# CTX

| Amino aci | Localizatio | Position | nalf_pvalu | U50_pval | log2_nalf_ | log2_U50_ | Protein | Protein na | Gene nam | Short sequence window |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 149 | 0.005316 | 0.002213 | -2.91602 | -3.1768 | Q9DCS2 | UPF0585 p | 0610011F | YAVNGKISPQSNVDF |
| S | 0.99993 | 211 | 0.030921 | 0.518768 | -1.62205 | -0.44023 | Q8R2R3 | Alpha- and | Aagab | HSEQQEPSPTAERTE |
| T | 0.999999 | 618 | 0.004484 | 0.613015 | -1.4438 | 0.205654 | Q3UHJ0 | AP2-associ | Aak1 | GQKVGSLTPPSSPKT |
| S | 0.999287 | 1178 | 0.019527 | 0.057566 | 3.467151 | 2.301082 | Q80YE4 | Serine/thr | Aatk | VQEPSEDSEEEPPAV |
| S | 1 | 2418 | 0.024757 | 0.121892 | -1.8137 | -1.00063 | P41234 | ATP-bindin | Abca2 | TEDEGLISFEEERAQ |
| S | 1 | 1327 | 0.89173 | 0.007686 | 0.39081 | -4.22995 | P41234 | ATP-bindin | Abca2 | KVSEEDQSLENSEAD |
| S | 1 | 1331 | 0.839844 | 0.003106 | 0.39081 | -4.18085 | P41234 | ATP-bindin | Abca2 | EDQSLENSEADVKES |
| S | 0.998174 | 657 | 0.010989 | 0.696774 | -1.03232 | -0.15311 | P21447 | Multidrug | Abcb1a | SSKDSGSSLIRRRST |
| S | 1 | 138 | 0.000694 | 0.003297 | -2.47225 | -1.57489 | Q6P542 | ATP-bindin | Abcf1 | EALIQDDSEEEEEEE |
| S | 1 | 103 | 0.036371 | 0.188021 | 1.771014 | 0.915035 | Q6P542 | ATP-bindin | Abcf1 | MERLKQLSVPASDEE |
| S | 1 | 107 | 0.036371 | 0.188021 | 1.771014 | 0.915035 | Q6P542 | ATP-bindin | Abcf1 | KQLSVPASDEEDEVP |
| S | 0.999999 | 904 | 0.39069 | 0.033273 | -0.67816 | -1.57624 | P00520-3 | Tyrosine-p | Abl1 | KAGKPAQSPSQEAGE |
| S | 1 | 499 | 0.006561 | 0.92371 | -1.93565 | -0.11409 | Q8K4G5 | Actin-bind | Ablim1 | HRSTSQGSINSPVYS |
| S | 0.867417 | 496 | 0.00305 | 0.713154 | -2.85927 | -0.30366 | Q8BL65-4 | Actin-bind | Ablim2 | RRLDVEDSSFDQDSR |
| S | 0.999609 | 365 | 0.009581 | 0.174951 | -1.38597 | -0.52426 | Q8BL65 | Actin-bind | Ablim2 | YKQCRTSSPSSAGSV |
| S | 1 | 383 | 0.020403 | 0.531077 | 2.18262 | -0.51949 | Q8BL65 | Actin-bind | Ablim2 | HYTPTSRSPQHYSRP |
| S | 0.999609 | 376 | 0.009581 | 0.174951 | -1.38597 | -0.52426 | Q8BL65-4 | Actin-bind | Ablim2 | YKQCRTSSPSSAGSV |
| S | 1 | 394 | 0.020403 | 0.531077 | 2.18262 | -0.51949 | Q8BL65-4 | Actin-bind | Ablim2 | HYTPTSRSPQHYSRP |
| S | 0.999902 | 521 | 0.005449 | 0.97578 | -2.4645 | 0.076675 | Q6ZQK5 | Arf-GAP w | Acap2 | DKYSALLSPSEQEKR |
| S | 0.999999 | 825 | 0.006563 | 0.089157 | -1.68135 | -0.74517 | Q9JIX8 | Apoptotic | Acin1 | KSFKRKISVVSATKG |
| S | 1 | 455 | 0.014062 | 0.651105 | -0.83767 | -0.14524 | Q3V117 | ATP-citrat | Acly | PAPSRTASFSESRAD |
| S | 1 | 1295 | 0.019075 | 0.016653 | -2.8315 | -2.62141 | P51830 | Adenylate | Adcy9 | SDKASLGSDDSTQAK |
| S | 1 | 1292 | 0.00977 | 0.198744 | -2.95765 | -1.06489 | P51830 | Adenylate | Adcy9 | VQYSDKASLGSDDST |
| S | 0.999809 | 12 | 0.027864 | 0.24956 | -1.19723 | 0.505774 | Q9QYC0 | Alpha-add | Add1 | TRAAVVTSPPPTTAP |
| S | 0.998507 | 555 | 0.031481 | 0.159886 | -1.7934 | -0.95192 | E9Q1K3 |  | Add1 | GLAEQTFSPAKSVSF |
| S | 0.999992 | 613 | 0.029295 | 0.005151 | 1.721194 | 2.362786 | Q9QYC0-2 | Alpha-add | Add1 | AVPNTPPSTPVKLEE |
| S | 1 | 629 | 0.038311 | 0.408523 | 1.147108 | 0.398338 | E9Q1K3 |  | Add1 | TREQKEKSPPDQSAV |
| S | 1 | 600 | 0.038311 | 0.408523 | 1.147108 | 0.398338 | Q9QYC0-2 | Alpha-add | Add1 | TREQKEKSPPDQSAV |
| S | 1 | 600 | 0.038311 | 0.408523 | 1.147108 | 0.398338 | Q9QYC0 | Alpha-add | Add1 | TREQKEKSPPDQSAV |
| T | 0.999968 | 639 | 0.040208 | 0.405335 | 1.147108 | 0.405975 | E9Q1K3 |  | Add1 | DQSAVPNTPPSTPVK |
| T | 0.999996 | 643 | 0.003076 | 0.016601 | 1.037548 | 0.623644 | E9Q1K3 |  | Add1 | VPNTPPSTPVKLEEG |
| T | 0.999968 | 610 | 0.040208 | 0.405335 | 1.147108 | 0.405975 | Q9QYC0-2 | Alpha-add | Add1 | DQSAVPNTPPSTPVK |
| T | 0.999996 | 614 | 0.003076 | 0.016601 | 1.037548 | 0.623644 | Q9QYC0-2 | Alpha-add | Add1 | VPNTPPSTPVKLEEA |
| T | 0.999993 | 610 | 0.040208 | 0.405335 | 1.147108 | 0.405975 | Q9QYC0 | Alpha-add | Add1 | DQSAVPNTPPSTPVK |
| T | 0.999998 | 614 | 0.003076 | 0.016601 | 1.037548 | 0.623644 | Q9QYC0 | Alpha-add | Add1 | VPNTPPSTPVKLEED |
| S | 1 | 692 | 0.00168 | 0.77615 | -1.09211 | 0.086945 | Q9QYB8 | Beta-addu | Add2 | SVTSGPLSPEGSPSK |
| S | 1 | 678 | 0.927136 | 0.014109 | -0.30736 | -3.55683 | Q9QYB8 | Beta-addu | Add2 | NADTDGDSYKDKTES |
| S | 1 | 594 | 0.003976 | 0.157126 | 1.58945 | 0.511675 | Q9QYB8 | Beta-addu | Add2 | IATEKPGSPVKSTPA |
| S | 1 | 598 | 0.003287 | 0.015906 | 1.444002 | 0.890469 | Q9QYB8 | Beta-addu | Add2 | KPGSPVKSTPASPVQ |
| S | 0.999984 | 677 | 0.007933 | 0.933896 | -1.41861 | 0.081027 | Q9QYB5 | Gamma-ac | Add3 | EVLSPDGSPSKSPSK |
| S | 0.987444 | 680 | 0.046176 | 0.082117 | -2.57529 | -1.9316 | Q80WT5 | Aftiphilin | Aftph | HLLETHSSPAKTREA |
| S | 0.832519 | 349 | 0.022123 | 0.2524 | 1.160231 | 0.458661 | Q3UHD9 | Arf-GAP w | Agap2 | ISGIFTKSTGGPPGP |
| S | 1 | 974 | 0.037311 | 0.948603 | 0.724276 | 0.053754 | Q8K3E5 | Jouberin | Ahi1 | PPKVKERSPPLTPKE |
| T | 1 | 978 | 0.037311 | 0.948603 | 0.724276 | 0.053754 | Q8K3E5 | Jouberin | Ahi1 | KERSPPLTPKEKTKP |
| S | 1 | 52 | 0.026751 | 0.998953 | -1.62504 | -0.01539 | O88845 | A-kinase a | Akap10 | KASVAVHSPQKSTKN |
| S | 0.997369 | 281 | 0.002227 | 0.632578 | -2.01388 | -0.23616 | O88845 | A-kinase a | Akap10 | GSRNSCSSPLRELSE |
| S | 1 | 467 | 0.015185 | 0.013876 | -2.89332 | -2.64652 | Q9WTQ5 | A-kinase a | Akap12 | HTQLTDLSPEEKMLP |
| S | 1 | 613 | 0.886846 | 0.001637 | -0.20178 | -3.02272 | Q9WTQ5 | A-kinase a | Akap12 | KKRVRRPSESDKEEE |
| S | 0.999137 | 234 | 0.700961 | 0.029689 | 0.693165 | -2.92908 | Q9WTQ5 | A-kinase a | Akap12 | GTLKQAQSSTEIPLQ |
| S | 1 | 682 | 0.155039 | 0.013083 | 0.940021 | -1.75559 | Q9WTQ5 | A-kinase a | Akap12 | KKRARKASSSDDEGG |
| S | 0.99999 | 36 | 0.021129 | 0.889597 | -2.20653 | 0.211451 | A2API8 |  | Akap2;Pak | EPAASSLSPDHKNME |
| S | 1 | 251 | 0.006492 | 0.53395 | -1.41129 | 0.25271 | D3YVF0 | A-kinase a | Akap5 | LESSAAGSPRSVTSA |
| S | 1 | 22 | 0.011566 | 0.151196 | -1.15035 | -0.48283 | D3YVF0 | A-kinase a | Akap5 | EKGPVAASPQKERQE |
| S | 0.996543 | 124 | 0.999928 | 0.046323 | 0.003403 | -0.85305 | P31750 | RAC-alpha | Akt1 | TMDFRSGSPSDNSGA |
| S | 0.999876 | 39 | 0.020114 | 0.481426 | -1.48607 | -0.38385 | P05064 | Fructose-b | Aldoa;Aldo | AADESTGSIAKRLQS |
| S | 1 | 477 | 0.006658 | 0.048908 | 2.25848 | 1.210051 | Q920R0 | Alsin | Als2 | EGGSRRLSLPGLLSQ |
| S | 1 | 486 | 0.006658 | 0.048908 | 2.25848 | 1.210051 | Q920R0 | Alsin | Als2 | PGLLSQVSPRLLRKA |
| S | 1 | 227 | 0.017297 | 0.735047 | -1.97983 | -0.3009 | Q8CCJ4 | APC memb | Amer2 | LPGSLTASLECVKEE |
| S | 1 | 262 | 0.013869 | 0.980862 | -5.39904 | -0.18617 | Q7TQF7 | Amphiphy | Amph | LRIAKTPSPPEEPSP |

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|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.994496 | 779 | 0.016616 | 0.131146 | -4.14113 | -2.00705 | Q91W96 | Anaphase- | Anapc4 | KEEVLSESETEAHQD |
| S | 1 | 3357 | 0.005267 | 0.569101 | -1.76741 | -0.28328 | S4R291 | Ankyrin-2 | Ank2 | KCPVKARSYIETETE |
| S | 1 | 2212 | 0.020859 | 0.909034 | -1.88134 | 0.161703 | S4R291 | Ankyrin-2 | Ank2 | LSFSPKKSEEQIGEA |
| S | 1 | 1925 | 0.02543 | 0.869324 | -1.61256 | 0.178097 | S4R291 | Ankyrin-2 | Ank2 | HEKHLPVSPGKTEKQ |
| S | 1 | 2491 | 0.007864 | 0.756242 | -1.9258 | -0.22909 | S4R291 | Ankyrin-2 | Ank2 | SSGKSPLSPDTPSSE |
| S | 0.999965 | 886 | 0.011256 | 0.962544 | -1.36118 | 0.062868 | Q8C8R3-2 | Ankyrin-2 | Ank2 | GMNYLRYSLEGGRSD |
| S | 0.999999 | 8 | 0.005323 | 0.368802 | -2.21658 | -0.50224 | Q8C8R3-3 | Ankyrin-2 | Ank2 | MTEVLDVSDEEGDDT |
| S | 0.998132 | 890 | 0.011256 | 0.962544 | -1.36118 | 0.062868 | S4R291 | Ankyrin-2 | Ank2 | GMNYLRYSLEGGRSD |
| S | 1 | 31 | 0.008522 | 0.49044 | -0.87069 | 0.179188 | S4R291 | Ankyrin-2 | Ank2 | KRPKKSDSNASFLRA |
| S | 1 | 7 | 0.010063 | 0.228397 | -3.04832 | -1.0383 | Q8C8R3-7 | Ankyrin-2 | Ank2 | _MAHAAASIKKVREA |
| S | 1 | 46 | 0.008522 | 0.49044 | -0.87069 | 0.179188 | Q8C8R3-7 | Ankyrin-2 | Ank2 | ERKRKSDSNASFLRA |
| S | 1 | 10 | 0.008522 | 0.49044 | -0.87069 | 0.179188 | S4R245 | Ankyrin-2 | Ank2 | TMLQKSDSNASFLRA |
| T | 0.994747 | 3713 | 7.98E-05 | 0.262007 | -5.16629 | 0.577271 | S4R291 | Ankyrin-2 | Ank2 | QQEYYVTTPGAEVED |
| T | 0.999985 | 2328 | 0.008519 | 0.965522 | -1.27226 | -0.05266 | S4R291 | Ankyrin-2 | Ank2 | SETQESLTPSEVTKP |
| S | 0.996941 | 2159 | 0.04464 | 0.93665 | 0.951805 | -0.08294 | S4R291 | Ankyrin-2 | Ank2 | QSGALGGSSESLKQE |
