN	6	7	14	6	-0.12641	0.057965745	0.285366268	0.184372484	0.411773007	0.227400523	0.795870014	0.463420335	0.732419047
sp|Q96A72|MGN2_HUMAN	2	4	6	3	-0.22958	0.154200522	0.145421695	0.383775543	0.374996716	-0.008778827	0.387573855	0.513709491	0.999543271
sp|Q14213|IL27B_HUMAN	2	15	28	12	-0.13393	-0.009977554	0.164186439	0.123952175	0.298116167	0.174163993	0.547280731	0.101320583	0.362833705
sp|P52597|HNRPF_HUMAN	16	7	14	6	-0.13317	-0.148799432	0.417620619	-0.01562567	0.550794381	0.566420051	0.998143243	0.224710333	0.134696174
sp|Q6ZMR3|LDH6A_HUMAN	27	40	76	33	-0.09341	-0.028550867	0.242722796	0.06485695	0.336130612	0.271273663	0.653489759	0.000639817	0.002101959
sp|O95803|NDST3_HUMAN	7	4	7	3	0.102677	0.049329383	0.089655466	-0.053348002	-0.013021919	0.040326084	0.728633786	0.987007237	0.859318
sp|Q08397|LOXL1_HUMAN	3	7	13	6	0.3771	0.290344449	0.243998255	-0.086755092	-0.133101286	-0.046346193	0.83028477	0.734157437	0.952937475
sp|Q969P0|IGSF8_HUMAN	1	10	21	10	-0.11057	0.022930109	-0.074410952	0.133498648	0.036157588	-0.09734106	0.801886683	0.988041589	0.888915836
sp|P25705|ATPA_HUMAN	3	8	13	6	0.001067	-0.265465586	0.712665497	-0.266532495	0.711598588	0.978131083	0.856756996	0.475862154	0.199065417
sp|P55010|IF5_HUMAN	22	4	7	3	-0.59973	-0.32072814	0.869485553	0.279004826	1.469218519	1.190213693	0.753177515	0.023505569	0.041065902
sp|P84085|ARF5_HUMAN	5	11	21	9	0.241137	0.259086088	0.274888544	0.017949429	0.033751885	0.015802456	0.996389743	0.99127047	0.997556378
sp|O75821|EIF3G_HUMAN	15	8	13	6	-0.40528	-0.447617256	0.219675868	-0.042341014	0.62495211	0.667293124	0.996442881	0.591693555	0.491500028
sp|Q6UXB4|CLC4G_HUMAN	6	12	21	9	-0.30135	-0.149380349	-0.054536803	0.151967967	0.246811513	0.094843546	0.187451429	0.056627679	0.573463908
sp|Q8N6G6|ATL1_HUMAN	3	4	7	3	-0.18692	-0.407801993	-0.5536664	-0.220880315	-0.366744722	-0.145864407	0.128829086	0.035418823	0.435640356
sp|P03971|MIS_HUMAN	9	4	7	3	0.340621	0.259253028	-0.012323823	-0.081368018	-0.352944869	-0.271576851	0.899663564	0.299748209	0.406511867
sp|Q96F85|CNRP1_HUMAN	8	11	21	9	-0.0877	-0.135857114	0.411997537	-0.04815756	0.499697092	0.547854652	0.96666576	0.096820296	0.031621468
sp|Q02223|TNR17_HUMAN	28	19	35	15	0.005062	-0.077278082	0.347746762	-0.082339755	0.34268509	0.425024844	0.62237323	0.005933509	0.000102744
sp|P35625|TIMP3_HUMAN	2	7	14	7	-0.03721	0.056059792	0.143654655	0.093269179	0.180864043	0.087594863	0.873128227	0.684852533	0.887141301
sp|Q14353|GAMT_HUMAN	446	4	7	3	-0.16289	-0.178496346	0.356494451	-0.01560923	0.519381567	0.534990797	0.998980402	0.491388599	0.40407771
sp|P14866|HNRPL_HUMAN	1	7	14	5	-0.41804	-0.430417606	0.736405412	-0.012379897	1.15444312	1.166823017	0.999467886	0.077345743	0.04067815
sp|Q16553|LY6E_HUMAN	2	25	48	21	0.019135	0.073633991	0.125110693	0.054499411	0.105976113	0.051476702	0.751827762	0.475310562	0.797433522
sp|P01611|KVD12_HUMAN	15	15	27	12	0.005928	-0.006959527	-0.017744453	-0.012887912	-0.023672838	-0.010784926	0.994385089	0.986953973	0.996608481

Supplemental Table II:

Description	SvsHC_padjust	SvsHC_Count	SvsM_padjust	SvsM_Count	MvsHC_padjust	MvsHC_Count
Neutrophil degranulation	3.92E-59	183	7.76E-59	177	0.000172546	23
Extracellular matrix organization	5.50E-40	120	4.05E-34	109	1.88E-09	25
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	3.40E-27	63	5.85E-24	58	0.005455229	9
Post-translational protein phosphorylation	5.76E-24	55	1.61E-20	50	0.002464872	9
Platelet degranulation	1.21E-23	60	7.65E-15	47	1.89E-16	24
Binding and Uptake of Ligands by Scavenger Receptors	6.84E-23	33	4.35E-18	29	NA	NA
Response to elevated platelet cytosolic Ca2+	9.84E-23	60	3.52E-14	47	2.41E-16	24
AUF1 (hnRNP D0) binds and destabilizes mRNA	9.84E-23	38	8.94E-20	35	NA	NA
ER-Phagosome pathway	2.67E-21	47	9.21E-14	37	NA	NA
Antigen processing-Cross presentation	2.67E-21	51	1.40E-13	40	NA	NA
The role of GTSE1 in G2/M progression after G2 checkpoint	5.29E-21	43	9.21E-14	34	NA	NA
Regulation of activated PAK-2p34 by proteasome mediated degradation	1.85E-20	34	1.89E-15	29	NA	NA
RUNX1 regulates transcription of genes involved in differentiation of HSCs	2.31E-20	56	2.89E-17	51	NA	NA
Vif-mediated degradation of APOBEC3G	3.82E-20	35	2.49E-15	30	NA	NA
FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	3.82E-20	35	2.49E-15	30	NA	NA
Negative regulation of NOTCH4 signaling	3.82E-20	35	3.17E-16	31	NA	NA
Cross-presentation of soluble exogenous antigens (endosomes)	8.25E-20	33	8.21E-15	28	NA	NA
SCF-beta-TrCP mediated degradation of Emi1	8.25E-20	35	4.73E-15	30	NA	NA
Vpu mediated degradation of CD4	8.25E-20	34	6.31E-15	29	NA	NA
NIK-->noncanonical NF-kB signaling	1.60E-19	36	5.71E-15	31	NA	NA
Regulation of Apoptosis	1.88E-19	34	1.07E-14	29	NA	NA
Dectin-1 mediated noncanonical NF-kB signaling	3.27E-19	36	9.02E-15	31	NA	NA
Regulation of RUNX3 expression and activity	9.00E-19	34	2.42E-13	28	NA	NA
Autodegradation of the E3 ubiquitin ligase COP1	9.00E-19	33	4.75E-14	28	NA	NA
Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	9.00E-19	33	4.75E-14	28	NA	NA
p53-Independent DNA Damage Response	9.00E-19	33	4.75E-14	28	NA	NA
p53-Independent G1/S DNA damage checkpoint	9.00E-19	33	4.75E-14	28	NA	NA
Ubiquitin-dependent degradation of Cyclin D	9.00E-19	33	4.75E-14	28	NA	NA
G2/M Checkpoints	9.33E-19	62	3.55E-16	57	NA	NA
SCF(Skp2)-mediated degradation of p27/p21	2.83E-18	35	6.24E-14	30	NA	NA
Degradation of GLI1 by the proteasome	2.83E-18	35	1.32E-15	32	NA	NA
Degradation of GLI2 by the proteasome	2.83E-18	35	1.32E-15	32	NA	NA
GLI3 is processed to GLI3R by the proteasome	2.83E-18	35	1.32E-15	32	NA	NA
Regulation of ornithine decarboxylase (ODC)	4.68E-18	32	2.14E-13	27	NA	NA
Degradation of AXIN	9.02E-18	33	2.42E-13	28	NA	NA
Regulation of mRNA stability by proteins that bind AU-rich elements	1.40E-17	42	4.45E-17	41	NA	NA
Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	1.61E-17	36	1.69E-13	31	NA	NA
Hh mutants are degraded by ERAD	1.83E-17	33	4.12E-13	28	NA	NA
Signaling by NOTCH	3.49E-17	73	2.86E-16	70	NA	NA
Degradation of DVL	3.54E-17	33	6.44E-13	28	NA	NA
Stabilization of p53	3.54E-17	33	6.44E-13	28	NA	NA
ROS sensing by NFE2L2	3.54E-17	33	9.40E-14	29	NA	NA
Interleukin-1 signaling	4.97E-17	45	3.41E-13	39	NA	NA
Hedgehog ligand biogenesis	7.20E-17	35	6.44E-13	30	NA	NA
Regulation of HMOX1 expression and activity	7.20E-17	35	1.04E-13	31	NA	NA
CLEC7A (Dectin-1) signaling	1.28E-16	44	3.17E-16	43	NA	NA
Hh mutants abrogate ligand secretion	1.33E-16	33	1.76E-12	28	NA	NA
CDT1 association with the CDC6:ORC:origin complex	1.33E-16	33	1.76E-12	28	NA	NA
FCERI mediated NF-kB activation	2.25E-16	39	6.44E-13	34	NA	NA
Activation of NF-kappaB in B cells	2.35E-16	35	1.65E-12	30	NA	NA
Defective CFTR causes cystic fibrosis	4.93E-16	33	4.73E-12	28	NA	NA
ECM proteoglycans	5.55E-16	37	6.33E-11	30	3.58E-05	10
Cellular response to chemical stress	6.16E-16	56	4.80E-13	50	NA	NA
Regulation of RUNX2 expression and activity	8.51E-16	36	2.09E-11	30	NA	NA
TNFR2 non-canonical NF-kB pathway	1.15E-15	43	5.56E-12	37	NA	NA
Metabolism of polyamines	1.25E-15	32	1.29E-11	27	NA	NA
Platelet activation, signaling and aggregation	1.32E-15	75	3.10E-11	64	2.33E-13	28
Signaling by NOTCH4	1.52E-15	38	6.44E-13	34	NA	NA
Orc1 removal from chromatin	2.15E-15	35	9.35E-12	30	NA	NA
Degradation of the extracellular matrix	2.15E-15	51	3.26E-17	53	NA	NA
Cellular response to hypoxia	2.30E-15	36	7.95E-12	31	NA	NA
Downstream signaling events of B Cell Receptor (BCR)	2.36E-15	38	3.66E-14	36	NA	NA
Autodegradation of Cdh1 by Cdh1:APC/C	2.68E-15	33	1.87E-11	28	NA	NA
Asymmetric localization of PCP proteins	2.68E-15	33	2.80E-12	29	NA	NA
Regulation of RAS by GAPs	3.12E-15	34	1.65E-11	29	NA	NA
MAPK6/MAPK4 signaling	5.61E-15	39	6.24E-14	37	NA	NA
p53-Dependent G1 DNA Damage Response	8.34E-15	33	4.30E-11	28	NA	NA
p53-Dependent G1/S DNA damage checkpoint	8.34E-15	33	4.30E-11	28	NA	NA
Signaling by Interleukins	1.02E-14	106	6.42E-13	98	NA	NA
Interleukin-1 family signaling	1.33E-14	50	3.32E-12	45	NA	NA
