Supplemental Materials

Molecular Biology of the Cell

Dou et al.

Supplemental Materials for:

Type II transmembrane domain hydrophobicity dictates the co-translational dependence for inversion

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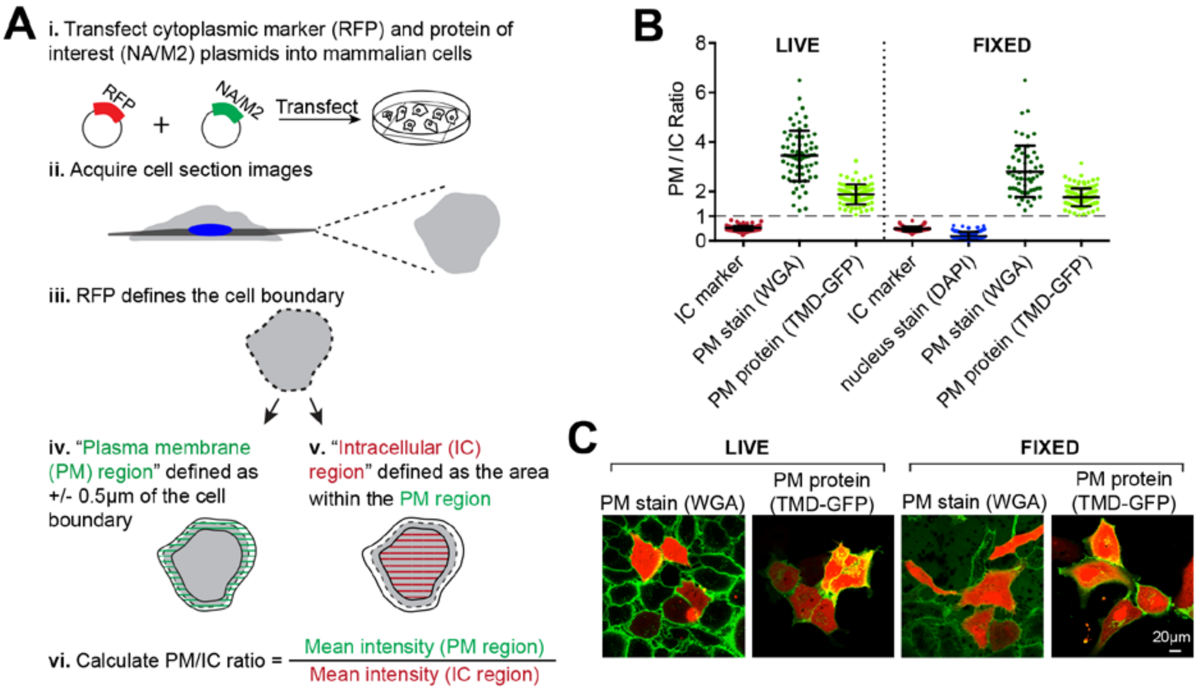
Single-cell approach to monitor plasma membrane localization

To monitor the plasma membrane (PM) localization of a protein in an unbiased manner, we established a semi-automated approach that compares the mean intensity of a substrate at the PM to the intracellular (IC) region at the single-cell level (Supplemental Fig. 1A). As a control for the approach, Vero cells were co-transfected with plasmids expressing GFP with an N-terminal TMD (TMD-GFP) and RFP for a cellular marker (step -i-). At 48 h post-transfection, live and fixed cells were prepared for confocal microscopy and multiple cell section images were taken (step -ii-). Each image was then processed using Cell profiler 2.0 software (Kamentsky et al., 2011) with the following parameters. The RFP signal identified each 'cell' boundary ≥ 350 um^2, the lower edge of the normal cell size distribution (step -iii-). The PM region was defined as the peripheral area 0.5 µm in-and-out from the RFP boundary (step -iv-). The intracellular (IC) region was defined as the area surrounded by the PM region (step -v-). The ratio of the mean fluorescent signal for the PM and IC regions were then calculated for each cell (step -vi-).

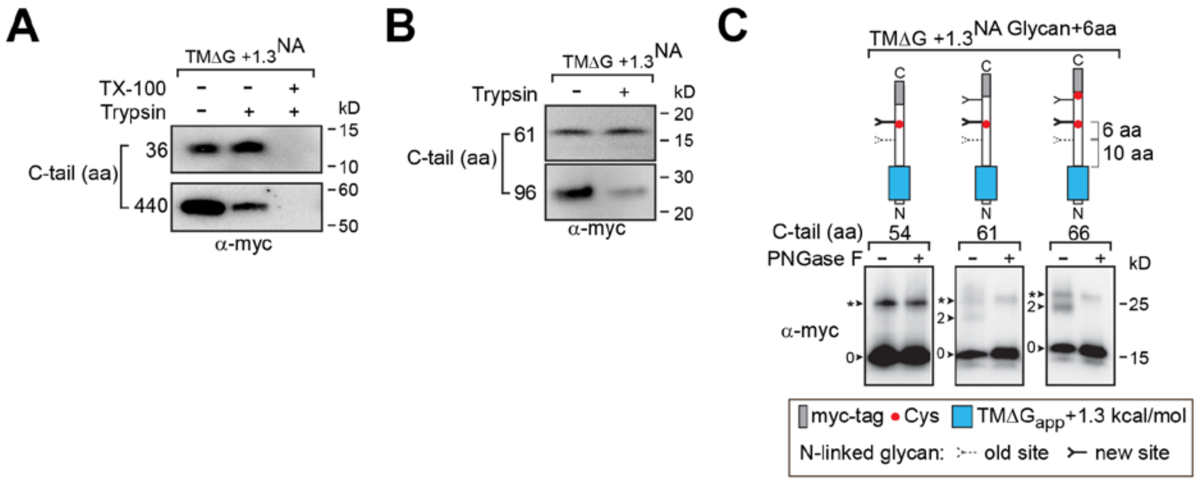
The signal from the RFP and the DAPI stained nucleus were used to determine the threshold IC value, and the signal from wheat germ agglutinin (WGA) and the protein marker TMD-GFP were used to establish the PM values. Analysis of the different cell populations gave average PM/IC ratios of ~0.5 for the IC localized targets and the ratios for the individual cells were all < 1 (Supplemental Fig. 1B and C). For the PM controls WGA and TMD-GFP, the average PM/IC ratios were ~3 and ~2, respectively for 100-200 cells, and all the individual cell PM/IC ratios were > 1. Both live and fixed cells showed cell-to-cell variation in the PM/IC ratios, but this was most notable for WGA, which was extremely sensitive to the image acquisition time after fixation or the staining time for the live cell analysis. Based on these results, PM localized substrates should have a PM/IC ratio > 1 and IC localized substrates should have a ratio < 1 using this approach.

SUPPLEMENTAL MATERIALS REFERENCE

Kamentsky, L., Jones, T.R., Fraser, A., Bray, M.A., Logan, D.J., Madden, K.L., Ljosa, V., Rueden, C., Eliceiri, K.W., and Carpenter, A.E. (2011). Improved structure, function and compatibility for CellProfiler: modular high-throughput image analysis software. Bioinformatics *27*, 1179-1180.



SUPPLEMENTAL FIGURE 1: Single-cell microscopy assay to monitor PM localization. **(**A) Outline of the experimental approach. Cells were transfected with a cytoplasmic marker (RFP) and the TMD construct of interest, and image sections were obtained by confocal microscopy. The images were then processed using Cell profiler 2.0 where RFP defines the cell boundary. The mean intensity of the TMD construct in the plasma membrane (PM) region, defined as 0.5 µm in-and-out from the cell boundary, was calculated. Finally, the PM mean intensity was normalized to that of the intracellular region (IC), defined as the area surrounded by the PM region. (B) The PM/IC values obtained from fixed and live cell controls are displayed with the IC marker RFP. (C) Representative images of fixed and live cell sections are shown for samples where the PM was labeled with WGA, or TMD-GFP, and the IC region with RFP.



SUPPLEMENTAL FIGURE 2: NA trypsin protection and glycosylation analysis of constructs with a shifted glycosylation site. (A) Immunoblots of lysates obtained from cells expressing the indicated constructs. Prior to harvesting, the cells were incubated in the absence and presence of trypsin to determine if the myc epitope was properly positioned on the extracellular side of the plasma membrane. The digestion was performed on detergent (TX-100) solubilized cells to confirm the epitope is sensitive to trypsin. Note the decrease in the signal on the full-length construct with the 440 aa C-tail, but not with the 36 aa C-tail. (B) Similar analysis using the PM localized, unglycosylated, NA construct with a 61 aa C-tail and the glycosylated construct with a 96 aa C-tail. The glycosylated construct (C-tail 96 aa) is properly orientated and trypsin sensitive, whereas the unglycosylated construct (C-tail 61 aa) is not properly inverted even though it localizes to the PM. (C) Glycosylation site positioning is not responsible for the low glycosylation efficiency of the NA constructs with a marginally hydrophobic TMD. Transfected cell lysates expressing the indicated constructs with the natural glycosylation site moved 6 aa further from the membrane were either untreated, or treated, with PNGase F, separated by SDS-PAGE, and immunoblotted. The number of N-linked glycans is indicated, and the SDS resistant TMD dimer is depicted with an asterisk.