| S | 0.996422 | 2162 | 0.04464 | 0.93665 | 0.951805 | -0.08294 | S4R291 | Ankyrin-2 | Ank2 | ALGGSSESLKQEVIA |
| S | 0.936215 | 2653 | 0.022615 | 0.147881 | 6.696935 | 3.356246 | S4R291 | Ankyrin-2 | Ank2 | PPSPLPSSIDSNSSP |
| S | 1 | 3759 | 0.000396 | 0.75353 | -6.05082 | 0.375455 | S4R291 | Ankyrin-2 | Ank2 | PVTSERGSPIVQEPE |
| S | 1 | 967 | 0.03707 | 0.962757 | -1.19824 | -0.07511 | S4R2K9 | Ankyrin-3 | Ank3 | TREFDSDSLRHYSWA |
| S | 0.998819 | 2041 | 0.098296 | 0.047474 | 1.697529 | 1.906858 | Q99NH0 | Ankyrin re | Ankrd17 | YPVSSPSSPSPPAQP |
| S | 0.978858 | 634 | 0.008965 | 0.5586 | -1.26788 | -0.23455 | Q3UMR0 | Ankyrin re | Ankrd27 | PSEVPAQSPTRSVDS |
| S | 1 | 260 | 0.028641 | 0.400868 | -0.71256 | -0.23145 | Q3UUF8 | Ankyrin re | Ankrd34b | KHQARVASLQEELQD |
| S | 1 | 272 | 0.00432 | 0.632563 | -2.14011 | -0.29111 | Q9JME5 | AP-3 comp | Ap3b2 | PEKAFYGSEEDEAKG |
| S | 1 | 282 | 0.005979 | 0.745329 | -1.07624 | 0.123417 | Q9JME5 | AP-3 comp | Ap3b2 | DEAKGPGSEEAATAA |
| S | 1 | 760 | 0.008539 | 0.928013 | -0.81787 | -0.04973 | O54774 | AP-3 comp | Ap3d1 | HSSLPTESDEDIAPA |
| S | 1 | 317 | 0.024387 | 0.932346 | -0.87155 | -0.06661 | B2RUJ5 | Amyloid b | Apba1 | PGGGHPDSPGLPAPA |
| S | 0.999714 | 84 | 0.016366 | 0.139242 | -2.42723 | -1.14587 | B2RUJ5 | Amyloid b | Apba1 | ECLARSASTESGFHN |
| S | 0.999994 | 573 | 0.592813 | 0.022313 | 0.233296 | -0.85587 | B2RUJ5 | Amyloid b | Apba1 | RRMPRSNSQENVEAS |
| S | 0.999965 | 289 | 0.574312 | 0.037876 | 0.568089 | -1.74696 | B2RUJ5 | Amyloid b | Apba1 | KQSMSSQSLDKAAED |
| S | 0.999984 | 2710 | 0.037746 | 0.999008 | -2.84235 | 0.028791 | B2RUG9 | Adenomat | Apc | KQSVGSGSPVQTVGL |
| S | 1 | 108 | 0.0138 | 0.324612 | -3.64997 | -1.12051 | Q9Z1K7 | Adenomat | Apc2 | AARTPEGSPVHGSGP |
| S | 1 | 187 | 0.042134 | 0.962485 | -2.33559 | 0.152356 | Q8R146 | Acylamino | Apeh | KALDVSASDEEMARP |
| S | 1 | 276 | 0.696702 | 0.042838 | 0.298983 | -1.13058 | P55088 | Aquaporin | Aqp4 | AAQQTKGSYMEVEDN |
| S | 1 | 285 | 0.696702 | 0.042838 | 0.298983 | -1.13058 | P55088 | Aquaporin | Aqp4 | MEVEDNRSQVETEDL |
| S | 0.99122 | 1550 | 0.03174 | 0.480025 | -1.67515 | -0.48934 | G3X9K3 | Brefeldin | Arfgef1 | SGEAEPPSPSAVSEK |
| T | 0.928318 | 623 | 0.973562 | 0.024505 | -0.17282 | -2.94146 | A2A5R2 | Brefeldin | Arfgef2 | MARRCSVTSVESTVS |
| S | 0.998395 | 314 | 0.009374 | 0.957719 | -2.08319 | -0.09801 | Q6DFV3 | Rho GTPas | Arhgap21 | KAASRTTSPASVPTA |
| S | 0.999229 | 1108 | 0.004644 | 0.580881 | -3.29846 | -0.50277 | Q6DFV3 | Rho GTPas | Arhgap21 | LLSKDDTSPPKDKGT |
| S | 1 | 874 | 0.01907 | 0.392312 | -1.53139 | -0.45368 | Q6DFV3 | Rho GTPas | Arhgap21 | SKTERSKSYDEGLDD |
| S | 1 | 1092 | 0.040244 | 0.121425 | -2.44444 | -1.54169 | Q6DFV3 | Rho GTPas | Arhgap21 | PKTQSPHSPKEESER |
| S | 0.999998 | 426 | 0.009269 | 0.30482 | -1.57732 | 0.455367 | B1AQY2 | Rho GTPas | Arhgap23 | YIGYRSYSPSFQRRT |
| S | 1 | 644 | 0.018537 | 0.586783 | 1.110473 | 0.233444 | B1AQY2 | Rho GTPas | Arhgap23 | RVLRRLPSRVPSLRV |
| S | 1 | 648 | 0.018537 | 0.586783 | 1.110473 | 0.233444 | B1AQY2 | Rho GTPas | Arhgap23 | RLPSRVPSLRVLRSF |
| S | 0.999193 | 850 | 0.021715 | 0.493034 | -0.82333 | 0.212664 | A6X8Z5 | Rho GTPas | Arhgap31 | NKGPGLPSPTKEVDI |
| S | 1 | 1823 | 0.038333 | 0.669549 | -1.39252 | -0.30251 | Q811P8 | Rho GTPas | Arhgap32 | RHPAKAVSPEGDERF |
| S | 0.999294 | 830 | 0.018882 | 0.538253 | -3.95208 | 0.910615 | Q811P8 | Rho GTPas | Arhgap32 | GYTRDKLSPSKKDAE |
| S | 0.997274 | 871 | 0.003095 | 0.569758 | -2.25852 | -0.32049 | Q811P8 | Rho GTPas | Arhgap32 | PFFTLDLSPTDDKSS |
| S | 1 | 597 | 0.009427 | 0.709368 | -1.41901 | 0.197222 | P59281 | Rho GTPas | Arhgap39 | GPVVRAFSEDEALAQ |
| S | 1 | 931 | 0.010141 | 0.407863 | -1.09595 | -0.27041 | Q60875 | Rho guani | Arhgef2 | REAQELGSPEDRLQD |
| S | 1 | 697 | 0.000962 | 0.071528 | -1.64467 | 0.510661 | E9QAQ7 | AT-rich int | Arid1a | LPGIRGPSPSPVGSP |
| S | 0.810603 | 246 | 0.022818 | 0.848926 | -0.95824 | -0.11164 | Q9D7A8 | Armadillo | Armc1 | DYLPEDESPTKEQDK |
| S | 1 | 67 | 0.010038 | 0.988577 | -2.13337 | -0.05236 | P60840 | cAMP-reg | Arpp19;En | KGQKYFDSGDYNMAK |
| S | 1 | 32 | 0.014317 | 0.851141 | -0.93349 | -0.09579 | Q9DCB4 | cAMP-reg | Arpp21 | NGILKSESLDEEEKL |
| T | 0.77221 | 852 | 0.015458 | 0.197272 | -2.32997 | -0.94173 | Q9QWY8 | Arf-GAP w | Asap1 | PPPGHKRTLSDPPSP |
| S | 1 | 704 | 0.00236 | 0.408114 | -3.59795 | -0.63476 | Q7SIG6 | Arf-GAP w | Asap2 | LHEDLDESDDDVDEK |
| S | 0.999733 | 317 | 0.006593 | 0.371255 | 1.277843 | 0.302988 | G3X963 | | Atad2 | RPRFRLSSTGPRSPY |
| S | 1 | 828 | 0.034694 | 0.910191 | -1.2478 | -0.12199 | Q3ZAQ4 | | Atg9a | EPVPEEGSEDELPPQ |
| S | 1 | 58 | 0.02456 | 0.933905 | -1.41809 | -0.10725 | Q6PIE5 | Sodium/p | Atp1a2 | RKYQVDLSKGLTNQR |
| S | 0.999552 | 442 | 0.028551 | 0.058959 | -1.54982 | -1.12816 | Q6PIC6 | Sodium/p | Atp1a3 | RDVAGDASESALLKC |
| S | 1 | 218 | 0.021578 | 0.927224 | -0.75256 | -0.0579 | Q6PIC6 | Sodium/p | Atp1a3 | ESEPQTRSPDCTHDN |

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|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.999997 | 663 | 0.001079 | 0.485457 | -1.35042 | 0.176271 | O55143 | Sarcoplasn | Atp2a2 | EFDELSPSAQRDACL |
| T | 1 | 1165 | 0.019906 | 0.963823 | -3.94992 | 0.206594 | G5E829 | Plasma me | Atp2b1 | HIPLIDDTDAEDDAP |
| S | 0.85441 | 19 | 0.003039 | 0.445525 | -3.27399 | -0.57359 | Q9R0K7 | Plasma me | Atp2b2 | KNQRNESSHGGEFGC |
| S | 1 | 1126 | 0.021354 | 0.710185 | -0.81105 | -0.13787 | A2ALL9 | Calcium-tr | Atp2b3 | STFKRSGSFQGAVRR |
| S | 1 | 1134 | 0.023809 | 0.070543 | -1.26519 | -0.83044 | Q0VF55 | Calcium-tr | Atp2b3 | EGLEKPESKSCIHNF |
| T | 1 | 45 | 0.008437 | 0.437128 | -3.89181 | -0.87461 | D3Z2Z6 | | Atp8a2 | EDEMSRATSVGDQLE |
| S | 0.980624 | 1467 | 0.001125 | 0.842664 | -1.40649 | 0.083328 | Q3UHD1 | Brain-spec | Bai1;Adgrb | VATLSVSSLERRKSR |
| S | 1 | 1220 | 0.01802 | 0.547419 | -1.07059 | -0.23986 | Q80ZF8 | Brain-spec | Bai3;Adgrb | TGTLSRISLNDDEEE |
| S | 0.997186 | 54 | 0.005832 | 0.412464 | -1.82496 | -0.39209 | Q91XV3 | Brain acid | Basp1 | DATEVKESTEEKPKD |
| S | 0.978393 | 192 | 0.005606 | 0.979912 | -1.07024 | 0.030471 | Q91XV3 | Brain acid | Basp1 | AASEAPSSAAKAPAP |
| T | 1 | 31 | 0.039542 | 0.997908 | -1.61201 | 0.024032 | Q91XV3 | Brain acid | Basp1 | KKAEGAGTEEEGTPK |
| S | 1 | 1464 | 0.002163 | 0.760146 | -1.28884 | -0.11317 | Q9Z277 | Tyrosine-p | Baz1b | LADDEGDSDSESVGQ |
| S | 1 | 525 | 0.021966 | 0.517391 | -1.00735 | 0.250268 | Q80YN3 | Breast carc | Bcas1 | NSVEKTPSPPEPEPA |
| S | 1 | 615 | 0.246852 | 0.007447 | -1.05082 | -2.75107 | Q80YN3 | Breast carc | Bcas1 | GLGPKRMSDAQVQTD |
| S | 0.999997 | 360 | 0.037758 | 0.540116 | -2.87385 | -0.79396 | Q80YN3 | Breast carc | Bcas1 | RHKDTENSPTTSANL |
| S | 1 | 271 | 0.021966 | 0.517391 | -1.00735 | 0.250268 | F7BNZ5 | | Bcas1 | NSVEKTPSPPEPEPA |
| S | 1 | 177 | 0.000437 | 0.946035 | -1.52536 | 0.041341 | Q8K019 | Bcl-2-asso | Bclaf1 | EGEPQEESPLKSKSQ |
| S | 0.999999 | 656 | 0.001324 | 0.758195 | -2.32374 | 0.184237 | Q8K019 | Bcl-2-asso | Bclaf1 | IHRRIDISPSALRKH |
| S | 1 | 646 | 0.017663 | 0.99664 | -2.22895 | 0.033995 | Q8K019 | Bcl-2-asso | Bclaf1 | EHSTRQKSPEIHRRI |
| S | 1 | 636 | 0.03488 | 0.227817 | -1.51355 | -0.7098 | Q6PGF5 | | Bms1 | GQKPASESLVDETSD |
| S | 1 | 642 | 0.014538 | 0.36798 | -1.73597 | -0.50064 | Q6PGF5 | | Bms1 | ESLVDETSDIESLLK |
| S | 1 | 119 | 0.030702 | 0.419911 | -1.58903 | -0.50924 | Q9Z2F7 | BCL2/aden | Bnip3l | SRDHSSQSEEEVVEG |
| S | 1 | 135 | 0.998283 | 0.023915 | -0.03272 | 1.028614 | P28028 | Serine/thr | Braf | ASRNNPKSPQKPIVR |
| S | 1 | 519 | 0.000347 | 0.102333 | -3.14843 | -0.7001 | Q5RJI5 | Serine/thr | Brsk1 | SGGTPLHSPLHTPRA |
| S | 1 | 3301 | 0.00549 | 0.87915 | -1.43357 | 0.104081 | O88737 | Protein ba | Bsn | YGRGEEESEEDSYDP |
| S | 1 | 3382 | 0.013425 | 0.71489 | -0.98902 | 0.147925 | O88737 | Protein ba | Bsn | EQKISKFSPIEEAKD |
| S | 0.954332 | 2822 | 0.130472 | 0.022175 | -0.68457 | 1.047501 | O88737 | Protein ba | Bsn | LLDTSFASSERLNKA |
| S | 0.999959 | 2866 | 0.001559 | 0.970742 | -5.99063 | -0.15521 | O88737 | Protein ba | Bsn | LSDPKPLSPTAEESA |
| S | 1 | 249 | 0.007268 | 0.035057 | -2.74279 | -1.64879 | O88737 | Protein ba | Bsn | PALSPAHSPAKQPLG |
| T | 1 | 2595 | 0.001219 | 0.337322 | -1.27156 | 0.219274 | O88737 | Protein ba | Bsn | IADSSVQTDDEEGEG |