Degradation of beta-catenin by the destruction complex	1.54E-14	37	2.91E-11	32	NA	NA
APC/C:Cdc20 mediated degradation of Securin	2.39E-14	33	9.42E-11	28	NA	NA
Assembly of the pre-replicative complex	2.39E-14	33	9.42E-11	28	NA	NA
G1/S DNA Damage Checkpoints	2.39E-14	33	9.42E-11	28	NA	NA
Amyloid fiber formation	3.43E-14	43	4.29E-12	39	NA	NA
Apoptosis	3.82E-14	57	3.11E-13	54	NA	NA
Host Interactions of HIV factors	3.82E-14	47	4.90E-11	41	NA	NA
Regulation of PTEN stability and activity	3.92E-14	33	1.39E-10	28	NA	NA
Hedgehog 'off' state	6.96E-14	43	6.24E-10	36	NA	NA
Transcriptional regulation by RUNX3	1.02E-13	39	1.79E-09	32	NA	NA
Formation of Fibrin Clot (Clotting Cascade)	1.44E-13	24	4.05E-08	18	0.009288971	5
UCH proteinases	1.86E-13	40	1.16E-10	35	NA	NA
Downstream TCR signaling	2.22E-13	39	1.58E-10	34	NA	NA
Integrin cell surface interactions	2.28E-13	36	2.88E-10	31	0.002532341	8
Regulation of APC/C activators between G1/S and early anaphase	2.50E-13	35	3.79E-10	30	NA	NA
ABC transporter disorders	2.68E-13	34	4.97E-10	29	NA	NA
Cdc20:Phospho-APC/C mediated degradation of Cyclin A	2.75E-13	33	6.31E-10	28	NA	NA
CDK-mediated phosphorylation and removal of Cdc6	2.75E-13	33	6.31E-10	28	NA	NA
Programmed Cell Death	2.96E-13	61	1.43E-12	58	NA	NA
C-type lectin receptors (CLRs)	3.32E-13	48	1.87E-14	49	NA	NA
APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	4.28E-13	33	8.96E-10	28	NA	NA
APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	4.28E-13	33	8.96E-10	28	NA	NA

Cyclin E associated events during G1/S transition	5.62E-13	35	7.34E-10	30	NA	NA
TCR signaling	7.06E-13	43	5.67E-11	39	NA	NA
APC/C:Cdc20 mediated degradation of mitotic proteins	1.07E-12	33	1.78E-09	28	NA	NA
Signaling by the B Cell Receptor (BCR)	1.17E-12	41	1.26E-12	40	NA	NA
Cyclin A:Cdk2-associated events at S phase entry	1.28E-12	35	1.37E-09	30	NA	NA
Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	1.63E-12	33	2.44E-09	28	NA	NA
PCP/CE pathway	3.56E-12	36	2.48E-11	34	NA	NA
Transcriptional regulation by RUNX1	3.87E-12	64	2.52E-09	56	NA	NA
APC/C-mediated degradation of cell cycle proteins	4.19E-12	35	3.33E-09	30	NA	NA
Regulation of mitotic cell cycle	4.19E-12	35	3.33E-09	30	NA	NA
Metabolism of carbohydrates	5.95E-12	73	1.12E-11	70	NA	NA
G2/M Transition	6.48E-12	56	7.83E-08	46	NA	NA
Mitotic G2-G2/M phases	1.02E-11	56	1.08E-07	46	NA	NA
Fc epsilon receptor (FCERI) signaling	1.09E-11	44	3.48E-11	42	NA	NA
Cytoprotection by HMOX1	1.10E-11	42	2.44E-09	37	NA	NA
Switching of origins to a post-replicative state	1.28E-11	35	7.89E-09	30	NA	NA
Non-integrin membrane-ECM interactions	3.73E-11	27	3.13E-09	24	0.000241742	8
Hedgehog 'on' state	4.06E-11	33	6.33E-09	29	NA	NA
DNA Replication Pre-Initiation	4.06E-11	33	2.83E-08	28	NA	NA
Scavenging by Class A Receptors	4.31E-11	15	9.05E-13	16	NA	NA
Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	9.32E-11	21	3.09E-09	19	0.048698799	4
Cell surface interactions at the vascular wall	1.02E-10	43	1.46E-06	34	4.85E-06	14
TCF dependent signaling in response to WNT	1.14E-10	60	3.37E-10	57	NA	NA
Signaling by Hedgehog	1.44E-10	45	4.40E-08	39	NA	NA
ABC-family proteins mediated transport	1.51E-10	36	4.61E-08	31	NA	NA
Scavenging of heme from plasma	1.75E-10	12	4.05E-05	8	NA	NA
RHO GTPases activate PKNs	2.59E-10	34	6.33E-11	34	NA	NA
Collagen degradation	3.56E-10	27	1.12E-10	27	NA	NA
Packaging Of Telomere Ends	4.35E-10	24	1.52E-10	24	NA	NA
M Phase	7.61E-10	87	3.06E-07	76	NA	NA
Cell Cycle Checkpoints	8.52E-10	68	3.36E-09	64	NA	NA
Common Pathway of Fibrin Clot Formation	1.27E-09	15	9.39E-05	10	0.009288971	4
Interleukin-12 signaling	1.95E-09	22	3.26E-08	20	NA	NA
Diseases of programmed cell death	2.28E-09	34	8.90E-09	32	NA	NA
Recognition and association of DNA glycosylase with site containing an affected purine	2.76E-09	24	9.19E-10	24	NA	NA
Cleavage of the damaged purine	2.76E-09	24	9.19E-10	24	NA	NA
Depurination	2.76E-09	24	9.19E-10	24	NA	NA
Diseases of metabolism	2.76E-09	59	2.39E-09	57	0.005049397	13
Interleukin-12 family signaling	4.26E-09	24	2.55E-07	21	NA	NA
Transcriptional regulation by RUNX2	5.72E-09	37	7.07E-07	32	NA	NA
Regulation of expression of SLITs and ROBOs	1.87E-08	45	7.26E-07	40	NA	NA
Recognition and association of DNA glycosylase with site containing an affected pyrimidine	2.16E-08	24	6.71E-09	24	NA	NA
Cleavage of the damaged pyrimidine	2.16E-08	24	6.71E-09	24	NA	NA
Depyrimidination	2.16E-08	24	6.71E-09	24	NA	NA
Elastic fibre formation	3.72E-08	20	3.00E-06	17	0.002763594	6
Base-Excision Repair, AP Site Formation	4.57E-08	24	1.39E-08	24	NA	NA
G1/S Transition	6.22E-08	37	4.50E-06	32	NA	NA
Molecules associated with elastic fibres	6.25E-08	18	7.26E-06	15	0.008831027	5
Synthesis of DNA	6.25E-08	35	5.86E-06	30	NA	NA
HSP90 chaperone cycle for steroid hormone receptors (SHR)	6.68E-08	22	0.000239457	16	NA	NA
Signaling by WNT	6.88E-08	69	5.65E-11	74	NA	NA
Nonhomologous End-Joining (NHEJ)	7.02E-08	25	2.15E-08	25	NA	NA
Meiotic synapsis	7.66E-08	27	2.17E-08	27	NA	NA
Metabolism of amino acids and derivatives	7.66E-08	75	0.000962166	58	NA	NA
Separation of Sister Chromatids	7.79E-08	47	7.64E-05	38	NA	NA
Plasma lipoprotein remodeling	8.53E-08	16	2.39E-06	14	0.000444061	6
Plasma lipoprotein assembly, remodeling, and clearance	9.54E-08	25	2.97E-08	25	0.004215306	7
Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	1.86E-07	26	2.43E-07	25	NA	NA
Diseases of glycosylation	2.23E-07	38	4.40E-08	38	NA	NA
RNA Polymerase I Promoter Opening	2.23E-07	23	7.31E-08	23	NA	NA
Inhibition of DNA recombination at telomere	2.38E-07	24	7.50E-08	24	NA	NA
DNA Double Strand Break Response	2.45E-07	26	3.17E-07	25	NA	NA
Mitotic Anaphase	2.47E-07	53	0.00019331	43	NA	NA
Mitotic Metaphase and Anaphase	2.85E-07	53	0.000211739	43	NA	NA
Signaling by ROBO receptors	2.94E-07	50	4.27E-08	50	NA	NA
MAPK family signaling cascades	3.42E-07	66	2.33E-09	69	NA	NA
DNA Replication	3.43E-07	35	2.38E-05	30	NA	NA
G2/M DNA damage checkpoint	3.54E-07	29	9.66E-08	29	NA	NA
Beta-catenin independent WNT signaling	3.83E-07	38	7.12E-09	40	NA	NA
Laminin interactions	3.97E-07	15	1.49E-06	14	0.023394658	4
MAPK1/MAPK3 signaling	4.08E-07	60	4.64E-08	60	NA	NA
DNA methylation	4.08E-07	23	1.40E-07	23	NA	NA
DNA Damage/Telomere Stress Induced Senescence	4.13E-07	26	1.28E-07	26	NA	NA
RAF/MAP kinase cascade	4.41E-07	59	5.22E-08	59	NA	NA
Intrinsic Pathway of Fibrin Clot Formation	4.53E-07	13	2.36E-06	12	NA	NA
L1CAM interactions	5.45E-07	33	0.000314061	26	0.013689406	8
Mitotic G1 phase and G1/S transition	6.54E-07	38	7.39E-05	32	NA	NA
Pre-NOTCH Expression and Processing	7.11E-07	31	1.91E-07	31	NA	NA
Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	7.47E-07	23	2.64E-07	23	NA	NA
SIRT1 negatively regulates rRNA expression	1.01E-06	23	3.55E-07	23	NA	NA
HIV Infection	1.11E-06	51	3.39E-05	45	NA	NA
Regulation of TLR by endogenous ligand	1.21E-06	12	0.000402886	9	NA	NA
Condensation of Prophase Chromosomes	1.32E-06	24	4.50E-07	24	NA	NA
Collagen formation	1.39E-06	27	4.32E-07	27	NA	NA
Formation of tubulin folding intermediates by CCT/TriC	1.59E-06	13	0.001629824	9	NA	NA
RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	2.01E-06	28	2.50E-05	25	NA	NA
Class I MHC mediated antigen processing & presentation	2.12E-06	71	0.000397383	60	NA	NA
Ub-specific processing proteases	2.40E-06	48	3.54E-05	43	NA	NA
Neddylation	2.67E-06	50	0.00015853	43	NA	NA
MET activates PTK2 signaling	2.96E-06	14	1.49E-06	14	NA	NA
PTEN Regulation	3.26E-06	35	0.000336898	29	NA	NA
MHC class II antigen presentation	3.84E-06	32	0.023821381	21	NA	NA
Metabolism of nucleotides	3.86E-06	28	4.29E-05	25	NA	NA

HCMV Early Events	3.88E-06	34	0.00017554	29	NA	NA
PRC2 methylates histones and DNA	3.96E-06	23	1.46E-06	23	NA	NA
Defective pyroptosis	3.96E-06	23	1.46E-06	23	NA	NA
RHO GTPase Effectors	4.17E-06	63	7.12E-09	68	NA	NA
Signaling by PDGF	4.20E-06	20	1.72E-06	20	0.039349738	5
Syndecan interactions	4.68E-06	13	0.002930495	9	0.000225937	6