SUPPLEMENTAL TABLE 1: Curation of human Nin-Cout type II membrane protein TMD sequences:hydrophobicity, positioning, topologies, and localization. The table displays all the human Nin-Cout type II membrane proteins obtained from the UniProtKB/Swiss-Prot database with the predicted length, hydrophobicity, and location of their TMDs, which were used to calculate their C-tail length and create the graph in Figure 8. References (Pubmed ID) for the proteins that localize to the mitochondria, have a likely Nout-Cin orientation, or have been documented as soluble or secreted are provided.

Uniprot ID	Protein length	TMD length	C-tail length	TMD sequence	TMD ΔG	Topology notes	PubMed reference
sp|Q5VT66|MOSC1_HUMAN	337	23	293	WLGVAALGLTAVALGAVAWRRAW	-1,04	Mitochondrial localization	23086957
sp|Q9BV23|ABHD6_HUMAN	337	33	296	FVIAGGTLAIPILAFVASFLLWPSALIRIYYWY	-2,9	Predicted mitochondrial localization	
sp|Q68CQ7|GL8D1_HUMAN	371	20	349	FRKVNIIILVLAVALFLLVL	-2,64	Predicted mitochondrial localization	
sp|P15144|AMPN_HUMAN	967	29	934	FYISKSLGILGILLGVAAVCTIIALSVVY	-2,3	Secreted	7904544, 7902291
sp|Q86X52|CHSS1_HUMAN	802	23	774	RRAWLSVLLGLVLGFVLASRLVL	-2,59	Secreted	21129727
sp|Q10471|GALT2_HUMAN	571	24	547	MRRRSRMLLCFAFLWVLGIAYYMY	-2,4	Secreted	9394011
sp|O75354|ENTP6_HUMAN	484	20	422	VAYPLGLCVGVFIYVAYIKW	-0,25	Secreted	14529283
sp|Q9H9S5|FKRP_HUMAN	495	27	468	MRLTRCQAALAAAITLNLLVLFYVSWL	-1,7	Secreted	19900540
sp|Q9NRQ2|PLS4_HUMAN	329	19	9	VKMKAMIFGACFLIDFMYF	0,93	Soluble	15035622, 16091359
sp|O15162|PLS1_HUMAN	318	19	13	VKMKAVMIGACFLIDFMFF	1	Soluble	15035622, 16091359
sp|Q9NRY6|PLS3_HUMAN	295	19	13	VRVKAVLLGATFLIDYMFF	1,15	Soluble	15035622, 16091359
sp|Q9NRY7|PLS2_HUMAN	224	19	4	VKMKAVMIGACFLIDYMFF	1,17	Soluble	15035622, 16091359
sp|Q8TC12|RDH11_HUMAN	318	21	297	MVELMFPLLLLLLPFLLYMAA	-1,28	Nout-Cin orientation	12036956
sp|P49788|TIG1_HUMAN	294	20	256	RPTAPLLALLLLLAPVAAPA	0,7	Nout-Cin orientation	21303978
sp|O75923|DYSF_HUMAN	2080	31	13	FILWRRFRWAIILFIILFILLLFLAIFIYAF	-9,8		
sp|Q9HC10|OTOF_HUMAN	1997	31	6	TYRWLLLKLLLLLLLLLLALFLYSVPGYLV	-7,7		
sp|Q9NZM1|MYOF_HUMAN	2061	31	13	FIVWRRFKWVIIGLLFLLILLLFVAVLLYSL	-7,32		
sp|Q13326|SGCG_HUMAN	291	33	228	WRKRCLYLFVLLLLIILVVNLALTIWILKVMWF	-7,17		
sp|Q9Y5Q5|CORIN_HUMAN	1042	30	970	LLRFLLLVLIPCICALVLLLVILLSYVGTL	-6,7		
sp|P21964|COMT_HUMAN	271	29	236	LLLAAVLLGLVLLVVLLLLLRHWGWGLCL	-6,45		
sp|Q9BY79|MFRP_HUMAN	579	30	487	CRFSWLCVLLLSSLLLLLLGLLVAIILAQL	-6,33		
sp|Q16585|SGCB_HUMAN	318	29	226	LAICVIILLFILAVINLIITLVIWAVIRI	-6,24		
sp|Q8IX19|MCEM1_HUMAN	187	30	81	CWLYRAILSLYILLALAFVLCIILSAFIMV	-6,23		
sp|Q9BXN2|CLC7A_HUMAN	247	29	176	WRLIAVILGILCLVILVIAVVLGTMAIWR	-6,1		
sp|Q9UMR7|CLC4A_HUMAN	237	28	168	FPKLLCASLLIFFLLLAISFFIAFVIFF	-5,97		
sp|Q92629|SGCD_HUMAN	289	31	230	WRKRCLYFFVLLLMILILVNLAMTIWILKVM	-5,96		
sp|Q10589|BST2_HUMAN	180	30	132	RCKLLLGIGILVLLIIVILGVPLIIFTIKA	-5,84		
sp|P41273|TNFL9_HUMAN	254	32	199	CRVLPWALVAGLLLLLLLAAACAVFLACPWAV	-5,68		
sp|Q9P126|CLC1B_HUMAN	229	29	172	WWRVMALILLILCVGMVVGLVALGIWSVM	-5,61		
sp|Q9BX97|PLVAP_HUMAN	442	29	393	CWYYLRYFFLFVSLIQFLIILGLVLFMVY	-5,55		
sp|Q8IU80|TMPS6_HUMAN	811	27	735	YLRLVPLFVLLALLVLASAGVLLWYFL	-5,51		
sp|Q9UNG2|TNF18_HUMAN	199	26	128	WKLWLFCSIVMLLFLCSFSWLIFIFL	-5,48		
sp|Q7RTY8|TMPS7_HUMAN	843	24	744	KIILFTVFLFILAVIAWTLLWLYI	-5,44		
sp|Q8NC01|CLC1A_HUMAN	280	27	204	VALTLLTLCLVLLIGLAALGLLFFQYY	-5,43		
sp|Q9UMD9|COHA1_HUMAN	1497	26	1008	WWKWLLGLLLTWLLLLGLLFGLIALA	-5,41		
sp|Q8NHY0|B4GN2_HUMAN	566	27	473	RFLWLLKILVIILVLGIVGFMFGSMFL	-5,37		
sp|P21854|CD72_HUMAN	359	29	240	TCLRYLLLGLLLTCLLLGVTAICLGVRYL	-5,36		
sp|O43451|MGA_HUMAN	1857	27	1822	FTTLEIVLSVLLLVLFIISIVLIVLLA	-5,27		
sp|Q9UHP7|CLC2D_HUMAN	191	30	130	ATLIWRLFFLIMFLTIIVCGMVAALSAIRA	-5,26		
sp|O60235|TM11D_HUMAN	418	32	375	RFLNPYVVCFIVVAGVVILAVTIALLVYFLAF	-5,23		