| S | 1 | 1100 | 0.038535 | 0.193886 | 1.37916 | 0.714711 | O88737 | Protein ba | Bsn | AQRRRERSKTPPSNL |
| S | 0.999982 | 1486 | 0.040489 | 0.982722 | 1.731757 | 0.075165 | O88737 | Protein ba | Bsn | TGSSPPLSPSTPSES |
| S | 0.982729 | 1493 | 0.03746 | 0.508458 | 1.364436 | 0.397404 | O88737 | Protein ba | Bsn | SPSTPSESPTFSPGK |
| S | 0.99998 | 464 | 0.619377 | 0.043306 | -0.2346 | -0.75532 | Q80X80 | C2 domain | C2cd2l | RVDGKLDSPSRSPSK |
| S | 0.998557 | 466 | 0.008149 | 0.221741 | -3.64367 | -1.19634 | Q80X80 | C2 domain | C2cd2l | DGKLDSPSRSPSKVE |
| S | 0.999995 | 396 | 0.004809 | 0.00063 | -2.51706 | -3.51411 | Q80X80 | C2 domain | C2cd2l | PGPGKSLSPAATVTA |
| S | 1 | 411 | 0.004809 | 0.00063 | -2.51706 | -3.51411 | Q80X80 | C2 domain | C2cd2l | ELHYEQGSPRNLGTP |
| S | 0.999971 | 659 | 0.047651 | 0.117663 | -2.80597 | -1.87866 | Q7TPS5 | C2 domain | C2cd5 | SRLLRSQSESSDEVT |
| S | 0.999962 | 1130 | 0.034072 | 0.799407 | -4.93653 | -0.7555 | E9Q5L4 | Uncharact | C530008M | PVLQSRHSLDGSKVT |
| S | 1 | 2303 | 0.016421 | 0.982267 | -2.8747 | -0.09947 | P97445 | Voltage-de | Cacna1a | ADYTEPDSPREPPGG |
| S | 1 | 15 | 0.056314 | 0.024823 | -1.04226 | -1.17259 | Q61290 | Voltage-de | Cacna1e | VVVGRPGSGDGDSDQ |
| S | 1 | 2054 | 0.001008 | 0.294512 | -1.78029 | -0.31807 | Q61290 | Voltage-de | Cacna1e | KERKHLLSPDVSRCN |
| S | 0.999968 | 152 | 0.487112 | 0.021235 | -0.62868 | -1.93877 | P54285 | Voltage-de | Cacnb3 | GDIGNRRSPPPSLAK |
| S | 1 | 248 | 0.021037 | 0.997178 | -0.78587 | 0.011484 | Q9JJV5 | Voltage-de | Cacng3 | EPRSRDLSPISKGFH |
| S | 1 | 1859 | 0.070964 | 0.046672 | -2.11857 | -2.14995 | B2RQC6 | CAD prote | Cad | PPRIHRASDPGLPAE |
| S | 1 | 96 | 0.206028 | 0.041449 | 1.16527 | 1.809636 | Q80TJ1 | Calcium-de | Cadps | SPSPSVVSEKEKEEL |
| S | 0.927414 | 275 | 0.001078 | 0.172176 | -4.81243 | -1.12015 | P11798 | Calcium/ca | Camk2a | HPWISHRSTVASCMH |
| S | 1 | 279 | 0.040669 | 0.757978 | -1.91923 | 0.346038 | P11798 | Calcium/ca | Camk2a | SHRSTVASCMHRQET |
| T | 1 | 287 | 0.028059 | 0.630141 | -1.25378 | 0.270635 | Q5SVJ0 | Calcium/ca | Camk2b | SMMHRQETVECLKKF |
| T | 0.988646 | 371 | 0.000166 | 0.853485 | -4.8069 | -0.18284 | Q923T9-2 | Calcium/ca | Camk2g | TDGIKGSTESCNTTT |
| T | 0.988646 | 348 | 0.000167 | 0.853855 | -4.80835 | -0.18284 | Q923T9-3 | Calcium/ca | Camk2g | TDGIKGSTESCNTTT |
| S | 1 | 734 | 0.03555 | 0.820546 | 0.803242 | 0.116448 | A2AHC3 | Calmoduli | Camsap1 | WTILRQDSDSDVVDV |
| S | 1 | 736 | 0.03555 | 0.820546 | 0.803242 | 0.116448 | A2AHC3 | Calmoduli | Camsap1 | ILRQDSDSDVVDVED |
| S | 1 | 1248 | 0.000412 | 0.359227 | -3.02893 | -0.39931 | Q8C1B1 | Calmoduli | Camsap2 | IHRDHIESPKTPIKG |
| T | 1 | 830 | 0.002536 | 0.197338 | -1.72865 | 0.45786 | Q80VC9 | Calmoduli | Camsap3 | SILLSEGTPPEEPTT |
| S | 0.999982 | 1077 | 0.003459 | 0.004649 | 2.304635 | 1.927707 | Q80VC9 | Calmoduli | Camsap3 | RPTSRAPSPSGLMSP |
| S | 1 | 362 | 0.004001 | 0.379461 | 1.420862 | 0.29617 | Q80VC9 | Calmoduli | Camsap3 | NFRHPLLSPGGPQSP |
| S | 1 | 368 | 0.004001 | 0.379461 | 1.420862 | 0.29617 | Q80VC9 | Calmoduli | Camsap3 | LSPGGPQSPLRGSTG |
| S | 0.998761 | 431 | 0.383005 | 0.044859 | 0.355154 | 0.749208 | Q80VC9 | Calmoduli | Camsap3 | PVLLRSVSSDSLGPP |
| S | 0.999984 | 434 | 0.383005 | 0.044859 | 0.355154 | 0.749208 | Q80VC9 | Calmoduli | Camsap3 | LRSVSSDSLGPPRPV |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 582 | 0.016959 | 0.955896 | -0.94748 | -0.05271 | P35564 | Calnexin | Canx | EDEILNRSPRNRKPR |
| S | 0.999659 | 34 | 0.013328 | 0.173744 | -1.66912 | -0.68608 | P40124 | Adenylyl c | Cap1 | MHCGYGDSPSKGAVP |
| S | 1 | 53 | 0.007171 | 0.986285 | -2.04856 | 0.050902 | Q9CR86 | Calcium-re | Carhsp1 | TRRTRTFSATVRASQ |
| S | 1 | 791 | 0.025743 | 0.767007 | -1.0527 | -0.16359 | Q6P9K8 | Caskin-1 | Caskin1 | PTKAQPGSPQALGGP |
| S | 1 | 1259 | 0.019424 | 0.558553 | -0.74498 | 0.1668 | Q6P9K8 | Caskin-1 | Caskin1 | VPLPGPGSPEVKRAH |
| S | 0.999767 | 423 | 0.000708 | 0.916678 | -4.50563 | 0.170167 | Q6P9K8 | Caskin-1 | Caskin1 | ATVLSQKSVSESSPG |
| S | 1 | 95 | 0.016715 | 0.392207 | 1.072758 | -0.30741 | Q9DCC5 | Chromobo | Cbx3 | GTKRKSLSDSESDDS |
| S | 1 | 50 | 0.000195 | 0.006757 | -3.3087 | -1.37065 | Q3TVA9 | Coiled-coil | Ccdc136 | MGKHRGLSLTETELE |
| T | 1 | 137 | 0.002782 | 0.773714 | -2.58347 | -0.23137 | Q9CR29 | Coiled-coil | Ccdc43 | LAQYADVTDEEDEAD |
| S | 0.999997 | 308 | 0.006278 | 0.494455 | -1.37987 | -0.26249 | Q5SP85 | Coiled-coil | Ccdc85a | PKHVLSGSPEHFQKH |
| S | 0.999994 | 194 | 0.0152 | 0.985687 | -1.39888 | 0.042591 | Q8VDN4 | Coiled-coil | Ccdc92 | RRMKKSLSAPLHPEF |
| S | 1 | 305 | 0.021384 | 0.959 | -3.26667 | -0.18566 | Q7TQK5 | Coiled-coil | Ccdc93 | SELSAEESPEKLGTS |
| S | 1 | 393 | 0.031221 | 0.970422 | -1.53749 | 0.081661 | Q8K2Y9 | Cerebral c | Ccm2 | GRGIITDSFGRHRRA |
| S | 1 | 358 | 0.014154 | 0.498064 | -0.70734 | 0.162511 | Q52KE7 | Cyclin-L1 | Ccnl1 | EVKAEEKSPVSINVK |
| S | 1 | 222 | 0.041448 | 0.608533 | -2.11793 | -0.53053 | Q8QZT2 | Centriole, | Ccsap | AQRQRAHSVDVEKNQ |
| S | 1 | 1692 | 0.985107 | 0.035226 | -0.13715 | -2.83375 | Q7TT50 | Serine/thr | Cdc42bpb | SNPSGPPSPNSPHRS |
| S | 1 | 64 | 0.000859 | 0.012196 | -2.67972 | -1.31636 | Q9JM96 | Cdc42 effe | Cdc42ep4 | AREADDESLDEQASA |
| S | 0.999939 | 110 | 0.019094 | 0.283831 | -1.32284 | -0.47435 | Q04735 | Cyclin-dep | Cdk16 | NHPPRKISTEDINKR |
| S | 0.999795 | 109 | 0.002819 | 0.735619 | -1.22628 | -0.1214 | Q04899 | Cyclin-dep | Cdk18 | TRMSRRASLSDIGFG |
| T | 0.999713 | 138 | 0.026712 | 0.85698 | -1.42975 | 0.168318 | P61809 | Cyclin-dep | Cdk5r1 | PAITSAGTPKRVIVQ |
| S | 1 | 347 | 0.036313 | 0.015018 | -0.65215 | -0.73538 | Q99J95 | Cyclin-dep | Cdk9 | APPRRKGSQITQQST |
| S | 0.985127 | 34 | 0.044404 | 0.669341 | 1.768147 | 0.40064 | Q99L43 | Phosphati | Cds2 | DGETASDSESRAETA |
| S | 0.998911 | 109 | 0.009905 | 0.246941 | 1.096633 | -0.35856 | Q9JKC6 | Cell cycle | Cend1 | DGAEEDESNTGGRGP |
| S | 0.999999 | 1341 | 0.011012 | 0.181533 | -1.42728 | -0.54981 | Q80U49 | Centrosom | Cep170b | GDGDSLGSPGPTRSP |
| S | 0.999532 | 981 | 0.068927 | 0.019522 | 0.600798 | -0.76537 | Q80U49 | Centrosom | Cep170b | PQKESPLSPPTVPDP |
| T | 1 | 25 | 0.02719 | 0.319387 | -0.86841 | -0.3202 | P18760 | Cofilin-1 | Cfl1 | MKVRKSSTPEEVKKR |
| S | 1 | 110 | 0.028302 | 0.363808 | -1.33564 | -0.46065 | Q8K327 | Chromoso | Champ1 | TESGKSPSPPERQNP |
| S | 0.999994 | 164 | 0.005238 | 0.031985 | -2.72022 | -1.55397 | Q91VN4 | MICOS cor | Chchd6 | SLPKKKASLTHEQQQ |
| S | 1 | 1997 | 0.021569 | 0.408854 | -1.14526 | 0.340537 | Q09XV5 | Chromodo | Chd8 | QCTSRTASPSPLRPD |
| S | 1 | 1997 | 0.00786 | 0.038418 | 0.832503 | 0.496921 | Q09XV5 | Chromodo | Chd8 | QCTSRTASPSPLRPD |
| S | 1 | 1999 | 0.00786 | 0.038418 | 0.832503 | 0.496921 | Q09XV5 | Chromodo | Chd8 | TSRTASPSPLRPDAP |
| S | 0.771396 | 99 | 0.031878 | 0.533741 | -5.86873 | -1.56471 | P16014 | Secretogra | Chgb | ASGTRWASSREDAGA |
| S | 0.968108 | 100 | 0.003788 | 0.520645 | -6.39516 | -1.03573 | P16014 | Secretogra | Chgb | SGTRWASSREDAGAP |
| S | 0.999999 | 199 | 0.011482 | 0.999045 | -3.30962 | -0.02416 | Q8BJF9 | Charged m | Chmp2b | STSKATISDEEIERQ |
| S | 0.999918 | 1080 | 0.016939 | 0.893632 | -1.12426 | -0.09976 | Q924A2 | Protein ca | Cic | PGKRRTQSLSALPKE |
| S | 1 | 148 | 0.05002 | 0.028122 | -2.52284 | -2.65092 | P30275 | Creatine ki | Ckmt1 | HTTDLDASKIRSGYF |
| S | 1 | 600 | 0.009046 | 0.010693 | -3.19766 | -2.74735 | E9QKH0 | CLIP-assoc | Clasp1 | GSLQRSRSDIDVNAA |
| S | 1 | 376 | 0.005102 | 0.032672 | -2.73369 | -1.54326 | F7DCH5 | CLIP-assoc | Clasp2 | GSLQRSRSDIDVNAA |
| T | 0.860257 | 600 | 0.000222 | 0.117895 | -3.90077 | -0.75192 | F7DCH5 | CLIP-assoc | Clasp2 | SAMRVLNTGSDVEEA |
| S | 1 | 14 | 0.939704 | 0.005779 | 0.143142 | -2.26634 | F7DCH5 | CLIP-assoc | Clasp2 | KRICDYKSFDDEESV |
| S | 0.999969 | 319 | 0.993918 | 0.013908 | -0.02518 | -1.04136 | F7DCH5 | CLIP-assoc | Clasp2 | TYLKSSGSVASLPQS |
| S | 0.99999 | 247 | 0.950134 | 0.041247 | 0.143142 | -1.52386 | Q8BRT1-5 | CLIP-assoc | Clasp2 | KSFDDEESVDGNRPS |
| S | 0.992603 | 58 | 0.01017 | 0.80428 | -1.98986 | -0.22019 | Q99LI2 | Chloride c | Clcc1 | KKEVSPDSSEAEELS |
| S | 1 | 419 | 0.005601 | 0.969878 | -1.68839 | 0.059101 | Q8C5W0 | Calmin | Clmn | KDGRRSNSLPVKKTV |
| S | 1 | 100 | 0.00148 | 0.508781 | -2.02645 | 0.272094 | Q923F1 | | Clns1a | EESKEPLSDEDEEDN |