Deposition of new CENPA-containing nucleosomes at the centromere	5.06E-06	23	1.86E-06	23	NA	NA
Nucleosome assembly	5.06E-06	23	1.86E-06	23	NA	NA
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	6.51E-06	33	0.0002921	28	NA	NA
Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	7.34E-06	14	0.002675233	10	NA	NA
Diseases associated with glycosaminoglycan metabolism	8.08E-06	16	3.89E-06	16	NA	NA
MET promotes cell motility	8.08E-06	16	6.68E-07	17	NA	NA
ERCC6 (CSB) and EHMT2 (G9a) positively regulate rRNA expression	8.33E-06	23	7.80E-07	24	NA	NA
Pre-NOTCH Transcription and Translation	9.33E-06	26	8.87E-07	27	NA	NA
COPI-independent Golgi-to-ER retrograde traffic	9.83E-06	18	0.010670328	12	NA	NA
Assembly of collagen fibrils and other multimeric structures	9.92E-06	20	9.23E-07	21	NA	NA
Transport to the Golgi and subsequent modification	9.96E-06	41	0.000436547	35	NA	NA
Diseases of signal transduction by growth factor receptors and second messengers	1.14E-05	71	5.37E-06	69	NA	NA
Asparagine N-linked glycosylation	1.49E-05	58	0.000647254	50	NA	NA
Aggrephagy	1.64E-05	16	0.007962825	11	NA	NA
Gluconeogenesis	1.68E-05	14	0.004327317	10	NA	NA
Signaling by MET	1.68E-05	23	1.68E-06	24	NA	NA
Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	1.95E-05	11	0.000600248	9	7.61E-05	6
Neurodegenerative Diseases	1.95E-05	11	0.000600248	9	7.61E-05	6
Chaperone Mediated Autophagy	1.95E-05	11	1.21E-05	11	NA	NA
Meiotic recombination	2.29E-05	24	8.80E-06	24	NA	NA
Glutathione synthesis and recycling	2.54E-05	8	0.002007169	6	NA	NA
Processing of DNA double-strand break ends	2.54E-05	26	9.23E-06	26	NA	NA
PIP3 activates AKT signaling	2.54E-05	52	0.000208567	47	NA	NA
Chondroitin sulfate/dermatan sulfate metabolism	3.20E-05	17	0.009060506	12	NA	NA
Glutathione conjugation	3.59E-05	14	0.001845358	11	NA	NA
COPI-mediated anterograde transport	4.55E-05	26	0.002513656	21	NA	NA
Toll-like Receptor Cascades	4.60E-05	35	0.000208567	32	NA	NA
Prefoldin mediated transfer of substrate to CCT/TriC	5.02E-05	12	0.000908139	10	NA	NA
Detoxification of Reactive Oxygen Species	5.11E-05	14	0.000143072	13	0.008475125	5
Defective B3GALTL causes Peters-plus syndrome (PpS)	5.11E-05	14	0.000635663	12	0.046379153	4
Defective B3GAT3 causes JDSSDHD	5.26E-05	10	0.000258445	9	NA	NA
Dissolution of Fibrin Clot	5.71E-05	8	0.003254419	6	NA	NA
Diseases associated with O-glycosylation of proteins	5.79E-05	20	9.49E-05	19	NA	NA
Formation of the beta-catenin:TCF transactivating complex	6.24E-05	24	2.50E-05	24	NA	NA
HCMV Infection	6.89E-05	35	0.001410284	30	NA	NA
O-glycosylation of TSR domain-containing proteins	7.13E-05	14	0.000817677	12	0.048698799	4
Base Excision Repair	7.53E-05	24	3.05E-05	24	NA	NA
Disorders of transmembrane transporters	8.74E-05	37	0.000698581	33	NA	NA
S Phase	9.00E-05	35	0.001685437	30	NA	NA
Retinoid metabolism and transport	0.000102323	15	0.003098587	12	0.013689406	5
Interconversion of nucleotide di- and triphosphates	0.000110685	12	0.001587191	10	NA	NA
CS/DS degradation	0.000115908	8	0.000755221	7	NA	NA
Deubiquitination	0.000122016	54	0.001241469	48	NA	NA
A tetrasaccharide linker sequence is required for GAG synthesis	0.000129489	11	0.00219405	9	NA	NA
Post-chaperonin tubulin folding pathway	0.000142712	10	NA	NA	NA	NA
Transcriptional regulation of granulopoiesis	0.000156027	23	6.60E-05	23	NA	NA
Collagen biosynthesis and modifying enzymes	0.000159742	19	7.62E-05	19	NA	NA
ER to Golgi Anterograde Transport	0.00017853	33	0.00655574	27	NA	NA
B-WICH complex positively regulates rRNA expression	0.00018563	23	2.50E-05	24	NA	NA
RNA Polymerase I Promoter Escape	0.00018563	23	2.50E-05	24	NA	NA
Mitotic Prophase	0.000207357	31	7.16E-05	31	NA	NA
Pentose phosphate pathway	0.000216613	8	0.001219647	7	NA	NA
Recycling pathway of L1	0.000235207	15	0.015736693	11	NA	NA
Glycosaminoglycan metabolism	0.000252833	28	0.000246678	27	NA	NA
Complement cascade	0.000252833	17	1.22E-08	23	NA	NA
Meiosis	0.000266728	27	0.000103247	27	NA	NA
Transcriptional regulation by small RNAs	0.000293402	25	0.000120101	25	NA	NA
Metabolism of fat-soluble vitamins	0.000303638	15	0.006534901	12	0.019256708	5
Ethanol oxidation	0.000307735	7	NA	NA	NA	NA
HDACs deacetylate histones	0.000308893	23	0.000135438	23	NA	NA
Defective B4GALT7 causes EDS, progeroid type	0.000376111	9	0.001548229	8	NA	NA
Defective B3GALT6 causes EDSP2 and SEMDJL1	0.000376111	9	0.001548229	8	NA	NA
Translocation of SLC2A4 (GLUT4) to the plasma membrane	0.00044238	19	0.001837812	17	NA	NA
Glucose metabolism	0.000528749	22	0.001648163	20	NA	NA
Estrogen-dependent gene expression	0.000582822	31	0.002213128	28	NA	NA
Advanced glycosylation endproduct receptor signaling	0.000588928	7	0.003254419	6	NA	NA
RHOBTB GTPase Cycle	0.000588928	12	0.001485548	11	NA	NA
O-linked glycosylation	0.000623949	25	0.001573624	23	NA	NA
MyD88 deficiency (TLR2/4)	0.000632962	8	0.014323589	6	NA	NA
Intracellular signaling by second messengers	0.000643979	53	1.82E-05	56	NA	NA
Senescence-Associated Secretory Phenotype (SASP)	0.000717819	25	0.000300099	25	NA	NA
Removal of aminoterminal propeptides from gamma-carboxylated proteins	0.000826653	6	0.000638339	6	NA	NA
Chylomicron assembly	0.000826653	6	0.000638339	6	0.010004681	3
Chylomicron remodeling	0.000826653	6	0.000638339	6	0.010004681	3
HDL remodeling	0.000826653	6	4.64E-05	7	NA	NA
Regulation of Complement cascade	0.000881679	14	2.97E-05	16	NA	NA
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	0.001002007	8	NA	NA	NA	NA
IRAK4 deficiency (TLR2/4)	0.001002007	8	0.018949236	6	NA	NA
Interleukin-4 and Interleukin-13 signaling	0.00100795	24	0.005644107	21	NA	NA
Attenuation phase	0.001020949	7	0.005000985	6	NA	NA
TGF-beta receptor signaling activates SMADs	0.001043282	11	0.002675233	10	NA	NA
Toll Like Receptor 4 (TLR4) Cascade	0.00107709	28	0.000982359	27	NA	NA
Reproduction	0.001253369	29	0.001092839	28	NA	NA
RHOBTB2 GTPase cycle	0.001264327	9	0.000862559	9	NA	NA
Plasma lipoprotein clearance	0.001399953	11	0.003372905	10	NA	NA
Transport of connexons to the plasma membrane	0.001524045	8	NA	NA	NA	NA
LDL clearance	0.001524045	8	0.024470873	6	NA	NA

Collagen chain trimerization	0.001556626	13	0.000920395	13	NA	NA
Endosomal/Vacuolar pathway	0.001571254	6	0.049623749	4	NA	NA
Gamma-carboxylation, transport, and amino-terminal cleavage of proteins	0.001571254	6	0.001196477	6	NA	NA
Oxidative Stress Induced Senescence	0.001640441	26	0.000691473	26	NA	NA
Activation of BAD and translocation to mitochondria	0.001658641	7	0.000156212	8	NA	NA
GRB2:SOS provides linkage to MAPK signaling for Integrins	0.001658641	7	NA	NA	NA	NA
Platelet Adhesion to exposed collagen	0.001658641	7	0.035312991	5	0.028806283	3
HDMs demethylate histones	0.001680419	14	0.00097685	14	NA	NA
Platelet Aggregation (Plug Formation)	0.001680419	12	NA	NA	NA	NA
RHO GTPases activate PAKs	0.001756173	9	3.37E-05	11	NA	NA
Positive epigenetic regulation of rRNA expression	0.0018227	23	0.000120101	25	NA	NA
Telomere Maintenance	0.0019187	24	0.000863046	24	NA	NA
Antigen processing: Ubiquitination & Proteasome degradation	0.001988697	51	0.007767537	46	NA	NA
NoRC negatively regulates rRNA expression	0.002078402	23	0.000959129	23	NA	NA
Chondroitin sulfate biosynthesis	0.002193527	8	0.031175551	6	NA	NA
Antimicrobial peptides	0.002420953	21	0.001168376	21	NA	NA
Defects of contact activation system (CAS) and kallikrein/kinin system (KKS)	0.002587482	7	0.001841868	7	NA	NA
Diseases of hemostasis	0.002587482	7	0.001841868	7	NA	NA
HCMV Late Events	0.002796947	24	0.001244581	24	NA	NA
SUMOylation of chromatin organization proteins	0.002997977	17	0.001573624	17	NA	NA
Glycolysis	0.002997977	17	0.001573624	17	NA	NA
Negative epigenetic regulation of rRNA expression	0.003038265	23	0.001402057	23	NA	NA
RNA Polymerase I Promoter Clearance	0.003038265	23	0.000587807	24	NA	NA
Gene Silencing by RNA	0.003272849	27	0.001381685	27	NA	NA
Toll Like Receptor TLR1:TLR2 Cascade	0.003300637	22	0.007962825	20	NA	NA
Toll Like Receptor 2 (TLR2) Cascade	0.003300637	22	0.007962825	20	NA	NA