sp|Q7L5N7|PCAT2_HUMAN	544	29	458	IVLLGIILLPIRVLLVALILLLAWPFAAI	-5,11		
sp|Q2M2H8|MGAL2_HUMAN	482	27	451	LSVLEVLLIIFCLIVVTIDILLLLLVL	-5,08		
sp|Q6Q4G3|AMPQ_HUMAN	990	29	953	FYVSRAVALLLAGLVAALLLALAVLAALY	-5,07		
sp|Q9UBQ6|EXTL2_HUMAN	330	25	290	IRVLRLSLVVILVLLLVAGALTALL	-5,03		
sp|Q9H3Q3|G3ST2_HUMAN	398	22	367	RYFRVILLLLLALTLLLLAGFL	-5,01		
sp|D3W0D1|KLRF2_HUMAN	207	30	151	LYPQYYCLLLIFGCIVILIFIMTGIDLKFW	-4,97		
sp|Q11203|SIAT6_HUMAN	375	28	345	LLVFVRNLLLALCLFLVLGFLYYSAWKL	-4,97		
sp|Q9UN42|AT1B4_HUMAN	357	28	219	LILLIYFFFYASLAAVITLCMYTLFLTI	-4,83		
sp|P23276|KELL_HUMAN	732	28	663	WAVARRVLTAILILGLLLCFSVLLFYNF	-4,77		
sp|Q9Y5Y6|ST14_HUMAN	855	29	773	RWVVLAAVLIGLLLVLLGIGFLVWHLQYR	-4,76		
sp|P19440|GGT1_HUMAN	569	23	543	KLVVLGLLAVVLVLVIVGLCLWL	-4,71		
sp|P36268|GGT2_HUMAN	569	23	543	KLVVLGLLAVVLVLVIVGLCLWL	-4,71		
sp|A6NGU5|GGT3_HUMAN	568	23	542	KLVVLGLLAVVLVLVIVGLCLWL	-4,71		
sp|Q7L211|ABHDD_HUMAN	337	31	277	LLPLIVTFHLYGGIILLLLIFISIAGILYKF	-4,64		
sp|Q8TDX6|CGAT1_HUMAN	532	28	497	LLAWISRVVVLLVLLCCAISVLYMLACT	-4,63		
sp|Q6AZY7|SCAR3_HUMAN	606	26	526	VRILYLFLALLLVAVAVLASLVFRKV	-4,62		
sp|Q96LD1|SGCZ_HUMAN	299	31	238	WRKRCLYFFVLLLLVTMIVNLAMTIWILKVM	-4,6		
sp|Q5QGZ9|CL12A_HUMAN	265	31	197	VWRPAALFLTLLCLLLLIGLGVLASMFHVTL	-4,52		
sp|Q16853|AOC3_HUMAN	763	24	735	TILVLLILAVITIFALVCVLLVGR	-4,49		
sp|P14410|SUIS_HUMAN	1827	27	1792	LEISLIVLFVIVTIIAIALIVVLATKT	-4,42		
sp|Q9Y328|NSG2_HUMAN	171	28	74	FTVTILVSLALAFLACIVFLVVYKAFTY	-4,4		
sp|P57727|TMPS3_HUMAN	454	32	383	ILSLLPLKFFPIIVIGIIALILALAIGLGIHF	-4,39		
sp|Q6ZMJ2|SCAR5_HUMAN	495	25	410	AVLGLYLLVFLILVGIFILAVSRPR	-4,38		
sp|Q5SRI9|MANEA_HUMAN	462	27	432	FRRRTCIILALFILFIFSLMMGLKMLR	-4,37		
sp|Q9NRB3|CHSTC_HUMAN	414	26	385	ARLFRLWLVLGSVFMILLIIVYWDSA	-4,33		
sp|Q9UKU6|TRHDE_HUMAN	1024	27	959	RLVLAFAVSLVALLAVTMLAVLLSLRF	-4,32		
sp|P61647|SIA8F_HUMAN	398	20	373	ALLALLASLLLLLLLRLLWC	-4,27		
sp|Q11130|FUT7_HUMAN	342	25	309	TRRLRGLGVLAGVALLAALWLLWLL	-4,24		
sp|Q01628|IFM3_HUMAN	133	28	1	CLNIWALILGILMTILLIVIPVLIFQAY	-4,22		
sp|Q8N3Y3|LARG2_HUMAN	721	24	690	RALGAAALLLLLLLLGFLLFGGDL	-4,22		
sp|Q9BYE2|TMPSD_HUMAN	581	24	397	LPLIGCVLLLIALVVSLIILFQFW	-4,2		
sp|P14415|AT1B2_HUMAN	290	29	227	TSWAFILLFYLVFYGFLTAMFTLTMWVML	-4,18		
sp|P42658|DPP6_HUMAN	865	26	747	WKGIAIALLVILVICSLIVTSVILLT	-4,18		
sp|O96024|B3GT4_HUMAN	378	22	354	LRLFRRLLLAALLLVIVWTLFG	-4,17		
sp|Q9Y231|FUT9_HUMAN	359	23	329	ILRPFLIVCIILGCFMACLLIYI	-4,17		
sp|Q9Y287|ITM2B_HUMAN	266	32	185	RRAWCWCMCFGLAFMLAGVILGGAYLYKYFAL	-4,17		
sp|Q8N539|FBCD1_HUMAN	461	27	407	CGYVLCTVLLALAVLLAVAVTGAVLFL	-4,16		
sp|P54709|AT1B3_HUMAN	279	30	214	WGLILLFYLVFYGFLAALFSFTMWVMLQTL	-4,13		
sp|O43909|EXTL3_HUMAN	919	29	865	RIRLTWLSFTLFVILVFFPLIAHYYLTTL	-4,13		
sp|P52848|NDST1_HUMAN	882	24	841	AVLFLLFIFCLFSVFISAYYLYGW	-4,09		
sp|Q9UKM7|MA1B1_HUMAN	699	28	594	LSRLQRNMILFLLAFLLFCGLLFYINLA	-4,07		
sp|P37059|DHB2_HUMAN	387	28	326	LWSWMVCLAGLCAVCLLILSPFWGLILF	-4,06		
sp|Q9UQ53|MGT4B_HUMAN	548	28	520	MRLRNGTFLTLLLFCLCAFLSLSWYAAL	-4,03		
sp|Q9BT22|ALG1_HUMAN	464	27	437	MAASCLVLLALCLLLPLLLLGGWKRWR	-4,02		
sp|P21757|MSRE_HUMAN	451	28	375	FKAALIALYLLVFAVLIPLIGIVAAQLL	-4,02		
sp|Q86UP2|KTN1_HUMAN	1357	27	1328	FYESAYFIVLIPSIVITVIFLFFWLFM	-4,01		
sp|Q5VUY2|ADCL4_HUMAN	407	25	382	MAVPWLVLLLALPIFFLGVFVWAVF	-4		
sp|Q8N608|DPP10_HUMAN	796	26	739	WKGIAIALLVILVVCSLITMSVILLT	-3,99		
sp|Q86T26|TM11B_HUMAN	416	30	375	WPLWTTIFIFLGVAAILGVTIGLLVHFLAV	-3,99		
sp|P08195|4F2_HUMAN	630	33	420	WVRTRWALLLLFWLGWLGMLAGAVVIIVRAPRC	-3,95		
sp|P98073|ENTK_HUMAN	1019	25	976	IMFAALFAILVVLCAGLIAVSCLTI	-3,95		
sp|P48023|TNFL6_HUMAN	281	27	176	TGLCLLVMFFMVLVALVGLGLGMFQLF	-3,95		
sp|Q8IV08|PLD3_HUMAN	490	25	430	ARWVLLVLILAVVGFGALMTQLFLW	-3,93		
sp|O43505|B3GN1_HUMAN	415	29	382	YAIRCAFYQLLLAALMLVAMLQLLYLSLL	-3,91		