| S | 1 | 103 | 0.012203 | 0.950773 | -2.42926 | -0.13184 | B1AWE0 | Clathrin lig | Clta | SEVDRLQSEPESIRK |
| S | 0.999998 | 329 | 0.00011 | 0.096472 | -1.32998 | -0.23787 | Q9D4C9 | Clavesin-1 | Clvs1 | KPMKRSQSVVEAGTL |
| S | 1 | 317 | 0.003428 | 0.212659 | -4.10172 | -1.12427 | P47746 | Cannabino | Cnr1 | IQRGTQKSIIIHTSE |
| S | 1 | 171 | 8.84E-05 | 0.834434 | -3.17567 | -0.11375 | Q5SU73 | Coilin | Coil | KKSKVTGSPAEEDEE |
| S | 0.968484 | 261 | 0.000315 | 7.87E-05 | -5.32695 | -6.34931 | O88587 | Catechol C | Comt | VYQGPGSSPVKS___ |
| S | 1 | 13 | 0.014695 | 0.013435 | -1.70404 | -1.55839 | O89079 | Coatomer | Cope | PGAVSGGSGEVDELF |
| S | 1 | 141 | 0.542335 | 0.011984 | -0.18243 | -0.71463 | Q9CQI6 | Coactosin- | Cotl1 | GANYDAQSE______ |
| S | 1 | 54 | 0.005773 | 0.641638 | -1.31942 | -0.18844 | Q6P1J1 | | Crmp1 | TIDFDAYSVGRRGSA |
| T | 1 | 623 | 0.00149 | 0.443199 | -2.24283 | 0.337167 | Q6P1J1 | Dihydropy | Crmp1 | PVYEVPATPKHAAPA |
| S | 0.999997 | 557 | 0.042354 | 0.999373 | -0.86999 | 0.007238 | Q9R194 | Cryptochr | Cry2 | ALSSGPASPKRKLEA |
| S | 0.999786 | 2 | 0.032834 | 0.939815 | -2.11202 | 0.164351 | P67871 | Casein kin | Csnk2b | ______MSSSEEVSW |
| S | 1 | 192 | 0.001155 | 0.264975 | -2.11977 | -0.41201 | P97315 | Cysteine a | Csrp1 | GAGALVHSE______ |
| S | 1 | 641 | 0.005152 | 0.268919 | -3.03174 | -0.81497 | P26231 | Catenin al | Ctnna1 | TPEELDDSDFETEDF |
| S | 1 | 640 | 0.010423 | 0.849564 | -2.36521 | -0.22591 | Q61301 | Catenin al | Ctnna2 | PEELEDDSDFEQEDY |
| S | 1 | 637 | 0.024594 | 0.345303 | -3.55953 | -1.22112 | Q65CL1 | Catenin al | Ctnna3 | PEELEDVSDLEDDHE |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 268 | 0.033214 | 0.998284 | -1.45891 | -0.01877 | P30999 | Catenin de | Ctnnd1 | PQVRVGGSSVDLHRF |
| S | 1 | 411 | 0.013033 | 0.311253 | -1.17513 | -0.36426 | E9QKH8 | Catenin de | Ctnnd2 | PELRALQSPEHHIDP |
| S | 1 | 533 | 0.017159 | 0.999971 | -2.54667 | 0.003591 | E9QKH8 | Catenin de | Ctnnd2 | ARSPSIDSIQKDPRE |
| S | 0.999513 | 456 | 0.031332 | 0.104551 | 4.260664 | 2.643581 | E9QKH8 | Catenin de | Ctnnd2 | FRTSTAPSSPGVDSV |
| S | 0.998618 | 457 | 0.292119 | 0.02697 | 0.686568 | 1.421259 | E9QKH8 | Catenin de | Ctnnd2 | RTSTAPSSPGVDSVP |
| S | 1 | 407 | 0.000284 | 0.091012 | -5.43189 | 1.205798 | Q60598 | Src substra | Cttn | QTPPASPSPQPIEDR |
| S | 0.999966 | 417 | 0.000628 | 0.853002 | 1.339968 | 0.067431 | Q60598 | Src substra | Cttn | PIEDRPPSSPIYEDA |
| S | 1 | 407 | 0.002592 | 0.014189 | 0.994132 | 0.598232 | Q60598 | Src substra | Cttn | QTPPASPSPQPIEDR |
| S | 0.999966 | 417 | 0.007493 | 0.059207 | 1.224783 | 0.637398 | Q60598 | Src substra | Cttn | PIEDRPPSSPIYEDA |
| T | 1 | 401 | 0.002277 | 0.012847 | 1.056727 | 0.633275 | Q60598 | Src substra | Cttn | QARAKKQTPPASPSP |
| S | 1 | 309 | 0.006506 | 0.169712 | -3.22944 | -1.12875 | Q9DBF7 | Pre-mRNA | Cwc25 | RKERDSPSPKKEAYQ |
| S | 0.999509 | 332 | 0.011853 | 0.989949 | -1.04937 | 0.025136 | P97792 | Coxsackiev | Cxadr | DFERAPQSPTLAPAK |
| S | 1 | 1163 | 0.004455 | 0.913838 | -3.49054 | -0.20085 | F6ZGR6 | | D430041D | RKRNVTASDEEEGAG |
| S | 1 | 978 | 0.001291 | 0.049283 | -1.86442 | -0.69042 | Q3UHC7 | Disabled h | Dab2ip | SSSSKGDSPELKPRA |
| S | 0.999999 | 409 | 0.013243 | 0.625828 | -1.49229 | 0.267937 | Q0PHV7 | Dapper ho | Dact3 | RKAARSQSETSLLGR |
| S | 0.999742 | 1032 | 0.021058 | 0.264903 | -1.72911 | -0.65883 | Q6WQJ1 | Sn1-specifi | Dagla | TPTGHGASPTKQDDL |
| S | 1 | 142 | 0.002094 | 0.253989 | -2.10455 | 0.475561 | Q9QXS6 | Drebrin | Dbn1 | NGLARLSSPVLHRLR |
| S | 1 | 100 | 0.001031 | 0.104417 | -4.15544 | -1.15603 | Q8N7N5 | DDB1- and | Dcaf8 | ESRGHGHSDEEDEEQ |
| S | 0.99999 | 545 | 0.011088 | 0.073093 | 2.495436 | 1.336164 | Q91YD3 | mRNA-dec | Dcp1a | ERKASSPSPLTVGTA |
| S | 1 | 33 | 0.001422 | 0.115929 | -1.07068 | -0.30772 | Q9CWS0 | N(G),N(G)- | Ddah1 | CRHALRRSQGEEVDF |
| S | 1 | 247 | 0.026786 | 0.99584 | 4.139352 | 0.078293 | Q7TNV0 | Protein DE | Dek | EKKNKEESSEDEEKE |
| S | 1 | 248 | 0.000811 | 0.344143 | 4.35922 | 0.680608 | Q7TNV0 | Protein DE | Dek | KKNKEESSEDEEKES |
| S | 0.999946 | 656 | 0.002252 | 0.968813 | -2.51354 | 0.072931 | Q8K382 | DENN dom | Dennd1a | PSKPSITSPEKPSAL |
| S | 0.997301 | 736 | 0.052659 | 0.006581 | -0.70944 | -1.08548 | Q3U1Y4 | DENN dom | Dennd4b | PSRSAPSSPAPRRTK |
| S | 1 | 22 | 0.027474 | 0.806061 | -0.93282 | -0.13199 | O08808 | Protein dia | Diaph1;Dia | RDKKKGRSPDELPAT |
| S | 0.999916 | 1256 | 0.001323 | 0.126533 | -1.6934 | -0.46421 | Q8C9B9 | Death-indu | Dido1 | TSTTPPGSPPPPPPL |
| S | 1 | 481 | 0.199672 | 0.044478 | 1.415211 | 2.124507 | Q9ESX5 | H/ACA ribo | Dkc1 | KPKTVLESGGETGDG |
| S | 1 | 40 | 0.04834 | 0.422714 | -5.41468 | -1.96178 | D3Z3B8 | | Dlg1 | KHWAKKGSSDELQAE |
| S | 1 | 28 | 0.035451 | 0.231494 | -1.21847 | -0.56972 | E9Q2L2 | | Dlg2 | EDGPHDHSLPRLTHE |
| S | 0.999665 | 328 | 0.016704 | 0.259972 | 0.880356 | 0.319167 | E9Q2L2 | | Dlg2 | PISPGRYSPIPKHML |
| S | 1 | 295 | 0.021932 | 0.719315 | -2.33013 | -0.3906 | Q62108 | Disks large | Dlg4 | PTSPRRYSPVAKDLL |
| S | 1 | 947 | 0.026543 | 0.542603 | -1.68899 | -0.42203 | Q9D415 | Disks large | Dlgap1 | APLIRERSLESSQRQ |
| S | 1 | 509 | 0.046303 | 0.996709 | -1.44532 | -0.02829 | Q9D415 | Disks large | Dlgap1 | RAIEKGCSQDDECVS |
| S | 1 | 154 | 0.002547 | 0.724338 | -3.85549 | -0.38332 | Q9D415 | Disks large | Dlgap1 | KLFTKSHSLEGPSKG |
| S | 1 | 930 | 0.033295 | 0.943734 | -0.98289 | -0.07411 | Q6PFD5 | Disks large | Dlgap3 | GVPVKERSLDSVDRQ |
| S | 1 | 415 | 0.003313 | 0.997852 | 1.004413 | 0.008234 | B1AZP2-2 | Disks large | Dlgap4 | EQSNPRRSLDRLDSV |
| S | 1 | 421 | 0.003313 | 0.997852 | 1.004413 | 0.008234 | B1AZP2-2 | Disks large | Dlgap4 | RSLDRLDSVDMLLPS |
| S | 1 | 87 | 0.043901 | 0.690528 | -1.417 | 0.305981 | Q9WV69 | Dematin | Dmtn | RSRECSLSPKSTSPP |
| S | 0.999978 | 289 | 0.016841 | 0.482665 | -1.23093 | 0.303241 | Q9WV69 | Dematin | Dmtn | SGTSKSSSLPSYGRT |
| S | 0.999982 | 110 | 0.031504 | 0.141294 | -2.22101 | -1.23726 | Q9WV69 | Dematin | Dmtn | SRTLGIISQASTPRT |
| S | 0.999771 | 572 | 0.003019 | 0.699036 | -1.37987 | 0.150911 | Q6PNC0 | DmX-like p | Dmxl1 | TGLTRSTSMLISSAH |
| S | 1 | 473 | 0.008938 | 0.526273 | -2.41182 | -0.47197 | Q8BPN8 | DmX-like p | Dmxl2 | EDGEREGSPRTHPRP |
| S | 1 | 1288 | 0.002461 | 0.274206 | -1.81528 | -0.409 | Q8BPN8 | DmX-like p | Dmxl2 | FGNVDADSPVEETIQ |
| S | 1 | 1856 | 0.003411 | 0.673186 | -0.96292 | 0.114403 | Q8BPN8 | DmX-like p | Dmxl2 | LIRRNLASPEGTLAT |
| T | 1 | 2017 | 5.22E-05 | 0.006858 | -4.32352 | -1.36105 | Q8BPN8 | DmX-like p | Dmxl2 | SDPRALLTPQDEECA |
| S | 1 | 1138 | 0.04293 | 0.128933 | 2.434139 | 1.529694 | Q8BPN8 | DmX-like p | Dmxl2 | KVGSVLDSRVSVDSN |
| S | 1 | 1141 | 0.009406 | 0.002341 | -3.03325 | -3.73127 | Q8BPN8 | DmX-like p | Dmxl2 | SVLDSRVSVDSNLFV |
| S | 1 | 1144 | 0.009406 | 0.002341 | -3.03325 | -3.73127 | Q8BPN8 | DmX-like p | Dmxl2 | DSRVSVDSNLFVYSK |
| S | 1 | 151 | 0.006482 | 0.044433 | -4.01077 | -2.19567 | P60904 | DnaJ homo | Dnajc5 | EETEFYVSPEDLEAQ |
| S | 0.999493 | 512 | 0.032336 | 0.00872 | -1.25505 | -1.5647 | P39053-4 | Dynamin-1 | Dnm1 | QMNKKKTSGNQDEIL |
| S | 0.989621 | 1629 | 0.032423 | 0.022068 | 2.338245 | 2.317103 | P59764 | Dedicator | Dock4 | NSAPASMSPDGTRVI |
| S | 1 | 440 | 0.002164 | 0.418134 | -2.99282 | -0.50928 | Q8R1A4 | Dedicator | Dock7 | WSERRNSSLVGRRSL |
| S | 1 | 527 | 0.010161 | 0.89558 | -0.99097 | 0.076748 | Q66L44 | Protein Do | Dos | ELPAPARSPPRSPRA |
| S | 1 | 297 | 0.043333 | 0.359151 | -0.96589 | -0.37781 | Q66L44 | Protein Do | Dos | TRLRRHASLDGASPY |
| T | 1 | 509 | 0.003061 | 0.708648 | -2.08058 | 0.223404 | O08553 | Dihydropy | Dpysl2 | PVCEVSVTPKTVTPA |
| T | 1 | 512 | 0.000166 | 0.615135 | -7.35313 | -0.51361 | O08553 | Dihydropy | Dpysl2 | EVSVTPKTVTPASSA |
| S | 0.998998 | 631 | 0.018467 | 0.525089 | -2.1623 | 0.506932 | E9PWE8 | | Dpysl3 | KGGTPAGSTRGSPTR |
| S | 0.999988 | 635 | 0.018467 | 0.525089 | -2.1623 | 0.506932 | E9PWE8 | | Dpysl3 | PAGSTRGSPTRPNPP |
| T | 1 | 627 | 0.018467 | 0.525089 | -2.1623 | 0.506932 | E9PWE8 | | Dpysl3 | TTTPKGGTPAGSTRG |
| S | 1 | 531 | 0.009178 | 0.025799 | 2.571559 | 1.775027 | Q9EQF6 | Dihydropy | Dpysl5 | GMRDLHESSFSLSGS |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 415 | 0.013263 | 0.872686 | -4.17058 | -0.38453 | S4R1P5 | Dystonin | Dst | PEDVDVSSPDEKSVI |
| S | 0.999881 | 7473 | 0.004651 | 0.4175 | -0.858 | -0.17352 | S4R1P5 | Dystonin | Dst | SKMLRSESNSSITAT |
