# Supplemental Materials Molecular Biology of the Cell

Dou et al.

## **Supplemental Materials for:**

## Type II transmembrane domain hydrophobicity dictates the cotranslational dependence for inversion

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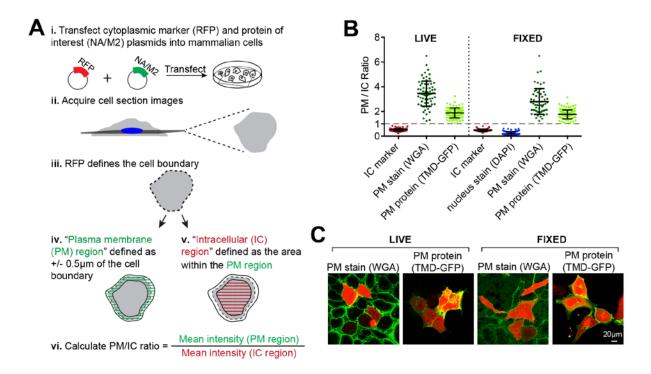
#### Single-cell approach to monitor plasma membrane localization

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  $\geq$  350 um², 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-).

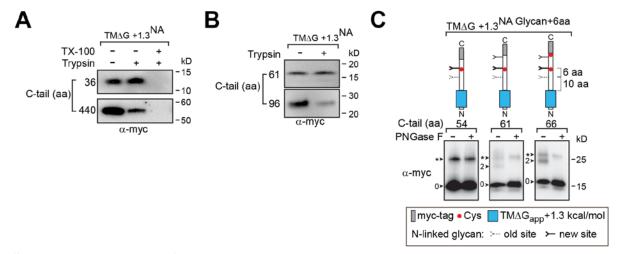
The signal from the RFP and the DAPI stained nucleus were used to determine the threshold IC value, and the signal from wheat germ agglutinin (WGA) and the protein marker TMD-GFP were used to establish the PM values. Analysis of the different cell populations gave average PM/IC ratios of ~0.5 for the 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 Nlinked 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<br>sp Q5VT66 MOSC1_HUMAN            | Protein length<br>337 | TMD length<br>23 | C-tail length<br>293 | TMD sequence WLGVAALGLTAVALGAVAWRRAW                              | -1,04          | Mitochondrial localization           | PubMed reference<br>23086957   |
| sp Q9BV23 ABHD6_HUMAN                          | 337                   | 33               | 296                  | FVIAGGTLAIPILAFVASFLLWPSALIRIYYWY                                 | -1,04          | Predicted mitochondrial localization |                                |
| sp Q68CQ7 GL8D1_HUMAN                          | 371                   | 20               | 349                  | FRKVNIIILVLAVALFLLVL  | -2,64          | Predicted mitochondrial localizatio  |                                |
| 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<br>sp Q9NRQ2 PLS4_HUMAN   | 495<br>329            | 27<br>19         | 468<br>9             | MRLTRCQAALAAAITLNLLVLFYVSWL<br>VKMKAMIFGACFLIDFMYF                | -1,7<br>0,93   | Secreted<br>Soluble                  | 19900540<br>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                  | MVELMFPLLLLLPFLLYMAA  | -1,28          | Nout-Cin orientation                 | 12036956                       |
| sp P49788 TIG1_HUMAN                           | 294                   | 20               | 256                  | RPTAPLLALLLLAPVAAPA   | 0,7            | Nout-Cin orientation                 | 21303978                       |
| sp O75923 DYSF_HUMAN                           | 2080                  | 31               | 13                   | FILWRRFRWAILFILLFILLLFLAIFIYAF                                    | -9,8           |                                      |                                |
| sp Q9HC10 OTOF_HUMAN<br>sp Q9NZM1 MYOF_HUMAN   | 1997<br>2061          | 31<br>31         | 6<br>13              | TYRWLLLKLLLLLLLLLALFLYSVPGYLV FIVWRRFKWVIIGLLFLLILLLFVAVLLYSL     | -7,7<br>-7,32  |                                      |                                |
| sp Q13326 SGCG_HUMAN                           | 291                   | 33               | 228                  | WRKRCLYLFVLLLLIILVVNLALTIWILKVMWF                                 | -7,32<br>-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<br>180            | 31<br>30         | 230<br>132           | WRKRCLYFFVLLLMILILVNLAMTIWILKVM                                   | -5,96<br>-5,84 |                                      |                                |
| sp Q10589 BST2_HUMAN<br>sp P41273 TNFL9_HUMAN  | 180<br>254            | 30<br>32         | 132<br>199           | RCKLLLGIGILVLLIIVILGVPLIIFTIKA<br>CRVLPWALVAGLLLLLLAAACAVFLACPWAV | -5,84<br>-5,68 |                                      |                                |
| sp Q9P126 CLC1B_HUMAN                          | 229                   | 29               | 172                  | WWRVMALILLILCVGMVVGLVALGIWSVM                                     | -5,66          |                                      |                                |
| 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                 | WWKWLLGLLTWLLLLGLLFGLIALA   | -5,41          |                                      |                                |
| sp Q8NHY0 B4GN2_HUMAN<br>sp P21854 CD72_HUMAN  | 566<br>359            | 27<br>29         | 473<br>240           | RFLWLLKILVIILVLGIVGFMFGSMFL TCLRYLLLGLLLTCLLLGVTAICLGVRYL         | -5,37<br>-5,36 |                                      |                                |
| sp O43451 MGA_HUMAN                            | 1857                  | 27               | 1822                 | FTTLEIVLSVLLLVLFIISIVLIVLLA                                       | -5,27          |                                      |                                |
| spiQ9UHP7 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                  | RYFRVILLLLALTLLLLAGFL   | -5,01          |                                      |                                |
| sp D3W0D1 KLRF2_HUMAN                          | 207<br>375            | 30<br>28         | 151<br>345           | LYPQYYCLLLIFGCIVILIFIMTGIDLKFW<br>LLVFVRNLLLALCLFLVLGFLYYSAWKL    | -4,97          |                                      |                                |
| sp Q11203 SIAT6_HUMAN<br>sp Q9UN42 AT1B4_HUMAN | 357                   | 28               | 219                  | LILLIYFFFYASLAAVITLCMYTLFLTI                                      | -4,97<br>-4,83 |                                      |                                |
| spiP23276 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                  | KLVVLGLLAVVLVIVGLCLWL   | -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<br>sp Q8TDX6 CGAT1_HUMAN | 337<br>532            | 31<br>28         | 277<br>497           | LLPLIVTFHLYGGIILLLLIFISIAGILYKF<br>LLAWISRVVVLLVLLCCAISVLYMLACT   | -4,64<br>-4,63 |                                      |                                |
| sp Q6AZY7 SCAR3_HUMAN                          | 606                   | 26               | 526                  | VRILYLFLALLLVAVAVLASLVFRKV  | -4,63          |                                      |                                |
| spiQ96LD1 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<br>sp Q5SRI9 MANEA_HUMAN | 495<br>462            | 25<br>27         | 410<br>432           | AVLGLYLLVFLILVGIFILAVSRPR<br>FRRRTCIILALFILFIFSLMMGLKMLR          | -4,38<br>-4,37 |                                      |                                |
| sp Q5SRI9 MANEA_HUMAN<br>sp Q9NRB3 CHSTC_HUMAN | 462<br>414            | 26               | 432<br>385           | ARLFRLWLVLGSVFMILLIIVYWDSA  | -4,37<br>-4,33 |                                      |                                |
| sp Q9UKU6 TRHDE_HUMAN                          | 1024                  | 27               | 959                  | RLVLAFAVSLVALLAVTMLAVLLSLRF                                       | -4,32          |                                      |                                |
| sp P61647 SIA8F_HUMAN                          | 398                   | 20               | 373                  | ALLALLASLLLLLLRLLWC   | -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                  | RALGAAALLLLLLLGFLLFGGDL   | -4,22          |                                      |                                |
| sp Q9BYE2 TMPSD_HUMAN<br>sp P14415 AT1B2 HUMAN | 581<br>200            | 24               | 397                  | LPLIGCVLLLIALVVSLIILFQFW  | -4,2<br>-4.18  |                                      |                                |
| spiP14415jA11B2_HUMAN<br>spiP42658jDPP6_HUMAN  | 290<br>865            | 29<br>26         | 227<br>747           | TSWAFILLFYLVFYGFLTAMFTLTMWVML<br>WKGIAIALLVILVICSLIVTSVILLT       | -4,18<br>-4,18 |                                      |                                |
| sp O96024 B3GT4_HUMAN                          | 378                   | 22               | 354                  | LRLFRRLLLAALLLVIVWTLFG  | -4,16          |                                      |                                |
| 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<br>sp Q9UKM7 MA1B1_HUMAN | 882<br>699            | 24<br>28         | 841<br>594           | AVLFLLFIFCLFSVFISAYYLYGW<br>LSRLQRNMILFLLAFLLFCGLLFYINLA          | -4,09<br>-4,07 |                                      |                                |
| sp Q9UKM/ MA1B1_HUMAN<br>sp P37059 DHB2_HUMAN  | 387                   | 28               | 326                  | LWSWMVCLAGLCAVCLLILSPFWGLILF                                      | -4,07<br>-4,06 |                                      |                                |
| sp Q9UQ53 MGT4B_HUMAN                          | 548                   | 28               | 520                  | MRLRNGTFLTLLLFCLCAFLSLSWYAAL                                      | -4,08          |                                      |                                |
| 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<br>630            | 30               | 375<br>420           | WPLWTTIFIFLGVAAILGVTIGLLVHFLAV                                    | -3,99<br>-3.95 |                                      |                                |
| sp P08195 4F2_HUMAN<br>sp P98073 ENTK_HUMAN    | 630<br>1019           | 33<br>25         | 420<br>976           | WVRTRWALLLLFWLGWLGMLAGAVVIIVRAPRO<br>IMFAALFAILVVLCAGLIAVSCLTI    | -3,95<br>-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          |                                      |                                |
|  |                       |                  |                      |   |                |                                      |                                |

| ## WORDSTRIPS - HANN ## 420 ## 27 ## 20 ## | sp Q5VSG8 MANEL_HUMAN                 | 457 | 27 | 428 | RRRRACIALFLVLLFAFGTLMGLRTL        | -3,88 |
|--|---------------------------------------|-----|----|-----|-----------------------------------|-------|
| SQUEEZISTIC   HANN   | sp Q9UL52 TM11E_HUMAN                 | 423 |    | 378 | WVIGLVIFISLIVLAVCIGLTVHYVRY       | -3,88 |
| SCIONAPPENDER   MINOR   100   20   20   20   20   20   20   2  |                                       |     |    |     |                                   |       |
| SCHOOLED   FUNDAM   102  | sp Q9H4F1 SIA7D_HUMAN                 | 302 | 33 | 264 | RLVLIILCSVVFSAVYILLCCWAGLPLCLATCL | -3,86 |
| SIGNERSPET   MINN  |                                       |     |    |     |                                   |       |
| SIGNERSHIPPS   HANN  | sp Q9H3R1 NDST4_HUMAN                 | 872 | 28 | 838 | LRRSFRTLIVLLATFCLVSIVISAYFLY      | -3,83 |
| SCIENCESTEEL   HAMM  |                                       |     |    |     |                                   |       |
| ### STATE   ST | sp Q9H0X4 ITFG3_HUMAN                 | 552 | 27 | 480 | RCRAAAFFLSLFLCLFVVFVVSFVIPC       | -3,73 |