Gamma carboxylation, hypusine formation and arylsulfatase activation	0.003340833	12	0.006679624	11	NA	NA
HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA)	0.003611063	26	0.001557407	26	NA	NA
RNA Polymerase I Transcription	0.003869433	23	0.000755818	24	NA	NA
EPH-Ephrin signaling	0.003872328	20	2.53E-06	26	NA	NA
RHO GTPases activate IQGAPs	0.004156637	10	0.002675233	10	NA	NA
Infection with Mycobacterium tuberculosis	0.004316415	9	0.011557951	8	NA	NA
Erythrocytes take up carbon dioxide and release oxygen	0.004316415	6	0.000436547	7	NA	NA
O2/CO2 exchange in erythrocytes	0.004316415	6	0.000436547	7	NA	NA
Trafficking and processing of endosomal TLR	0.004316415	6	0.019354134	5	NA	NA
Keratan sulfate degradation	0.004316415	6	4.05E-05	8	NA	NA
Purine salvage	0.004316415	6	0.019354134	5	NA	NA
Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	0.004316415	6	0.003254419	6	NA	NA
Heparan sulfate/heparin (HS-GAG) metabolism	0.004316415	14	0.045848681	11	NA	NA
Post-translational modification: synthesis of GPI-anchored proteins	0.004324987	20	0.011705452	18	NA	NA
Selective autophagy	0.005057682	18	NA	NA	NA	NA
Activation of Matrix Metalloproteinases	0.00523388	10	0.003372905	10	NA	NA
Pre-NOTCH Processing in Golgi	0.005498592	7	0.003974798	7	NA	NA
Metabolism of Angiotensinogen to Angiotensins	0.005498592	7	NA	NA	NA	NA
Sulfur amino acid metabolism	0.005658755	9	NA	NA	NA	NA
Phase II - Conjugation of compounds	0.005924181	22	0.026648914	19	NA	NA
NCAM signaling for neurite out-growth	0.005924181	15	0.00334773	15	NA	NA
Keratan sulfate/keratin metabolism	0.006615454	10	5.20E-05	13	NA	NA
Homology Directed Repair	0.00663756	26	0.002930495	26	NA	NA
Gamma-carboxylation of protein precursors	0.007221244	5	0.005603758	5	NA	NA
Folding of actin by CCT/TriC	0.007221244	5	4.64E-05	7	NA	NA
Metabolism of vitamins and cofactors	0.007226646	33	0.009694596	31	NA	NA
Glycogen metabolism	0.007284199	9	0.00496138	9	NA	NA
Apoptotic execution phase	0.007335592	13	0.00443201	13	NA	NA
Assembly of active LPL and LIPC lipase complexes	0.007676325	7	0.005557148	7	NA	NA
Triglyceride catabolism	0.00772085	8	0.000221681	10	NA	NA
Semaphorin interactions	0.008021306	15	0.001648163	16	0.002763594	7
Signaling by Nuclear Receptors	0.008040292	47	0.002470854	47	NA	NA
Golgi-to-ER retrograde transport	0.008087523	25	NA	NA	NA	NA
GPVI-mediated activation cascade	0.008120336	10	0.017683844	9	NA	NA
Biological oxidations	0.008241539	37	NA	NA	NA	NA
trans-Golgi Network Vesicle Budding	0.008646441	16	NA	NA	NA	NA
Signaling by CSF3 (G-CSF)	0.009190361	9	0.021558731	8	NA	NA
Prolactin receptor signaling	0.009696333	6	0.007312466	6	NA	NA
p130Cas linkage to MAPK signaling for integrins	0.009696333	6	NA	NA	NA	NA
Activation of anterior HOX genes in hindbrain development during early embryogenesis	0.010045639	23	0.004880256	23	NA	NA
Activation of HOX genes during differentiation	0.010045639	23	0.004880256	23	NA	NA
Receptor-type tyrosine-protein phosphatases	0.010350013	7	0.007560886	7	NA	NA
NCAM1 interactions	0.010350013	11	0.006679624	11	NA	NA
MyD88:MAL(TIRAP) cascade initiated on plasma membrane	0.011176935	20	0.025834797	18	NA	NA
Toll Like Receptor TLR6:TLR2 Cascade	0.011176935	20	0.025834797	18	NA	NA
Dermatan sulfate biosynthesis	0.011393367	5	0.008959336	5	NA	NA
DNA Double-Strand Break Repair	0.012445536	29	0.010202569	28	NA	NA
Downregulation of TGF-beta receptor signaling	0.012885256	8	NA	NA	NA	NA
Nuclear Envelope (NE) Reassembly	0.012885256	16	NA	NA	NA	NA
Glycogen synthesis	0.013695241	6	NA	NA	NA	NA
Signal regulatory protein family interactions	0.013695241	6	0.001841868	7	NA	NA
Signal transduction by L1	0.013784594	7	NA	NA	0.008699543	4
ESR-mediated signaling	0.015324819	36	0.003254419	37	NA	NA
Metabolism of porphyrins	0.016392045	8	NA	NA	NA	NA
Integrin signaling	0.016392045	8	NA	NA	NA	NA
Caspase-mediated cleavage of cytoskeletal proteins	0.017245803	5	NA	NA	NA	NA
HSF1 activation	0.017245803	5	0.013662988	5	NA	NA
GP1b-IX-V activation signalling	0.017245803	5	NA	NA	NA	NA
Purine ribonucleoside monophosphate biosynthesis	0.017245803	5	0.002007169	6	NA	NA
TAK1 activates NFkB by phosphorylation and activation of IKKs complex	0.017495455	9	0.03665047	8	NA	NA
Intra-Golgi and retrograde Golgi-to-ER traffic	0.0176637	33	NA	NA	NA	NA
Signaling by ERBB2 TMD/JMD mutants	0.017941042	7	0.047323229	6	NA	NA
PKMTs methylate histone lysines	0.017966218	15	0.010645707	15	NA	NA
Glycosphingolipid metabolism	0.020745945	11	0.035510466	10	NA	NA
Autophagy	0.020898154	26	NA	NA	NA	NA
RMTs methylate histone arginines	0.020957759	16	0.012080994	16	NA	NA
Nucleotide salvage	0.023154118	7	0.016859694	7	NA	NA

RHOBTB1 GTPase cycle	0.023154118	7	0.016859694	7	NA	NA
Activation of AMPK downstream of NMDARs	0.025332545	8	NA	NA	NA	NA
Signaling by TGFB family members	0.02595621	19	NA	NA	NA	NA
Regulation of PLK1 Activity at G2/M Transition	0.026510185	17	NA	NA	NA	NA
HSF1-dependent transactivation	0.029516368	7	0.00542735	8	NA	NA
Activation of BH3-only proteins	0.031072616	8	0.00628775	9	NA	NA
EPHA-mediated growth cone collapse	0.031072616	8	NA	NA	0.023394658	4
Chromosome Maintenance	0.03153092	24	0.015672058	24	NA	NA
Ephrin signaling	0.033017058	6	0.005557148	7	NA	NA
Plasma lipoprotein assembly	0.033017058	6	0.000161907	9	0.048999353	3
Methylation	0.034678478	5	0.026460847	5	NA	NA
Heme biosynthesis	0.034678478	5	NA	NA	NA	NA
Golgi Associated Vesicle Biogenesis	0.034768198	12	NA	NA	NA	NA
IKK complex recruitment mediated by RIP1	0.036265016	7	0.00706967	8	NA	NA
Signaling by ERBB2 KD Mutants	0.036265016	7	NA	NA	NA	NA
Inactivation of CSF3 (G-CSF) signaling	0.036265016	7	NA	NA	NA	NA
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	0.036265016	7	NA	NA	NA	NA
Diseases of Immune System	0.036819132	8	NA	NA	NA	NA
Uptake and actions of bacterial toxins	0.036819132	8	0.007844962	9	NA	NA
Diseases associated with the TLR signaling cascade	0.036819132	8	NA	NA	NA	NA
Sealing of the nuclear envelope (NE) by ESCRT-III	0.036819132	8	NA	NA	NA	NA
Cell-Cell communication	0.039665264	22	0.001117136	26	NA	NA
Apoptotic cleavage of cellular proteins	0.042669498	9	0.02915956	9	NA	NA
DNA Damage Recognition in GG-NER	0.042669498	9	0.02915956	9	NA	NA
EPH-ephrin mediated repulsion of cells	0.042769695	11	0.010670328	12	NA	NA
Signaling by ERBB2 in Cancer	0.044033774	7	NA	NA	NA	NA
Purinergic signaling in leishmaniasis infection	0.044033774	7	NA	NA	NA	NA
Cell recruitment (pro-inflammatory response)	0.044033774	7	NA	NA	NA	NA
Iron uptake and transport	0.044033774	12	0.011449431	13	NA	NA
Urea cycle	0.044990414	4	NA	NA	NA	NA
Signaling by NOTCH1 HD Domain Mutants in Cancer	0.045086085	5	0.035312991	5	NA	NA
Constitutive Signaling by NOTCH1 HD Domain Mutants	0.045086085	5	0.035312991	5	NA	NA
ERBB2 Regulates Cell Motility	0.045086085	5	NA	NA	NA	NA
Nucleobase biosynthesis	0.045086085	5	0.007312466	6	NA	NA
Recruitment of NuMA to mitotic centrosomes	0.046770436	17	NA	NA	NA	NA
TP53 Regulates Metabolic Genes	0.047968599	16	NA	NA	NA	NA
Signaling by TGF-beta Receptor Complex	0.049572079	14	NA	NA	NA	NA
Smooth Muscle Contraction	NA	NA	1.53E-05	15	0.010004681	5
Initial triggering of complement	NA	NA	2.09E-05	11	NA	NA
DARPP-32 events	NA	NA	0.000473668	10	NA	NA
Striated Muscle Contraction	NA	NA	0.000480462	12	NA	NA
EPHB-mediated forward signaling	NA	NA	0.000582218	13	NA	NA
Calcineurin activates NFAT	NA	NA	0.001196477	6	NA	NA
eNOS activation	NA	NA	0.003254419	6	NA	NA
Adherens junctions interactions	NA	NA	0.003372905	10	NA	NA
Keratan sulfate biosynthesis	NA	NA	0.003811283	9	NA	NA
Creation of C4 and C2 activators	NA	NA	0.005000985	6	NA	NA
CREB1 phosphorylation through the activation of Adenylate Cyclase	NA	NA	0.005000985	6	NA	NA
Fcgamma receptor (FCGR) dependent phagocytosis	NA	NA	0.005139349	18	NA	NA
Regulation of actin dynamics for phagocytic cup formation	NA	NA	0.006691711	14	NA	NA
Triglyceride metabolism	NA	NA	0.008044861	10	NA	NA
CaMK IV-mediated phosphorylation of CREB	NA	NA	0.013662988	5	NA	NA