sp|Q5VSG8|MANEL_HUMAN	457	27	428	RRRRRACIALFLVLLFAFGTLMGLRTL	-3,88
sp|Q9UL52|TM11E_HUMAN	423	27	378	WVIGLVIFISLIVLAVCIGLTVHYVRY	-3,88
sp|O14638|ENPP3_HUMAN	875	31	827	LKKYKIACIVLLALLVIMSLGLGLGLGLRKL	-3,87
sp|Q92935|EXTL1_HUMAN	676	25	642	LWLALSASWLLLVLLGGFSLLRLAL	-3,87
sp|Q9H4F1|SIA7D_HUMAN	302	33	264	RLVLIILCSVVFSAVYILLCCWAGLPLCLATCL	-3,86
sp|Q9UH99|SUN2_HUMAN	717	25	483	LKTFLWFLLPLLLLTCLTYGAWYFY	-3,86
sp|Q9UIQ6|LCAP_HUMAN	1025	29	889	ARTMVVCAFVIVVAVSVIMVIYLLPRCTF	-3,85
sp|Q9H3R1|NDST4_HUMAN	872	28	838	LRRSFRTLIVLLATFCLVSIVISAYFLY	-3,83
sp|Q96JF0|SIAT2_HUMAN	529	24	498	WRQRMLFGIFAWGLLFLLIFIYFT	-3,83
sp|Q9NRS4|TMPS4_HUMAN	437	32	374	VGIPIIIALLSLASIIIVVVLIKVILDKYYFL	-3,75
sp|Q9H0X4|ITFG3_HUMAN	552	27	480	RCRAAAFFLSLFLCLFVVFVVSFVIPC	-3,73
sp|Q5KU26|COL12_HUMAN	742	29	680	WALKFSIILLYILCALLTITVAILGYKVV	-3,71
sp|Q6ZMR5|TM11A_HUMAN	421	30	377	LKPWMIAVLIVLSLTVVAVTIGLLVHFLVF	-3,71
sp|O60476|MA1A2_HUMAN	641	28	584	TLRLSEKFILLLILSAFITLCFGAFFFL	-3,68
sp|Q07837|SLC31_HUMAN	685	28	570	ILFWLTVASVLVLIAATIAIIALSPKCL	-3,68
sp|Q6P4E1|CASC4_HUMAN	433	28	398	RRAGRLPSLVLVVLLVVIVVLAFNYWSI	-3,64
sp|Q16842|SIA4B_HUMAN	350	23	323	LRVWFLSVAFLLVFIMSLLFTYS	-3,64
sp|Q9NQX7|ITM2C_HUMAN	267	28	182	VCYLSMGMVVLLMGLVFASVYIYRYFFL	-3,63
sp|Q96E93|KLRG1_HUMAN	195	25	134	CLVAIALGLLTAVLLSVLLYQWILC	-3,63
sp|Q00973|B4GN1_HUMAN	533	28	505	MWLGRRALCALVLLLACASLGLLYASTR	-3,62
sp|Q6ZS10|CL17A_HUMAN	378	26	185	RWMVYLCLLVVTSLFLGCLGLTVTLI	-3,62
sp|Q2HXU8|CL12B_HUMAN	276	28	211	IWRHAALGLVTLCLMLLIGLVTLGMMFL	-3,61
sp|A0PJZ3|GXLT2_HUMAN	443	25	416	LRSKAAALLLLALAALLLALLSLRA	-3,6
sp|O43508|TNF12_HUMAN	249	33	199	TALLVPLALGLGLALACLGLLLAVVSLGSRASL	-3,59
sp|Q04609|FOLH1_HUMAN	750	25	707	RWLCAGALVLAGGFFLLGFLFGWFI	-3,58
sp|P51164|ATP4B_HUMAN	291	30	228	LSRWVWISLYYVAFYVVMTGLFALCLYVLM	-3,56
sp|Q9C0J1|B3GN4_HUMAN	378	28	325	MLCRLCWLVSYSLAVLLLGCLLFLRKAA	-3,55
sp|Q8N6G5|CGAT2_HUMAN	542	23	510	TRTHWLLLGLALLCSLVLFMYLL	-3,55
sp|Q8N3T1|GLT15_HUMAN	639	22	606	CRLQFLLLLLMLGCVLMMVAML	-3,55
sp|O95502|NPTXR_HUMAN	500	28	470	FLAVLLAAGMLAFLGAVICIIASVPLAA	-3,55
sp|P16442|BGAT_HUMAN	354	22	317	ALRPMILFLIMLVLVLFGYGVL	-3,54
sp|Q9UJ37|SIA7B_HUMAN	374	24	343	FFWLLLLLTAACSGLLFALYFSAV	-3,54
sp|Q9Y673|ALG5_HUMAN	324	29	292	LLLQLAVLGAALAAAALVLISIVAFTTAT	-3,53
sp|Q9NR71|ASAH2_HUMAN	780	26	746	LETFLIFLLVMMSAITVALLSLLFIT	-3,51
sp|P42857|NSG1_HUMAN	185	27	79	RFKVSVLVLFALAFLTCVVFLVVYKVY	-3,49
sp|P28907|CD38_HUMAN	300	24	253	LCLGVSILVLILVVVLAVVVPRWR	-3,46
sp|P33908|MA1A1_HUMAN	653	29	591	AALRLTEKFVLLLVFSAFITLCFGAIFFL	-3,45
sp|Q8N1L4|CP4Z2_HUMAN	340	25	307	LMAHPFLLLILLCMSLLLFQVIRLY	-3,44
sp|Q86W10|CP4Z1_HUMAN	505	25	472	LMAHPFLLLILLCMSLLLFQVIRLY	-3,44
sp|O43529|CHSTA_HUMAN	356	25	327	WLLLAACFWVIFMFMVASKFITLTF	-3,41
sp|P32971|TNFL8_HUMAN	234	25	172	YFYLTTATLALCLVFTVATIMVLVV	-3,41
sp|P26572|MGAT1_HUMAN	445	25	414	AGLVLWGAILFVAWNALLLLFFWTR	-3,4
sp|Q96FL9|GLT14_HUMAN	552	25	525	RLTRRLVLPVFGVLWITVLLFFWVT	-3,38
sp|P06734|FCER2_HUMAN	321	30	276	RCCRRGTQIVLLGLVTAALWAGLLTLLLLW	-3,37
sp|Q495T6|MMEL1_HUMAN	779	25	731	FLEGGLLLLLLLVTAALVALGVLYA	-3,37
sp|Q96AG4|LRC59_HUMAN	307	27	36	WAVLKLLLLLLLFGVAGGLVACRVTEL	-3,34
sp|P78380|OLR1_HUMAN	273	32	213	FLYSPWWCLAAATLGVLCLGLVVTIMVLGMQL	-3,34
sp|P05026|AT1B1_HUMAN	303	30	242	WFKILLFYVIFYGCLAGIFIGTIQVMLLTI	-3,33
sp|Q6UXB4|CLC4G_HUMAN	293	27	240	WSRRPLFLALAVLVTTVLWAVILSILL	-3,31
sp|P36269|GGT5_HUMAN	586	31	555	MARGYGATVSLVLLGLGLALAVIVLAVVLSR	-3,31
sp|Q8NF37|PCAT1_HUMAN	534	30	457	LMTLTLFPVRLLVAAAMMLLAWPLALVASL	-3,31
sp|Q11128|FUT5_HUMAN	374	26	338	WLWRRCLAGLLFQLLVAVCFFSYLRV	-3,28