| SCORDSPINATE   HUMAN   |                                       |     |    |     |                                   |       |
| GODEPHE   CASE   HUMAN   433   28   388   RRAGER PE INVOLVINIVAPINES   -3,64   | sp O60476 MA1A2_HUMAN                 |     |    |     |                                   |       |
| GODGESTING HAMN   20   |                                       |     |    |     |                                   |       |
| GOODES   GENERAL   JUNIAN   195   25   134   CEMANGEL TAVELS (CHAPTER   3.02   105   |                                       |     |    |     | LRVWFLSVAFLLVFIMSLLFTYS           |       |
| SEGORATION   STATE     |                                       |     |    |     |                                   |       |
| ## SQUANDERCH JERUMN 276 28 28 211 MORPHAGENT CAMER. 3.01   ## SQUANDERCH JERUMN 279 32   ## SQUANDERCH JERUMN 378 28   ## SQUANDERCH JERUMN 374 24   ## SQUANDERCH JERUMN 374 25   ## SQUANDERCH JERUMN 374 26   ## SQU |                                       |     |    |     | MWLGRRALCALVLLLACASLGLLYASTR      |       |
| ### ### ### ### ### ### ### ### ### ##   |                                       |     |    |     |                                   |       |
| SOCIATION  FILMAN   750   25   707   |                                       |     |    |     |                                   |       |
| Sephential Princip   Human   291   30   228   ISSNW/WISLY/WAPV/WINGER/ALVICLE/LIPEN   3.55    |                                       |     |    |     |                                   |       |
| SQGMNSGCGATZ_HUMAN   |                                       |     |    |     |                                   |       |
| SQIGNEST_HAMAN   S90   22   606   CRICFILLUM_GCYUMMAM,   3.55  |                                       |     |    |     |                                   |       |
| SOGEOSCHPTER, HUMAN   500   28   470   FLAVILAGENIA, FLAVICIA, SOCIEDATION   3.54   2.57      |                                       |     |    |     |                                   |       |
| ### SQUAYSTRANDS JULYAN ### SQ | sp O95502 NPTXR_HUMAN                 |     |    |     |                                   |       |
| SQUAYETALCE_HUMAN   324   29   292   LLIQAM_GRAQAAALVUSINAFTTAT   -3.53  |                                       |     |    |     |                                   |       |
| September   Sept   | sp Q9Y673 ALG5_HUMAN                  | 324 | 29 | 292 | LLLQLAVLGAALAAALVLISIVAFTTAT      | -3,53 |
| SPP380FCD39 HUMAN  |                                       |     |    |     |                                   |       |
| SQCORDINGENERAL   HUMAN   340   25   307   LIMAMPELLILICONSILLEFOURITY   -3.44   | sp P28907 CD38_HUMAN                  | 300 | 24 | 253 | LCLGVSILVLILVVVLAVVVPRWR          | -3,46 |
| SOIGNESPHI   |                                       |     |    |     |                                   |       |
| Sep-2857  TINELE   HUMAN   | sp Q86W10 CP4Z1_HUMAN                 |     | 25 |     |                                   |       |
| September   Sept   |                                       |     |    |     |                                   |       |
| SpiPost3/ifCER2_HUMAN   321   30   276   RCCRRGTONLIGLYTALWAGILYA   3.37   35   SpiCo86AgilRCES9_HUMAN   307   27   36   WAVKILLILLIEGVAGGLVACKYTEL   3.34   30   32   21   FLYPPWICLAATI, GULL, GLVYTMIN, GMOL   3.34   33   32   22   SpiPyWICLAATI, GULL, GLVYTMIN, GMOL   3.34   33   32   22   SpiPyWICLAATI, GULL, GLVYTMIN, GMOL   3.34   33   35   35   WAVKILLILLIEGVAGGLVACKYTEL   3.33   35   35   WAVKILLILLIEGVAGGLVACKYTEL   3.33   35   35   WAVKILLILLIEGVAGGLVACKYTEL   3.35   33   35   35   WAVKILLILLIEGVAGGLVACKYTEL   3.35   33   35   WAVKILLIELLIEGVAGGLVACKYTEL   3.35   33   35   WAVKILLIELLIEGVAGGLVACKYTEL   3.35   WAVKILLIELLIEGVAGGLVACKYTEL   3.35   WAVKILLIEGVAGGLVACKYTEL   3.35   WAVKILLIEGVAGGLVACKYTEL   3.35   WAVKILLIEGVAGGLVACKYTEL   3.35   WAVKILLIEGVAGGLVACKYTEL   3.35   WAVKILLIEGVAGGLVACKYTEL   3.36   WAVKILLIEGVAGGLVACKYTEL   3.36   WAVKILLIEGVAGGLVACKYTEL   3.36   WAVKILLIEGVAGGLVACKYTEL   3.36   WAVKILLIEGVAGGLVACKYTEL   3.36   WAVKILLIEGVAGGLVACKYTEL   3.36   WAVKILLIEGVAGGLVACKYTEL   3.37   WAVKILLIEGVAGGLVACKYTEL   3.37   WAVKILLIEGVAGGLVACKYTEL   3.38   WAVKILLIEGVAGGLVACKYTEL   3.32   WAVKILLIEGVAGGLVACKYTEL   3.3   |                                       |     |    |     |                                   |       |
| ### SPORTSHIMMEL   HUMAN   779   25   731   FLEGGILLILLYTALVALGULYA   3,37   ### SPORTSHIMMEN   737   32   213   FLYSPYWICLANTLGVLGLUYTAM   3,34   ### SPORTSHIP   HUMAN   273   32   213   FLYSPYWICLANTLGVLGLUYTAM   3,34   ### SPORTSHIP   HUMAN   233   27   240   WSRRFIP FLAURIUTY   WSRRFIP   START   S |                                       |     |    |     |                                   |       |
| SipPrassion_CRT_HUMAN         273         32         213         FLYSFWICLARATLOVICLG_CIVTINVLGMOL         3,34           SipPoso26paTrib_HUMAN         293         27         240         WSRRPELRALAVLYTTVLWAVILSILL         -3,33           SipPoso26paTrib_HUMAN         293         27         240         WSRRPERLALAVLYTTVLWAVILSILL         -3,31           SipPoso26paTrib_HUMAN         584         30         457         LMTLTEPVRLLVAAAMILLAVVILS (GLALAVIVLSVS         -3,31           SipComposition_FL_HUMAN         374         26         338         MUMRCHAGLELARICA         -3,28           SipComposition_FL_HUMAN         390         25         348         RRIVLGARLVACICLEPALVLLARICA         -3,28           SipComposition_FL_HUMAN         241         29         197         FIFT FOCPARAMGIRFIBMYARIVSAVIL         -3,27           SipPosition_FL_HUMAN         210         27         187         FIFT CORPAMORIPRIBMYARIVSAVIL         -2,52           SipPosition_FL_HUMAN         25         30         668         RWTPLESIS.SIV.LULTHAVITMALYATY         -2,22           SipOreasitivite_HUMAN         30         23         344         LKORVVLLARILAVITOLOVIC -3,22         -2,23           SipOreasitivite_HUMAN         30         26         RWTPLESIS.SIV.LULTHAVITMALYATY <td< td=""><td></td><td></td><td></td><td></td><td></td><td></td></td<>  |                                       |     |    |     |                                   |       |
| SpiPoSogiaTriBI_HUMAN   303   30   242   WFIKILETVIFYGCIAGFIERTOLVMLTIT   3.33     SpiPoSogiaGTE   HUMAN   293   27   240   WSRRPLFALAVITYTUMAVISI   3.31     SpiPoSogiaGTE   HUMAN   586   31   555   MARGYGATVSLVLI.GI.GI.AAVIULAVUS.R   3.31     SpiPoSogiaGTE   HUMAN   534   30   457   MARGYGATVSLVLI.GI.GI.AAVIULAVUS.R   3.31     SpiPoSogiaGTE   HUMAN   374   26   338   WLWBRCI.AGULFQLLVAVICEFSYIRV   3.28     SpiPoSogiaTriPC   HUMAN   374   26   338   WLWBRCI.AGULFQLLVAVICEFSYIRV   3.28     SpiPoSogiaTriPC   HUMAN   244   29   197   LILLAVIGATSLVTLLAVIPTIVALVALU   3.27     SpiPoSogiaTriPC   HUMAN   216   27   137   FFFCCPLAVMARIFERIMAVINSAVIL   3.26     SpiPoSogiaTriPC   HUMAN   775   26   680   VCLI.SQLYPAGCI.CALAMALAKIL   3.25     SpiPoSogiaTriPC   HUMAN   45   20   432   MARGYGATSLVTLLAVIPTIVALVALU   3.27     SpiPoSogiaTriPC   HUMAN   45   20   432   MARGYGATSLVTLLAVIPTIVALVALU   3.25     SpiPoSogiaTriPC   HUMAN   45   20   432   MARGYGATSLVTLLAVIPTIVALVALU   3.25     SpiPoSogiaTriPC   HUMAN   45   20   432   MARGYGATSLVTLLAVIPTIVALVALU   3.25     SpiPoSogiaTriPC   HUMAN   400   20   432   MARGYGATSLVTLLAVIPTIVALVALU   3.20     SpiPoSogiaTriPC   HUMAN   400   20   432   MARGYGATSLVTLLAVIPTIVALU   3.20     SpiPoSogiaTriPC   HUMAN   400   20   433   MARGYGATSLVTLLAVIPTIVALVALU   3.20     SpiPoSogiaTriPC   HUMAN   400   20   432   MARGYGATSLVTLLAVIPTIVALVALU   3.20     SpiPoSogiaTriPC   HUMAN   400   20   433   MARGYGATSLVTLLAVIPTIVALVALU   3.20     SpiPoSogiaTriPC   HUMAN   400   20   433   MARGYGATSLVTLLAVIPTIVALVALU   3.20     SpiPoSogiaTriPC   HUMAN   400   20   400   MARGYGATSLVTLLAVIPTIVALVALU   3.20     SpiPoSogiaTriPC   HUMAN   400   20   400   MARGYGATSLVTLLAVIPTIVALVALU   3.10     SpiPoSogiaTriPC   HUMAN   400   20   400   MARGYGATSLVTLLAVIPTIVALVALU   3.11     SpiPoSogiaTriPC   HUMAN   400   400   MARGYGATSLVTLLAVIPTIVALVALU   400   MARGYGATSLVTLLAVIPTIVALVALU   400   MARGYGATSLVTLLAVIPTIVALVALU   400   MARGYGATSLVTLLAVIPTIVALVALU   400   MARGYGATSLVTLAVIPTIVALVALU   400   MARGYGATSLVTLAVIPTIVALVALU    |                                       |     |    |     |                                   |       |
| SpiGEUKRICILOG HUMAN   |                                       |     |    |     |                                   |       |
| Spicestary   Figure   State    | sp Q6UXB4 CLC4G_HUMAN                 |     |    |     | WSRRPLFLALAVLVTTVLWAVILSILL       | -3,31 |
| Signature   Sign   |                                       |     |    |     |                                   |       |
| Spicoge-843 TINFC_HUMAN   244   29   | sp Q11128 FUT5_HUMAN                  | 374 | 26 | 338 | WLWRRCLAGLLFQLLVAVCFFSYLRV        | -3,28 |
| Spipe2f7is NKC2D_HUMAN   216   27   137   FFFCCFIAVMAIGRINA/MINSAVFL   3.26   3.26   3.29   3.26   3.27   3.27   3.27   3.27   3.27   3.28     |                                       |     |    |     |                                   |       |
| SpiPadziafria.PezB. Human  | sp P26718 NKG2D_HUMAN                 | 216 | 27 | 137 | FFFCCFIAVAMGIRFIIMVAIWSAVFL       | -3,26 |
| Spinoration      |                                       |     |    |     |                                   |       |
| Spi075063 XYIL HUMAN   409   23   384  | sp P08473 NEP_HUMAN                   | 750 | 30 | 698 | RWTPLEISLSVLVLLLTIIAVTMIALYATY    | -3,22 |
| Spicitification   Spicitific   |                                       |     |    |     |                                   |       |
| Spicon   S   |                                       |     |    |     | LLGSRTLLFIFICAFALVTLLQQILY        |       |
| Spice     |                                       |     |    |     |                                   |       |
| Description  |                                       |     |    |     |                                   |       |
| Spin      |                                       |     |    |     |                                   |       |
|  |                                       |     |    |     |                                   |       |