Metabolism of nitric oxide: NOS3 activation and regulation	NA	NA	0.014323589	6	NA	NA
Signaling by BRAF and RAF fusions	NA	NA	0.015611743	14	NA	NA
Epigenetic regulation of gene expression	NA	NA	0.015736693	25	NA	NA
Signaling by moderate kinase activity BRAF mutants	NA	NA	0.015736693	11	NA	NA
Signaling by RAS mutants	NA	NA	0.015736693	11	NA	NA
Paradoxical activation of RAF signaling by kinase inactive BRAF	NA	NA	0.015736693	11	NA	NA
Signaling downstream of RAS mutants	NA	NA	0.015736693	11	NA	NA
HATs acetylate histones	NA	NA	0.01684925	24	NA	NA
Downstream signal transduction	NA	NA	0.017806081	8	NA	NA
Crosslinking of collagen fibrils	NA	NA	0.018949236	6	NA	NA
Uptake and function of anthrax toxins	NA	NA	0.019354134	5	NA	NA
Cell junction organization	NA	NA	0.020432009	17	NA	NA
RHO GTPases Activate WASPs and WAVEs	NA	NA	0.021079591	9	NA	NA
RAF activation	NA	NA	0.021079591	9	NA	NA
Cytosolic tRNA aminoacylation	NA	NA	0.02121053	7	NA	NA
MyD88-independent TLR4 cascade	NA	NA	0.021474363	18	NA	NA
TRIF(TICAM1)-mediated TLR4 signaling	NA	NA	0.021474363	18	NA	NA
Clathrin-mediated endocytosis	NA	NA	0.022928951	24	NA	NA
Signaling by RAF1 mutants	NA	NA	0.023135898	10	NA	NA
Protein methylation	NA	NA	0.024470873	6	NA	NA
Calmodulin induced events	NA	NA	0.02479162	9	NA	NA
CaM pathway	NA	NA	0.02479162	9	NA	NA
Activated NOTCH1 Transmits Signal to the Nucleus	NA	NA	0.025961493	8	NA	NA
Cellular Senescence	NA	NA	0.027033861	30	NA	NA
PKA activation	NA	NA	0.031175551	6	NA	NA
Parasite infection	NA	NA	0.031816869	12	NA	NA
Leishmania phagocytosis	NA	NA	0.031816869	12	NA	NA
FCGR3A-mediated phagocytosis	NA	NA	0.031816869	12	NA	NA
Ca-dependent events	NA	NA	0.034214398	9	NA	NA
Anchoring fibril formation	NA	NA	0.035312991	5	NA	NA
CREB1 phosphorylation through the activation of CaMKII/CaMKK/CaMKIV cascasde	NA	NA	0.036049905	4	NA	NA
STAT5 activation downstream of FLT3 ITD mutants	NA	NA	0.036049905	4	NA	NA
VEGFR2 mediated cell proliferation	NA	NA	0.038871267	6	NA	NA
PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	NA	NA	0.039986865	18	NA	NA
TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	NA	NA	0.041540161	16	NA	NA
VEGFA-VEGFR2 Pathway	NA	NA	0.042747921	17	NA	NA
Oncogenic MAPK signaling	NA	NA	0.043998945	15	NA	NA
Muscle contraction	NA	NA	0.045104075	29	NA	NA
MyD88 dependent cascade initiated on endosome	NA	NA	0.045473832	16	NA	NA
Spry regulation of FGF signaling	NA	NA	0.045764395	5	NA	NA
Sema3A PAK dependent Axon repulsion	NA	NA	0.045764395	5	NA	NA

Signaling by ERBB2 ECD mutants	NA	NA	0.045764395	5	NA	NA
Interleukin-3, Interleukin-5 and GM-CSF signaling	NA	NA	0.046079633	10	NA	NA
Translation of structural proteins	NA	NA	0.046096413	7	NA	NA
Signaling by VEGF	NA	NA	0.04667717	18	NA	NA
PKA-mediated phosphorylation of CREB	NA	NA	0.047323229	6	NA	NA
NOTCH2 Activation and Transmission of Signal to the Nucleus	NA	NA	0.047323229	6	NA	NA
Toll Like Receptor 7/8 (TLR7/8) Cascade	NA	NA	0.048861225	16	NA	NA
Regulation of localization of FOXO transcription factors	NA	NA	0.049623749	4	NA	NA
Constitutive Signaling by Overexpressed ERBB2	NA	NA	0.049623749	4	NA	NA
N-glycan trimming in the ER and Calnexin/Calreticulin cycle	NA	NA	0.049623749	8	NA	NA
Sema4D induced cell migration and growth-cone collapse	NA	NA	NA	NA	0.000823938	5
Sema4D in semaphorin signaling	NA	NA	NA	NA	0.001896423	5
PECAM1 interactions	NA	NA	NA	NA	0.016233959	3
Metabolic disorders of biological oxidation enzymes	NA	NA	NA	NA	0.03563081	4
Other semaphorin interactions	NA	NA	NA	NA	0.048999353	3

Supplemental Table III:

	Metabolite	N_HC	N_Mild	N_Severe	Mean_HC	Mean_Mild	Mean_Severe	Log2FC_MvsHC	Log2FC_SvsHC	Log2FC_SvsM	Adj_Pvalue_MvsHC	Adj_Pvalue_SvsHC	Adj_Pvalue_SvsM
1	1,5-anhydroglucitol*	39	74	33	2.258717	2.232249644	1.100972136	-0.026467215	-1.157744723	-1.131277508	0.990340108	9.24E-06	9.67E-07
2	1H-pyrrole-2,5-dione*	39	74	33	3.569952	3.157935613	2.818393171	-0.412016615	-0.751559057	-0.339542442	0.342165897	0.085338469	0.520074093
3	2,4-dihydroxybutanoic acid*	39	74	33	-3.53612	-3.514166238	-3.62395165	0.021949489	-0.087835923	-0.109785412	0.976275601	0.764607687	0.586367931
4	2-aminobutanoic acid	39	74	33	0.865915	0.684656532	0.495757932	-0.181258372	-0.370156972	-0.1888986	0.707386211	0.366665795	0.714615413
5	2-aminomalonic acid*	39	74	33	-2.74367	-2.835537866	-2.786744639	-0.091869762	-0.043076535	0.048793227	0.883322549	0.981069368	0.969180576
6	2-hydroxybutyric acid	39	74	33	-0.98074	-0.899189477	-0.699341749	0.081554667	0.281402395	0.199847728	0.842062382	0.243307625	0.400498211
7	2-hydroxyisopentanoic acid*	39	74	33	0.965316	1.014410903	0.952162693	0.04909462	-0.01315359	-0.06224821	0.88026827	0.993605071	0.832689392
8	2-ketoisocaproic acid	39	74	33	-2.3118	-2.197012565	-2.542510069	0.114787908	-0.230709595	-0.345497504	0.448443292	0.107182405	0.002141952
9	3,4-dihydroxybutanoic acid*	39	74	33	-3.22469	-3.309905283	-2.764042942	-0.085211429	0.460650913	0.545862341	0.854058771	0.043854951	0.004192373
10	3-aminopiperidine-2,6-dione*	39	74	33	4.379419	4.443755751	3.933498653	0.06433663	-0.445920469	-0.510257098	0.798289449	0.000856348	1.18E-05
11	5-methylhydantoin*	39	74	33	-0.5709	-0.562861429	-0.873622542	0.008039145	-0.302721967	-0.310761112	0.996610301	0.038555346	0.013132951
12	aconitic acid	39	74	33	-0.91178	-0.76602275	-1.023482957	0.145760602	-0.111699605	-0.257460208	0.547399069	0.779881244	0.189936174
13	adipic acid (contaminated?)	39	74	33	-1.68085	-1.523894823	-1.630778038	0.156950418	0.050067202	-0.106883216	0.603326527	0.964475122	0.810524572
14	alpha-tocopherol	39	74	33	2.330629	1.411284926	1.469777338	-0.919343904	-0.860851492	0.058492412	0.000166724	0.004065037	0.966234413
15	benzoic acid	39	74	33	0.707619	0.634729448	0.504074364	-0.072889592	-0.203544676	-0.130655084	0.699129537	0.146444137	0.360463572
16	beta-alanine	39	74	33	-2.17937	-1.959309062	-1.726042243	0.220063197	0.453330015	0.233266819	0.554920641	0.177638227	0.553607183
17	beta-sitosterol	39	72	33	-2.44424	-2.58426056	-1.939475214	-0.140023089	0.504762257	0.644785347	0.785113406	0.113533508	0.012376256
18	capric acid	39	74	33	-2.14626	-2.024212206	-1.287509461	0.122048343	0.858751089	0.736702745	0.871368622	0.010509258	0.01367807
19	carbonate ion	39	74	33	3.871691	3.787083072	3.690215955	-0.084608048	-0.181475165	-0.096867117	0.505836486	0.115294643	0.450540763
20	cholest-7-en-3-ol*	39	74	33	-1.99293	-1.971140897	-1.818431591	0.021785553	0.174494859	0.152709306	0.993898161	0.760316807	0.764927791
21	cholestan-3-ol*	39	74	33	-1.90192	-1.826180612	-0.955989235	0.075738499	0.945929876	0.870191377	0.948514721	0.004271694	0.002820436
22	cholesterol	39	74	33	6.376818	6.368245588	6.408369167	-0.008572351	0.031551229	0.040123579	0.989830727	0.907720495	0.818984244
23	citric acid	39	74	33	2.332407	2.34428339	2.093860763	0.01187674	-0.238545886	-0.250422626	0.994800887	0.23478325	0.131785127
24	creatinine	39	74	33	0.065332	-0.085225044	0.131593897	-0.150557543	0.066261398	0.216818941	0.621071115	0.937199709	0.415237897
25	dehydroalanine	39	74	33	-2.27595	-2.005150548	-1.64357635	0.270798909	0.632373107	0.361574198	0.154143071	0.001124478	0.052569536
26	D-fructose	39	74	33	2.364601	2.314893584	2.433092914	-0.049707507	0.068491823	0.11819933	0.946752416	0.929884437	0.758954403
27	D-gluconic acid	39	74	33	-2.94591	-2.784881561	-2.013864814	0.161031343	0.93204809	0.771016746	0.682544335	0.000256498	0.000681116
28	D-glucose	39	74	33	7.982834	8.035088871	7.885109589	0.052255208	-0.097724074	-0.149979282	0.766441079	0.522871662	0.146069103
29	D-glucuronic acid	39	74	33	-2.31403	-2.222406887	-1.282496169	0.091623856	1.031534573	0.939910718	0.904665079	0.00027803	0.000176501
30	D-mannose	39	74	33	3.170393	3.289055416	3.65188024	0.118662801	0.481487625	0.362824824	0.644781408	0.007979228	0.028776106
31	D-ribitol	39	74	33	-3.2467	-3.090229308	-2.899399801	0.156465887	0.347295394	0.190829507	0.362822049	0.033067777	0.261089302
32	D-sorbitol	39	74	33	0.427151	0.401638501	1.326221849	-0.025512863	0.899070486	0.924583349	0.992762203	0.002637665	0.000382294