sp|O75900|MMP23_HUMAN	390	25	348	RRWLGAALVALCLLPALVLLARLGA	-3,28
sp|Q06643|TNFC_HUMAN	244	29	197	LLLAVAGATSLVTLLLAVPITVLAVLALV	-3,27
sp|P26718|NKG2D_HUMAN	216	27	137	FFFCCFIAVAMGIRFIIMVAIWSAVFL	-3,26
sp|O95672|ECEL1_HUMAN	775	26	690	VCLLSGLVFAAGLCAILAAMLALKYL	-3,25
sp|P42167|LAP2B_HUMAN	454	22	20	VWIKILLFVVVAVFLFLVYQAM	-3,23
sp|P08473|NEP_HUMAN	750	30	698	RWTPLEISLSVLVLLLTIIAVTMIALYATY	-3,22
sp|Q96MM7|H6ST2_HUMAN	605	20	432	LLLALVMLFLFAVIVLQYVC	-3,2
sp|O75063|XYLK_HUMAN	409	23	384	LKQRVVLLAILLVIFIFTKVFLI	-3,2
sp|O15466|SIA8E_HUMAN	376	26	339	LLGSRTLLFIFICAFALVTLLQQILY	-3,17
sp|P26715|NKG2A_HUMAN	233	28	135	LIVGILGIICLILMASVVTIVVIPSTLI	-3,16
sp|Q9Y3Q0|NALD2_HUMAN	740	28	706	RLYLWMCLAAALASFLMGFMVGWFIKPL	-3,14
sp|Q6L9W6|B4GN3_HUMAN	998	28	953	LLRRRFRLLLALAVVSVGLWTLYLELVA	-3,13
sp|Q6ZWK6|TM11F_HUMAN	438	30	385	FWDSVRLALFTLAIVAIIGIAIGIVTHFVV	-3,13
sp|Q9NR34|MA1C1_HUMAN	630	27	587	LRLPQKFLFLLFLSGLVTLCFGALFLL	-3,07
sp|Q9UP52|TFR2_HUMAN	801	27	696	RRAAPYLVLTALLIFTGAFLLGYVAFR	-3,06
sp|Q8IUN9|CLC10_HUMAN	316	20	256	LLLSLGLGLLLLVIICVVGF	-3,02
sp|O43736|ITM2A_HUMAN	263	28	184	RCMLTLLGLSFILAGLIVGGACIYKYFM	-2,98
sp|Q9UJ71|CLC4K_HUMAN	328	28	260	TVRAALICLTLVLVASVLLQAVLYPRFM	-2,96
sp|Q92838|EDA_HUMAN	391	26	326	CLLFLGFFGLSLALHLLTLCCYLELR	-2,96
sp|Q9Y2C3|B3GT5_HUMAN	310	23	282	MRLMYICLLVLGALCLYFSMYSL	-2,91
sp|Q6NSJ0|K1161_HUMAN	714	24	634	LLGSAVLGLLLVLAAVVAWCYYSV	-2,91
sp|P01375|TNFA_HUMAN	233	24	182	RRCLFLSLFSFLIVAGATTLFCLL	-2,9
sp|Q6UXN8|CLC9A_HUMAN	241	28	182	ACCLVMVISCVFCMGLLTASIFLGVKLL	-2,89
sp|O60909|B4GT2_HUMAN	372	29	336	TLERVCKAVLLLCLLHFLVAVILYFDVYA	-2,87
sp|Q93063|EXT2_HUMAN	718	24	672	RIYYITLFSIVLLGLIATGMFQFW	-2,85
sp|O43173|SIA8C_HUMAN	380	28	347	MARVASVLGLVMLSVALLILSLISYVSL	-2,84
sp|Q6EIG7|CLC6A_HUMAN	209	33	162	WLSLRLWSVAGISIALLSACFIVSCVVTYHFTY	-2,82
sp|O43825|B3GT2_HUMAN	422	22	379	LFRTHLIGVLSLVFLFAMFLFF	-2,81
sp|P02786|TFR1_HUMAN	760	24	671	ICYGTIAVIVFFLIGFMIGYLGYC	-2,81
sp|Q8WXI8|CLC4D_HUMAN	215	25	173	LIPSVIAVVFILLLSVCFIASCLVT	-2,77
sp|Q07108|CD69_HUMAN	199	24	135	VLCAVMNVVFITILIIALIALSVG	-2,76
sp|P21217|FUT3_HUMAN	361	24	325	WRRCLAALLFQLLVAVCFFSYLRV	-2,75
sp|Q9ULY5|CLC4E_HUMAN	219	29	170	MFLWTVAGIPILFLSACFITRCVVTFRIF	-2,74
sp|O60344|ECE2_HUMAN	883	27	680	LELVLAGASLLLAALLLGCLVALGVQY	-2,73
sp|Q9NXG6|P4HTM_HUMAN	502	28	420	ICSRAYFLVLMVFVHLYLGNVLALLLFV	-2,73
sp|Q9NPZ5|B3GA2_HUMAN	323	26	294	ALFTRFFILLPWILIVIIMLDVDTRR	-2,72
sp|Q6IAN0|DRS7B_HUMAN	325	28	280	FITSTAILPLLFGCLGVFGLFRLLQWVR	-2,7
sp|Q3V5L5|MGT5B_HUMAN	792	26	751	LVTLRPFRLFVLGIGFFTLCFLMTSL	-2,67
sp|Q9NUM4|T106B_HUMAN	274	25	157	RTKLYVMASVFVCLLLSGLAVFFLF	-2,67
sp|Q13061|TRDN_HUMAN	729	24	658	AAWLLVIALIITWSAVAIVMFDLV	-2,67
sp|Q9HCQ5|GALT9_HUMAN	603	24	573	IRTLLTVNILVFVGIVLFSVYCRL	-2,65
sp|Q76KP1|B4GN4_HUMAN	1039	19	1008	MKLLLLLLLLSCAAWLTYV	-2,64
sp|P07306|ASGR1_HUMAN	291	22	230	RLLLLSLGLSLLLLVVVCVIGS	-2,62
sp|Q7L1S5|CHST9_HUMAN	443	23	408	VFLSVLIFGVAGLLLFMYLQVWI	-2,59
sp|Q7Z7M9|GALT5_HUMAN	940	29	905	FFRGSGRVLAFIFVASVIWLLFDMAALRL	-2,59
sp|O43557|TNF14_HUMAN	240	27	179	VARVGLGLLLLLMGAGLAVQGWFLLQL	-2,58
sp|O95150|TNF15_HUMAN	251	24	195	ARWALTCCLVLLPFLAGLTTYLLV	-2,58
sp|Q9H2S6|TNMD_HUMAN	317	22	267	LKICGLVFGILALTLIVLFWGS	-2,58
sp|P07307|ASGR2_HUMAN	311	29	234	LAQRLCSMVCFSLLALSFNILLLVVICVT	-2,57
sp|Q9Y644|RFNG_HUMAN	331	23	302	ALCRACLALAAALAALLLLPLPL	-2,57
sp|O15393|TMPS2_HUMAN	492	26	383	ALCITLTLGTFLVGAALAAGLLWKFM	-2,57
sp|Q96SE0|ABHD1_HUMAN	405	26	368	TWADTFSLLLALAVALYLGYYWACVL	-2,56
sp|O75752|B3GL1_HUMAN	331	24	293	LRSLKWSLLLLSLLSFFVMWYLSL	-2,55