| spipolyutricloak_human         328         28         260         TVRAALICITULVLASVLLOAVLYPRFM         -2,96           spipolyszosiastafilman         391         26         326         CLIFLGFFGLSLALHLLTLCCYLELR         -2,96           spipolyszosiastafilman         310         23         282         MRLMYICLULVLAQUACYYSV         -2,91           spipolstafilman         714         24         634         LLGSAVLGLLLVLAVAWCYYSV         -2,91           spipolstafilman         714         24         634         LLGSAVLGLLVLAAVAWCYYSV         -2,91           spipolstafilman         714         24         634         LLGSAVLGLLVLAAVAWCYYSV         -2,91           spipolstafilman         714         28         182         ACCLVMVISCVFCMGLITASIFLGVKLL         -2,9           spipolstafilman         72         29         336         TLEYDIKTLGLIATGMFOFW         -2,85           spipol331saBC_HUMAN         380         28         347         MARYASVLGLVMLSVALLILISLISVVSL         -2,85           spipo2786ITFRI HUMAN         422         22         379         LFRTHLIGVISLVFLFAMFLF         -2,81           spipo38WSIGLCAD HUMAN         429         24         671         LCYGTAWINVFILLILALISLISVVCY         -2,21           spipo38WSIGLCAD HU   | sp Q8IUN9 CLC10_HUMAN                 |     |    |     |                                   |       |
| Sping2838 EDA_HUMAN   391   26   326   CLIFLGFFGLSLAHLLTLCCYLELR   2,96     Sping3Y2C3 B3GT5_HUMAN   310   23   282   MRIMYICLLVLGALCLYFSMYSL   2,91     Sping3Y2C3 B3GT5_HUMAN   714   24   634   LLGSAVIGLLLVLAAVVAWCYYSV   2,91     Sping3X15 INFA_HUMAN   233   24   182   RRCLFLSLFSFLIVAGATTLFCLL   2,9     Sping3X15 INFA_HUMAN   231   24   28   RRCLFLSLFSFLIVAGATTLFCLL   2,9     Sping3X15 INFA_HUMAN   231   24   28   RRCLFLSLFSFLIVAGATTLFCLL   2,9     Sping3X15 INFA_HUMAN   372   29   336   TLERVCKAVLLLCLLHFLVAVILYFDVYA   2,87     Sping3X15 IAGS_HUMAN   718   24   672   RIYYITLFSIVLLGLIATGMFQFW   2,85     Sping3X15 ISAGS_HUMAN   300   28   347   MARVASVLGLVMLSVALLILSLLSVYSL   2,84     Sping3X15 ISAGS_HUMAN   209   33   162   WLSLRLWSVAGISIALLSACFIVSCVYTYHFTY   2,82     Sping3X15 ISAGS_HUMAN   422   22   379   LFRTHLIGVLSLVFLFAMFLFF   2,81     Sping3X15 ISAGS_HUMAN   425   25   173   LIPSVAVVELLLSVGFIASCLVT   2,77     Sping3X15 ISAGS_HUMAN   215   25   173   LIPSVAVVFLLLSVGFIASCLVT   2,77     Sping3X15 ISAGS_HUMAN   361   24   325   WRRCLAALLFOLLVAVCFFSYLRV   2,76     Sping3V15 ICAGB_HUMAN   361   24   325   WRRCLAALLFOLLVAVCFFSYLRV   2,75     Sping3V15 ISAGS_HUMAN   363   27   860   LELVLAGASLLAALLLEGLVALGVY   2,73     Sping3X15 ISAGS_HUMAN   323   26   294   ALFTFFTMIVPHLYRIVENIVALLLEV   2,73     Sping3X15 ISAGS_HUMAN   325   28   280   FITSTAILPLLFGUSFFFTLF   2,67     Sping3X15 ISAGS_HUMAN   326   28   280   FITSTAILPLLFGUSFFTLFLHTSL   2,67     Sping3X15 ISAGS_HUMAN   327   26   751   LIVLFFRHEYULGINIBLUTY   2,67     Sping3X15 ISAGS_HUMAN   329   24   658   ARVILLYALITYSAVAVIVEDLY   2,67     Sping3X15 ISAGS_HUMAN   329   24   658   ARVILLYALITYSVAVIVEDLY   2,67     Sping3X15 ISAGS_HUMAN   329   26   751   LIVLFFRHEYULGINGFFTLCFLMTSL   2,67     Sping3X15 ISAGS_HUMAN   329   26   751   LIVLFFRHEYULGINGFFTLCFLMTSL   2,67     Sping3X15 ISAGS_HUMAN   329   24   658   ARVILLYALITYSVAVIVEDLY   2,67     Sping3X15 ISAGS_HUMAN   321   22   230   RILLLSLG_ISLLLLVVCVIGS   2,66     Sping3X15 ISAGS_HUMAN   340   29   905     |                                       |     |    |     |                                   |       |
| spions/signt161_Human         714         24         634         LLGSAVLGLLLVLAAVVAWCYYSV         2.91           spi01375 TNFA_Human         233         24         182         RRCLFLSLFSFLIVAGATTLFCLL         -2.9           spi060VNB(CLO9A_HUMAN         241         28         182         ACCLVMVISCVFCMGLLTASIFLGVKLL         -2.89           spi0600909B4GT2_HUMAN         372         29         336         TLERVCK4VLLLCLHFLVAVILYPDVYA         -2.87           spi043173 SIA8C_HUMAN         380         28         347         MARVASVLGLVMLSVALILSLISYVSL         -2.84           spi043825 B3GT2_HUMAN         209         33         162         WLSIALWSVAGISIALLSACFIVSCVVTYHFTY         -2.82           spi063825 B3GT2_HUMAN         209         33         162         WLSIALWSVAGISIALLSACFIVSCVVTYHFTY         -2.81           spi063825 B3GT2_HUMAN         42         22         379         LFITHLIGYLSLVFLFAMFLF         -2.81           spi08W18 CLC4D_HUMAN         215         25         173         LIPSVIAVVFILLSVCFIASCLYT         -2.77           spi09T1217 FUT3_HUMAN         361         24         325         WRRCLAALLFOLLVAVCFFSYLRV         -2.75           spi02W145 CLC4E_HUMAN         219         29         170         MFLWAYSGPITHACHUMAN         24  | sp Q92838 EDA_HUMAN                   | 391 | 26 | 326 | CLLFLGFFGLSLALHLLTLCCYLELR        | -2,96 |
| spiP01375 TNFA_HUMAN         233         24         182         RRCLFLSLFSFLIVAGATTLFCLL         -2,9           spiQ6UXN8 CLC9A_HUMAN         241         28         182         ACCLVMVISCVFCMGLLTASIFLGVKLL         -2,89           spiQ600909 B4GT2_HUMAN         372         29         336         TLFRVCKAVLLLCLIHFLVAVILYFDVVA         -2,87           spiQ33173 SIA8C_HUMAN         718         24         672         RIYVITLFSIVLLGLIATGMF0FW         -2,85           spiQ43173 SIA8C_HUMAN         380         28         347         MARVASVLGUMLSVLGUAVLLILSLISYVSL         -2,84           spiQ6EIGT/CLC6A_HUMAN         209         33         162         WLSIRLWSVAGISIALLSACFIVSCVVTYHFTY         -2,82           spiQ6EIGT/ERT_HUMAN         422         22         379         LFRTHLIGVELYFLFAMFLFF         -2,81           spiQ3BWXI8]CLC4D_HUMAN         215         25         173         LIPSVIAVVFILLLSVCFIASCLVT         -2,77           spiQ3BWXI8]CLC4B_HUMAN         199         24         135         VLCAVMNVVFITHLIALLASVG         -2,76           spiP21217[FIPT3 HUMAN         361         24         325         WRGALALLFOLLVAVCFFSYLRV         -2,76           spiP21217[FIPT3 HUMAN         83         27         680         LELVLAGASLLHALLGCLVALGVQT         -2,73   |                                       |     |    |     |                                   |       |
| sp)C6909(B)BGTZ_HUMAN         372         29         336         TLERVCKAYLLCLLHFLVAVILYFDVYA         -2,87           sp)Q39363 EXTZ_HUMAN         718         24         672         RIYYITLSIVLLGLIATGMFQFW         -2,85           sp)Q3373 SABC_HUMAN         380         28         347         MARVASVLGLVMLSVALILISLISYVSL         -2,84           sp)Q643173 SABC_HUMAN         209         33         162         WLSLRLWSVAGISIALLSACFIVSCVVTYHFTY         -2,84           sp)Q43825 B3GT2_HUMAN         422         22         379         LFRTHLIGVLSLVFLFAMFLFF         -2,81           sp)P02786 TFR1_HUMAN         760         24         671         ICYGTIAVIVFFLIGFMIGYLGYC         -2,81           sp)Q97108 CD69_HUMAN         215         25         173         LIPSVIAVVFILLLSVCFIASCLVT         -2,76           sp)Q91178 CLC4E_HUMAN         361         24         325         WRCLAALLFQLVACVFFSYLRV         -2,75           sp)Q981LY5 CLC4E_HUMAN         383         27         680         LELVLGAGSLLLAALLGCLVALGYOY         -2,73           sp)Q981LY5 CLC4E_HUMAN         383         27         680         LEVLGAGSLLLAALLGCLVALGYOY         -2,73           sp)Q981LY5 CLC4E_HUMAN         323         26         294         ALFTREFILLPWILLVIIMILDYDTRR         -2,72   | sp P01375 TNFA_HUMAN                  | 233 | 24 | 182 | RRCLFLSLFSFLIVAGATTLFCLL          | -2,9  |
| Sp Q93063 EXT2_FUMAN         718         24         672         RIYYITLFSIVLLGILATGMFQFW         -2,85           Sp Q08167 CLGA_HUMAN         380         28         347         MARVASVLGUMLSVAGIALISLISYVSL         -2,84           Sp Q08167 CLGA_HUMAN         209         33         162         WLSRLWSVAGISIALISAGFIVSCVVTYHFTY         -2,82           Sp Q04788 ERT1_HUMAN         422         22         379         LFRTHLIGVLSLVFLAMFLEF         -2,81           Sp Q08788 ECLGA_HUMAN         760         24         671         ICYGTIAVIVFILLISVCFIASCLVT         -2,77           Sp Q08788 CLGA_HUMAN         215         25         173         LIPSVIAVVFILLISVCFIASCLVT         -2,77           Sp Q08718 CLCAB_HUMAN         199         24         135         VLCAVIMIVYFIILIALISVG         -2,76           Sp Q381CC4E_HUMAN         361         24         325         WRRCLAALLFQLLVAVCFFSVLRV         -2,75           Sp Q39N25 BGGP4HTM_HUMAN         502         28         420         ICSRAFLLLARILLIGUAVCFFSVLRV         -2,73           Sp Q39N25 B3G3C2_HUMAN         323         26         294         ALFTRFFILLPWILIVIIMLDVDTRR         -2,72           Sp Q39N25 B3G7S2_HUMAN         325         28         220         ICSRAFLLYARIVAVAVIVITUTOVAR         -2,67 </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>  |                                       |     |    |     |                                   |       |
| Sp OGEIG7[CLCGA_HUMAN         209         33         162         WLSLR_WSAGISIALLSACFIVSCVVTYHFTY         -2,82           Sp O43825 B3GT2_HUMAN         422         22         379         LFRTHLIGVLSLVFLFAMFLFF         -2,81           Sp O2786]FFR1_HUMAN         760         24         671         ICYGTIAVIVFFLIGFMIGYLGYC         -2,81           Sp O27108 CD69_HUMAN         215         25         173         LIPSVIAVVFIILLISVGFIASGLVT         -2,76           Sp O21717 FUT3_HUMAN         361         24         325         WRRCLAALLFQLLVAVCFFSYLRV         -2,75           Sp O2034 ECE2_HUMAN         361         24         325         WRRCLAALLFQLLVAVCFFSYLRV         -2,75           Sp O3034 ECE2_HUMAN         383         27         680         LELVLAGASLLLAGLLGCVALGVQY         -2,73           Sp O304PEGEP_HUMAN         302         28         420         ICSRAYFLVLMVFVHLYLGNVLALLFV         -2,73           Sp O3NPZ5 B3GA2_HUMAN         323         26         294         ALFTRFFILLPWILLWIIMLDVDTRR         -2,27           Sp O3NPZ5 B3GA2_HUMAN         323         26         294         ALFTRFFILLPWILLWIIMLDVDTRR         -2,27           Sp O3NPZ5 B3GA2_HUMAN         792         26         751         LVTLRPFRLPVLGIGFFTLCFLMTSL         -2,67   | sp Q93063 EXT2_HUMAN                  | 718 | 24 | 672 | RIYYITLFSIVLLGLIATGMFQFW          | -2,85 |
| spj0a3825jB3GTZ_HUMAN         422         22         379         LFRTHLIGVLSLVFLFAMFLEF         -2,81           spjP02786jTFR1_HUMAN         760         24         671         ICYGTIAVIVFFLIGFMIGYLGYC         -2,81           spjQgWXI8jCLC4D_HUMAN         215         25         173         LIPSVIAVVFILLLSVCFIASCLVT         -2,77           spjQ301718jCLG6B_HUMAN         199         24         135         VLCAVMNVVFIILIALIALSVG         -2,75           spjP21217jFUT3_HUMAN         361         24         325         WRRCLAALLFQLLVAVCFFSYLRV         -2,75           spjQ3UY5jCLC4E_HUMAN         219         29         170         MFLWTVAGIPILFSACFITRCVVTFRIF         -2,74           spjQ3U4EjCE2_HUMAN         883         27         680         LELVLAGASILLAALLLGCLVALGVQY         -2,73           spjQ3MPZ5jB3GA2_HUMAN         323         26         294         ALFTRFILLFOCLGVFGLFRLLQWVR         -2,72           spjQ3MSL5jMGT5B_HUMAN         325         28         280         FITSTAILPLIFGGCGYFGLFRLLQWVR         -2,72           spjQ3MSL5jMGT5B_HUMAN         792         26         751         LYTLRPFRLFGCLGFFTLCFLMTSL         -2,67           spjQ3MSL5jMGT5B_HUMAN         729         24         658         AAWLLVIALITWSAVAIVMFDLV         -2,67   |                                       |     |    |     |                                   |       |