| S | 1 | 168 | 0.000403 | 0.000145 | 3.187081 | 3.523479 | S4R1P5 | Dystonin | Dst | DFSQKSGSASPAPGD |
| S | 1 | 170 | 0.000448 | 0.00014 | 2.425474 | 2.761872 | S4R1P5 | Dystonin | Dst | SQKSGSASPAPGDTL |
| S | 1 | 3 | 0.001689 | 0.53557 | -0.87095 | 0.11489 | Q9R0P5 | Destrin | Dstn | ______MASGVQVADE |
| S | 1 | 205 | 0.00227 | 0.919335 | -3.12164 | 0.149062 | Q9DD18 | D-tyrosyl-t | Dtd1 | GAEGDVSSEREP___ |
| S | 1 | 196 | 0.003577 | 0.587373 | -2.59267 | 0.368068 | Q9DD18 | D-tyrosyl-t | Dtd1 | RKEDRSASSGAEGDV |
| S | 1 | 306 | 0.008269 | 0.912668 | -1.86257 | -0.12463 | Q9D2N4 | Dystrobrev | Dtna | LTNALSKSLSCASSR |
| S | 0.965045 | 500 | 0.425029 | 0.025834 | -1.3229 | 3.48887 | Q8CFR5 | Dystrobrev | Dtna | LKTQGASSPRSSPSH |
| S | 0.994322 | 531 | 0.617144 | 0.04111 | 0.84464 | -2.74829 | O70585-2 | Dystrobrev | Dtnb | QAAQATGSPHTSPTH |
| S | 1 | 162 | 0.00656 | 0.728208 | -3.35495 | 0.409764 | O88485 | Cytoplasm | Dync1i1 | TPLATHQSEEDEEDE |
| S | 0.9948 | 510 | 0.068424 | 0.037589 | 1.022132 | 1.090589 | Q8R1Q8 | Cytoplasm | Dync1li1 | TRKPASVSPTTPTSP |
| S | 0.9966 | 516 | 0.001198 | 0.150327 | -4.33838 | 1.090589 | Q8R1Q8 | Cytoplasm | Dync1li1 | VSPTTPTSPTEGEAS |
| Y | 1 | 312 | 0.029275 | 0.896464 | -1.73591 | 0.175031 | A1L341 | Dual specif | Dyrk1a;Dy | LGQRIYQYIQSRFYR |
| S | 1 | 768 | 0.011086 | 0.998122 | -4.93245 | -0.05008 | Q8C008 | Double zin | Dzank1 | QGLEDQLSPPGNRIL |
| S | 1 | 106 | 0.005773 | 0.719918 | -4.215 | -0.50953 | O70251 | Elongation | Eef1b | DDIDLFGSDDEEESE |
| S | 1 | 157 | 0.015492 | 0.862893 | -1.35441 | -0.13529 | Q91VK2 | Elongation | Eef1d | KDIDLFGSDEEEEDK |
| S | 0.987009 | 220 | 0.704273 | 0.009396 | -0.50816 | -2.89399 | Q8BG67 | Protein EFI | Efr3a | SRLGPPSSPSAADKE |
| S | 1 | 540 | 0.004225 | 0.157011 | -1.03229 | -0.33702 | Q8CHW4 | Translatior | Eif2b5 | ELDSRAGSPQLDDIR |
| S | 0.999983 | 75 | 0.004692 | 0.23947 | -2.04028 | 0.568361 | Q8JZQ9 | Eukaryotic | Eif3b | SEEETATSPAASPTP |
| S | 1 | 166 | 0.075851 | 0.030783 | -0.76442 | -0.8902 | Q8R1B4 | Eukaryotic | Eif3c | YKQNPEQSADEDAEK |
| S | 0.999953 | 42 | 0.043149 | 0.777507 | 0.816237 | 0.142095 | Q9Z1D1 | Eukaryotic | Eif3g | PLPTGDTSPEPELLP |
| T | 0.998571 | 41 | 0.043149 | 0.777507 | 0.816237 | 0.142095 | Q9Z1D1 | Eukaryotic | Eif3g | IPLPTGDTSPEPELL |
| S | 0.998648 | 504 | 0.800494 | 0.015841 | -0.26627 | -2.38642 | Q8BGD9 | Eukaryotic | Eif4b | SSDTEQPSPTSGGGK |
| S | 0.999964 | 422 | 0.783007 | 0.016528 | 0.277283 | -0.82724 | Q8BGD9 | Eukaryotic | Eif4b | RERSRTGSESSQTGA |
| S | 0.999956 | 425 | 0.783007 | 0.016528 | 0.277283 | -0.82724 | Q8BGD9 | Eukaryotic | Eif4b | SRTGSESSQTGASAT |
| S | 1 | 1211 | 0.047313 | 0.994938 | -1.4687 | 0.035895 | Q6NZJ6 | Eukaryotic | Eif4g1 | EGLRKAASLTEDRGR |
| S | 0.999955 | 108 | 0.000831 | 0.008595 | -1.7312 | -0.91876 | Q05D44 | Eukaryotic | Eif5b | GQKGKKTSFDENDSE |
| S | 1 | 114 | 0.000831 | 0.008595 | -1.7312 | -0.91876 | Q05D44 | Eukaryotic | Eif5b | TSFDENDSEELEDKD |
| S | 0.999997 | 191 | 0.00265 | 0.978289 | 3.583093 | -0.08958 | Q80Y81 | Zinc phosp | Elac2 | GKQQPSQSPRTSPNR |
| S | 0.9739 | 154 | 0.002036 | 0.858731 | 3.633919 | 0.230367 | E9QK48 | | Eml2 | GYATSPSSPKKEASS |
| S | 1 | 263 | 0.013718 | 0.413925 | -1.21189 | -0.31862 | P17182 | Alpha-eno | Eno1 | KYDLDFKSPDDPSRY |
| S | 1 | 508 | 0.005712 | 0.259257 | -1.20396 | -0.33758 | A2A842 | Protein 4.1 | Epb4.1;Epl | ASKRASRSLDGAAAA |
| S | 1 | 737 | 0.047855 | 0.665611 | -1.06197 | 0.247793 | E9PV14 | | Epb4.1l1 | QTEARADSSDETDTS |
| S | 1 | 69 | 0.009266 | 0.875677 | -2.04281 | 0.170371 | A2AUK5 | Band 4.1-li | Epb4.1l1;E | DMDDKDYSEADGLSE |
| S | 1 | 677 | 0.04885 | 0.99766 | -1.1971 | -0.02006 | A2AUK5 | Band 4.1-li | Epb4.1l1;E | ESGGLEDSPDRGACS |
| S | 1 | 544 | 0.024938 | 0.006699 | -1.21945 | -1.5089 | A2AUK5 | Band 4.1-li | Epb4.1l1;E | RLPSSPASPSPKGTP |
| S | 1 | 378 | 0.005759 | 0.516554 | -1.93899 | 0.348048 | A2AUK5 | Band 4.1-li | Epb4.1l1;E | HTFFRLVSPEPPPKG |
| T | 0.999967 | 475 | 0.012552 | 0.721302 | -1.9808 | -0.28713 | A2AUK5 | Band 4.1-li | Epb4.1l1;E | AEEGEVRTPTKIKEL |
| T | 1 | 685 | 0.007366 | 0.980056 | -5.54803 | 0.167723 | A2AUK5 | Band 4.1-li | Epb4.1l1;E | PDRGACSTPEMPQFE |
| S | 1 | 540 | 0.049272 | 0.006388 | 3.204136 | 4.841084 | A2AUK5 | Band 4.1-li | Epb4.1l1;E | DRERRLPSSPASPSP |
| S | 1 | 544 | 0.000108 | 0.60931 | 2.824917 | 0.182555 | A2AUK5 | Band 4.1-li | Epb4.1l1;E | RLPSSPASPSPKGTP |
| S | 1 | 639 | 0.047921 | 0.539775 | -4.02765 | -1.19168 | Q9Z2H5 | Band 4.1-li | Epb41l1 | AFEDFSRSLPELDRD |
| S | 1 | 639 | 0.001817 | 0.000679 | -4.33254 | -4.78976 | Q9Z2H5 | Band 4.1-li | Epb41l1 | AFEDFSRSLPELDRD |
| S | 1 | 116 | 0.019343 | 0.986982 | -2.54506 | -0.0785 | O70318 | Band 4.1-li | Epb41l2 | QILGKEESLPEEESR |
| S | 0.999977 | 470 | 0.031507 | 0.818894 | -3.25456 | -0.4589 | Q9WV92 | Band 4.1-li | Epb41l3 | IYMKDSVSAAEVGTG |
| S | 1 | 451 | 0.015358 | 0.470214 | -3.34941 | -0.8235 | Q9WV92-8 | Band 4.1-li | Epb41l3 | KRYTMSRSLDGEVGT |
| T | 1 | 518 | 0.003037 | 0.604935 | -2.81421 | 0.372741 | Q9WV92 | Band 4.1-li | Epb41l3 | RKKAEEATPVTALRH |
| T | 0.999998 | 923 | 0.009098 | 0.702962 | -1.74796 | 0.244365 | Q9WV92 | Band 4.1-li | Epb41l3 | VHKETEITPEDGED_ |
| T | 1 | 495 | 0.000672 | 0.998566 | -2.64793 | 0.012532 | Q9WV92 | Band 4.1-li | Epb41l3 | TNLITTVTPEKKAEE |
| S | 0.999638 | 99 | 0.024316 | 0.865178 | -2.10596 | -0.23392 | Q9WV92 | Band 4.1-li | Epb41l3 | DDKLSQRSSSSKLSR |
| S | 0.999881 | 453 | 0.010005 | 0.41014 | -1.78667 | -0.43772 | Q80VP1 | Epsin-1 | Epn1 | SLAESVGSPPPAATP |
| S | 0.993316 | 416 | 0.861458 | 0.000328 | 0.13138 | -2.47649 | Q80VP1 | Epsin-1 | Epn1 | LRTALPTSGSSTGEL |
| T | 0.920544 | 415 | 0.001414 | 0.870354 | 4.039721 | -0.22536 | Q80VP1 | Epsin-1 | Epn1 | RLRTALPTSGSSTGE |
| S | 0.999691 | 173 | 0.006461 | 0.328386 | -1.10044 | -0.27975 | Q8CHU3 | Epsin-2 | Epn2 | ITFGRGSSQPNLSTS |
| S | 1 | 255 | 0.000685 | 0.99987 | -2.27499 | -0.00325 | Q60902 | Epidermal | Eps15l1 | LNSTGSLSPKHSVKQ |
| S | 1 | 211 | 0.006543 | 0.34663 | -3.04673 | -0.75239 | Q5EBJ4 | Ermin | Ermn | KRKHREGSPLKEESL |
| T | 1 | 234 | 0.031997 | 0.782371 | -2.20754 | -0.34881 | Q5EBJ4 | Ermin | Ermn | SPGSQPGTPDEQPVF |
| S | 0.925195 | 343 | 0.155919 | 0.009202 | 1.155959 | -2.35647 | Q925F2 | Endothelia | Esam | TPTPSVSSQALSSPR |
| S | 0.99972 | 663 | 0.016973 | 0.733527 | 2.608227 | 0.39596 | Q3TZZ7 | Extended s | Esyt2 | DLGRSSSSLLASPSH |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 650 | 0.556838 | 0.048346 | 0.907445 | 2.522321 | Q3TZZ7 | Extended s | Esyt2 | KPQPPEASPLGHRDL |
| T | 1 | 313 | 0.000316 | 0.750132 | -2.95568 | 0.176424 | Q6PGF7 | Exocyst co | Exoc8 | EDDEELATPEAEEEK |
| S | 0.991245 | 119 | 0.004506 | 0.999647 | -1.76804 | -0.0063 | Q8VE88 | Protein FA | Fam114a2 | ETSLGIPSPTEISAE |
| S | 1 | 140 | 0.000171 | 0.000954 | 1.363056 | 0.849375 | Q9DB52 | Protein FA | Fam122a | RIDFIPVSPAPSPTR |
| S | 0.999456 | 144 | 0.000171 | 0.000954 | 1.363056 | 0.849375 | Q9DB52 | Protein FA | Fam122a | IPVSPAPSPTRGIGK |
| T | 0.999909 | 306 | 0.00098 | 0.282605 | -2.60679 | 0.473235 | Q8C729-2 | Protein FA | Fam126b | KVLKVEVTPTVPRIS |
| S | 1 | 320 | 0.005266 | 0.052056 | -3.32227 | -1.65518 | Q9CQV4 | Protein FA | Fam134c | SEDLDGHSDPEESFA |
| T | 0.999954 | 448 | 0.019604 | 0.68748 | -1.72365 | -0.30132 | A2ATK9 | | Fam171a1 | QTSFDNLTPSGTLGK |
| S | 1 | 533 | 0.021925 | 0.232157 | -1.83524 | -0.75343 | Q6PGL7 | WASH com | Fam21 | KTQKGLFSDEEDSED |
| S | 1 | 723 | 0.030519 | 0.630158 | -2.46573 | 0.544414 | Q6PGL7 | WASH com | Fam21 | PKVPLLFSDEEDSEV |
| S | 1 | 157 | 0.024091 | 0.013177 | -3.79475 | -3.95649 | Q6PGL7 | WASH com | Fam21 | LDIKAGNSDSEEDDA |
| S | 1 | 613 | 0.036388 | 0.034 | -1.1459 | -1.04434 | Q6PGL7 | WASH com | Fam21 | KTSALLFSSDEEDQW |
| S | 1 | 614 | 0.036388 | 0.034 | -1.1459 | -1.04434 | Q6PGL7 | WASH com | Fam21 | TSALLFSSDEEDQWN |
| S | 0.999995 | 168 | 0.139091 | 0.027366 | -0.48261 | 0.71561 | Q8BGR5 | Protein FA | Fam53b | SPMQRSSSFSLPARA |
| S | 1 | 103 | 0.003857 | 0.973739 | -3.57385 | 0.107084 | Q76LS9 | Protein FA | Fam63a | RPQELPQSPRIQQPE |
| S | 0.996027 | 129 | 0.043844 | 0.962542 | -2.02071 | -0.13322 | E9PYD1 | | Fam98c | LRLQRDSSPVPSFGE |
| S | 1 | 476 | 0.012547 | 0.92188 | -1.80914 | -0.12609 | Q6NS60 | F-box only | Fbxo41 | QRRPRRHSTEGEEGD |