33	D-xylitol	39	74	33	-1.51925	-1.417680569	-1.627852353	0.101568206	-0.108603578	-0.210171784	0.833218283	0.864103563	0.499427579
34	dopamine	39	74	33	-1.45695	-1.468079798	-1.684221496	-0.011125806	-0.227267504	-0.216141698	0.994127744	0.184668805	0.14292145
35	EDTA [major]	39	74	33	8.606051	8.530070058	8.278870439	-0.075981044	-0.327180664	-0.251199619	0.769372578	0.037061021	0.082040816
36	EDTA [minor]	39	74	33	2.670986	2.704961756	2.666024342	0.033976177	-0.004961237	-0.038937413	0.944168539	0.999142499	0.93480426
37	erythritol	39	74	33	0.100895	-0.04185635	0.188420365	-0.142751661	0.087525054	0.230276715	0.841537381	0.955562607	0.67019497
38	erythronic acid	39	74	33	-0.28	-0.394577605	0.228529106	-0.114579522	0.508527188	0.623106711	0.681796624	0.006529867	9.52E-05
39	fumaric acid	39	74	33	0.11458	0.052985812	0.433868765	-0.061594024	0.319288929	0.380882953	0.900354536	0.144307213	0.031372377
40	glyceric acid	39	74	33	-0.15249	-1.269282945	-1.3023105	-1.116790668	-1.149818223	-0.033027555	7.23E-12	2.15E-09	0.974967897
41	glycerol	39	74	33	5.019067	4.96825257	4.956532895	-0.050814363	-0.062534039	-0.011719676	0.896692304	0.890856301	0.994824385
42	glycerol 3-phosphate	39	74	33	0.49184	0.554680649	0.416532567	0.062840279	-0.075307803	-0.138148082	0.575491326	0.573865036	0.096199881
43	glycine	39	74	33	4.897205	4.953353077	4.715128227	0.056148079	-0.182076772	-0.238224851	0.834632213	0.268667265	0.05917539
44	glycolic acid	39	74	33	-0.95133	-0.992351747	-1.067793768	-0.041022605	-0.116464627	-0.075442021	0.702293075	0.140897359	0.346464459
45	heptadecanoic acid	39	74	33	0.8576	0.818743437	0.599534064	-0.03885698	-0.258066353	-0.219209373	0.917211445	0.074462376	0.090911918
46	hypoxanthine	39	74	33	0.167798	1.337003646	1.450483345	1.169205636	1.282685335	0.1134797	7.12E-05	0.000288464	0.915392784
47	inosine	39	74	33	-4.57783	-3.459710848	-3.836039772	1.118120577	0.741791652	-0.376328924	0.007655366	0.211588054	0.596861828
48	inositol phosphate	39	74	33	-2.02445	-2.047156842	-2.540455572	-0.02270192	-0.51600065	-0.49329873	0.981037796	0.001538748	0.000561681
52	internal standard - creatinine-d3	39	74	33	0.127152	-0.397612959	-0.380825668	-0.524765166	-0.507977876	0.016787291	0.061550425	0.157792718	0.997377342
58	internal standard - tryptophan -d3	39	74	33	10.31714	10.23395924	10.03918339	-0.083177384	-0.277953238	-0.194775855	0.277944154	9.67E-05	0.002530497
59	internal standard - tyrosine 13C6	39	74	33	1.644392	1.544808034	1.593218101	-0.099584258	-0.051174191	0.048410067	0.297608929	0.797412004	0.772154555
60	lactic acid	39	74	33	6.856348	7.227829257	7.434542889	0.371481431	0.578195064	0.206713632	0.000510894	4.55E-06	0.1093796
61	L-alanine	39	74	33	4.861541	4.89860976	4.677545629	0.037068676	-0.183995456	-0.221064131	0.95755244	0.476014184	0.256887118
62	L-aspartic acid	39	74	33	2.541342	2.293359106	2.279315588	-0.247983098	-0.262026617	-0.014043518	0.064038606	0.115242533	0.991923814
63	lauric acid	39	74	33	-0.35774	-0.559024109	-0.914942366	-0.201284246	-0.557202502	-0.355918257	0.42901726	0.012587542	0.097528556
64	L-cysteine	39	74	33	1.687302	1.969798743	2.088693118	0.282496498	0.401390873	0.118894375	0.003649661	0.000423418	0.393637326
65	L-cystine	39	74	33	-4.4104	0.159927892	1.655743949	4.570332793	6.06614885	1.495816057	0	0	5.20E-07
66	L-glutamic acid	39	74	33	2.098891	1.631444472	2.119978613	-0.467446555	0.021087586	0.488534141	0.007784742	0.992751129	0.00869898
67	L-glutamine	39	74	33	0.749781	1.310597489	1.39495025	0.560816979	0.64516974	0.084352761	0.177360852	0.201058071	0.965020092
68	linoleic acid	39	74	33	0.888911	0.713000799	0.788522456	-0.175909777	-0.100388119	0.075521658	0.639497229	0.902771942	0.928733451
69	L-isoleucine	39	74	33	3.56852	3.565730027	3.520874776	-0.002789801	-0.047645053	-0.044855251	0.999707815	0.942126865	0.934767804
70	L-leucine	39	74	33	4.165779	4.143353326	3.812494364	-0.022425493	-0.353284455	-0.330858963	0.991871843	0.247438094	0.209879982
71	L-lysine	39	74	33	3.778293	3.826268014	4.00763541	0.047975184	0.22934258	0.181367396	0.894823592	0.174375533	0.246666135
72	L-malic acid	39	74	33	-1.5561	-1.369814995	-0.995851565	0.186284725	0.560248155	0.37396343	0.299113523	0.000753351	0.014805825
73	L-methionine	39	74	33	0.798596	0.740628887	0.725925127	-0.057967251	-0.072671011	-0.01470376	0.906570916	0.897734172	0.994370709
74	L-ornithine	39	74	33	3.778267	3.69627731	3.917014117	-0.081990082	0.138746725	0.220736807	0.697658513	0.487340168	0.101816506
75	L-phenylalanine	39	74	33	2.027119	2.047518848	1.925752636	0.020400227	-0.101365984	-0.121766211	0.994617356	0.911034853	0.842384723
76	L-proline	39	74	33	4.207605	4.069263648	4.09310557	-0.138340898	-0.114498976	0.023841922	0.66939975	0.824590945	0.989358734
77	L-pyroglutamic acid	39	74	33	4.330487	4.349493422	4.41396617	0.019006298	0.083479046	0.064472748	0.96159856	0.591010224	0.669603234
78	L-serine	39	74	33	3.031949	2.935482762	2.648483913	-0.096466356	-0.383465205	-0.286998849	0.679170038	0.016329276	0.050927226
79	L-threonine	39	74	33	3.179093	3.185276024	3.03687539	0.006183342	-0.142217291	-0.148400634	0.997223957	0.361307796	0.244294519
80	L-tryptophan	39	74	33	6.442334	6.41538639	6.104576801	-0.026947181	-0.33775677	-0.310809589	0.924820287	0.000358454	0.000197561
81	L-tyrosine	39	74	33	1.787962	1.863698363	2.068091137	0.075736737	0.280129512	0.204392775	0.817423802	0.150225837	0.273435916
82	L-valine	39	74	33	5.215604	5.228520006	5.111846762	0.012916258	-0.103756986	-0.116673244	0.989848077	0.632163564	0.477987971
83	maltose	39	74	33	-1.56724	-1.448002051	-0.724807312	0.119242567	0.842437306	0.723194739	0.820646982	0.001543856	0.002214983
84	myristic acid	39	74	33	4.856915	4.329056297	4.20424188	-0.527858369	-0.652672787	-0.124814417	2.76E-11	6.81E-12	0.224238287
85	nonanoic acid	39	74	33	1.414495	1.350085583	1.131794578	-0.06440976	-0.282700765	-0.218291005	0.812385093	0.065382565	0.123661281
86	oleic acid	39	74	33	2.258491	2.129187466	2.228825087	-0.129303043	-0.029665423	0.099637621	0.84117488	0.993637215	0.912239791
87	O-phosphocolamine	39	74	33	-0.20918	-0.093950485	-0.0943086	0.115227404	0.114869289	-0.000358115	0.590689068	0.692939993	0.99999543
88	oxalic acid	39	74	33	-0.60866	-0.732956593	-0.719635345	-0.12429293	-0.110971681	0.013321249	0.633294896	0.77459328	0.995298994
89	palmitic acid	39	74	33	1.207671	0.911010128	0.863469426	-0.296660466	-0.344201168	-0.047540702	0.003260413	0.004464429	0.870031237
90	phosphate ion	39	74	33	7.254326	7.281284712	7.044272547	0.026958492	-0.210053674	-0.237012165	0.884710771	0.007086985	0.000400354
91	pipecolic acid	39	74	33	-2.48554	-2.096760896	-1.818360921	0.388777751	0.667177725	0.278399975	0.224420714	0.048283555	0.501274326
92	pseudouridine	39	74	33	-2.51293	-2.37070842	-2.202968657	0.142220193	0.309959956	0.167739763	0.162243985	0.003011915	0.105350594
93	pyrophosphate	39	74	33	-1.09599	-1.141913963	-1.399887678	-0.045920216	-0.303893931	-0.257973715	0.944112278	0.177024376	0.202832548
94	pyrrole -2-carboxylic acid	39	74	33	-4.38165	-4.075317296	-3.898889197	0.306331254	0.482759352	0.176428099	0.30207451	0.127220431	0.699042914
95	pyruvic acid	39	74	33	1.378261	1.665836574	1.649717559	0.287575473	0.271456458	-0.016119015	0.360795269	0.528158394	0.997110541
96	sedoheptulose	39	74	33	4.418601	4.412133951	4.237585947	-0.00646749	-0.181015495	-0.174548004	0.999220415	0.653365638	0.603595743
97	S-methylcysteine*	39	74	33	-0.64542	-0.64668391	-0.709962399	-0.001268864	-0.064547353	-0.063278489	0.999957993	0.926797004	0.910951467
98	stearic acid	39	74	33	5.117182	4.898514975	4.827230748	-0.218667066	-0.289951294	-0.071284228	0.016537897	0.006721384	0.667017033
99	succinic acid	39	74	33	-0.9171	-1.025636135	-0.727779533	-0.108538352	0.18931825	0.297856602	0.816627439	0.650323717	0.260126714
100	tagatose	39	74	33	0.946803	0.904709086	1.138568874	-0.042094077	0.191765712	0.233859789	0.979218895	0.73778799	0.562289506