| Sp QBWXIB CLCAD_HUMAN         215         25         173         LIPSVIAVYFILLISVCFIASCLYT         -2,77           sp Q07108 CD69_HUMAN         199         24         135         VLCAVMNVVFITILIALIALSVG         -2,76           sp P21217 FUT3_HUMAN         361         24         325         WRRCLAALLFQLLVAVCFFSYLRV         -2,75           sp QBQILY5 CLC4E_HUMAN         219         29         170         MFLWTVAGPIPLESACFITRCVVTFRIF         -2,74           sp QS034 ECE2_HUMAN         883         27         680         LELVLAGASLLLAALLGCLVALGVQY         -2,73           sp QSNPZ5 B3GA2_HUMAN         323         26         294         ALFTRFFILLPWILWIMLDVDTRR         -2,73           sp QGANDIDRS7B_HUMAN         323         26         294         ALFTRFFILLPWILWIMLDVDTRR         -2,72           sp Q3NPZ5 B3GA2_HUMAN         323         26         294         ALFTRFFILLPWILWIMLDVDTRR         -2,72           sp Q3NPZ5 B3GA5_HUMAN         325         28         280         FITSTALPLYFGCLGYFGLFRLLQWVR         -2,7           sp Q3NUM4 T106B_HUMAN         792         26         751         LVTLRPFILLPWILWIMLDVDTRR         -2,67           sp Q3NUM4 T106B_HUMAN         274         25         157         RTKLYYMASYVCLLLSGLSLLLLY         -2,67      <   |                                       |     |    |     |                                   |       |
| sp]007108 CD69_HUMAN         199         24         135         VLCAVMNVYFITILIIALIALSVG         -2,76           sp P21217 FUT3_HUMAN         361         24         325         WRRCLAALLFQLLVAVCFFSYLRV         -2,75           sp QSULYS CLC4E_HUMAN         219         29         170         MFLWTVAGIPILE-ISACFITRCVVTFRIF         -2,74           sp QS0NSG P4HTM_HUMAN         883         27         680         LELVLAGASILLAALLLGCUVALGVQY         -2,73           sp QS0NSG P4HTM_HUMAN         502         28         420         ISRAFFLVLMIVPVHYLYGNVLALLEFV         -2,73           sp QSNPZS B3GA2_HUMAN         323         26         294         ALFTRFFILLPWILIVIIMLDVDTRR         -2,72           sp QSNSL5 MGTSB_HUMAN         325         28         280         FITSTAILPLFIGCLGYFGLFRILQWVR         -2,72           sp QSNUM4 T106B_HUMAN         792         26         751         LYTLRPFRLFVLGIGFTLCFLMTSL         -2,67           sp Q3V5L5 MGTSB_HUMAN         729         24         658         AAWILLVIALITWSAVFVCLLLSGLAVFFLF         -2,67           sp Q3V5L5 MGTSB_HUMAN         729         24         658         AAWILLVIALITWSAVAIVMFDLV         -2,65           sp Q3F6KP1 B4GN4_HUMAN         1039         19         1008         MKLLLLLLSCAWLTYV         -2,65  |                                       |     |    |     |                                   |       |
| SP QSULYS CLC4E + HUMAN         219         29         170         MFLWTVAGIPILFLSACFITRCVVTFRIF         -2,74           Sp QS0344 ECE2 + HUMAN         883         27         680         LELVLAGASLLIAALLLGCLVALGVQY         -2,73           Sp QS0NXG6 P4HTM, HUMAN         502         28         420         ICSRAYFLVLMVFVHYLGNVLALLLFV         -2,73           Sp QS0NPZ5 B3GA2 + HUMAN         323         26         294         ALFTRFILLPWILIVIIMLDVDTRR         -2,72           Sp QG1AN0 DRS7B_HUMAN         325         28         280         FITSTAILPLLFGCLGVFGLFRLLQWVR         -2,7           Sp QSV5L5 MGT5B_HUMAN         792         26         751         LVTLRPFRLFVLGIGFFTLCFLMTSL         -2,67           Sp Q3NUM4 T106B_HUMAN         274         25         157         RTKLYYMASVFVCLLLSGLAVFFLF         -2,67           Sp Q39C1ALT9_HUMAN         729         24         658         AAWLVIALITWASVFVCLLLSGLAVFFLF         -2,67           Sp Q36CALT9_HUMAN         603         24         573         IRTLLTVNILVFVGIVLFSVYCRL         -2,65           Sp Q36KAPT_HUMAN         1039         19         1008         MKLLLLLLSCASULTYV         -2,64           Sp Q36ASGR1_HUMAN         291         22         230         RILLSGLSLLLLVVCVIGS         -2,62   |                                       |     |    |     |                                   |       |
| Sp C60344 ECE2_HUMAN         883         27         680         LELVLAGASLLLAALLLGCUALGVQY         -2,73           Sp C9NXG6 P4HTM_HUMAN         502         28         420         ICSRAYFLVLMVFVHLYLGNVLALLLFV         -2,73           Sp C9NXG6 P4HTM_HUMAN         323         26         294         ALFTRFFILLPWILIMIMLDVDTRR         -2,72           Sp C6IAN0 DRS7B_HUMAN         325         28         280         FITSTAILPLLFGCLGVFGLFRLLQWVR         -2,7           Sp C9SV5L5 MGT5B_HUMAN         792         26         751         LVTLRPFRLFVLGIGFFTLCFLMTSL         -2,67           Sp C9SV5L5 MGT5B_HUMAN         792         26         751         LVTLRPFRLFVLGIGFFTLCFLMTSL         -2,67           Sp C91013061 TRDN_HUMAN         729         24         658         AAWLLVIALLITWASVFVCLLLSGLAVFFLF         -2,67           Sp C9104C05 GALT9_HUMAN         603         24         573         IRTLLTVNILVFVGIVLFSVYCRL         -2,65           Sp C946CS HBGAVA_HUMAN         1039         19         1008         MKLLLLLLSVCSVLFSVYCRL         -2,64           Sp C975TSP BGAVA_HUMAN         291         22         230         RLLLLSLGSLLLLVVCVGIGS         -2,62           Sp C972TSP GALT5_HUMAN         443         23         408         VFLSVLIFGVAGLLEFMYLQWI         -2,59 </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>  |                                       |     |    |     |                                   |       |
| spiQonXG6jiP4HTM_HUMAN         502         28         420         ICSRAYFLVLMVFVHLYLGNVLALLEFV         -2,73           spiQonXG6jiP4HTM_HUMAN         323         26         294         ALFTRFFILLPWILIVIIMLDVDTRR         -2,72           spiQoIANGIPRSTB_HUMAN         325         28         280         FITSTAILPLLFGCLGVFGLFRLLQWVR         -2,7           spiQoIANGIPRSTB_HUMAN         792         26         751         LVTLRPFRLFVLGIGFFTLCFLMTSL         -2,67           spiQoSMLMIT106B_HUMAN         274         25         157         RTKLYVMASVFVCLLLSGLAVFFLF         -2,67           spiQo13061TRDN_HUMAN         729         24         658         AAWILVIALIITWSAVAIVMFDLV         -2,67           spiQO361TRDN_HUMAN         603         24         573         IRTLLTYNILVFVGIVLFSVYCRL         -2,67           spiQO36ASGR1_HUMAN         1039         19         1008         MKLLLLLSLGAWLTYV         -2,64           spiQO7L1S5(CHST9_HUMAN         291         22         230         RILLLSLGSLLLLLVVCVVIGS         -2,62           spiQO7L1S5(CHST9_HUMAN         443         23         408         VFLSVLIFGVAGLLIFMYLQVVI         -2,59           spiQO3557[TNF14_HUMAN         240         27         179         VARVGLGLLLLMGAGLAVGCWFLLQL         -2,58 <tr< td=""><td>· · · · · · · · · · · · · · · · · · ·</td><td></td><td></td><td></td><td></td><td></td></tr<>   | · · · · · · · · · · · · · · · · · · · |     |    |     |                                   |       |
| Sp QGIAN0 DRS7B_HUMAN         325         28         280         FITSTAILPILFGCLGVFGLFRLLQWVR         -2,7           Sp Q3V5L5 MGT5B_HUMAN         792         26         751         LVTLRPFRLFVLGIGFFTLCFLMTSL         -2,67           Sp Q3NUM4 T106B_HUMAN         274         25         157         RTKLYYMASVFVCLLLSGLAVFFLF         -2,67           Sp Q31061 TRDN_HUMAN         729         24         658         AAWLLVIALIITWSQIAVISVMFDLV         -2,67           Sp Q36F13HUMAN         603         24         573         IRTLLTVNILIVFVGIVLFSVYCRL         -2,65           Sp Q76F8F1B4GN4_HUMAN         1039         19         1008         MKLLLLLLLSCASULLLVVCVIGS         -2,64           Sp Q757L155 CHST9_HUMAN         291         22         230         RLLLLSLGSLLLLVVVCVIGS         -2,62           Sp Q72TXF19GALT5_HUMAN         443         23         408         VFLSVLIFGVAGLLEFMYLQVWI         -2,59           Sp Q72TXF19GALT5_HUMAN         940         29         905         FFRGSGVLAFIFVASVIWLLFDMAALRL         -2,59           Sp Q4557 TNF14_HUMAN         240         27         179         VARVGLGLLLLMGAGLAVQGWFLLQL         -2,58           Sp Q9156150 TNF15_HUMAN         251         24         195         ARWALTCCLVLLPFLAGLTTYLLV         -2,58  | sp Q9NXG6 P4HTM_HUMAN                 | 502 | 28 | 420 | ICSRAYFLVLMVFVHLYLGNVLALLLFV      | -2,73 |
| Sp Q395L5 MGT5B_HUMAN         792         26         751         LVTLRPFRLFVLGIGFFTLCFLMTSL         -2,67           Sp Q390LMM4 T106B_HUMAN         274         25         157         RTKLYVMASVFVCLLLSGLAVFFLF         -2,67           Sp Q31601 TRDN_HUMAN         274         25         658         AWILLVIALIHWSAVAIVMFDLV         -2,67           Sp Q36BCS GALT9_HUMAN         603         24         573         IRTLLTYNILVFVGIVLFSVYCRL         -2,65           Sp Q76KP1 B4GN4_HUMAN         1039         19         1008         MKLLLLLLSCAWLTYV         -2,64           Sp Q7036 ASGR1_HUMAN         291         22         230         RLLLSLGSLLLLVVCVVIGS         -2,62           Sp Q72TM9 GALT5_HUMAN         443         23         408         VFLSVLIFGVAGLLLFMYLQVVI         -2,59           Sp Q72TM9 GALT5_HUMAN         940         29         905         FFRGSGRVLAFIFVASVIWLLFDMAALRL         -2,59           Sp Q355TJTNF14_HUMAN         240         27         179         VARVGLGLLLLMGAGLAVGGWFLLQL         -2,58           Sp Q95150 TNF15_HUMAN         317         22         267         LKICGLVFGILALTLIVLFWGS         -2,58           Sp Q942S6 TNMD_HUMAN         317         22         267         LKICGLVFGILALTLIVLFWGS         -2,58  |                                       |     |    |     |                                   |       |
| Sp O13061 TRDN_HUMAN         729         24         658         AAWLLVIALIITWSAVAIVMFDLV         -2,67           Sp O9HCQ5 GALT9 HUMAN         603         24         573         IRTLLTVNILIVFGIVLFSVYCRL         -2,65           Sp O76KP1B4GN4_HUMAN         1039         19         1008         MKLLLLLLLSCAWLTYV         -2,64           Sp P07306 ASGR1_HUMAN         291         22         230         RLLLSLGLSLLLLVVVCVIGS         -2,62           Sp O72TN59 GALT5_HUMAN         443         23         408         VFLSVLIFGVAGLLEFMYLQVWI         -2,59           Sp O72TN9 GALT5_HUMAN         940         29         905         FFRGSGRVLAFIFVASVIWLLEDMAALRL         -2,59           Sp O43557 TNF14_HUMAN         240         27         179         VARVGLGLLLLMGAGLAVQGWFLLQL         -2,58           Sp O95150 TNF15_HUMAN         251         24         195         ARWALTCCLVLLPFLAGLTTYLLV         -2,58           Sp O95156 TNMD_HUMAN         317         22         267         LIGGLYFGILALTIVLFWGS         -2,58           Sp P07307 ASGR2_HUMAN         311         29         234         LAQRLCSMVCFSLLALSFNILLLVICVT         -2,57           Sp O15593 TMPS2_HUMAN         331         23         302         ALCRACLALAALAALLLLPLP         -2,57   | sp Q3V5L5 MGT5B_HUMAN                 | 792 | 26 | 751 | LVTLRPFRLFVLGIGFFTLCFLMTSL        | -2,67 |