| S | 1 | 280 | 5.79E-06 | 5.56E-06 | -1.82952 | -1.65005 | Q9D824 | Pre-mRNA | Fip1l1 | DRYGRAESPDLRRLP |
| S | 1 | 1091 | 0.012982 | 0.931605 | -1.77474 | -0.11622 | Q6P9Q6 | FK506-bin | Fkbp15 | QGNSRRLSLTPDPEK |
| S | 0.999999 | 9 | 0.014827 | 0.646704 | -0.94281 | 0.167102 | P26883 | Peptidyl-p | Fkbp1a | GVQVETISPGDGRTF |
| S | 1 | 493 | 0.016973 | 0.542477 | -0.91449 | 0.203568 | Q9JL04 | Formin-2 | Fmn2 | ADDSGGGSPVLAAKA |
| S | 1 | 171 | 0.036654 | 0.911101 | -1.05776 | -0.10442 | A2APV2 | Formin-lik | Fmnl2 | KSKPWSRSIEDLHRG |
| S | 0.998572 | 432 | 0.019396 | 0.734366 | -1.67776 | 0.262969 | Q8K2I1 | Protein far | Fntb | ECEDEVTSDPATD__ |
| S | 1 | 415 | 0.003856 | 0.143498 | 1.088172 | 0.360381 | Q3UCQ1 | Forkhead | Foxk2 | QEARFAQSAPGSPLS |
| S | 0.999989 | 419 | 0.003856 | 0.143498 | 1.088172 | 0.360381 | Q3UCQ1 | Forkhead | Foxk2 | FAQSAPGSPLSSQPV |
| S | 0.999974 | 270 | 0.010577 | 0.603822 | 2.017558 | -0.35756 | F6XM46 | FERM dom | Frmd5 | AGMVPSRSCPSITHG |
| S | 0.998795 | 21 | 0.03927 | 0.752579 | -1.88921 | -0.34196 | Q3UFK8 | FERM dom | Frmd8 | AERSHRSSVSSVGAR |
| S | 0.999999 | 2815 | 0.018063 | 0.999716 | -1.33509 | 0.005944 | E9Q8I9 | Protein fur | Fry | KATFAGGSRDGVITC |
| S | 0.949183 | 1939 | 0.982495 | 0.01806 | -0.06205 | -1.4098 | E9Q8I9 | Protein fur | Fry | FTVLSRSSSPDLSSS |
| S | 0.999999 | 1940 | 0.984188 | 0.020607 | -0.06205 | -1.4351 | E9Q8I9 | Protein fur | Fry | TVLSRSSSPDLSSSS |
| S | 0.885877 | 3013 | 0.994809 | 0.032162 | 0.049393 | 1.779509 | E9Q8I9 | Protein fur | Fry | LTAFLPDSSVSGTSL |
| S | 1 | 313 | 0.020401 | 0.138468 | 3.930194 | 1.966617 | Q7TPM6 | Fibronecti | Fsd1 | EGKGRTASPVNSPAR |
| S | 1 | 317 | 0.461392 | 0.001172 | 0.174202 | 1.006967 | Q7TPM6 | Fibronecti | Fsd1 | RTASPVNSPARGTPS |
| S | 1 | 335 | 0.107853 | 0.003779 | -0.70833 | -1.54852 | Q9DBE9 | pre-rRNA | Ftsj3 | KALDISLSSEEEEEG |
| S | 1 | 336 | 0.107853 | 0.003779 | -0.70833 | -1.54852 | Q9DBE9 | pre-rRNA | Ftsj3 | ALDISLSSEEEEEGD |
| S | 1 | 602 | 0.000739 | 0.203077 | 1.027791 | 0.205778 | Q9WVR4 | Fragile X m | Fxr2 | RGNRTDGSISGDRQP |
| S | 1 | 604 | 0.000739 | 0.203077 | 1.027791 | 0.205778 | Q9WVR4 | Fragile X m | Fxr2 | NRTDGSISGDRQPVT |
| S | 1 | 68 | 0.036059 | 0.152157 | 1.611877 | 0.905634 | P59648 | FXYD dom | Fxyd7 | PTCKSCKSELPSSAP |
| T | 1 | 929 | 0.001252 | 0.993101 | -1.42269 | -0.01691 | Q9WV18 | Gamma-ar | Gabbr1 | RSRRHPPTPPDPSGG |
| S | 1 | 193 | 0.021005 | 0.207675 | -5.59164 | -2.38872 | P06837 | Neuromod | Gap43 | PTETAESSQAEEEKD |
| S | 0.828055 | 208 | 0.025022 | 0.319454 | -0.75643 | 0.272794 | P16858 | Glyceralde | Gapdh;Gm | AQNIIPASTGAAKAV |
| S | 0.969622 | 758 | 0.175354 | 0.008459 | -0.7028 | -1.53269 | Q6PAR5 | GTPase-ac | Gapvd1 | TDVREVSSRPSTPGL |
| S | 0.999999 | 103 | 0.040821 | 0.752807 | 1.447426 | 0.264724 | Q8CHY6 | Transcripti | Gatad2a | SPDVIVLSDSEQPSS |
| S | 0.998212 | 259 | 0.008558 | 0.686596 | -0.98278 | 0.140333 | P47856 | Glutamine | Gfpt1 | CGLSRVDSTTCLFPV |
| S | 0.999519 | 413 | 0.309001 | 0.039431 | -1.05563 | 2.030689 | Q99MR1 | PERQ amir | Gigyf1 | SLSPRISSPPGPPGD |
| S | 1 | 368 | 0.946841 | 0.047966 | -0.25143 | -2.47897 | P23242 | Gap juncti | Gja1 | QRPSSRASSRASSRP |
| S | 1 | 261 | 0.003436 | 0.990829 | -2.84113 | -0.04867 | Q921C1 | Gap juncti | Gjc3 | KDTTDELSVVEAKEP |
| S | 0.992348 | 121 | 0.000871 | 0.710733 | -3.35815 | -0.27283 | Q64516 | Glycerol ki | Gk;Gyk;Gy | WLDLRTQSTVENLSK |
| S | 1 | 139 | 0.029471 | 0.237342 | -1.23266 | -0.54157 | Q8K3I9 | Glucocorti | Glcci1 | PERRSPGSPVCRVDR |
| T | 0.999999 | 2503 | 0.015288 | 0.77907 | -1.53531 | 0.201974 | E9Q2E4 | | Gm15800 | GWERTEGTPPPPGQP |
| S | 0.976319 | 8 | 0.021138 | 0.175855 | -2.53646 | -1.16549 | J3QPK1 | | Gm21833 | KKQEDNPSTKLKEDS |
| S | 0.999963 | 99 | 0.499116 | 0.003142 | 0.331178 | -1.64409 | Q3UPT2 | | Gm26596 | RENRLGASPSRSGLF |
| S | 1 | 319 | 0.007661 | 0.580407 | -1.29438 | 0.221784 | A2AJA9 | Uncharact | Gm996 | SEEPPRPSPRRGGSY |
| S | 1 | 207 | 0.023609 | 0.090732 | -1.07573 | -0.64945 | P18872 | Guanine n | Gnao1 | FDVGGQRSERKKWIH |
| S | 1 | 21 | 0.035768 | 0.964006 | -2.30692 | -0.14069 | P62881-2 | Guanine n | Gnb5 | SLKSEAESLKGKLEE |
| S | 0.999763 | 8 | 0.006781 | 0.439817 | -1.23684 | -0.26281 | Q9CXP8 | Guanine n | Gng10 | MSSGASVSALQRLVE |
| S | 0.999949 | 324 | 0.000872 | 0.009473 | -1.83268 | -0.96023 | P36916 | Guanine n | Gnl1 | GASWGNVSGEEEEEE |
| S | 1 | 188 | 0.007755 | 0.817101 | 1.370592 | 0.136588 | Q8BUV3 | Gephyrin;I | Gphn | DELEDLPSPPPPLSP |
| S | 1 | 194 | 0.007755 | 0.817101 | 1.370592 | 0.136588 | Q8BUV3 | Gephyrin;I | Gphn | PSPPPPLSPPPTTSP |
| S | 1 | 318 | 0.044397 | 0.116938 | -0.83686 | -0.55019 | P35803 | Neuronal r | Gpm6b | QELQDIQSRSKEQLN |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.998107 | 869 | 0.008257 | 0.195797 | -0.92071 | 0.32052 | Q8C419 | Probable | Gpr158 | KEDSEAESTESVPLV |
| S | 1 | 904 | 0.0332 | 0.485604 | -1.54192 | -0.45168 | Q8C419 | Probable | Gpr158 | SMLQKSLSVIASAKE |
| S | 1 | 539 | 0.044324 | 0.707031 | -0.86648 | -0.18092 | Q3UN16 | Probable | Gpr162 | GFSPRRLSLGSPDSR |
| S | 1 | 626 | 0.024938 | 0.474957 | -2.69626 | 0.744695 | Q5U4C1 | G-protein | Gprasp1 | SVEAEVNSKSSLEDE |
| S | 0.996129 | 679 | 0.003593 | 0.659167 | -1.66785 | 0.206374 | Q3UNH4 | G protein- | Gprin1 | REPSASTSQKDLAAA |
| S | 1 | 694 | 0.043295 | 0.078435 | -2.28879 | -1.71041 | Q80TI0-4 | GRAM do | Gramd1b | LAEIHRQSPKEKASK |
| S | 1 | 885 | 0.021635 | 0.215422 | -0.85477 | -0.36197 | H7BX90 | Glutamate | Grip1 | SQLGRQASFQERSSS |
| S | 1 | 900 | 0.005921 | 0.185756 | -0.81046 | 0.26693 | Q68ED2 | Metabotr | Grm7 | CENVDPNSPAAKKKY |
| S | 1 | 163 | 0.038566 | 0.834318 | -1.07196 | -0.15175 | D3Z7I0 | General tr | Gtf3c2;Gm | KGLDQPESPHPKRPP |
| S | 1 | 206 | 0.020391 | 0.800842 | -1.58685 | 0.21095 | Q9JKS5 | Intracellul | Habp4 | PGNRAFDSFDQRGKR |
| S | 1 | 114 | 0.010244 | 0.704347 | -1.58298 | 0.22699 | Q8K2C9 | Very-long- | Hacd3 | FDRWLDESDAEMELR |
| S | 1 | 588 | 0.015339 | 0.661017 | -1.98436 | 0.344591 | O88704 | Potassium | Hcn1 | DRIGKKNSILLQKFQ |
| S | 0.995639 | 818 | 0.017525 | 0.992467 | -4.888 | 0.111587 | O88703 | Potassium | Hcn2 | SARPASSSTPRLGPA |
| S | 1 | 119 | 1.67E-05 | 0.728003 | -5.41063 | 0.18653 | O88703 | Potassium | Hcn2 | SAAEEAGSEEAGPAG |
| S | 1 | 131 | 0.000401 | 0.214029 | -0.85748 | 0.147351 | O88703 | Potassium | Hcn2 | PAGEPRGSQASFLQR |
| S | 1 | 834 | 0.743567 | 0.016211 | 0.394464 | 2.154887 | O88703 | Potassium | Hcn2 | TARTAAPSPDRRDSA |
| S | 0.999863 | 807 | 0.019447 | 0.111706 | -1.17142 | 0.626238 | O88703 | Potassium | Hcn2 | PHGVPAPSPAASARP |
| S | 0.999458 | 465 | 0.328882 | 0.003065 | -0.82269 | -3.07179 | Q6NZM9 | Histone de | Hdac4 | RPLGRTQSAPLPQNA |
| S | 1 | 165 | 0.001421 | 0.994949 | -2.28214 | -0.02384 | P51859 | Hepatoma | Hdgf | AGDVLEDSPKRPKES |
| S | 0.999915 | 659 | 0.726484 | 0.019914 | -0.27819 | -1.38412 | Q3UMU9 | Hepatoma | Hdgfrp2 | HERTRLASESANDDN |
| S | 1 | 31 | 0.046123 | 0.963526 | -1.23686 | 0.081611 | Q8VDJ3 | Vigilin | Hdlbp | IKVATLNSEEENDPP |
| S | 0.999951 | 388 | 0.015938 | 0.642557 | -2.54354 | 0.462822 | Q6NVF4 | DNA helic | Helb | AKPNDPGSAEAVEGS |
| S | 1 | 301 | 0.016873 | 0.881397 | -2.04695 | 0.192668 | Q640R3 | Hepatocyt | Hepacam | EADTLPRSGEQERKN |
| T | 1 | 297 | 0.008446 | 0.752251 | -3.23531 | 0.395428 | Q640R3 | Hepatocyt | Hepacam | RLKSEADTLPRSGEQ |
| S | 0.996022 | 323 | 0.036115 | 0.211321 | -2.28925 | -1.1218 | Q8VD75 | Huntingtin | Hip1 | AEVSSPDSEPVLEKD |
| S | 1 | 2 | 0.010012 | 0.257422 | -0.92565 | 0.297315 | P43277 | Histone H | Hist1h1d | _______MSETAPAAP |
| S | 1 | 302 | 0.024717 | 0.230746 | -3.06472 | -1.30198 | Q8R1M0 | Embryonic | Hmces | PKKEVPDSPKKDASG |
| S | 1 | 6 | 0.014915 | 0.864434 | -0.99288 | 0.097621 | Q9DCB1 | High mobi | Hmgn3 | __MPKRKSPENTEGK |
| S | 1 | 4 | 0.030284 | 0.960509 | -2.357 | -0.14406 | Q5EBP8 | Heterogen | Hnrnpa1 | ____MSKSESPKEPE |
| S | 0.999993 | 359 | 0.028076 | 0.948886 | -1.18865 | 0.081387 | Q8BG05 | Heterogen | Hnrnpa3; | FGGRSSGSPYGGGYG |
| S | 1 | 116 | 0.067656 | 0.040853 | -1.5615 | -1.62181 | Q8BG05 | Heterogen | Hnrnpa3; | RAVSREDSVKPGAHL |
| S | 1 | 226 | 0.040354 | 0.97909 | -2.91637 | -0.13933 | Q00PI9 | Heterogen | Hnrnpul2 | AYHSRSKSPPPPEEE |
| S | 1 | 226 | 0.041009 | 0.971399 | -0.80843 | -0.04552 | P11499 | Heat shoc | Hsp90ab1 | KEREKEISDDEAEEE |