101	taurine	39	74	33	1.203558	1.391116324	1.189744995	0.187558291	-0.013813038	-0.201371329	0.451109911	0.996956786	0.440531903
102	urea	39	74	33	9.027862	9.084553305	9.213236604	0.056691265	0.185374565	0.1286833	0.898140249	0.450248468	0.61105484
103	uric acid	39	74	33	4.240503	4.364625656	4.191925775	0.124122198	-0.048577683	-0.172699881	0.483284211	0.924501635	0.286250556
104	Unknown 001	39	74	33	0.55874	0.454994924	0.119123277	-0.103745198	-0.439616845	-0.335871647	0.687324964	0.010967387	0.033323481
105	Unknown 002	39	74	33	-0.44623	0.084338764	0.140607234	0.530573247	0.586841717	0.05626847	0.283372347	0.339004925	0.987237168

106	Unknown 003	39	74	33	-1.77166	-1.884480017	-2.219016821	-0.112817767	-0.447354571	-0.334536804	0.258866383	1.75E-06	5.72E-05
107	Unknown 004	39	74	33	-0.88967	-0.947458161	-0.925476297	-0.057786523	-0.035804659	0.021981865	0.909018522	0.974676286	0.987730245
108	Unknown 005	39	74	33	1.323075	1.56873333	1.59330191	0.245658483	0.270227063	0.02456858	0.599745359	0.648344974	0.995415829
109	Unknown 006	39	74	33	-2.12565	-2.025838115	-2.062469315	0.099815353	0.063184153	-0.0366312	0.542147573	0.841548022	0.928568149
110	Unknown 007	39	74	33	0.143794	-0.238663866	-0.025425348	-0.382457675	-0.169219156	0.213238519	0.268021684	0.833088716	0.691084892
111	Unknown 008	39	74	33	-0.51502	-0.537098751	-0.954542847	-0.022077463	-0.43952156	-0.417444097	0.981852811	0.00797828	0.003982978
112	Unknown 009	39	74	33	-0.96472	-1.018678959	-1.594254595	-0.053957436	-0.629533073	-0.575575636	0.931902194	0.001834094	0.001231867
113	Unknown 010	39	73	33	-0.90913	-0.903513611	-0.838531303	0.005618907	0.070601214	0.064982307	0.999481254	0.944056066	0.939878564
114	Unknown 011	39	74	33	1.645347	1.48689251	1.322538874	-0.158454028	-0.322807664	-0.164353636	0.557082238	0.18643854	0.569734106
115	Unknown 012	39	74	33	1.484225	1.274154182	1.2218215	-0.210070678	-0.26240336	-0.052332682	0.332545485	0.300886441	0.9401225
116	Unknown 013	39	74	33	0.136522	0.227572977	0.642180643	0.091051421	0.505659087	0.414607667	0.829958155	0.020852078	0.035429288
117	Unknown 014	39	74	33	1.707932	1.889165011	1.590197041	0.181233244	-0.117734726	-0.29896797	0.643985982	0.877725691	0.345412448
118	Unknown 015	39	74	33	2.561528	2.65037149	2.034134673	0.088843437	-0.527393379	-0.616236817	0.923523325	0.14604756	0.03667455
119	Unknown 016	39	74	33	-3.15119	-2.943529694	-3.126726518	0.207663869	0.024467045	-0.183196824	0.413598901	0.991378503	0.540241961
120	Unknown 017	39	74	33	-1.38626	-1.357706955	-1.789058233	0.028549076	-0.402802202	-0.431351278	0.959862641	0.004523914	0.000440689
121	Unknown 018	39	74	33	-0.40465	-0.561085497	-0.134719815	-0.156432874	0.269932808	0.426365682	0.422333891	0.168837847	0.004266051
122	Unknown 019	39	74	33	-4.10777	-3.517471502	-3.521761028	0.590300908	0.586011381	-0.004289527	1.14E-06	5.68E-05	0.999262654
123	Unknown 020	39	74	33	-3.24372	-3.082603378	-2.811841744	0.161116948	0.431878582	0.270761634	0.765993357	0.265685507	0.511787272
124	Unknown 021	39	74	33	-1.42938	-1.526442269	-2.049434253	-0.097059027	-0.62005101	-0.522991983	0.735054897	0.000296723	0.000594771
125	Unknown 022	39	74	33	-3.0661	-3.203002409	-3.430466018	-0.136906058	-0.364369667	-0.227463609	0.49285671	0.033059849	0.177915936
126	Unknown 023	39	73	33	-2.96581	-2.988169204	-3.293331461	-0.022357524	-0.327519781	-0.305162257	0.978734386	0.043376096	0.031676768
127	Unknown 024	39	74	32	-0.34443	-0.248643154	-0.42431828	0.095783411	-0.079891716	-0.175675126	0.91910639	0.960397083	0.780549162
128	Unknown 025	39	74	33	-1.87751	-1.720503607	-1.983623363	0.157006757	-0.106112998	-0.263119755	0.193402153	0.5877101	0.017902582
129	Unknown 026	39	74	33	0.425196	0.476457069	0.427128788	0.051260936	0.001932655	-0.049328281	0.839758937	0.999825942	0.865402622
130	Unknown 027	39	74	33	-1.02035	-1.056280425	-1.095584969	-0.035931138	-0.075235683	-0.039304544	0.87725301	0.669861089	0.869342837
131	Unknown 028	39	74	33	0.073129	0.266293724	-0.365731861	0.193165017	-0.438860568	-0.632025585	0.521017644	0.098851198	0.002715798
132	Unknown 029	12	23	12	-4.7284	-4.915376484	-3.996834245	-0.186976407	0.731565831	0.918542238	0.973358034	0.731877283	0.526713209
133	Unknown 030	39	74	33	-1.50808	-1.418581572	-1.66932242	0.089495222	-0.161245626	-0.250740848	0.612183714	0.330367078	0.035424934
134	Unknown 031	39	74	33	-1.64108	-1.630846031	-1.106482047	0.010231157	0.534595141	0.524363984	0.997329077	0.007766687	0.002724
135	Unknown 032	4	8	10	0.648028	0.419621978	0.799908784	-0.228406229	0.151880576	0.380286806	0.965521794	0.98349785	0.851336019
136	Unknown 033	39	74	33	0.090941	-0.625701617	-0.336216366	-0.716642891	-0.42715764	0.289485251	2.16E-06	0.02871913	0.120864867
137	Unknown 034	39	74	33	-3.73172	-3.446270094	-3.651881591	0.285445027	0.07983353	-0.205611497	0.21694533	0.918544746	0.489340474
138	Unknown 035	39	74	33	-1.28787	-1.837411179	-1.932508354	-0.549544841	-0.644642016	-0.095097175	0.000205736	0.000275212	0.781223938
139	Unknown 036	39	74	33	-0.96805	-1.181906433	-1.143067263	-0.213855182	-0.175016013	0.03883917	0.088345895	0.315742129	0.929288814
140	Unknown 037	39	74	33	-3.91437	-3.603787366	-3.504900194	0.310584462	0.409471634	0.098887172	0.024011066	0.011094624	0.704661332
141	Unknown 038	39	74	33	-1.79303	-1.626575372	-1.297895018	0.166452871	0.495133224	0.328680354	0.734527142	0.152762548	0.344293619
142	Unknown 039	39	73	33	-3.51713	-4.40957706	-4.204023185	-0.892447091	-0.686893216	0.205553875	0.144630516	0.44257029	0.910701302
143	Unknown 040	39	74	33	2.990792	2.906559887	2.522003652	-0.084232573	-0.468788808	-0.384556235	0.600010602	4.24E-05	0.00015746
144	Unknown 041	39	74	33	3.848689	3.841320365	3.729823029	-0.007368763	-0.1188661	-0.111497336	0.99677782	0.557617635	0.51910796
145	Unknown 042	39	74	33	7.598106	7.593278517	7.504044217	-0.00482748	-0.094061781	-0.0892343	0.99658204	0.406172729	0.355642543
146	Unknown 043	39	74	33	4.17127	4.081114192	3.850854731	-0.090155389	-0.320414851	-0.230259461	0.510942344	0.00355367	0.022631998
147	Unknown 044	39	74	33	1.630782	1.475907002	1.637211408	-0.154874859	0.006429547	0.161304407	0.806433742	0.999739929	0.811759067
148	Unknown 045	39	74	33	-0.00816	-0.031086683	-0.585295705	-0.022924659	-0.577133681	-0.554209022	0.983039887	0.000859292	0.000269272
149	Unknown 046	39	74	33	3.774661	3.704232701	3.57756929	-0.070428306	-0.197091717	-0.126663411	0.717221932	0.166372654	0.385097948
150	Unknown 047	39	74	33	-2.10572	-1.728737763	-1.260526133	0.376978296	0.845189926	0.46821163	0.753434283	0.372143617	0.677184418
151	Unknown 048	39	74	33	-1.3509	-1.394541577	-1.102394819	-0.043644997	0.248501762	0.292146758	0.963030992	0.428591572	0.226511251
152	Unknown 049	39	74	33	-0.18613	0.156855614	0.132637338	0.342983505	0.318765229	-0.024218276	0.615124675	0.744999023	0.997825986
153	Unknown 050	39	74	33	2.79875	2.76177089	2.736962375	-0.036978984	-0.061787499	-0.024808516	0.95797332	0.919562389	0.982875164
154	Unknown 051	39	74	33	3.171386	3.032831389	2.935917142	-0.13855421	-0.235468458	-0.096914247	0.619957997	0.382344709	0.810880345
155	Unknown 052	39	74	33	0.392426	0.028125463	-0.083727622	-0.364300801	-0.476153886	-0.111853085	0.130880534	0.088793257	0.839678735
156	Unknown 053	39	74	33	1.344447	1.475568631	1.28524087	0.131121975	-0.059205786	-0.190327761	0.622030298	0.934218026	0.410700017
157	Unknown 054	39	74	33	2.490648	2.504647417	2.647005078	0.013999408	0.156357069	0.142357661	0.994076659	0.597008957	0.579400284
158	Unknown 055	39	74	33	1.42603	1.486535709	0.97805283	0.060505366	-0.447977513	-0.508482879	0.86037962	0.004252164	0.00016572
159	Unknown 056	39	74	33	-3.21598	-3.04872778	-3.126605462	0.167249293	0.089371612	-0.077877682	0.339949158	0.804418057	0.809765211
160	Unknown 057	39	74	33	-3.34147	-3.138676588	-3.173066741	0.202788932	0.168398778	-0.034390154	0.185051485	0.439637231	0.956830507