| Sp Q9HCQ5 GALT9_HUMAN         603         24         573         IRTLLTVNILVFVGIVLFSVYCRL         -2,65           Sp Q76KP1 BaGNA_HUMAN         1039         19         1008         MKLLLLLLSCAAWLTYV         -2,64           Sp PQ7306 ASGR1_HUMAN         291         22         230         RILLLSLGSLLILLVVCVIGS         -2,62           Sp Q72TM9 GALT5_HUMAN         443         23         408         VFLSVLIFGVAGLLIFMYLQVWI         -2,59           Sp Q72TM9 GALT5_HUMAN         940         29         905         FFRGSGRVLAFIFVASVIWLIFDMAALRL         -2,59           Sp Q3557 TNF14_HUMAN         240         27         179         VARVGLGLILLIMGAGLAVQGWFILQL         -2,58           Sp Q96156 TNF15_HUMAN         251         24         195         ARWALTCCLVILPFLAGLTTYLLV         -2,58           Sp Q9629E36 TNMD_HUMAN         317         22         267         LKICGLVFGILALTLIVLFWGS         -2,58           Sp PQ7307 ASGR2_HUMAN         311         29         234         LAQRLCSMVCFSLLALSFNILLLVVICVT         -2,57           Sp O15393 TMPS2_HUMAN         331         23         302         ALCRACLALAALALLLLPLP         -2,57           Sp O29664 RFNG_HUMAN         492         26         383         ALCITLTGFTLVGAALAAGLLWKFM         -2,57  |                                       |     |    |     |                                   |       |
| Sp P07306 ASGR1_HUMAN         291         22         230         RLLLLSLGLSLLLLVVVCVIGS         -2,62           Sp P07306 ASGR1_HUMAN         443         23         408         VFLSVLIFGVAGLLEFMYLQVWI         -2,59           Sp OZTATIONGALTS_HUMAN         940         29         905         FFRGSGRVLAFIFVASVIWLLFDMAALRL         -2,59           Sp O43557 TNF14_HUMAN         240         27         179         VARVGLGLLLLMGAGLAVQGWFLLQL         -2,58           Sp O95150 TNF15_HUMAN         251         24         195         ARWALTCCLVLLPFLAGLETTYLLV         -2,58           Sp O91505 TNMD_HUMAN         317         22         267         LKIGSUYFGILATIVLFWGS         -2,58           Sp P07307 ASGR2_HUMAN         311         29         234         LAQRLCSMVCFSLLALSFNILLLVVICVT         -2,57           Sp O155393 TMPS2_HUMAN         331         23         302         ALCRACLALAALAALLLLPLP         -2,57           Sp O36580 ABHD1_HUMAN         405         26         368         TWADTFSLLLALAVALYLGYYWACVL         -2,56  | sp Q9HCQ5 GALT9_HUMAN                 | 603 | 24 | 573 | IRTLLTVNILVFVGIVLFSVYCRL          | -2,65 |
| Sp Q7L155 CHST9_HUMAN         443         23         408         VFLSVLIFGVAGLLLFMYLQVWI         -2,59           Sp Q7Z7M9 GALT5_HUMAN         940         29         905         FFRGSGRVLAFIFVASVIWLIFDMAALRL         -2,59           Sp Q3557 TNF14_HUMAN         240         27         179         VARVGLGLLLLLMGAGLAVQGWFLLQL         -2,58           Sp Q96156 TNF15_HUMAN         251         24         195         ARWALTCCLVILPFLAGLTTYLLV         -2,58           Sp Q9942S6 TNMD_HUMAN         317         22         267         LKICGLYFGILALTLIVLFWGS         -2,58           Sp PO7307 ASGR2_HUMAN         311         29         234         LAQRLCSMVCFSLLALSFNILLLVVICVT         -2,57           Sp O15393 TMPS2_HUMAN         331         23         302         ALCRACLALAAALALLLLPLP         -2,57           Sp Q365E0 ABHD1_HUMAN         492         26         383         ALCITLTLGFFLVGAALAAGLLWKFM         -2,57           Sp Q365E0 ABHD1_HUMAN         405         26         368         TWADTFSLLLALAVALYLGYYWACVL         -2,56  |                                       |     |    |     |                                   |       |
| Sp O43557 TNF14_HUMAN         240         27         179         VARVGLGLLLLMGAGLAVQGWFLLQL         -2,58           sp O95150 TNF15_HUMAN         251         24         195         ARWALTCCLVLLPFLAGLTTYLLV         -2,58           sp Q9H256 TMND_HUMAN         317         22         267         LKIGGLVFGILALTIVLFWGS         -2,58           sp P07307 ASGR2_HUMAN         311         29         234         LAQRLCSMVCFSLLALSFNILLLVVICVT         -2,57           sp O15939 TMPS2_HUMAN         331         23         302         ALCRACLALAAALAALLLLPLP         -2,57           sp O15939 TMPS2_HUMAN         492         26         383         ALCITL1GFFLVGAALAAGLLWKFM         -2,57           sp O9685E0 ABHD1_HUMAN         405         26         368         TWAD1FSLLLALAVALYLGYYWACVL         -2,56   | sp Q7L1S5 CHST9_HUMAN                 | 443 | 23 | 408 | VFLSVLIFGVAGLLLFMYLQVWI           | -2,59 |
| Sp O95150 TNF15_HUMAN         251         24         195         ARWALTCCLV/LLPFLAGLTTYLLV         -2,58           Sp Q9812S6 TNMD_HUMAN         317         22         267         LIKICGLVFGILALTLIVLFWGS         -2,58           Sp PO7307 ASGR2_HUMAN         311         29         234         LAORLCSMVCFSLLALSFNILLLVVICVT         -2,57           Sp O99644 RFNG_HUMAN         331         23         302         ALCRACLALAAALAALLLLPLP         -2,57           Sp O3533 TMPS2_HUMAN         492         26         383         ALCITLTLGTFLVGAALAAGLLWKFM         -2,57           Sp O365E0 ABHD1_HUMAN         405         26         368         TWADTFSLLLALAVALYLGYYWACVL         -2,56   |                                       |     |    |     |                                   |       |
| sp P07307 ASGR2_HUMAN         311         29         234         LAQRLCSMVCFSLLALSFNILLLVVICVT         -2,57           sp Q9564 RFNG_HUMAN         331         23         302         ALCRACLALAALAALLLLPLPL         -2,57           sp O156393 TMPS2_HUMAN         492         26         383         ALCITLTLGTFLVGAALAAGLLWKFM         -2,57           sp Q96SE0 ABHD1_HUMAN         405         26         368         TWADTFSLLIALAVALYLGYYWACVL         -2,56  | sp O95150 TNF15_HUMAN                 | 251 | 24 | 195 | ARWALTCCLVLLPFLAGLTTYLLV          | -2,58 |
| spiQ9Y644 RFNG_HUMAN         331         23         302         ALCRACLALAAALAALLLLPLPL         -2,57           spiQ15393 TMPS2_HUMAN         492         26         383         ALCITLTLGTFLVGAALAAGLLWKFM         -2,57           spiQ96SE0 ABHD1_HUMAN         405         26         368         TWADTFSLLLALAVALYLGYYWACVL         -2,56  |                                       |     |    |     |                                   |       |
| sp[015393]TMPS2_HUMAN         492         26         383         ALCITLTLGTFLVGAALAAGLLWKFM         -2,57           sp[Q96SE0]ABHD1_HUMAN         405         26         368         TWADTFSLLLALAVALYLGYYWACVL         -2,56  |                                       |     |    | 302 |                                   |       |
|  | sp O15393 TMPS2_HUMAN                 |     |    |     | ALCITLTLGTFLVGAALAAGLLWKFM        |       |
|  |                                       |     |    |     |                                   |       |

| emiO442001CIA4C LILIMANI                       | 222        | 20       | 200        | RWKLLAMLALVLVVMVWYSI   | 2.55           |
|--|------------|----------|------------|--|----------------|
| sp Q11206 SIA4C_HUMAN<br>sp Q8NFS9 GNT2C_HUMAN | 333<br>402 | 20<br>23 | 308<br>377 | FWRYCFFAFTLLSVVIFVRFYSS  | -2,55<br>-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<br>sp Q58DX5 NADL2_HUMAN | 633<br>795 | 20<br>22 | 594<br>649 | FWKLGAVIFFFIIVLVLMQR<br>VLKILCTATILFIFGILIGYYV                 | -2,51<br>-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<br>sp Q8NES3 LFNG_HUMAN   | 365<br>379 | 19<br>23 | 338<br>353 | LCLAFLLVCVLSVIFFLHI<br>RCGRRLLLALAGALLACLLVLTA                 | -2,45<br>-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<br>sp O94901 SUN1_HUMAN  | 390<br>812 | 24<br>30 | 338<br>476 | VRRKLALLFAMLCVWLYMFLYSCA<br>FLLTRCLRNICKFLVLLIPLFLLLAGLSLR     | -2,42<br>-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<br>sp P51993 FUT6_HUMAN  | 375<br>359 | 22<br>26 | 349<br>323 | FRSWMLAALTLLVVFLIFADIS WSWRCCLTTLLFQLLMAVCFFSYLRV              | -2,34<br>-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<br>sp Q9H1B5 XYLT2_HUMAN | 388<br>865 | 29<br>29 | 353<br>827 | LLRLPRRSLLAALFFFSLSSSLLYFVYVA<br>LVRRYKLAIATALAILLLQGLVVWSFSGL | -2,28<br>-2,27 |
| sp Q6lCH7 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<br>sp O00461 GOLI4_HUMAN | 457<br>696 | 29<br>25 | 384<br>660 | MRRGCAVLGALGLLAGAGVGSWLLVLYLC<br>RIFQTLLLLTVVFGFLYGAMLYYEL     | -2,22<br>-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<br>sp Q5H943 KKLC1_HUMAN | 581<br>113 | 26<br>22 | 542<br>89  | LRRGREALLVLLALLALAGLGSVLRA FYLLLASSILCALIVFWKYRRF              | -2,18<br>-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<br>sp P52849 NDST2_HUMAN | 486<br>883 | 22<br>25 | 454<br>845 | YCKFALLLVLYTLVLLLVPSVL<br>LELHRLILLLIAFSLGSMGFLAYYV            | -2,07<br>-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<br>sp Q9UBM8 MGT4C_HUMAN | 271<br>478 | 19<br>24 | 219<br>435 | QVALLGLSLLLMLLLYVGL<br>LRKRSTVSFLGVLVIFLLFMNLYI                | -2,02<br>-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<br>sp P27487 DPP4_HUMAN  | 399<br>766 | 21<br>24 | 329<br>738 | ALVLQLLSFMLLAGVLVAILV<br>WKVLLGLLGAAALVTIITVPVVLL              | -1,99<br>-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<br>sp Q8NDV1 SIA7C_HUMAN  | 617<br>305 | 19<br>25 | 589<br>277 | YKTLIIICALFTLVTVLLW<br>ILKRKSVIAVSFIAAFLFLLVVRLV               | -1,95<br>-1,94 |
| sp O60513 B4GT4_HUMAN                          | 344        | 22       | 314        | LSYKFRLLLLTLCLTVVGWAT  | -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<br>sp Q8NET6 CHSTD_HUMAN | 240<br>341 | 27<br>27 | 143<br>310 | LTAEVLGIICIVLMATVLKTIVLIPFL<br>CCRRRVLAAACLGAALLLLCAAPRSLR     | -1,88<br>-1,87 |
| spiQ92185 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<br>sp Q9Y274 SIA10_HUMAN | 376<br>331 | 28<br>26 | 310<br>305 | LLLPSMLMFAVIVASSGLLLMIERGILA<br>MRGYLVAIFLSAVFLYYVLHCILWGT     | -1,85<br>-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<br>sp Q49A17 GLTL6 HUMAN | 657<br>601 | 27<br>25 | 630<br>570 | MQWRALVLGLVLLRLGLHGVLWLVFGL<br>RFLQMTLLFTVALIFLPNVGLWSLY       | -1,78<br>-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<br>sp P32970 CD70 HUMAN  | 622<br>193 | 19<br>28 | 593<br>151 | LRLAMVGCAFVLFLFLLHR YGCVLRAALVPLVAGLVICLVVCIQRFA               | -1,74<br>-1,73 |
| sp P22413 ENPP1_HUMAN                          | 925        | 24       | 828        | TYKVLSLVLSVCVLTTILGCIFGL                                       | -1,73          |