| S | 0.999999 | 24 | 0.048878 | 0.995577 | -4.23724 | 0.097705 | Q8K0U4 | Heat shoc | Hspa12a | APTSTYSSPARSLGD |
| S | 0.999993 | 631 | 0.005127 | 0.865737 | -0.77172 | -0.05849 | Q8K0U4 | Heat shoc | Hspa12a | LRLDLTGSGGTAVPA |
| S | 1 | 276 | 0.034727 | 0.961521 | -1.09697 | 0.068678 | Q9CZJ2 | Heat shoc | Hspa12b | GRLGERRSIDSSFRH |
| T | 1 | 545 | 0.00672 | 0.115136 | -2.86358 | -1.16877 | P48722 | Heat shoc | Hspa4l | QKCHAEHTPEEEIDH |
| S | 1 | 810 | 0.038973 | 0.560377 | -2.24755 | 0.604368 | Q61699 | Heat shoc | Hsph1 | QPKPKIESPKLERTP |
| S | 1 | 441 | 0.988775 | 0.019675 | 0.058402 | -1.62529 | Q8BGC0 | HIV Tat-sp | Htatsf1 | KAEEGGESEGDASEK |
| S | 1 | 242 | 0.017406 | 0.231141 | -2.35545 | -0.91331 | Q8BGC0 | HIV Tat-sp | Htatsf1 | KDYKKKLSLQQKQLD |
| S | 1 | 679 | 0.038978 | 0.474084 | -2.40665 | -0.75169 | Q8BGC0 | HIV Tat-sp | Htatsf1 | DEKLFDDSDEKEDEE |
| S | 1 | 705 | 8.43E-05 | 0.456811 | -4.68145 | -0.37628 | Q8BGC0 | HIV Tat-sp | Htatsf1 | DKVFEDNSNEKLFDE |
| S | 1 | 1395 | 0.005545 | 0.188515 | -1.1512 | 0.371101 | Q7TMY8 | E3 ubiquit | Huwe1 | PMDQRAESPEEVACR |
| S | 0.994727 | 3818 | 0.1084 | 0.030277 | -1.68981 | -2.22701 | Q7TMY8 | E3 ubiquit | Huwe1 | PMDVDQPSPSAQDTQ |
| S | 0.99999 | 1215 | 0.016049 | 0.83942 | -1.8948 | 0.208925 | E9PZ19 | | Igsf9b | PLSSRTGSPELAARA |
| S | 0.999895 | 437 | 0.032704 | 0.987009 | -1.37834 | 0.048798 | P46660 | Alpha-inte | Ina | RILSSTASKVSSAGL |
| S | 1 | 941 | 0.035206 | 0.673923 | -1.66915 | 0.350902 | Q8CDA1 | Phosphati | Inpp5f | LESPLKKSPSADSIH |
| S | 1 | 943 | 0.035292 | 0.781726 | -1.60182 | -0.26048 | Q8CDA1 | Phosphati | Inpp5f | SPLKKSPSADSIHTR |
| S | 0.996133 | 266 | 0.00349 | 0.994586 | -1.79011 | -0.02361 | P59644 | Phosphati | Inpp5j | RAAGPATSPPRAQAF |
| S | 1 | 872 | 0.146145 | 0.048482 | 0.852019 | 1.097911 | P59644 | Phosphati | Inpp5j | LLAPKSRSPSPGKSK |
| S | 1 | 874 | 0.146145 | 0.048482 | 0.852019 | 1.097911 | P59644 | Phosphati | Inpp5j | APKSRSPSPGKSKRH |
| S | 0.999916 | 183 | 0.059007 | 0.037088 | 3.134732 | 3.207984 | E9PUA3 | IQ motif a | Iqsec1 | YFEGKQVSVTNDGSQ |
| S | 1 | 412 | 0.023132 | 0.271351 | -2.08947 | -0.80591 | A4GZ26 | IQ motif a | Iqsec2 | YFEGKPASLDEGAMA |
| S | 0.985662 | 228 | 0.049011 | 0.280088 | -4.03924 | -1.88482 | A4GZ26 | IQ motif a | Iqsec2 | HSTSTSTSPATTLQR |
| S | 1 | 256 | 0.002472 | 0.249538 | -1.30495 | -0.30855 | Q3TES0 | IQ motif a | Iqsec3 | ERPGAVGSPRAGPLR |
| S | 0.932357 | 1072 | 0.015488 | 0.128174 | 3.772496 | 1.811686 | Q3TES0 | IQ motif a | Iqsec3 | PAPSPPTSPPPLPPD |
| S | 1 | 195 | 0.023801 | 0.136157 | -0.90759 | 0.475724 | Q8K3X4 | Interferon | Irf2bpl | PPELNRQSPNSSSAA |
| S | 0.999963 | 303 | 0.018334 | 0.972263 | -3.0993 | 0.138494 | P81122 | Insulin rec | Irs2 | EFRPRSKSQSSGSSA |
| S | 1 | 30 | 0.003714 | 0.973205 | -1.82772 | -0.05486 | Q9D7P6 | Iron-sulfur | Iscu | RLPARELSAPARLYH |
| S | 1 | 1573 | 0.003546 | 0.69841 | -2.15856 | -0.24508 | P11881-4 | Inositol 1, | Itpr1 | RNAARRDSVLAASRD |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 335 | 0.009589 | 0.891041 | -0.93707 | 0.073257 | Q9Z0R4 | Intersectin | Itsn1 | RLPEEPSSEDEQQPE |
| S | 1 | 623 | 0.001355 | 0.023737 | -2.42662 | -1.11115 | Q9Z0R4 | Intersectin | Itsn1 | QQLQKQRSLEAARLK |
| S | 1 | 75 | 0.011394 | 0.008494 | 2.306774 | -2.21419 | Q9QXM1 | Junction-m | Jmy | DGSRGPGSPAARGRS |
| S | 0.997127 | 172 | 0.007266 | 0.638095 | -1.1184 | -0.16971 | Q8K0T4 | Katanin p6 | Katnal1 | KNVQDGASDSEIPKF |
| S | 1 | 441 | 0.004331 | 0.99953 | -1.35653 | 0.005524 | P63141 | Potassium | Kcna2 | SCPKIPSSPDLKKSR |
| S | 1 | 14 | 0.015021 | 0.273908 | 0.869978 | 0.299102 | P62482 | Voltage-ga | Kcnab2 | TGSPARLSLRQTGSP |
| S | 1 | 552 | 0.024667 | 0.005152 | -2.31893 | -3.04057 | Q9Z0V2 | Potassium | Kcnd2 | VSGSHRGSVQELSTI |
| S | 1 | 552 | 0.016109 | 0.000482 | -1.25568 | -2.47681 | Q9Z0V2 | Potassium | Kcnd2 | VSGSHRGSVQELSTI |
| S | 1 | 546 | 0.261604 | 0.001524 | -0.60052 | -2.3128 | Q9Z0V2 | Potassium | Kcnd2 | RIPNANVSGSHRGSV |
| S | 1 | 548 | 0.016109 | 0.000482 | -1.25568 | -2.47681 | Q9Z0V2 | Potassium | Kcnd2 | PNANVSGSHRGSVQE |
| S | 1 | 938 | 0.026832 | 0.002956 | 1.463137 | 2.2247 | Q08460 | Calcium-ac | Kcnma1 | HGMLRQPSITTGVNI |
| S | 1 | 479 | 0.024108 | 0.0491 | 0.754381 | 0.554351 | B7ZBW2 | Potassium | Kcnq2 | GAASRQNSEEASLPG |
| S | 1 | 47 | 0.000144 | 0.975143 | -3.16031 | 0.045538 | Q6ZPR4 | Potassium | Kcnt1 | RGGGSVGSDVGQRVQ |
| S | 0.977506 | 178 | 0.039189 | 0.159934 | -1.52911 | -0.86222 | Q6WVG3 | BTB/POZ d | Kctd12 | GASAGAPSPTLELAS |
| S | 0.935653 | 200 | 0.008542 | 0.578214 | -4.43532 | -0.78294 | Q6WVG3 | BTB/POZ d | Kctd12 | AGPLLTPSQSLDGSR |
| S | 1 | 221 | 0.451015 | 0.030018 | 0.308081 | -0.8155 | Q7TSH8 | Uncharact | Kiaa0195 | GDLFPPFSPPPSPRG |
| S | 1 | 225 | 0.451015 | 0.030018 | 0.308081 | -0.8155 | Q7TSH8 | Uncharact | Kiaa0195 | PPFSPPPSPRGEVKR |
| S | 1 | 275 | 0.012473 | 0.91136 | -1.22403 | 0.091165 | Q8R0A7 | Uncharact | Kiaa0513; | TKTVTMISPEDEQKG |
| T | 1 | 47 | 0.034962 | 0.30425 | -2.24762 | -0.91164 | Q80TL4 | Protein KI | Kiaa1045; | LPGSRRGTVEGSVQE |
| S | 1 | 180 | 0.023744 | 0.056313 | -1.20461 | -0.84663 | Q148V7 | LisH doma | Kiaa1468; | GQLNRAGSISTLDSL |
| S | 1 | 966 | 0.009067 | 0.86287 | -1.5712 | -0.13771 | A2A7S8-2 | Uncharact | Kiaa1522 | LQLERPVSPEAQADL |
| S | 1 | 205 | 0.027359 | 0.981615 | -1.80796 | -0.07272 | Q8BRV5 | Uncharact | Kiaa1671 | KSPRRDESDEEPPRV |
| S | 1 | 1578 | 0.001273 | 0.834006 | -1.50731 | 0.094601 | E9Q9B7 | | Kidins220 | KAERVAKSPEHSVEP |
| S | 0.99985 | 1660 | 0.020008 | 0.566622 | -2.57206 | -0.57195 | Q9QXL2 | Kinesin-lik | Kif21a | NLQDGQLSDTGDLGE |
| S | 0.998655 | 1217 | 0.025628 | 0.542062 | -1.08117 | 0.267907 | Q9QXL1 | Kinesin-lik | Kif21b | SRGATDTSPLTRRKS |
| S | 0.993818 | 545 | 0.035009 | 0.890346 | -3.6732 | -0.40132 | P28740-1 | Kinesin-lik | Kif2a | GGSRPDLSPSYDYDD |
| T | 1 | 396 | 0.042729 | 0.503546 | -1.14828 | 0.350047 | P28738 | Kinesin he | Kif5c | SLEPCDNTPIIDNIT |
| S | 1 | 151 | 0.026326 | 0.889697 | -2.5507 | 0.258805 | Q91YS4 | | Klc2 | RKLDEDASPNEEKGD |
| S | 1 | 60 | 0.00782 | 0.417766 | -1.44393 | 0.329301 | O35344 | Importin s | Kpna3 | QEESLEDSDVDADFK |
| S | 1 | 60 | 0.0108 | 1 | -2.36484 | -0.00024 | O35343 | Importin s | Kpna4 | QEDICEDSDIDGDYR |
| S | 1 | 518 | 0.022732 | 0.41105 | -3.06209 | -0.9196 | Q61097 | Kinase sup | Ksr1 | EEPEAGKSEAEDDEE |
| S | 1 | 81 | 0.020567 | 0.895775 | -1.27947 | 0.117978 | Q6ZQ58 | La-related | Larp1 | AAEAPAGSDGEDGGR |
| S | 1 | 739 | 0.000678 | 0.375711 | -1.92785 | -0.27439 | Q6A0A2 | La-related | Larp4b | EQNTPPKSPQ_____ |
| S | 1 | 299 | 0.009489 | 0.648279 | -1.48671 | -0.23555 | Q8C351 | Layilin | Layn | YNVIRKQSEADLAEP |
| S | 1 | 631 | 0.049043 | 0.381676 | -2.74961 | -1.07247 | Q5XJE5 | RNA polym | Leo1 | LKAKKLNSDEEGESS |
| S | 1 | 659 | 0.001474 | 0.56112 | -1.81574 | -0.22224 | Q5XJE5 | RNA polym | Leo1 | KHKKYVISDEEEEED |
| S | 0.85895 | 371 | 0.006484 | 0.960575 | -1.12879 | -0.04695 | Q9ERG0 | LIM domai | Lima1 | RTSSLPESSPSKTAK |
| S | 0.912144 | 523 | 0.838579 | 0.001582 | -0.20291 | -2.50758 | D3YU59 | LIM and ca | Limch1 | IASAGTGSPSKIITP |
| S | 0.999999 | 390 | 0.276185 | 0.008246 | 0.590085 | 1.595262 | P48678 | Prelamin- | Lmna | EEERLRLSPSPTSQR |
| S | 0.999907 | 392 | 0.008371 | 0.778543 | -1.64897 | -0.18763 | P48678 | Prelamin- | Lmna | ERLRLSPSPTSQRSR |
| S | 1 | 411 | 0.01028 | 0.768333 | -1.02837 | 0.126358 | Q7TQ95 | Protein lur | Lnp | SPVLRADSVPNLEPS |
| S | 1 | 982 | 0.000818 | 0.672378 | 2.742587 | 0.238931 | E9Q3Y4 | Lipopolysa | Lrba | DRKDSPISPHFTRNS |
| S | 1 | 660 | 0.004987 | 0.023448 | -2.04368 | -1.25421 | Q8R4U7 | Leucine zi | Luzp1 | SGREKPDSDDDLDIE |
| S | 1 | 280 | 0.019132 | 0.966217 | -1.13762 | -0.05686 | E9QA63 | Microtubu | Macf1 | AEDVDVPSPDEKSVI |
| S | 1 | 3883 | 0.014777 | 0.052724 | -1.54816 | -0.98307 | E9QA63 | Microtubu | Macf1 | SLLKRQGSFSEDVIS |
| S | 1 | 266 | 0.042735 | 0.861711 | -1.49091 | 0.195991 | Q3UYG8 | O-acetyl-A | Macrod2 | GPEPKGLSPPHKKSK |
| S | 1 | 1229 | 0.164024 | 0.005188 | -1.62883 | -3.87501 | A2AGQ7 | | Madd | PKEKPAGSPIRSSED |
| S | 0.99999 | 1038 | 4.63E-06 | 0.868891 | -6.94914 | -0.11978 | A2AGQ7 | | Madd | EPDKRKRSPTENVNT |
| S | 0.994094 | 547 | 0.002381 | 0.010988 | -1.73402 | -1.09026 | P20917 | Myelin-ass | Mag | KNVTESSSFSGGDNP |