sp|Q11206|SIA4C_HUMAN	333	20	308	RWKLLAMLALVLVVMVWYSI	-2,55
sp|Q8NFS9|GNT2C_HUMAN	402	23	377	FWRYCFFAFTLLSVVIFVRFYSS	-2,54
sp|Q9Y275|TN13B_HUMAN	285	26	213	LLAATLLLALLSCCLTVVSFYQVAAL	-2,53
sp|Q6UVW9|CLC2A_HUMAN	174	24	125	WKIGLMCFLSIIITTVCIIMIATW	-2,51
sp|Q14435|GALT3_HUMAN	633	20	594	FWKLGAVIFFFIIVLVLMQR	-2,51
sp|Q58DX5|NADL2_HUMAN	795	22	649	VLKILCTATILFIFGILIGYYV	-2,5
sp|Q11201|SIA4A_HUMAN	340	20	314	RTLKVLTFLVLFIFLTSFFL	-2,5
sp|O95803|NDST3_HUMAN	873	25	838	FQRTVILLATFCMVSIIISAYYLYS	-2,48
sp|Q09327|MGAT3_HUMAN	533	27	504	MRRYKLFLMFCMAGLCLISFLHFFKTL	-2,46
sp|P19526|FUT1_HUMAN	365	19	338	LCLAFLLVCVLSVIFFLHI	-2,45
sp|Q8NES3|LFNG_HUMAN	379	23	353	RCGRRLLLALAGALLACLLVLTA	-2,45
sp|Q9H2A9|CHST8_HUMAN	424	25	393	TMRLACMFSSILLFGAAGLLLFISL	-2,43
sp|P05981|HEPS_HUMAN	417	28	372	VAALTAGTLLLLTAIGAASWAIVAVLLR	-2,43
sp|Q6IS24|GLTL3_HUMAN	598	26	569	LRRVKVLLVLNLIAVAGFVLFLAKCR	-2,42
sp|Q9Y662|HS3SB_HUMAN	390	24	338	VRRKLALLFAMLCVWLYMFLYSCA	-2,42
sp|O94901|SUN1_HUMAN	812	30	476	FLLTRCLRNICKFLVLLIPLFLLLAGLSLR	-2,42
sp|P42892|ECE1_HUMAN	770	24	679	RLVVLVVLLAAGLVACLAALGIQY	-2,39
sp|Q96L58|B3GT6_HUMAN	329	32	295	LLRRAWRRRAALGLGTLALCGAALLYLARCAA	-2,36
sp|Q8IXA5|SACA3_HUMAN	215	23	133	LRRRWCPAGIMLLALVCLLSCLL	-2,34
sp|Q92186|SIA8B_HUMAN	375	22	349	FRSWMLAALTLLVVFLIFADIS	-2,34
sp|P51993|FUT6_HUMAN	359	26	323	WSWRCCLTTLLFQLLMAVCFFSYLRV	-2,33
sp|Q12918|KLRB1_HUMAN	225	28	159	FALKLSCAGIILLVLVVTGLSVSVTSLI	-2,3
sp|Q9UEW3|MARCO_HUMAN	520	32	443	LAVVVIYLILLTAGAGLLVVQVLNLQARLRVL	-2,29
sp|Q12797|ASPH_HUMAN	758	27	680	TSFFTWFMVIALLGVWTSVAVVWFDLV	-2,28
sp|O43286|B4GT5_HUMAN	388	29	353	LLRLPRRSLLAALFFFSLSSSLLYFVYVA	-2,28
sp|Q9H1B5|XYLT2_HUMAN	865	29	827	LVRRYKLAIATALAILLLQGLVVWSFSGL	-2,27
sp|Q6ICH7|ASPH2_HUMAN	369	19	293	TTAVITVACLLVLFVWYCY	-2,26
sp|Q86SF2|GALT7_HUMAN	657	28	628	RLKIGFILRSLLVVGSFLGLVVLWSSLT	-2,22
sp|Q86SR1|GLT10_HUMAN	603	26	571	RLLQAVALVLAALVLLPNVGLWALYR	-2,22
sp|Q9H3S3|TMPS5_HUMAN	457	29	384	MRRGCAVLGALGLLAGAGVGSWLLVLYLC	-2,22
sp|O00461|GOLI4_HUMAN	696	25	660	RIFQTLLLLTVVFGFLYGAMLYYEL	-2,2
sp|Q9BYC5|FUT8_HUMAN	575	19	550	SWRWIMLILFAWGTLLFYI	-2,19
sp|P29965|CD40L_HUMAN	261	28	211	IFMYLLTVFLITQMIGSALFAVYLHRRL	-2,18
sp|Q9H1C3|GL8D2_HUMAN	349	25	322	LLRKINQVLLFLLIVTLCVILYKKV	-2,18
sp|Q8IXK2|GLT12_HUMAN	581	26	542	LRRGREALLVLLALLALAGLGSVLRA	-2,18
sp|Q5H943|KKLC1_HUMAN	113	22	89	FYLLLASSILCALIVFWKYRRF	-2,16
sp|Q5U4P2|ASPH1_HUMAN	390	33	292	LIMLPWPLPLASSALTLLFGALTSLFLWYCYRL	-2,14
sp|Q8IUS5|EPHX4_HUMAN	362	33	319	LMLTLRSLLFWSLVYCYCGLCASIHLLKLLWSL	-2,09
sp|Q16706|MA2A1_HUMAN	1144	20	1118	FTVFGSAIFCVVIFSLYLML	-2,09
sp|Q9NS84|CHST7_HUMAN	486	22	454	YCKFALLLVLYTLVLLLVPSVL	-2,07
sp|P52849|NDST2_HUMAN	883	25	845	LELHRLILLLIAFSLGSMGFLAYYV	-2,07
sp|P78562|PHEX_HUMAN	749	24	709	RGTRIALVVFVGGTLVLGTILFLV	-2,07
sp|Q8N5D6|GBGT1_HUMAN	347	25	320	RRRLALGLGFCLLAGTSLSVLWVYL	-2,04
sp|Q4G148|GXLT1_HUMAN	440	23	417	MRRYLRVVVLCVACGFCSLLYAF	-2,04
sp|Q9BUJ0|ABHEA_HUMAN	271	19	219	QVALLGLSLLLMLLLYVGL	-2,02
sp|Q9UBM8|MGT4C_HUMAN	478	24	435	LRKRSTVSFLGVLVIFLLFMNLYI	-2,02
sp|Q10472|GALT1_HUMAN	559	25	531	FAYCKVVLATSLIWVLLDMFLLLYF	-2,01
sp|O00587|MFNG_HUMAN	321	26	293	CRLPRGLAGALLTLLCMGLLCLRYHL	-2,01
sp|Q969X2|SIA7F_HUMAN	333	19	273	RSAVFVILFALITILILYS	-2,01
sp|Q9H2X3|CLC4M_HUMAN	399	21	329	ALVLQLLSFMLLAGVLVAILV	-1,99
sp|P27487|DPP4_HUMAN	766	24	738	WKVLLGLLGAAALVTIITVPVVLL	-1,99
sp|Q9NSC7|SIA7A_HUMAN	600	21	565	VQWSLLLAVLVFFLFALPSFI	-1,98
sp|Q5T4J0|GCNT6_HUMAN	391	21	368	VWSCYLCIITLQIIIIVTVLY	-1,97
sp|Q8NBJ4|GOLM1_HUMAN	401	20	366	LVLAALVACIIVLGFNYWIA	-1,96
sp|O94923|GLCE_HUMAN	617	19	589	YKTLIIICALFTLVTVLLW	-1,95
sp|Q8NDV1|SIA7C_HUMAN	305	25	277	ILKRKSVIAVSFIAAFLFLLVVRLV	-1,94
sp|O60513|B4GT4_HUMAN	344	22	314	LSYKFRLLLLLTLCLTVVGWAT	-1,93
sp|Q7Z410|TMPS9_HUMAN	1059	28	1009	AACCRAASIGVVATSLVVLTLGVLLAFL	-1,92
sp|P26717|NKG2C_HUMAN	231	27	134	LTAEVLGIICIVLMATVLKTIVLIPFL	-1,88
sp|Q07444|NKG2E_HUMAN	240	27	143	LTAEVLGIICIVLMATVLKTIVLIPFL	-1,88
sp|Q8NET6|CHSTD_HUMAN	341	27	310	CCRRRVLAAACLGAALLLLCAAPRSLR	-1,87
sp|Q92185|SIA8A_HUMAN	356	27	305	RTRLPMGASALCVVVLCWLYIFPVYRL	-1,87
sp|Q8NBI6|XXLT1_HUMAN	393	19	351	YCALLLAAALAVCAFYYLG	-1,87
sp|Q13241|KLRD1_HUMAN	179	26	148	TTLWRLISGTLGIICLSLMSTLGILL	-1,86
sp|Q8NCH0|CHSTE_HUMAN	376	28	310	LLLPSMLMFAVIVASSGLLLMIERGILA	-1,85
sp|Q9Y274|SIA10_HUMAN	331	26	305	MRGYLVAIFLSAVFLYYVLHCILWGT	-1,84
sp|Q9NS00|C1GLT_HUMAN	363	26	332	WLNFLTFLCGSAIGFLLCSQLFSILL	-1,83
sp|P15291|B4GT1_HUMAN	398	25	355	LQRACRLLVAVCALHLGVTLVYYLA	-1,82
sp|Q9P2E5|CHPF2_HUMAN	772	29	738	LLALLRPALPLILGLSLGCSLSLLRVSWI	-1,81
sp|Q92611|EDEM1_HUMAN	657	27	630	MQWRALVLGLVLLRLGLHGVLWLVFGL	-1,78
sp|Q49A17|GLTL6_HUMAN	601	25	570	RFLQMTLLFTVALIFLPNVGLWSLY	-1,78
sp|Q9P2W7|B3GA1_HUMAN	334	21	310	RRDILAIVLIVLPWTLLITVW	-1,77
sp|Q6Y288|B3GLT_HUMAN	498	24	470	ACWWLLAPPALLALLTCSLAFGLA	-1,77
sp|Q06430|GNT2B_HUMAN	400	23	375	LSMRYLFIISVSSVIIFIVFSVF	-1,77
sp|Q8NCL4|GALT6_HUMAN	622	19	593	LRLAMVGCAFVLFLFLLHR	-1,74
sp|P32970|CD70_HUMAN	193	28	151	YGCVLRAALVPLVAGLVICLVVCIQRFA	-1,73
sp|P22413|ENPP1_HUMAN	925	24	828	TYKVLSLVLSVCVLTTILGCIFGL	-1,73
sp|P23510|TNFL4_HUMAN	183	27	133	LLLVASVIQGLGLLLCFTYICLHFSAL	-1,73
sp|Q9HDC9|APMAP_HUMAN	416	25	355	RVFRVTFLMLAVSLTVPLLGAMMLL	-1,72
sp|Q9Y2A9|B3GN3_HUMAN	372	19	343	ATLILAIGAFTLLLFSLLV	-1,71
sp|Q6UWU4|CF089_HUMAN	347	23	268	LLIVVYKVLATLGLILLTAYFVI	-1,71
sp|Q8NFL0|B3GN7_HUMAN	401	24	371	TVYRSLCLALALLVAVTVFQRSLT	-1,7
sp|Q9Y4C5|CHST2_HUMAN	530	25	456	VFRRKALVLCAGYALLLVLTMLNLL	-1,68
sp|O43908|NKG2F_HUMAN	158	24	64	LTAEVLGIICIVLMATVLKTIVLI	-1,66
sp|P50591|TNF10_HUMAN	281	28	242	LGQTCVLIVIFTVLLQSLCVAVTYVYFT	-1,65
sp|Q8WVQ1|CANT1_HUMAN	401	20	340	RWKVILTFFVGAAILWLLCS	-1,62
sp|Q8N4A0|GALT4_HUMAN	578	28	549	AVRWTWAGKSCLLLAFLTVAYIFVELLV	-1,62
sp|Q8N428|GLT16_HUMAN	558	25	533	MRKIRANAIAILTVAWILGTFYYLW	-1,61
sp|P15907|SIAT1_HUMAN	406	19	379	KFSCCVLVFLLFAVICVWK	-1,61
sp|Q8WTT0|CLC4C_HUMAN	213	29	171	LWWFQLKVWSMAVVSILLLSVCFTVSSVV	-1,59
sp|O95395|GCNT3_HUMAN	438	24	405	LHYLWALGCYMLLATVALKLSFRL	-1,59
sp|O14788|TNF11_HUMAN	317	25	245	MFVALLGLGLGQVVCSVALFFYFRA	-1,58
sp|Q8IUC8|GLT13_HUMAN	556	28	528	MRRFVYCKVVLATSLMWVLVDVFLLLYF	-1,56
sp|P46695|IEX1_HUMAN	156	19	55	AKRLLFLLLTIVFCQILMA	-1,54
sp|P22760|AAAD_HUMAN	399	19	378	RKSLYLLIVGILIAYYIYT	-1,53
sp|Q0P6D2|FA69C_HUMAN	419	22	374	TLLAFAAWTAGWVLAAALLLRA	-1,52
sp|Q9UBV7|B4GT7_HUMAN	327	25	276	RKCSVFHLFVACLSLGFFSLLWLQL	-1,51
sp|Q6P531|GGT6_HUMAN	493	23	415	TWARVVAALLLLAVGCSLAVRQL	-1,5
sp|Q07075|AMPE_HUMAN	957	23	916	VAILCAVVVGVGLIVGLAVGLTR	-1,49
sp|Q9UQQ1|NALDL_HUMAN	740	26	712	WTKVLGLGLGAAALLGLGIILGHFAI	-1,49
sp|Q96BA8|CR3L1_HUMAN	519	23	125	TGTCLMVAALCFVLVLGSLVPCL	-1,48
sp|Q8TEY5|CR3L4_HUMAN	395	20	82	TSTCVLILLFSLALIILPSF	-1,48
sp|P55073|IOD3_HUMAN	278	24	236	CLVLFPRFLGTAFMLWLLDFLCIR	-1,47
sp|O95461|LARGE_HUMAN	756	23	726	RRKFLAASLSLLCIPAITWIYLF	-1,47
sp|P09172|DOPO_HUMAN	617	20	580	AAFMYSTAVAIFLVILVAAL	-1,46