| sp P23510 TNFL4_HUMAN                          | 183        | 27       | 133        | LLLVASVIQGLGLLLCFTYICLHFSAL                                    | -1,73          |
| spiQ9HDC9 APMAP_HUMAN                          | 416<br>372 | 25<br>19 | 355<br>343 | RVFRVTFLMLAVSLTVPLLGAMMLL<br>ATLILAIGAFTLLLFSLLV               | -1,72<br>-1,71 |
| sp Q9Y2A9 B3GN3_HUMAN<br>sp Q6UWU4 CF089 HUMAN | 372<br>347 | 19<br>23 | 343<br>268 | LLIVVYKVLATLGLILLTAYFVI  | -1,71<br>-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<br>242  | LTAEVLGIICIVLMATVLKTIVLI<br>LGQTCVLIVIFTVLLQSLCVAVTYVYFT       | -1,66<br>1.65  |
| sp P50591 TNF10_HUMAN<br>sp Q8WVQ1 CANT1_HUMAN | 281<br>401 | 28<br>20 | 242<br>340 | RWKVILTFFVGAAILWLLCS   | -1,65<br>-1,62 |
| sp Q8N4A0 GALT4_HUMAN                          | 578        | 28       | 549        | AVRWTWAGKSCLLLAFLTVAYIFVELLV                                   | -1,62          |
| sp Q8N428 GLT16_HUMAN                          | 558        | 25       | 533        | MRKIRANAIAILTVAWILGTFYYLW                                      | -1,61          |
| spiO8WTTOICLC4C HUMAN                          | 406<br>213 | 19<br>29 | 379<br>171 | KFSCCVLVFLLFAVICVWK<br>LWWFQLKVWSMAVVSILLLSVCFTVSSVV           | -1,61<br>-1.59 |
| sp Q8WTT0 CLC4C_HUMAN<br>sp O95395 GCNT3 HUMAN | 213<br>438 | 29<br>24 | 171<br>405 | LHYLWALGCYMLLATVALKLSFRL                                       | -1,59<br>-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<br>sp P22760 AAAD_HUMAN   | 156<br>399 | 19<br>19 | 55<br>378  | AKRLLFLLLTIVFCQILMA<br>RKSLYLLIVGILIAYYIYT                     | -1,54<br>-1,53 |
| spiQ0P6D2jFA69C HUMAN                          | 399<br>419 | 19<br>22 | 378<br>374 | TLLAFAAWTAGWVLAAALLLRA   | -1,53<br>-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<br>sp Q9UQQ1 NALDL_HUMAN  | 957<br>740 | 23<br>26 | 916<br>712 | VAILCAVVVGVGLIVGLAVGLTR WTKVLGLGLGAAALLGLGIILGHFAI             | -1,49<br>-1,49 |
| spiQ96BA8iCR3L1 HUMAN                          | 740<br>519 | 26       | 125        | TGTCLMVAALCFVLVLGSLVPCL  | -1,49<br>-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<br>sp P09172 DOPO_HUMAN  | 756<br>617 | 23<br>20 | 726<br>580 | RRKFLAASLSLLCIPAITWIYLF AAFMYSTAVAIFLVILVAAL                   | -1,47<br>-1,46 |
| SPIT USTIZIDOFO_HUIVIAIN                       | 617        | 20       | 300        | 70 TWITOTA VAIL EVIEVAAL                                       | -1,40          |

| IO40004IOEDD LIIIMANI  | 700  | 05   | 700   | TIAN (KINEO) (ATO AN II ALLI VIA CON II D   | 4.40   |
|--|--|--|---|---|--|
| sp Q12884 SEPR_HUMAN<br>sp Q9Y2B1 TMEM5_HUMAN  | 760<br>443   | 25<br>27   | 733<br>414  | TWVKIVFGVATSAVLALLVMCIVLR<br>LTRKRLCSFLIALYCLFSLYAAYHVFF  | -1,46<br>-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<br>sp Q9NPF2 CHSTB_HUMAN   | 402<br>352   | 23<br>25   | 375<br>315  | LRLRRDALLTLLLGASLGLLLYA<br>RICRMVLATCLGSFILVIFYFQSML  | -1,39<br>-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<br>409   | 23<br>27   | 363<br>360  | IFRKFLLMLCSLLTSLYVFYCLA<br>VRVGFFGSGVGLSLILGFSVAYAFYYL  | -1,37<br>-1,36   |
| sp Q8WU67 ABHD3_HUMAN<br>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<br>sp Q7LGC8 CHST3 HUMAN  | 837  | 29   | 771   | RSTAGGVALAVVVLSLALGMSGRWVLAWY   | -1,29  |
| sp Q7EGC8 CHS13_HUMAN<br>sp Q5T7M9 FA69A_HUMAN   | 479<br>428   | 19<br>28   | 441<br>378  | MRSKYALFLVFVVIVFVFI YVRMKYLFFSWLVVFVGSWIIYVQYSTY  | -1,28<br>-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<br>sp Q8WZA1 PMGT1_HUMAN   | 319<br>660   | 22<br>26   | 255<br>601  | WLRTAGLGAGFVLTALLLWSSL<br>ALRRFCQTGAVLFLLVTVIVNIKLIL  | -1,2<br>-1,18  |
| spiQ86Y22 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<br>sp Q9NZS2 KLRF1_HUMAN   | 500<br>232   | 24<br>30   | 476<br>164  | MRNWLVLLCPCVLGAALHLWLRLR ILLGISGTVNGILTLTLISLILLVSQGVLL   | -1,12<br>-1,12   |
| sp Q9NZ5Z KERF1_HUMAN<br>sp Q6P4F1 FUT10_HUMAN   | 479  | 25   | 449   | RRKLLASCLCVTATVFLLVTLQVMV   | -1,12<br>-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<br>353   | 23<br>25   | 339<br>310  | LRDYGFCMATLLVFCLGSLLYQL<br>RVCTLFIIGFKFTFFVSIMIYWHVV  | -1,07<br>-1,04   |
| sp Q9NPC4 A4GAT_HUMAN<br>sp Q9NY28 GALT8_HUMAN   | 637  | 25   | 610   | FWRKLPKALFIGLTLAIAVNLLLVF   | -1,04  |
| 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<br>sp A8MXE2 Yl036_HUMAN   | 384<br>369   | 23<br>29   | 353<br>336  | LTAKTLACLLVGVSFLALQQWFL<br>FCRLRTHQWCFILFNVILFHALLFGTDFV  | -0,97<br>-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<br>sp Q99999 G3ST1_HUMAN   | 395<br>423   | 20<br>23   | 367<br>389  | TAVTALLLAQTFLLLFLVSR<br>MAKGLVLGALFTSFLLLVYSYAV   | -0,87<br>-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<br>sp Q8NCG5 CHST4_HUMAN   | 326<br>386   | 22<br>21   | 300<br>359  | VSCLYVLTVVCWASALWYLSIT<br>MKLLLFLVSQMAILALFFHMY   | -0,74<br>-0,72   |
| sp Q68CJ9 CR3L3_HUMAN  | 461  | 20   | 122   | TGTCVAVLLLSFALIILPSI  | -0,72  |
| 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<br>258   | 26<br>23   | 913<br>54   | FLPLKWSLATMSFLLSSLLALLTVST<br>LGLSVFSMLCCFWPLGIAAFYLS   | -0,65<br>-0,65   |
| sp Q9H7V2 SYNG1_HUMAN<br>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<br>455   | 31   | 507   | WGLRGALAAVALLSALNAAGTVFALCQWRGL   | -0,57  |
| sp P07099 HYEP_HUMAN<br>sp Q9UM21 MGT4A HUMAN  | 455<br>535   | 21<br>27   | 434<br>508  | MWLEILLTSVLGFAIYWFISR<br>MRLRNGTVATALAFITSFLTLSWYTTW  | -0,55<br>-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  | 378<br>602   | 20<br>25   | 346<br>475  | WQLIIQLFATCFLASLMFFW<br>RLGRALNFLFYLALVAAAAFSGWCV   | -0,47<br>-0,47   |
| sp Q07065 CKAP4_HUMAN<br>sp Q9BVH7 SIA7E_HUMAN   | 378<br>602<br>336  | 20<br>25<br>24   | 346<br>475<br>310   | WQLIIQLFATCFLASLMFFW<br>RLGRALNFLFYLALVAAAAFSGWCV<br>TLMRHGLAVCLALTTMCTSLLLVY   | -0,47<br>-0,47<br>-0,43  |
| sp Q07065 CKAP4_HUMAN  | 378<br>602   | 20<br>25   | 346<br>475  | WQLIIQLFATCFLASLMFFW<br>RLGRALNFLFYLALVAAAAFSGWCV   | -0,47<br>-0,47   |
| sp Q07065 CKAP4_HUMAN<br>sp Q9BVH7 SIA7E_HUMAN<br>sp Q4G0N0 GGTA1_HUMAN<br>sp Q9Y661 H3354_HUMAN<br>sp Q7Z7M8 B3GN8_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397   | 20<br>25<br>24<br>20<br>22<br>19   | 346<br>475<br>310<br>75<br>403<br>374   | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,4  |
| sp Q07065 CKAP4_HUMAN<br>sp Q9BVH7 SIA7E_HUMAN<br>sp Q4G0N0 GGTA1_HUMAN<br>sp Q97661 HS3S4_HUMAN<br>sp Q7Z7M8 B3GN8_HUMAN<br>sp Q86VU5 CMTD1_HUMAN   | 378<br>602<br>336<br>100<br>456<br>397<br>262  | 20<br>25<br>24<br>20<br>22<br>19<br>29   | 346<br>475<br>310<br>75<br>403<br>374<br>227  | WQLIIOLFATCFLASLMFFW RLGRAINFIFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,4<br>-0,39   |
| sp Q07065 CKAP4_HUMAN<br>sp Q9BVH7 SIA7E_HUMAN<br>sp Q4G000) GGTA1_HUMAN<br>sp Q9Y661 HS3S4_HUMAN<br>sp Q727M8 B3GN8_HUMAN<br>sp Q86VU5 CMTD1_HUMAN<br>sp Q81ZT8 HS3S5_HUMAN   | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315   | WQLIIQLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTTMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPALALLGSAALGAAFATGLFLGRRC AWLRQKLLVLGSLAVGSLLYLVARV   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,4<br>-0,39<br>-0,35  |
| sp Q07065 CKAP4_HUMAN<br>sp Q9BVH7 SIA7E_HUMAN<br>sp Q4G0N0 GGTA1_HUMAN<br>sp Q97661 HS384_HUMAN<br>sp Q7Z7M8 B3GN8_HUMAN<br>sp Q86VU5 CMTD1_HUMAN<br>sp Q8IZT8 HS385_HUMAN<br>sp Q9941 ATF6B_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703  | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291  | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,4<br>-0,4<br>-0,39<br>-0,35   |
| sp Q07065 CKAP4_HUMAN<br>sp Q9BVH7 SIA7E_HUMAN<br>sp Q4G000) GGTA1_HUMAN<br>sp Q9Y661 HS3S4_HUMAN<br>sp Q727M8 B3GN8_HUMAN<br>sp Q86VU5 CMTD1_HUMAN<br>sp Q81ZT8 HS3S5_HUMAN   | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315   | WQLIIQLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTTMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPALALLGSAALGAAFATGLFLGRRC AWLRQKLLVLGSLAVGSLLYLVARV   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,4<br>-0,39<br>-0,35  |
| sp Q07065 CKAP4_HUMAN<br>sp Q9BVH7 SIA7E_HUMAN<br>sp Q4G001 GGTA1_HUMAN<br>sp Q9Y661 HS3S4_HUMAN<br>sp Q8F0V5 CMTD1_HUMAN<br>sp Q86VU5 CMTD1_HUMAN<br>sp Q89241 ATF6B_HUMAN<br>sp Q99241 ATF6B_HUMAN<br>sp Q9GZS9 CHST5_HUMAN<br>sp Q9BY50 SC11C_HUMAN<br>sp Q3T906 GNPTA_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256  | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219  | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHIGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAOTTCLLLFIISR LYYQVLNFAMIVSSALMIWKGLIVLT RYGLYVOFLGVVVTIVSAFQF  | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,4<br>-0,39<br>-0,35<br>-0,28<br>-0,28<br>-0,23<br>-0,2<br>-0,19   |
| sp Q07065 CKAP4_HUMAN<br>sp Q98VH7 SIA7E_HUMAN<br>sp Q4G0N0 GGTA1_HUMAN<br>sp Q37561 H5354_HUMAN<br>sp Q3727M8 B3GN8_HUMAN<br>sp Q86VU5 CMTD1_HUMAN<br>sp Q88IZT8 H5355_HUMAN<br>sp Q9941 ATF6B_HUMAN<br>sp Q99545 CH5T5_HUMAN<br>sp Q3950 GCNFT5_HUMAN<br>sp Q31906 GNPTA_HUMAN<br>sp Q31906 GNPTA_HUMAN<br>sp Q31906 GNPTA_HUMAN   | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376   | WOLIIOLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAQTTCLLLFIISR LYYQVLNFAMIVSSALMWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,4<br>-0,39<br>-0,35<br>-0,28<br>-0,23<br>-0,2<br>-0,19   |
| sp Q07065 CKAP4_HUMAN<br>sp Q98VH7 SIA7E_HUMAN<br>sp Q4G010 GGTA1_HUMAN<br>sp Q3727M8 B3GN8_HUMAN<br>sp Q36015 CMTD1_HUMAN<br>sp Q89015 CMTD1_HUMAN<br>sp Q89214 ATF6B_HUMAN<br>sp Q99941 ATF6B_HUMAN<br>sp Q9925 CH3T5_HUMAN<br>sp Q3905 CH3T6_HUMAN<br>sp Q31306 GNPTA_HUMAN<br>sp Q8N005 GNT2A_HUMAN<br>sp Q8N005 GNT2A_HUMAN<br>sp Q8N005 GNT2A_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402<br>420  | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385  | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAQTTCLLLFIISR LYYQVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLLGIALLAVVASVWG   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,39<br>-0,28<br>-0,28<br>-0,22<br>-0,19<br>-0,16<br>-0,16   |
| sp Q07065 CKAP4_HUMAN<br>sp Q98VH7 SIA7E_HUMAN<br>sp Q4G0N0 GGTA1_HUMAN<br>sp Q9Y661 HS3S4_HUMAN<br>sp Q3E5MB B3GN8_HUMAN<br>sp Q86VU5 CMTD1_HUMAN<br>sp Q86VU5 CMTD1_HUMAN<br>sp Q9941 ATF6B_HUMAN<br>sp Q995S0 SC11C_HUMAN<br>sp Q3E59 CHST5_HUMAN<br>sp Q3E50 GMPTA_HUMAN<br>sp Q8N0V5 GMT2A_HUMAN<br>sp Q8N0V5 GMT2A_HUMAN<br>sp Q8NBZ7 UXS1_HUMAN<br>sp Q6NBZ7 UXS1_HUMAN<br>sp Q6NBZ7 UXS1_HUMAN   | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402<br>420<br>156   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104   | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHIGLAVCLALTTMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLRQKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAOTTCLLLFIISR LYYQVLNFAMIVSSALMWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLLGIALLAYVASVWG KQTLLALLILVLYLSTEIW   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,4<br>-0,39<br>-0,35<br>-0,28<br>-0,23<br>-0,2<br>-0,19<br>-0,16<br>-0,16<br>-0,09  |