161	Unknown 058	39	74	33	-0.69092	-0.290669697	-0.505171684	0.400253641	0.185751654	-0.214501987	0.14432838	0.743095371	0.603854279
162	Unknown 059	39	74	33	-0.10186	0.223860219	0.433884059	0.325724439	0.535748278	0.210023839	0.084657807	0.010302821	0.39362277
163	Unknown 060	39	74	33	0.478817	0.50638845	0.313291332	0.027571292	-0.165525827	-0.193097119	0.915971507	0.114694547	0.024644409
164	Unknown 061	39	74	33	-1.24489	-1.167345735	-1.946946297	0.077545418	-0.702055144	-0.779600562	0.894592548	0.00244922	0.000102827
165	Unknown 062	39	74	33	-0.08492	-0.099892493	-0.491353954	-0.014970445	-0.406431906	-0.391461461	0.987992616	0.002836333	0.001029415
166	Unknown 063	39	74	33	0.000616	-0.099984169	-0.485928118	-0.100600181	-0.486544129	-0.385943948	0.537940716	9.10E-05	0.00050199
167	Unknown 064	39	74	33	-0.15406	-0.139241139	-0.491370583	0.014818711	-0.337310732	-0.352129444	0.987622231	0.013337701	0.002705988
168	Unknown 065	39	74	33	-1.15987	-1.225547126	-1.45891011	-0.065681113	-0.299044097	-0.233362984	0.944756998	0.441435545	0.528861157
169	Unknown 066	39	74	33	0.108702	0.031816078	0.062944427	-0.076886238	-0.045757889	0.031128349	0.781243886	0.94052223	0.964406525
170	Unknown 067	39	74	33	0.518708	0.643390886	0.816140436	0.124682482	0.297432032	0.17274955	0.711181778	0.261077084	0.558149051
171	Unknown 068	39	74	33	-1.12346	-1.123810739	-1.844464924	-0.000354632	-0.721008817	-0.720654185	0.999997903	0.003289472	0.000755285
172	Unknown 069	39	74	33	-1.42071	-1.104633301	-1.474647564	0.316072478	-0.053941784	-0.370014262	0.350363965	0.978614625	0.277704842
173	Unknown 070	39	74	33	-1.81281	-1.984478327	-2.030271087	-0.171664517	-0.217457278	-0.045792761	0.035174869	0.023654144	0.80251545
174	Unknown 071	39	74	33	-0.17137	-0.080892017	-0.526234745	0.090476392	-0.354866336	-0.445342728	0.868563902	0.224182384	0.051769733
175	Unknown 072	39	74	33	1.086682	1.089513572	0.957282546	0.002831371	-0.129399655	-0.132231026	0.999269245	0.347657378	0.245749189
176	Unknown 073	39	74	33	6.944682	6.929978755	6.602363403	-0.014703343	-0.342318695	-0.327615352	0.9897188	0.023092481	0.012531041
177	Unknown 074	39	74	33	-2.14625	-2.134793238	-2.296320623	0.011451824	-0.150075561	-0.161527385	0.997516328	0.742340111	0.644030952
178	Unknown 075	39	72	33	-3.40806	-3.683535025	-4.057526643	-0.275474272	-0.64946589	-0.373991619	0.531277612	0.087462372	0.354095508
179	Unknown 076	39	74	33	-3.34872	-3.563960159	-3.492178682	-0.215240707	-0.14345923	0.071781477	0.687327045	0.889673211	0.963290273
180	Unknown 077	39	74	33	-2.73741	-2.596929336	-2.792540901	0.140478938	-0.055132627	-0.195611565	0.420759182	0.910188598	0.225375942
181	Unknown 078	39	74	33	-1.5669	-1.381661352	-2.03161464	0.185241535	-0.464711753	-0.649953288	0.558342838	0.080868059	0.00233437
182	Unknown 079	39	74	33	-4.2185	-4.318584358	-3.654997017	-0.100085253	0.563502088	0.663587341	0.881166664	0.065210387	0.008773501
183	Unknown 080	39	74	33	-0.47814	-0.285719424	-1.492036461	0.192420914	-1.013896123	-1.206317037	0.793570918	0.013498334	0.000532597
184	Unknown 081	39	74	33	-2.42938	-2.36962419	-2.244059002	0.059758749	0.185323937	0.125565188	0.855054149	0.352043243	0.540779981
185	Unknown 082	39	74	33	-3.60667	-3.456276173	-3.940233212	0.150391771	-0.333565268	-0.483957039	0.397990459	0.045036676	0.000355395
186	Unknown 083	39	74	33	-1.72511	-2.310133941	-2.448621559	-0.585019139	-0.723506757	-0.138487618	1.30E-07	4.90E-08	0.400272505
187	Unknown 084	39	74	33	-0.89243	-0.93818929	-1.599986696	-0.045756429	-0.707553835	-0.661797406	0.958631917	0.001348534	0.000655208
188	Unknown 085	39	74	33	-0.9422	-0.773080888	-0.791887042	0.169120915	0.150314761	-0.018806154	0.74052616	0.84677031	0.996675561
189	Unknown 086	39	74	33	-2.33279	-2.446507932	-2.895437011	-0.113718257	-0.562647335	-0.448929078	0.563951937	0.000121422	0.000587876
190	Unknown 087	39	74	33	0.030176	0.073068249	0.132026309	0.042892435	0.101850496	0.058958061	0.947924648	0.81002458	0.913694808
191	Unknown 088	39	72	33	0.004447	-0.288637088	0.011933471	-0.293084083	0.007486476	0.300570559	0.633610174	0.999788586	0.650881791
192	Unknown 089	39	74	33	-3.333	-3.317049519	-3.212752646	0.015952541	0.120249414	0.104296873	0.989245934	0.65178285	0.662850192
193	Unknown 090	39	74	33	-1.5538	-1.547602386	-1.390202693	0.006202605	0.163602298	0.157399693	0.999317383	0.717987264	0.676189982
194	Unknown 091	39	74	33	-2.87333	-2.721607155	-3.266681882	0.151719873	-0.393354853	-0.545074727	0.89262816	0.587460813	0.274297283
195	Unknown 092	39	73	32	-3.35162	-3.678600331	-3.878867451	-0.326980077	-0.527247197	-0.200267121	0.012076219	0.000458601	0.22426002
196	Unknown 093	39	74	32	1.688379	0.714967779	0.580605135	-0.97341171	-1.107774353	-0.134362644	4.04E-12	4.43E-11	0.575444817
197	Unknown 094	39	74	33	1.299567	1.157334048	0.889025593	-0.142232843	-0.410541298	-0.268308455	0.80820727	0.292833727	0.509791036
198	Unknown 095	39	74	33	-0.18717	-1.113023304	-1.158390971	-0.925849151	-0.971216818	-0.045367667	0.001654201	0.006729967	0.98543024
199	Unknown 096	39	74	33	-1.72277	-1.681506985	-1.453590123	0.041263185	0.269180047	0.227916862	0.978601538	0.527313098	0.556480956
200	Unknown 097	39	74	33	2.761275	2.908066387	2.433086007	0.14679137	-0.32818901	-0.47498038	0.643768143	0.218052841	0.018857427
201	Unknown 098	39	74	33	-0.72195	-0.843674559	-0.912619293	-0.121729474	-0.190674208	-0.068944734	0.802833012	0.68627865	0.938888771
202	Unknown 099	39	74	33	2.900109	2.749293819	2.490485769	-0.150815187	-0.409623238	-0.25880805	0.052987706	1.13E-06	0.000614356
203	Unknown 100	39	74	33	1.628652	1.574013628	1.346401505	-0.054638644	-0.282250767	-0.227612123	0.762020078	0.007907047	0.017409097

204	Unknown 101	39	74	33	-2.22748	-2.261232904	-2.358659818	-0.033749888	-0.131176802	-0.097426914	0.993087642	0.929335817	0.949682941
205	Unknown 102	39	73	33	-3.51935	-1.981837844	-1.641701816	1.537507857	1.877643885	0.340136028	1.69E-05	1.04E-05	0.586642877
206	Unknown 103	39	74	33	0.011495	0.172496474	0.154895125	0.161001151	0.143399801	-0.01760135	0.591706571	0.74670605	0.994379888
207	Unknown 104	39	70	32	-1.64607	-4.286801006	-5.077334368	-2.640731845	-3.431265207	-0.790533362	8.66E-08	6.60E-09	0.228642052
208	Unknown 105	39	74	33	0.44489	0.336857909	0.281883988	-0.108032012	-0.163005933	-0.054973921	0.811256064	0.716876499	0.952671057
209	Unknown 106	39	74	33	-0.65443	-0.650681906	-0.677986907	0.003748679	-0.023556323	-0.027305002	0.999834414	0.995434048	0.992180286
210	Unknown 107	39	74	33	4.079474	4.187140091	4.252216362	0.10766614	0.172742411	0.065076271	0.833517076	0.720677336	0.942209108
211	Unknown 108	39	74	33	-1.60148	-1.531654425	-1.474809211	0.06982402	0.126669234	0.056845214	0.950927434	0.890638518	0.970631518
212	Unknown 109	39	74	33	-2.04133	-1.727937458	-1.950211685	0.31339412	0.091119892	-0.222274227	0.510154406	0.960698314	0.738046604
213	Unknown 110	38	74	33	-1.07312	-0.557021525	-0.37689771	0.516100639	0.696224454	0.180123815	0.264552258	0.183479702	0.861466226

Supplemental Table IV:

Protein	uniprot_url	Cor_w_NET
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P11047	https://www.uniprot.org/uniprot/P11047	0.762476326
P0DOY3	https://www.uniprot.org/uniprot/P0DOY3	0.684550547
P06744	https://www.uniprot.org/uniprot/P06744	0.808941074
P24821	https://www.uniprot.org/uniprot/P24821	0.682467661
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P14625	https://www.uniprot.org/uniprot/P14625	0.739693826
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P69905	https://www.uniprot.org/uniprot/P69905	0.619340603
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P18428	https://www.uniprot.org/uniprot/P18428	0.769097603
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P20333	https://www.uniprot.org/uniprot/P20333	0.641866
Q15485	https://www.uniprot.org/uniprot/Q15485	0.606446189
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