sp|Q12884|SEPR_HUMAN	760	25	733	TWVKIVFGVATSAVLALLVMCIVLR	-1,46
sp|Q9Y2B1|TMEM5_HUMAN	443	27	414	LTRKRLCSFLIALYCLFSLYAAYHVFF	-1,46
sp|Q02742|GCNT1_HUMAN	428	20	394	TKYYFMVLVLSLITFSVLRI	-1,42
sp|Q9P109|GCNT4_HUMAN	453	23	415	VFILFLTLWLLSLLKLLNVRRLF	-1,42
sp|Q96QI5|HS3S6_HUMAN	342	24	295	ALRASRAPMLLVALVLGAYCLCAL	-1,41
sp|Q5VUD6|FA69B_HUMAN	431	22	383	LRVRCIFLAWLGVFAGSWLVYV	-1,4
sp|Q6UX72|B3GN9_HUMAN	402	23	375	LRLRRDALLTLLLGASLGLLLYA	-1,39
sp|Q9NPF2|CHSTB_HUMAN	352	25	315	RICRMVLATCLGSFILVIFYFQSML	-1,39
sp|Q7Z4J2|GL6D1_HUMAN	308	21	284	KRMLLLVLFAFSLMLVERYFR	-1,38
sp|P49641|MA2A2_HUMAN	1150	20	1124	VTVCGAAIFCVAVFSLYLML	-1,38
sp|Q9UBX8|B4GT6_HUMAN	382	23	347	RSLLAFIFFFSLSSSCLYFIYVA	-1,37
sp|Q16394|EXT1_HUMAN	746	22	720	KRYFILLSAGSCLALLFYFGGL	-1,37
sp|Q9Y663|HS3SA_HUMAN	406	23	363	IFRKFLLMLCSLLTSLYVFYCLA	-1,37
sp|Q8WU67|ABHD3_HUMAN	409	27	360	VRVGFFGSGVGLSLILGFSVAYAFYYL	-1,36
sp|Q9UNP4|SIAT9_HUMAN	418	19	333	ILKCTLLVFGVWILYILKL	-1,36
sp|O43889|CREB3_HUMAN	395	20	124	STCILVLLVSFCLLLVPAMY	-1,35
sp|P22083|FUT4_HUMAN	530	26	358	RGLPWTVCVLAAAGLTCTALITYACW	-1,35
sp|Q7LFX5|CHSTF_HUMAN	561	20	463	RCSLVFGLIIMTLVMASYIL	-1,34
sp|Q13724|MOGS_HUMAN	837	29	771	RSTAGGVALAVVVLSLALGMSGRWVLAWY	-1,29
sp|Q7LGC8|CHST3_HUMAN	479	19	441	MRSKYALFLVFVVIVFVFI	-1,28
sp|Q5T7M9|FA69A_HUMAN	428	28	378	YVRMKYLFFSWLVVFVGSWIIYVQYSTY	-1,27
sp|Q9NX62|IMPA3_HUMAN	359	27	327	IRLSPLGVAVFCLLGLGVLYHLYSGFL	-1,27
sp|Q9H5K3|SG196_HUMAN	350	22	312	VPPAVGLLLIMALMNTLLYLCL	-1,27
sp|P04233|HG2A_HUMAN	296	25	224	ALYTGFSILVTLLLAGQATTAYFLY	-1,25
sp|Q9NY25|CLC5A_HUMAN	188	25	161	WHMIISGLIVVVLKVVGMTLFLLYF	-1,21
sp|Q6PK18|OGFD3_HUMAN	319	22	255	WLRTAGLGAGFVLTALLLWSSL	-1,2
sp|Q8WZA1|PMGT1_HUMAN	660	26	601	ALRRFCQTGAVLFLLVTVIVNIKLIL	-1,18
sp|Q86Y22|CONA1_HUMAN	540	28	479	RAVSALCLLLSVGSAAACLLLGVQAAAL	-1,17
sp|O75477|ERLN1_HUMAN	346	20	323	ARVLVAAVVGLVAVLLYASI	-1,16
sp|P61009|SPCS3_HUMAN	180	22	148	LFAFSLSVMAALTFGCFITTAF	-1,15
sp|Q9Y278|HS3S2_HUMAN	367	27	326	RRARRLLFAFTLSLSCTYLCYSFLCCC	-1,14
sp|Q8NCR0|B3GL2_HUMAN	500	24	476	MRNWLVLLCPCVLGAALHLWLRLR	-1,12
sp|Q9NZS2|KLRF1_HUMAN	232	30	164	ILLGISGTVNGILTLTLISLILLVSQGVLL	-1,12
sp|Q6P4F1|FUT10_HUMAN	479	25	449	RRKLLASCLCVTATVFLLVTLQVMV	-1,11
sp|Q9BXS0|COPA1_HUMAN	654	23	598	CAVLAALLSVVAVVSCLYLGVKT	-1,08
sp|Q09328|MGT5A_HUMAN	741	21	707	LGFFLVTFGFIWGMMLLHFTI	-1,08
sp|Q10469|MGAT2_HUMAN	447	25	420	FRIYKRKVLILTLVVAACGFVLWSS	-1,07
sp|Q9Y2C2|UST_HUMAN	406	23	339	LRDYGFCMATLLVFCLGSLLYQL	-1,07
sp|Q9NPC4|A4GAT_HUMAN	353	25	310	RVCTLFIIGFKFTFFVSIMIYWHVV	-1,04
sp|Q9NY28|GALT8_HUMAN	637	25	610	FWRKLPKALFIGLTLAIAVNLLLVF	-1,03
sp|O60704|TPST2_HUMAN	377	23	353	RLSVRRVLLAAGCALVLVLAVQL	-1,03
sp|Q70SY1|CR3L2_HUMAN	520	25	125	LAGTQTGTCLMVVVLCFAVAFGSFF	-1
sp|Q8NCW6|GLT11_HUMAN	608	25	580	VTVRYFCYGCLFTSATWTVLLFVYF	-1
sp|Q6ZNI0|GCNT7_HUMAN	430	19	404	KSGLVVRAVICIFIFLYLR	-0,98
sp|Q6ZMB0|B3GN6_HUMAN	384	23	353	LTAKTLACLLVGVSFLALQQWFL	-0,97
sp|A8MXE2|YI036_HUMAN	369	29	336	FCRLRTHQWCFILFNVILFHALLFGTDFV	-0,93
sp|Q8IZP7|H6ST3_HUMAN	471	20	445	KWLLTPVLTLLFVVIMYQYV	-0,9
sp|Q6PIU2|NCEH1_HUMAN	408	23	385	MRSSCVLLTALVALAAYYVYIPL	-0,9
sp|Q7Z412|PEX26_HUMAN	305	19	35	FKKSLLAALILCLLVVRFD	-0,9
sp|P18850|ATF6A_HUMAN	670	19	277	KRRVVCVMIVLAFIILNYG	-0,88
sp|Q9GZX3|CHST6_HUMAN	395	20	367	TAVTALLLAQTFLLLFLVSR	-0,87
sp|Q99999|G3ST1_HUMAN	423	23	389	MAKGLVLGALFTSFLLLVYSYAV	-0,85
sp|Q7Z4T8|GLTL5_HUMAN	443	24	416	AIIQGLFYGSLTFGIWTALLFIYL	-0,85
sp|Q8N1N0|CLC4F_HUMAN	589	25	529	RLVQATPAFMAVTLVFSLVTLFVVV	-0,77
sp|O75072|FKTN_HUMAN	461	22	432	VVLALLTLTSSAFLLFQLYYYK	-0,76
sp|Q9UNA3|A4GCT_HUMAN	340	21	315	LQLSLSVTLLLVCGFLYQFTL	-0,75
sp|Q9Y5Z6|B3GT1_HUMAN	326	22	300	VSCLYVLTVVCWASALWYLSIT	-0,74
sp|Q8NCG5|CHST4_HUMAN	386	21	359	MKLLLFLVSQMAILALFFHMY	-0,72
sp|Q68CJ9|CR3L3_HUMAN	461	20	122	TGTCVAVLLLSFALIILPSI	-0,7
sp|Q9UJ14|GGT7_HUMAN	662	26	530	LTVIVTACLTFATGVTVALVMQIYFG	-0,67
sp|O94766|B3GA3_HUMAN	335	21	310	LKNVFLAYFLVSIAGLLYALV	-0,66
sp|O60243|H6ST1_HUMAN	411	19	375	FVLVVAGSVCFMLILYQYA	-0,66
sp|Q9NZ08|ERAP1_HUMAN	941	26	913	FLPLKWSLATMSFLLSSLLALLTVST	-0,65
sp|Q9H7V2|SYNG1_HUMAN	258	23	54	LGLSVFSMLCCFWPLGIAAFYLS	-0,65
sp|Q96RP7|G3ST4_HUMAN	486	26	451	LRLWGPRSLGVALGVFMTIGFALQLL	-0,64
sp|Q5TAT6|CODA1_HUMAN	717	22	651	CGLLTLALCSLALSLLAHFRTA	-0,62
sp|Q9NY97|B3GN2_HUMAN	397	21	372	RRRIKLLGILMMANVFIYFIM	-0,6
sp|Q70JA7|CHSS3_HUMAN	882	23	854	RRPWMSVALGLVLGFTAASWLIA	-0,57
sp|Q6ZMI3|GLDN_HUMAN	551	31	507	WGLRGALAAVALLSALNAAGTVFALCQWRGL	-0,57
sp|P07099|HYEP_HUMAN	455	21	434	MWLEILLTSVLGFAIYWFISR	-0,55
sp|Q9UM21|MGT4A_HUMAN	535	27	508	MRLRNGTVATALAFITSFLTLSWYTTW	-0,52
sp|O43916|CHST1_HUMAN	411	26	383	CSWKAVLLLALASIAIQYTAIRTFTA	-0,5
sp|Q86Y38|XYLT1_HUMAN	959	29	921	LARRSHSALLAALTVLLLQTLVVWNFSSL	-0,5
sp|Q9BYG0|B3GN5_HUMAN	378	20	346	WQLIIQLFATCFLASLMFFW	-0,47
sp|Q07065|CKAP4_HUMAN	602	25	475	RLGRALNFLFYLALVAAAAFSGWCV	-0,47
sp|Q9BVH7|SIA7E_HUMAN	336	24	310	TLMRHGLAVCLALTTMCTSLLLVY	-0,43
sp|Q4G0N0|GGTA1_HUMAN	100	20	75	KVILSMLVVSTVIIVFWEFI	-0,42
sp|Q9Y661|HS3S4_HUMAN	456	22	403	ARKLLFMCTLSLSVTYLCYSLL	-0,41
sp|Q7Z7M8|B3GN8_HUMAN	397	19	374	KCLLCLSALLTLLGLKVYI	-0,4
sp|Q86VU5|CMTD1_HUMAN	262	29	227	RLSVPAALALGSAALGAAFATGLFLGRRC	-0,39
sp|Q8IZT8|HS3S5_HUMAN	346	25	315	AWLRQKLLVLGSLAVGSLLYLVARV	-0,35
sp|Q99941|ATF6B_HUMAN	703	19	291	NRKVVCIMVFLLFIAFNFG	-0,28
sp|Q9GZS9|CHST5_HUMAN	411	20	361	TVTVLLLAQTTCLLLFIISR	-0,23
sp|Q9BY50|SC11C_HUMAN	192	26	137	LYYQVLNFAMIVSSALMIWKGLIVLT	-0,2
sp|Q3T906|GNPTA_HUMAN	1256	21	1219	RYGLYVCFLGVVVTIVSAFQF	-0,19
sp|Q8N0V5|GNT2A_HUMAN	402	19	376	CLFSASLISALIFVFVYNT	-0,16
sp|Q8NBZ7|UXS1_HUMAN	420	21	385	RRRMKLLLGIALLAYVASVWG	-0,12
sp|A6NLE4|CE050_HUMAN	156	19	104	KQTLLALLILVLYLSTEIW	-0,09
sp|Q8IZS7|CLCL1_HUMAN	167	24	81	FSGTSFVVFSLFLICAMAGDVVYA	-0,07
sp|Q8NAT1|PMGT2_HUMAN	580	23	555	LSAVFNALLVSVLAAVLWKHVRL	-0,06
sp|Q92187|SIA8D_HUMAN	359	19	337	IRKRWTICTISLLLIFYKT	-0,03
sp|P0C7V7|SC11B_HUMAN	166	28	135	WRLYYQVLNFGMIVSSALMIWKGLMVIT	0
sp|Q7LGA3|HS2ST_HUMAN	356	25	329	LLRIMMPPKLQLLAVVAFAVAMLFL	0,01
sp|Q9ULG6|CCPG1_HUMAN	757	24	519	LNKCVILALVIAISMGFGHFYGTI	0,02
sp|Q96EU7|C1GLC_HUMAN	318	23	288	FLKGVMLGSIFCALITMLGHIRI	0,03
sp|Q92478|CLC2B_HUMAN	149	23	121	KKCFIIVGVLITTNIITLIVKLT	0,05
sp|Q6P9A2|GLT18_HUMAN	607	25	574	TLVSTCVILSGMTNIICLLYVGWVT	0,05
sp|O60512|B4GT3_HUMAN	393	29	355	CTLALLVGSQLAVMMYLSLGGFRSLSALF	0,08
sp|Q8IZ52|CHSS2_HUMAN	775	30	741	LLLSVLRPAGPVAVGISLGFTLSLLSVTWV	0,08
sp|Q86WD7|SPA9_HUMAN	417	20	396	ASYLYGVLFAVGLCAPIYCV	0,17
sp|O60507|TPST1_HUMAN	370	20	346	LKQNLLLACLVISSVTVFYL	0,24
sp|Q6UWH4|F198B_HUMAN	519	23	459	LLLGTACAIYLGFLVSQVGRASL	0,35
sp|Q9NNX6|CD209_HUMAN	404	25	346	LAGCLGHGPLVLQLLSFTLLAGLLV	0,38
sp|Q495W5|FUT11_HUMAN	492	20	471	AAGPIRVVLVLLGVLSVCAA	0,46
sp|P28845|DHI1_HUMAN	292	21	269	FMKKYLLPILGLFMAYYYYSA	0,51