| sp Q07065 CKAP4_HUMAN<br>sp Q98VH7 SIA7E_HUMAN<br>sp Q4G010 GGTA1_HUMAN<br>sp Q3727M8 B3GN8_HUMAN<br>sp Q36015 CMTD1_HUMAN<br>sp Q89015 CMTD1_HUMAN<br>sp Q89214 ATF6B_HUMAN<br>sp Q99941 ATF6B_HUMAN<br>sp Q9925 CH3T5_HUMAN<br>sp Q3905 CH3T6_HUMAN<br>sp Q31306 GNPTA_HUMAN<br>sp Q8N005 GNT2A_HUMAN<br>sp Q8N005 GNT2A_HUMAN<br>sp Q8N005 GNT2A_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402<br>420  | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385  | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAQTTCLLLFIISR LYYQVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLLGIALLAVVASVWG   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,39<br>-0,28<br>-0,28<br>-0,22<br>-0,19<br>-0,16<br>-0,16   |
| sp 007065 CKAP4_HUMAN<br>sp 03BVH7 SIA7E_HUMAN<br>sp 03G0N0 GGTA1_HUMAN<br>sp 03Y661 HS3S4_HUMAN<br>sp 03E5V15 CMTD1_HUMAN<br>sp 086VU5 CMTD1_HUMAN<br>sp 088VU5 CMTD1_HUMAN<br>sp 09941 ATF6B_HUMAN<br>sp 09941 ATF6B_HUMAN<br>sp 039BY50 SG11C_HUMAN<br>sp 03BY50 SG11C_HUMAN<br>sp 08NBZ7 UXS1_HUMAN<br>sp 08NBZ7 UXS1_HUMAN<br>sp 08IES7 CLCL1_HUMAN<br>sp 08IES7 CLCL1_HUMAN<br>sp 08IES7 CLCL1_HUMAN<br>sp 08NAT1 PMGT2_HUMAN<br>sp 08NAT1 PMGT2_HUMAN<br>sp 08NAT1 PMGT2_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402<br>420<br>156<br>167<br>580<br>359  | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>21<br>19<br>24<br>23   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337   | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLICLSALLTLLGLKVYI RLSVPAALALGSAALGAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAOTTCLLLFIISR LYYQVLNFAMIVSSALMWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLEGIALLAYVASVWG KQTLLALLILVLYLSTEIW FSGTSFVVFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVRL IRKRWTICTISLLLIFVKT  | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,39<br>-0,35<br>-0,28<br>-0,23<br>-0,2<br>-0,19<br>-0,16<br>-0,12<br>-0,09<br>-0,07<br>-0,06  |
| sp Q07065 CKAP4_HUMAN<br>sp Q98VH7 SIA7E_HUMAN<br>sp Q4G0N0 GGTA1_HUMAN<br>sp Q375M8 B3GN8_HUMAN<br>sp Q3727M8 B3GN8_HUMAN<br>sp Q88VU5 CMTD1_HUMAN<br>sp Q88U25 HS155_HUMAN<br>sp Q9941 ATF6B_HUMAN<br>sp Q39259 CHST5_HUMAN<br>sp Q37906 GNPTA_HUMAN<br>sp Q8NB27 UXS1_HUMAN<br>sp Q8NB27 UXS1_HUMAN<br>sp Q8NB27 UXS1_HUMAN<br>sp Q8NB27 UXS1_HUMAN<br>sp Q8NB27 CLC1_HUMAN<br>sp Q8NB27 CLC1_HUMAN<br>sp Q8NB27 CLC1_HUMAN<br>sp Q81257 CLC1_HUMAN<br>sp Q92187 SIA8D_HUMAN<br>sp Q92187 SIA8D_HUMAN<br>sp Q92187 SIA8D_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402<br>420<br>156<br>167<br>580<br>359<br>166   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>21<br>19<br>24<br>23   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135  | WOLIIOLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLICLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAQTTCLLLFIISR LYYOVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLLGIALLAYVASVWG KOTLLALLLIVLYLSTEIW FSGTSFVVFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVPL IRKRWTICTISLLLIFYKT WRLYYQVLNFGMIVSSALMIWKGLMVIT   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,4<br>-0,39<br>-0,35<br>-0,23<br>-0,23<br>-0,2<br>-0,19<br>-0,16<br>-0,16<br>-0,19<br>-0,09<br>-0,07<br>-0,06<br>-0,03<br>0                         |
| Sp 007065 CKAP4_HUMAN<br>sp 039VH7 SIA7E_HUMAN<br>sp 0360N0 GGTA1_HUMAN<br>sp 03727M8 B3GN8_HUMAN<br>sp 0367015 CMTD1_HUMAN<br>sp 036V15 CMTD1_HUMAN<br>sp 03812T8 HS3S5_HUMAN<br>sp 039941 ATF6B_HUMAN<br>sp 039959 CHST5_HUMAN<br>sp 039059 CHST5_HUMAN<br>sp 031906 GNT2A_HUMAN<br>sp 031906 GNT2A_HUMAN<br>sp 031097 CLC1_HUMAN<br>sp 031075 CLC1_HUMAN<br>sp 031075 CLC1_HUMAN<br>sp 03187 CLC1_HUMAN<br>sp 03187 CLC1_HUMAN<br>sp 03187 CLC1_HUMAN<br>sp 03187 SC11B_HUMAN<br>sp 03187 SC11B_HUMAN<br>sp 071C71SC11B_HUMAN<br>sp 071C71SC11B_HUMAN<br>sp 071CA3]HS2ST_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402<br>420<br>156<br>167<br>580<br>359<br>166<br>356  | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>24<br>23<br>19<br>28<br>25   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135<br>329   | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHIGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAGTTCLLLFIISR LYYOVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLGIALLAYVASVWG KOTLLALLILVLYLSTEIW FSGTSFVVFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVRL IRKRWTICTISLLLIFVKT WRLYYOVLNFGMIVSSALMIWKGLMVIT LLRIMMPPKLQLLAVVAFAVAMLFL   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,39<br>-0,35<br>-0,28<br>-0,23<br>-0,2<br>-0,19<br>-0,16<br>-0,16<br>-0,12<br>-0,09<br>-0,07<br>-0,06<br>-0,03<br>0                                 |
| sp Q07065 CKAP4_HUMAN<br>sp Q98VH7 SIA7E_HUMAN<br>sp Q4G0N0 GGTA1_HUMAN<br>sp Q37M8 B3GN8_HUMAN<br>sp Q37M8 B3GN8_HUMAN<br>sp Q88VU5 GMTD1_HUMAN<br>sp Q88VU5 GMTD1_HUMAN<br>sp Q98V3 SGT1C_HUMAN<br>sp Q99SS9 CHST5_HUMAN<br>sp Q9BY50 SGT1C_HUMAN<br>sp Q8N0V5 GNPTA_HUMAN<br>sp Q8N0V5 GNPTA_HUMAN<br>sp Q8N0V5 GNT2A_HUMAN<br>sp Q8N0V5 GNT2A_HUMAN<br>sp Q8N0V5 GNT2A_HUMAN<br>sp Q8NAT1 PMGT2_HUMAN<br>sp Q92187 SIA8D_HUMAN<br>sp Q92187 SIA8D_HUMAN<br>sp Q7LGA3 HS2ST_HUMAN<br>sp Q7LGA3 HS2ST_HUMAN<br>sp Q7LGA3 HS2ST_HUMAN   | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402<br>420<br>156<br>167<br>580<br>359<br>166<br>356<br>757   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>24<br>23<br>19<br>28<br>25<br>24   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135<br>329<br>519  | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLRGKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAOTTCLLLFIISR LYYQVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLLGIALLAYVASVWG KQTLLALLILVLYLSTEIW FSGTSFVVFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVRL IRRRWTICTISLLIFYKT WRLYYQVLNFGMIVSSALMIWKGLMVIT LLRIMMPPKLQLLAVVAFAVAMLFL LNKCVILALVIAISMGFGHFYGTI   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,4<br>-0,39<br>-0,28<br>-0,23<br>-0,2<br>-0,19<br>-0,16<br>-0,12<br>-0,09<br>-0,07<br>-0,06<br>-0,03<br>0<br>0,01                                   |
| Sp 007065 CKAP4_HUMAN<br>sp 039VH7 SIA7E_HUMAN<br>sp 0360N0 GGTA1_HUMAN<br>sp 03727M8 B3GN8_HUMAN<br>sp 0367015 CMTD1_HUMAN<br>sp 036V15 CMTD1_HUMAN<br>sp 03812T8 HS3S5_HUMAN<br>sp 039941 ATF6B_HUMAN<br>sp 039959 CHST5_HUMAN<br>sp 039059 CHST5_HUMAN<br>sp 031906 GNT2A_HUMAN<br>sp 031906 GNT2A_HUMAN<br>sp 031097 CLC1_HUMAN<br>sp 031075 CLC1_HUMAN<br>sp 031075 CLC1_HUMAN<br>sp 03187 CLC1_HUMAN<br>sp 03187 CLC1_HUMAN<br>sp 03187 CLC1_HUMAN<br>sp 03187 SC11B_HUMAN<br>sp 03187 SC11B_HUMAN<br>sp 071C71SC11B_HUMAN<br>sp 071C71SC11B_HUMAN<br>sp 071CA3]HS2ST_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402<br>420<br>156<br>167<br>580<br>359<br>166<br>356  | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>24<br>23<br>19<br>28<br>25   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135<br>329   | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHIGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAGTTCLLLFIISR LYYOVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLGIALLAYVASVWG KOTLLALLILVLYLSTEIW FSGTSFVVFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVRL IRKRWTICTISLLLIFVKT WRLYYOVLNFGMIVSSALMIWKGLMVIT LLRIMMPPKLQLLAVVAFAVAMLFL   | -0,47<br>-0,47<br>-0,43<br>-0,42<br>-0,41<br>-0,39<br>-0,35<br>-0,28<br>-0,23<br>-0,2<br>-0,19<br>-0,16<br>-0,16<br>-0,12<br>-0,09<br>-0,07<br>-0,06<br>-0,03<br>0                                 |
| sp Q07065 CKAP4_HUMAN<br>sp Q98VH7 SIA7E_HUMAN<br>sp Q4G0N0 GGTA1_HUMAN<br>sp Q37Z7M8 B3GN8_HUMAN<br>sp Q35V15 CMTD1_HUMAN<br>sp Q88VU5 CMTD1_HUMAN<br>sp Q88V15 CMTD1_HUMAN<br>sp Q9941 ATF6B_HUMAN<br>sp Q998Y50 SC11C_HUMAN<br>sp Q398Y50 SC11C_HUMAN<br>sp Q8N0V5 GNT2A_HUMAN<br>sp Q8N0V5 GNT2A_HUMAN<br>sp Q8N0V5 GNT2A_HUMAN<br>sp Q8N0V5 GNT2A_HUMAN<br>sp Q8N2T UXS1_HUMAN<br>sp Q8N2T IPMGT2_HUMAN<br>sp Q8NAT1 PMGT2_HUMAN<br>sp Q7LGA3 HS2ST_HUMAN<br>sp Q7LGA3 HS2ST_HUMAN<br>sp Q96EU7 C1GLC_HUMAN<br>sp Q96EU7 C1GLC_HUMAN<br>sp Q96EU7 CLC2B_HUMAN<br>sp Q92478 CLC2B_HUMAN<br>sp Q694Z GLC2B_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402<br>420<br>156<br>167<br>580<br>359<br>166<br>356<br>757<br>318<br>149<br>607                      | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>24<br>23<br>19<br>28<br>25<br>24<br>23<br>23<br>23<br>25   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135<br>329<br>519<br>288<br>121<br>574   | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLICLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLRGKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAOTTCLLLFIISR LYYQVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLLGIALLAYVASVWG KQTLLALLILVLYLSTEIW FSGTSFVVFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVRL IRRRWTICTISLLIFYKT WRLYYQVLNFGMIVSSALMIWKGLMVIT LLRIMMPPKLQLLAVVAFAVAMLFL LNKCVILALVIAISMGFGHFYGTI FLKGVMLGSIFCALITMLGHIRI KKCFIIVGVLITTNIITLIVKLT TLVSTOVILSGMTNIICLLYVGWVT   | -0,47 -0,47 -0,43 -0,42 -0,41 -0,4 -0,39 -0,35 -0,28 -0,23 -0,2 -0,19 -0,16 -0,12 -0,09 -0,07 -0,06 -0,03 0 0,01 0,02 0,03 0,05  |
| Sp 007065 CKAP4_HUMAN<br>sp 039VH7 SIA7E_HUMAN<br>sp 03460N0 GGTA1_HUMAN<br>sp 034561 H5354_HUMAN<br>sp 0345727M8 B3GN8_HUMAN<br>sp 0365VU5 CMTD1_HUMAN<br>sp 03812T8 H5355_HUMAN<br>sp 039259 CHST5_HUMAN<br>sp 039550 SC11C_HUMAN<br>sp 031906 GNPTA_HUMAN<br>sp 0380827 UX51_HUMAN<br>sp 0380827 UX51_HUMAN<br>sp 0381257 CLC1_HUMAN<br>sp 0381257 CLC1_HUMAN<br>sp 031257 CLC1_HUMAN<br>sp 031267 CS11B_HUMAN<br>sp 031267 CS11B_HUMAN<br>sp 031267 CS1B_HUMAN<br>sp 032478 CLC2B_HUMAN<br>sp 032478 CLC2B_HUMAN<br>sp 03612 B4GT3_HUMAN<br>sp 06512 B4GT3_HUMAN   | 378 602 336 100 456 397 262 346 703 411 192 1256 402 420 156 167 580 359 166 356 757 318 149 607   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>24<br>23<br>19<br>28<br>25<br>24<br>23<br>23<br>23<br>23<br>23<br>25<br>29   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135<br>329<br>519<br>288<br>121<br>574<br>355                                    | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHIGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLVLUSSLAVSSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAGTTCLLFIISR LYYOVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLLGIALLAYVASVWG KOTLLALLILVLYLSTEIW FSGTSFVYFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVRL IRKRWTICTISLLLIFVKT WRLYYQVLNFGMIVSSALMIWKGLMVIT LLRIMMPPKLQLLAVVAFAVAMLFL LNKCVILALVIASIGMGFHFYCTI FLKGVMLGSIFCALTIMLGHIRI KKCFIIVGVLITTNIITLIVKLT TLVSTCVILSGMTNIICLLYVGWVT CTLALLVGSOLAVMMYLSLGGFRSLSALF  | -0.47<br>-0.47<br>-0.43<br>-0.42<br>-0.41<br>-0.39<br>-0.28<br>-0.23<br>-0.2<br>-0.19<br>-0.16<br>-0.12<br>-0.07<br>-0.06<br>-0.03<br>0<br>0.01<br>0.02<br>0.03<br>0<br>0.03                       |
| sp 007065 CKAP4_HUMAN<br>sp 028VH7 SIA7E_HUMAN<br>sp 024G0N0 GGTA1_HUMAN<br>sp 024G0N0 GGTA1_HUMAN<br>sp 0375XM8 B3GN8_HUMAN<br>sp 038V15 CMTD1_HUMAN<br>sp 038V14 ATF6B_HUMAN<br>sp 03994 ATF6B_HUMAN<br>sp 03995Y50 SC11C_HUMAN<br>sp 038N0V5 GNT7A_HUMAN<br>sp 08N0V5 GNT2A_HUMAN<br>sp 08N0V5 GNT2A_HUMAN<br>sp 08N0V5 GNT2A_HUMAN<br>sp 08N0Z7 UXS1_HUMAN<br>sp 08N0Z7 UXS1_HUMAN<br>sp 08N2Z7 CLCL1_HUMAN<br>sp 08N2Z7 CLC11_HUMAN<br>sp 03N2Z7 CLC2B_HUMAN<br>sp 03N2Z7 CLC2B_HUMAN<br>sp 03P2Z7 CLC2B_HUMAN<br>sp 03N2Z7 CLC2B_HUMAN<br>sp 03N2Z7 CLC2B_HUMAN<br>sp 03N2Z7 CLC3B_HUMAN<br>sp 03N2Z7 CLC3B_HUMAN<br>sp 03N2Z2 CLC3B_HUMAN<br>sp 03N2Z2 CLC3B_HUMAN<br>sp 03N2Z2 CLCSB_HUMAN   | 378 602 336 100 456 397 262 346 703 411 192 1256 402 420 156 167 580 359 166 356 757 318 149 607 393 775   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>24<br>23<br>19<br>28<br>25<br>24<br>23<br>25<br>24<br>23<br>25<br>24<br>23<br>25<br>26<br>21<br>29<br>20<br>20<br>20<br>20<br>21<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135<br>329<br>519<br>288<br>121<br>574<br>355<br>741                             | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAGTTCLLLFIISR LYYOVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLGIALLAYVASVWG KQTLLALLILVLYLSTEIW FSGTSFVVFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVBL IRKRWTICTISLLLIFYKT WRLYYQVLNFGMIVSSALMIWKGLMVIT LLRIMMPPKLQLLAVVAFAVAMLFL LNKCVILALVIALSMGFGHFYGTI FLKGVMLGSIFCALITMLGHIRI KKCFIIVGVLITTNIITLIVKLT TLYSTCVILSGMTNIICLLYYGWVT CTLALLVGSQLAVMMYLSLGGFRSLSALF LLLSVLRPAGPVAVGISLGFTLSLLSVTWV  | -0.47<br>-0.47<br>-0.43<br>-0.42<br>-0.41<br>-0.4<br>-0.39<br>-0.28<br>-0.28<br>-0.23<br>-0.2<br>-0.19<br>-0.16<br>-0.16<br>-0.12<br>-0.09<br>-0.07<br>-0.06<br>-0.03<br>0<br>0.01<br>0.02<br>0.03 |
| Sp 007065 CKAP4_HUMAN<br>Sp 039VH7 SIA7E_HUMAN<br>Sp 03460N0 GGTA1_HUMAN<br>Sp 03727M8 B3GN8_HUMAN<br>Sp 0365VU5 CMTD1_HUMAN<br>Sp 0365VU5 CMTD1_HUMAN<br>Sp 0395VU5 CMTD1_HUMAN<br>Sp 0395VI5 CHST5_HUMAN<br>Sp 0395V5 CHST5_HUMAN<br>Sp 03105 CMPTA_HUMAN<br>Sp 03105 CMPTA_HUMAN<br>Sp 03808Z7 UXS1_HUMAN<br>Sp 03808Z7 UXS1_HUMAN<br>Sp 03105 CMPTA_HUMAN<br>Sp 03107 CMT1PMGT2_HUMAN<br>Sp 03127 CLC11_HUMAN<br>Sp 03127 CLC11_HUMAN<br>Sp 03127 CS11B_HUMAN<br>Sp 03125 CHS12_HUMAN<br>Sp 03165 CCPG1_HUMAN<br>Sp 03165 CCPG1_HUMAN<br>Sp 032478 CLC2B_HUMAN<br>Sp 032478 CLC2B_HUMAN<br>Sp 032478 CLC2B_HUMAN<br>Sp 060512 B4GT3_HUMAN<br>Sp 060512 B4GT3_HUMAN<br>Sp 031252 CHSS2_HUMAN<br>Sp 031252 CHSS2_HUMAN<br>Sp 031252 CHSS2_HUMAN<br>Sp 031252 CHSS2_HUMAN<br>Sp 031252 CHSS2_HUMAN  | 378<br>602<br>336<br>100<br>456<br>397<br>262<br>346<br>703<br>411<br>192<br>1256<br>402<br>420<br>156<br>167<br>580<br>359<br>166<br>356<br>757<br>318<br>149<br>607<br>393<br>775<br>417 | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>24<br>23<br>19<br>28<br>25<br>24<br>23<br>25<br>29<br>30<br>20   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135<br>329<br>519<br>288<br>121<br>574<br>355<br>741<br>396                      | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLRGKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAOTTCLLLFIISR LYYQVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLLGIALLAYVASVWG KQTLLALLILVLYLSTEIW FSGTSFVVFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVRL IRRRWTICTISLLLIFVKT WRLYYQVLNFGMIVSSALMIWKGLMVIT LLRIMMPPKLQLLAVVAFAVAMLFL LNKCVILALVIAISMGFGHFYGTI FLKGVMLGSIFCALITMLGHIRI KKCFIIVGVLITTNIITLIVKLT TLVSTCVILSGMTNIICLLYVGWVT CTLALLIGSGMTNIICLLYVGWVT CTLALLICSGALVMMYLSLGGFRSLSALF LLLSVLPAGPVAVGISLGFTLSLLSVTWV ASYLYGVLFAVOLGPIVCV   | -0,47 -0,47 -0,43 -0,42 -0,41 -0,4 -0,39 -0,35 -0,28 -0,23 -0,2 -0,19 -0,16 -0,12 -0,09 -0,07 -0,06 -0,03 0 0,01 0,02 0,03 0,05 0,08 0,08 0,08 0,08  |
| sp 007065 CKAP4_HUMAN<br>sp 028VH7 SIA7E_HUMAN<br>sp 024G0N0 GGTA1_HUMAN<br>sp 024G0N0 GGTA1_HUMAN<br>sp 0375XM8 B3GN8_HUMAN<br>sp 038V15 CMTD1_HUMAN<br>sp 038V14 ATF6B_HUMAN<br>sp 03994 ATF6B_HUMAN<br>sp 03995Y50 SC11C_HUMAN<br>sp 038N0V5 GNT7A_HUMAN<br>sp 08N0V5 GNT2A_HUMAN<br>sp 08N0V5 GNT2A_HUMAN<br>sp 08N0V5 GNT2A_HUMAN<br>sp 08N0Z7 UXS1_HUMAN<br>sp 08N0Z7 UXS1_HUMAN<br>sp 08N2Z7 CLCL1_HUMAN<br>sp 08N2Z7 CLC11_HUMAN<br>sp 03N2Z7 CLC2B_HUMAN<br>sp 03N2Z7 CLC2B_HUMAN<br>sp 03P2Z7 CLC2B_HUMAN<br>sp 03N2Z7 CLC2B_HUMAN<br>sp 03N2Z7 CLC2B_HUMAN<br>sp 03N2Z7 CLC3B_HUMAN<br>sp 03N2Z7 CLC3B_HUMAN<br>sp 03N2Z2 CLC3B_HUMAN<br>sp 03N2Z2 CLC3B_HUMAN<br>sp 03N2Z2 CLCSB_HUMAN   | 378 602 336 100 456 397 262 346 703 411 192 1256 402 420 156 167 580 359 166 356 757 318 149 607 393 775   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>24<br>23<br>19<br>28<br>25<br>24<br>23<br>25<br>24<br>23<br>25<br>24<br>23<br>25<br>26<br>21<br>29<br>20<br>20<br>20<br>20<br>21<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135<br>329<br>519<br>288<br>121<br>574<br>355<br>741                             | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAGTTCLLLFIISR LYYOVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFVYNT RRRMKLLGIALLAYVASVWG KQTLLALLILVLYLSTEIW FSGTSFVVFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVBL IRKRWTICTISLLLIFYKT WRLYYQVLNFGMIVSSALMIWKGLMVIT LLRIMMPPKLQLLAVVAFAVAMLFL LNKCVILALVIALSMGFGHFYGTI FLKGVMLGSIFCALITMLGHIRI KKCFIIVGVLITTNIITLIVKLT TLYSTCVILSGMTNIICLLYYGWVT CTLALLVGSQLAVMMYLSLGGFRSLSALF LLLSVLRPAGPVAVGISLGFTLSLLSVTWV  | -0.47<br>-0.47<br>-0.43<br>-0.42<br>-0.41<br>-0.4<br>-0.39<br>-0.28<br>-0.28<br>-0.23<br>-0.2<br>-0.19<br>-0.16<br>-0.16<br>-0.12<br>-0.09<br>-0.07<br>-0.06<br>-0.03<br>0<br>0.01<br>0.02<br>0.03 |
| Sp 007065 CKAP4_HUMAN  Sp 039VH7 SIA7E_HUMAN  Sp 0360N0 GGTA1_HUMAN  Sp 037Z7M8 B3GN8_HUMAN  Sp 036VU5 CMTD1_HUMAN  Sp 038VU5 CMTD1_HUMAN  Sp 0395VI5 CHST5_HUMAN  Sp 0395VI5 CHST5_HUMAN  Sp 0395VI5 CHST5_HUMAN  Sp 038VI5 GNFT2_HUMAN  Sp 038NBZ7 UXS1_HUMAN  Sp 031S7 CLC1_HUMAN  Sp 031S7 SIA8D_HUMAN  Sp 07LGA3 HS2ST_HUMAN  Sp 07LGA3 HS2ST_HUMAN  Sp 095U7 SC11B_HUMAN  Sp 095U7 SC11B_HUMAN  Sp 095U7 CLC2B_HUMAN  Sp 096EU7 C1GLC_HUMAN  Sp 036U7 SP3_HUMAN  Sp 060512 B4GT3_HUMAN  Sp 0605T PST1_HUMAN  Sp 060507 TPST1_HUMAN  Sp 06050HHIMAN  Sp 06050HHIMAN  Sp 06050HHIMAN  Sp 06050HHIMAN  Sp 06050HHIMAN  Sp 060HM4 F198B_HUMAN  Sp 060WH4 F198B_HUMAN  Sp 060WH4 F198B_HUMAN  | 378 602 336 100 456 397 262 346 703 411 192 1256 402 420 156 167 580 359 166 356 757 318 149 607 393 775 417 370 519 404   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>21<br>19<br>24<br>23<br>19<br>28<br>25<br>24<br>23<br>23<br>25<br>29<br>30<br>20<br>20<br>20<br>20<br>22<br>25<br>21<br>21<br>21<br>21<br>21<br>22<br>24<br>25<br>26<br>21<br>21<br>21<br>22<br>24<br>25<br>26<br>27<br>27<br>28<br>28<br>28<br>28<br>28<br>28<br>28<br>28<br>28<br>28<br>28<br>28<br>28 | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135<br>329<br>519<br>288<br>121<br>574<br>355<br>741<br>396<br>346<br>459<br>346 | WOLIIGLFATCFLASIMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLIVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAQTTCLLLFIISR LYYQVLNFAMIVSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFOF CLFSASLISALFVFLYNT RRMKLLGJALLAYVASVWG KQTLLALLILIVLYLSTEIW FSGTSFVYCSFLFICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVRL IRKRWTICTISLLLIFYKT WRLYYQVLNFGMIVSSALMIWKGLMVIT LLRIMMPPKLQLLAVVAFAVAMLFL LNKCVILALVIAISMGFGHFYGTI FLKGVMLGSIFCALITMLGHIRI KKCFIIVGVLITTNIITLIVKLT TLYSTCVILSGMTNIICLLYYGWVT CTLALLVGSQLAVMMYLSLGGFRSLSALF LLLSVLRPAGFQVAGISLGFTLSLLSVTWV ASYLYGVLFAVGLCAPIYCV LKONLLLGLVISSVTVFYL LLGGACHGFLVSQVGRASL LAGCLGHGPLVLOLLSFTLLAGLLV  | -0.47 -0.47 -0.47 -0.43 -0.42 -0.41 -0.49 -0.39 -0.28 -0.23 -0.2 -0.19 -0.16 -0.12 -0.09 -0.06 -0.03 0 0.01 0.02 0.03 0.05 0.08 0.08 0.08 0.08 0.08 0.08 0.08                                      |
| Sp 007065 CKAP4_HUMAN<br>Sp 0490VH7 SIA7E_HUMAN<br>Sp 04G0N0 GGTA1_HUMAN<br>Sp 034G0N0 GGTA1_HUMAN<br>Sp 0375MB B33GN8_HUMAN<br>Sp 0385V1 SCMTD1_HUMAN<br>Sp 0381ZT8 HS3355_HUMAN<br>Sp 03941 ATF6B_HUMAN<br>Sp 039850 SC11C_HUMAN<br>Sp 039850 SC11C_HUMAN<br>Sp 038050 SC11C_HUMAN<br>Sp 038057 SC11C_HUMAN<br>Sp 08N0Z7 UXS1_HUMAN<br>Sp 08N0Z7 UXS1_HUMAN<br>Sp 08NAT1 PMGT2_HUMAN<br>Sp 032137 SIA8D_HUMAN<br>Sp 032137 SIA8D_HUMAN<br>Sp 03137 SIA8D_HUMAN<br>Sp 03165 CCPG1_HUMAN<br>Sp 03165 CCPG1_HUMAN<br>Sp 03167 CC2B_HUMAN<br>Sp 0317 CC3B_HUMAN<br>Sp 0317 CC3B_HUMAN<br>Sp 0317 CC3B_HUMAN<br>Sp 0317 CC3B_HUMAN<br>Sp 0317 CC3B_HUMAN<br>Sp 0317 CT3B_HUMAN<br>Sp 0317 CT3B_HUMAN | 378 602 336 100 456 397 262 346 703 411 192 1256 402 420 156 167 580 359 166 356 757 318 149 607 393 775 417 370 519   | 20<br>25<br>24<br>20<br>22<br>19<br>29<br>25<br>19<br>20<br>26<br>21<br>19<br>24<br>23<br>19<br>28<br>25<br>24<br>23<br>25<br>24<br>23<br>25<br>24<br>23<br>25<br>26<br>21<br>29<br>20<br>20<br>20<br>20<br>21<br>20<br>21<br>21<br>20<br>21<br>21<br>21<br>22<br>21<br>21<br>22<br>21<br>21<br>22<br>21<br>22<br>21<br>21   | 346<br>475<br>310<br>75<br>403<br>374<br>227<br>315<br>291<br>361<br>137<br>1219<br>376<br>385<br>104<br>81<br>555<br>337<br>135<br>329<br>519<br>288<br>121<br>574<br>355<br>741<br>396<br>346<br>459        | WOLIIGLFATCFLASLMFFW RLGRALNFLFYLALVAAAAFSGWCV TLMRHGLAVCLALTIMCTSLLLVY KVILSMLVVSTVIIVFWEFI ARKLLFMCTLSLSVTYLCYSLL KCLLCLSALLTLLGLKVYI RLSVPAALALGSAALGAAFATGLFLGRRC AWLROKLLVLGSLAVGSLLYLVARV NRKVVCIMVFLLFIAFNFG TVTVLLLAOTTCLLFIISR LYYOVLNFAMINSSALMIWKGLIVLT RYGLYVCFLGVVVTIVSAFQF CLFSASLISALIFVFYYNT RRRMKLLGIALLAYVASVWG KQTLLALLILVLYLSTEIW FSGTSFVVFSLFLICAMAGDVVYA LSAVFNALLVSVLAAVLWKHVRL IRKRWTICTISLLLIFYKT WRLYYQVLNFGMIVSSALMIWKGLMVIT LLRIMMPPKLQLLAVVAFAVAMLFL LNKCVILALVIALSMGFGHFYGTI FLKGVMLGSIFCALITMLGHIRI KKCFIIVGVLITTNIITLIVKLT TLVSTCVILSGMTNICLLYVGWVT CTLALLVGSQLAVMMYLSLGGFRSLSALF LLSVLRPAGPVAVGISLGFTLSLLSVTWV ASYLYGVLFAVGLCAPIYCV LKQNLLACLVISSVTYFYL LLLGLACAVIGSLCFTLSLLSVTWV LKQNLLACLVISSVTYFYL LLLLGLACAVIGSLCFTLSLLSVTWV LKQNLLLACLVISSVTYFYL LLLLGLACAVIGSLCFTLSLLSVTWV LKQNLLLACLVISSVTYFYL LLLGLACAVIGSLCFRISCL | -0.47 -0.47 -0.43 -0.42 -0.41 -0.4 -0.39 -0.28 -0.23 -0.2 -0.19 -0.16 -0.12 -0.09 -0.07 -0.06 -0.03 0 0.01 0.02 0.03 0 0.01 0.02 0.03 0 0.05 0.05 0.08 0.17 0.24 0.35                              |

| sp Q96A11 G3ST3_HUMAN  | 431  | 19 | 397  | SRRKILLLVLGCSTVSLLI        | 0,54 |
|------------------------|------|----|------|----------------------------|------|
| sp P08910 ABHD2_HUMAN  | 425  | 22 | 392  | AVFDGVKLAAVAAVLYVIVRCL     | 0,57 |
| sp P67812 SC11A_HUMAN  | 179  | 26 | 136  | LYYQVLNFGMIVSSALMIWKGLMVIT | 0,57 |
| sp O75356 ENTP5_HUMAN  | 428  | 20 | 407  | ATSWGTVFFMLVVSCVCSAV       | 0,59 |
| sp Q10981 FUT2_HUMAN   | 343  | 19 | 317  | FSFPMAHFILFVFTVSTIF        | 0,87 |
| sp O00468 AGRIN_HUMAN  | 2067 | 22 | 2036 | LRPLLPLLVVAACVLPGAGGTC     | 0,97 |
| sp Q14494 NF2L1_HUMAN  | 772  | 26 | 740  | YLTEGLLQFTILLSLIGVRVDVDTYL | 0,98 |
| sp Q9UIR0 BTNL2_HUMAN  | 455  | 21 | 431  | FPGYNLSGAVASFLFILLTMK      | 1,19 |
| sp O94905 ERLN2_HUMAN  | 339  | 20 | 316  | LGAVVAVASSFFCASLFSAV       | 1,38 |
| sp Q9NST1 PLPL3_HUMAN  | 481  | 24 | 452  | RGWSLSFAGCGFLGFYHVGATRCL   | 1,47 |
| sp Q96AD5 PLPL2_HUMAN  | 504  | 24 | 474  | TWNISFAGCGFLGVYYVGVASCLR   | 1,51 |
| SNIO6P179IFRAP2 HIIMAN | 960  | 21 | 920  | RGEYCLTAIL POLCICSOESV     | 2 10 |