<table>
<tr><td>sp|Q96A11|G3ST3_HUMAN</td><td>431</td><td>19</td><td>397</td><td>SRRKILLLVLGCSTVSLLI</td><td>0,54</td></tr>
<tr><td>sp|P08910|ABHD2_HUMAN</td><td>425</td><td>22</td><td>392</td><td>AVFDGVKLAAVAAVLYVIVRCL</td><td>0,57</td></tr>
<tr><td>sp|P67812|SC11A_HUMAN</td><td>179</td><td>26</td><td>136</td><td>LYYQVLNFGMIVSSALMIWKGLMVIT</td><td>0,57</td></tr>
<tr><td>sp|O75356|ENTP5_HUMAN</td><td>428</td><td>20</td><td>407</td><td>ATSWGTVFFMLVVSCVCSAV</td><td>0,59</td></tr>
<tr><td>sp|Q10981|FUT2_HUMAN</td><td>343</td><td>19</td><td>317</td><td>FSFPMAHFILFVFTVSTIF</td><td>0,87</td></tr>
<tr><td>sp|O00468|AGRIN_HUMAN</td><td>2067</td><td>22</td><td>2036</td><td>LRPLLPLLVVAACVLPGAGGTC</td><td>0,97</td></tr>
<tr><td>sp|Q14494|NF2L1_HUMAN</td><td>772</td><td>26</td><td>740</td><td>YLTEGLLQFTILLSLIGVRVDVDTYL</td><td>0,98</td></tr>
<tr><td>sp|Q9UIR0|BTNL2_HUMAN</td><td>455</td><td>21</td><td>431</td><td>FPGYNLSGAVASFLFILLTMK</td><td>1,19</td></tr>
<tr><td>sp|O94905|ERLN2_HUMAN</td><td>339</td><td>20</td><td>316</td><td>LGAVVAVASSFFCASLFSAV</td><td>1,38</td></tr>
<tr><td>sp|Q9NST1|PLPL3_HUMAN</td><td>481</td><td>24</td><td>452</td><td>RGWSLSFAGCGFLGFYHVGATRCL</td><td>1,47</td></tr>
<tr><td>sp|Q96AD5|PLPL2_HUMAN</td><td>504</td><td>24</td><td>474</td><td>TWNISFAGCGFLGVYYVGVASCLR</td><td>1,51</td></tr>
<tr><td>sp|Q6P179|ERAP2_HUMAN</td><td>960</td><td>21</td><td>920</td><td>RGFYCLTAILPQICICSQFSV</td><td>2,19</td></tr>
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