| S | 0.994094 | 547 | 0.002381 | 0.010988 | -1.73402 | -1.09026 | P20917-2 | Myelin-ass | Mag | KNVTESSSFSGGDNP |
| S | 0.994094 | 547 | 0.734337 | 0.03516 | -0.82148 | -3.57958 | P20917 | Myelin-ass | Mag | KNVTESSSFSGGDNP |
| S | 0.994094 | 547 | 0.81418 | 0.045766 | -0.82148 | -4.1352 | P20917-2 | Myelin-ass | Mag | KNVTESSSFSGGDNP |
| S | 1 | 667 | 0.001207 | 0.578112 | -2.08765 | -0.23732 | Q9QYR6 | Microtubu | Map1a | EMEEVHPSDEEEEET |
| S | 1 | 1606 | 0.000185 | 0.959583 | -2.01575 | -0.03928 | Q9QYR6 | Microtubu | Map1a | RALGLEESPEEEGKA |
| S | 1 | 644 | 0.016398 | 0.842759 | -2.26285 | -0.24785 | Q9QYR6 | Microtubu | Map1a | IAAAREESEPEVKED |
| S | 1 | 908 | 0.000593 | 0.002431 | -1.20303 | -0.79341 | Q9QYR6 | Microtubu | Map1a | EEDKGFKSPPCEDFS |
| S | 0.996349 | 384 | 0.006324 | 0.193694 | -2.48725 | -0.8171 | Q9QYR6 | Microtubu | Map1a | PERVRTESSEALKAE |
| S | 1 | 1205 | 0.370845 | 0.048975 | 0.390101 | 0.785767 | Q9QYR6 | Microtubu | Map1a | DISSKQLSPESLGTL |
| S | 1 | 2162 | 0.018393 | 0.157374 | -1.30102 | -0.60335 | Q9QYR6 | Microtubu | Map1a | PSPAEPRSAPCGSLA |
| S | 0.999989 | 1023 | 0.001232 | 0.72312 | -4.32406 | 0.367787 | Q9QYR6 | Microtubu | Map1a | PQDFQEDSWGDTKHA |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.999465 | 895 | 0.005839 | 0.328973 | -0.80251 | 0.199061 | Q9QYR6 | Microtubu | Map1a | VPSAGTISPTSSLEE |
| T | 1 | 633 | 3.98E-05 | 0.320549 | -3.09441 | 0.269311 | Q9QYR6 | Microtubu | Map1a | KPREAELTPENIAAA |
| T | 0.999991 | 504 | 0.026381 | 0.985295 | -5.49895 | 0.195601 | Q9QYR6 | Microtubu | Map1a | ELSSEPRTPPAQKGA |
| S | 0.985263 | 1634 | 0.027212 | 0.999094 | -4.09864 | -0.03628 | Q9QYR6 | Microtubu | Map1a | VQGWRETSPTRGEPV |
| S | 1 | 1205 | 0.011458 | 0.047236 | 1.575836 | 0.970665 | Q9QYR6 | Microtubu | Map1a | DISSKQLSPESLGTL |
| S | 1 | 1208 | 0.01513 | 0.066866 | 1.575836 | 0.936628 | Q9QYR6 | Microtubu | Map1a | SKQLSPESLGTLQFG |
| S | 1 | 1218 | 0.000769 | 0.004451 | 1.91684 | 1.166218 | Q9QYR6 | Microtubu | Map1a | TLQFGELSLGKEEKG |
| S | 1 | 995 | 0.015295 | 0.054938 | 5.44373 | 3.444177 | Q9QYR6 | Microtubu | Map1a | KMASPPPSGPPSAAH |
| S | 0.961767 | 898 | 0.047154 | 0.124991 | 1.04539 | 0.682681 | Q9QYR6 | Microtubu | Map1a | AGTISPTSSLEEDKG |
| S | 0.992914 | 899 | 0.04105 | 0.126474 | 1.028149 | 0.642482 | Q9QYR6 | Microtubu | Map1a | GTISPTSSLEEDKGF |
| S | 1 | 1523 | 0.007024 | 0.874847 | -1.37184 | -0.10755 | P14873 | Microtubu | Map1b | SISEGTVSDKSATPV |
| S | 0.999476 | 1815 | 0.015019 | 0.389297 | -0.85749 | 0.240401 | P14873 | Microtubu | Map1b | AAHQASSSPPIDAAT |
| S | 1 | 974 | 0.022444 | 0.744169 | -3.77224 | 0.599468 | P14873 | Microtubu | Map1b | SPTEDDESAKAEADV |
| S | 1 | 2068 | 0.000401 | 0.620198 | -7.52032 | 0.625405 | P14873 | Microtubu | Map1b | CYTTEKKSPSEARQD |
| S | 1 | 1775 | 0.046073 | 0.980928 | -2.50306 | -0.11852 | P14873 | Microtubu | Map1b | SLEGEKLSPKSDISP |
| S | 1 | 1781 | 0.010305 | 0.556226 | -1.50941 | 0.289945 | P14873 | Microtubu | Map1b | LSPKSDISPLTPRES |
| S | 1 | 2267 | 0.001347 | 0.522994 | -2.12777 | -0.27312 | P14873 | Microtubu | Map1b | KSKPLAASPKPGALK |
| S | 0.983029 | 2094 | 0.000393 | 0.966134 | -3.982 | 0.082898 | P14873 | Microtubu | Map1b | KHPKTELSPSFINPN |
| T | 1 | 905 | 9.93E-06 | 0.687287 | -2.5919 | 0.088138 | P14873 | Microtubu | Map1b | GEGECEQTPEELEPV |
| T | 1 | 1629 | 0.023046 | 0.176363 | -1.56502 | -0.73459 | P14873 | Microtubu | Map1b | PKTAKSRTPVQDHRS |
| S | 0.999878 | 608 | 0.009305 | 0.179568 | -1.17262 | -0.43573 | P14873 | Microtubu | Map1b | SVTEKEVSSKEEQSP |
| S | 1 | 1508 | 0.614863 | 0.02171 | 0.370008 | -1.42481 | P14873 | Microtubu | Map1b | IDVSQFGSFKEDTKM |
| S | 1 | 1395 | 0.032496 | 0.306121 | 0.782151 | 0.309882 | P14873 | Microtubu | Map1b | KVLSPLRSPPLLGSE |
| S | 1 | 1391 | 0.032496 | 0.306121 | 0.782151 | 0.309882 | P14873 | Microtubu | Map1b | SPVEKVLSPLRSPPL |
| S | 1 | 1247 | 0.031232 | 0.268251 | 1.032693 | 0.434021 | P14873 | Microtubu | Map1b | DVSDERLSPAKSPSL |
| S | 1 | 1251 | 0.031232 | 0.268251 | 1.032693 | 0.434021 | P14873 | Microtubu | Map1b | ERLSPAKSPSLSPSP |
| S | 1 | 1161 | 0.04607 | 0.893094 | -1.06679 | -0.12421 | P20357 | Microtubu | Map2 | DEGKKETSPETSLIQ |
| S | 0.999998 | 447 | 0.011457 | 0.100157 | -2.72137 | -1.32424 | P20357 | Microtubu | Map2 | LDEKSTVSIEEAVAK |
| S | 0.999982 | 520 | 0.016572 | 0.682454 | -1.58104 | -0.2677 | P20357 | Microtubu | Map2 | KTLGKVTSEPEAVSE |
| T | 1 | 1620 | 0.030114 | 0.50566 | -1.38568 | 0.381931 | P20357 | Microtubu | Map2 | YSSRTPGTPGTPSYP |
| T | 0.999458 | 1260 | 0.03044 | 0.017834 | -1.72282 | -1.77255 | P20357 | Microtubu | Map2 | KLLFRSDTLQISDLL |
| S | 0.999395 | 1796 | 0.720608 | 0.001785 | 0.399309 | -3.44446 | P20357 | Microtubu | Map2 | VASPRRLSNVSSSGS |
| T | 0.999834 | 1609 | 0.00031 | 0.000354 | 2.962518 | 2.577767 | P20357 | Microtubu | Map2 | STAITPGTPPSYSSR |
| S | 1 | 1161 | 0.045656 | 0.252959 | 2.109955 | 1.015511 | P20357 | Microtubu | Map2 | DEGKKETSPETSLIQ |
| S | 0.997436 | 1165 | 0.014064 | 0.057371 | 2.818018 | 1.723573 | P20357 | Microtubu | Map2 | KETSPETSLIQDEVA |
| T | 0.999999 | 43 | 0.048594 | 0.343414 | -2.14509 | -0.89124 | Q60700 | Mitogen-a | Map3k12 | CTPEKDLTPTQCVLR |
| S | 1 | 667 | 0.023536 | 0.971555 | -1.39 | 0.06711 | P27546-3 | Microtubu | Map4 | PNKEPPPSPEKKAKP |
| S | 0.999371 | 261 | 0.00219 | 0.436623 | -1.97188 | 0.326122 | Q7TSJ2 | Microtubu | Map6 | KPLPPAQSQTQEGGP |
| S | 1 | 544 | 0.003611 | 0.302081 | -0.87053 | 0.202991 | A2AJI0 | MAP7 do | Map7d1 | KEPAAPASPAPSPVP |
| S | 1 | 401 | 0.004906 | 0.979164 | -3.40329 | -0.09573 | A2AJI0 | MAP7 do | Map7d1 | RKPGAGGSPALARRR |
| S | 1 | 460 | 0.00342 | 0.843288 | -2.34357 | 0.176857 | A2AJI0 | MAP7 do | Map7d1 | LSTGSELSPKSKARP |
| S | 1 | 357 | 0.004811 | 0.083609 | -1.35514 | 0.570944 | A2AG50 | MAP7 do | Map7d2 | AKPTYLGSPVKYYFP |
| S | 0.995086 | 415 | 0.00165 | 0.52126 | -2.94032 | 0.3956 | Q80W82 | Mitogen-a | Mapk10 | GVVKGQPSPSAQVQQ |
| S | 1 | 28 | 2.08E-05 | 0.960806 | -2.84229 | -0.03485 | Q9WVI9 | C-Jun-ami | Mapk8ip1 | FLGLHIASPPNFRLT |
| T | 1 | 42 | 0.040873 | 0.999586 | -4.42892 | -0.02964 | P10637-5 | Microtubu | Mapt | EEAGIGDTPNQEDQA |
| S | 0.999929 | 486 | 0.035171 | 0.435183 | 1.248125 | 0.404588 | A2A5Y6 | Microtubu | Mapt | IPAKTTPSPKTPPGS |
| T | 1 | 489 | 0.035171 | 0.435183 | 1.248125 | 0.404588 | A2A5Y6 | Microtubu | Mapt | KTTPSPKTPPGSGEP |
| S | 1 | 704 | 0.04203 | 0.982618 | 0.894724 | 0.039367 | A2A5Y6 | Microtubu | Mapt | GAEIVYKSPVVSGDT |
| S | 1 | 708 | 0.037476 | 0.986671 | 0.918697 | 0.034214 | A2A5Y6 | Microtubu | Mapt | VYKSPVVSGDTSPRH |
| S | 1 | 112 | 0.001992 | 0.545634 | -0.73742 | 0.099077 | P26645 | Myristoyla | Marcks | EAEPAEPSSPAAEAE |
| S | 1 | 113 | 0.001992 | 0.545634 | -0.73742 | 0.099077 | P26645 | Myristoyla | Marcks | AEPAEPSSPAAEAEG |
| T | 1 | 79 | 0.001682 | 0.996054 | -1.59992 | 0.015314 | P26645 | Myristoyla | Marcks | PASGSAATPAAAEKD |
| S | 1 | 22 | 0.003081 | 0.049159 | -1.72058 | -0.77196 | P28667 | MARCKS-r | Marcksl1 | AEEAAGASPAKANGQ |
| T | 1 | 85 | 0.008128 | 0.160598 | -2.0072 | -0.75586 | P28667 | MARCKS-r | Marcksl1 | GEVAPKETPKKKKKF |
| T | 0.985734 | 613 | 0.022353 | 0.98707 | -1.54766 | 0.049384 | Q8VHJ5 | Serine/thr | Mark1 | RGSSSRSTFHGEQLR |
| S | 1 | 1414 | 0.018421 | 0.999671 | -1.81916 | 0.008764 | Q9R1L5 | Microtubu | Mast1 | ALAKAALSPVQEHET |
| S | 0.998783 | 1112 | 0.922332 | 0.02887 | -0.22499 | 2.092567 | Q9R1L5 | Microtubu | Mast2;Ma | SLLHTSRSLSSLNRS |
| S | 0.979775 | 935 | 0.009215 | 0.008536 | 0.867204 | 0.789944 | E9Q8S5 | Microtubu | Mast3 | NPSSRDSSPSRDPSP |
| S | 0.99999 | 2517 | 0.003422 | 0.340286 | -0.95759 | 0.20614 | Q811L6 | Microtubu | Mast4 | SQMIKSDSLPSFRLS |
| S | 1 | 139 | 0.010109 | 0.400955 | -1.5411 | 0.384428 | P04370-4 | Myelin ba | Mbp | GLSLSRFSWGAEGQK |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| T | 1 | 174 | 0.018796 | 0.895747 | -3.46519 | 0.312267 | P04370-4 | Myelin bas | Mbp | GAYDAQGTLSKIFKL |
| S | 0.980749 | 547 | 0.003992 | 0.000233 | -1.29729 | -2.13874 | Q99J21 | Mucolipin | Mcoln1 | YIEQCQDSPTSGKFR |
| S | 1 | 4827 | 0.004896 | 0.139977 | -1.16719 | -0.41204 | A2ANY6 | | Mdn1 | HQDEKEDSEPEDVEQ |
| S | 1 | 5012 | 0.024882 | 0.728698 | -1.19093 | -0.20186 | A2ANY6 | | Mdn1 | EEEEGEQSDAEEQVP |
| S | 1 | 438 | 0.040887 | 0.857202 | -3.56398 | -0.47112 | Q9Z2D6-2 | Methyl-Cp | Mecp2 | EKMPRGGSLESDGCP |
| T | 1 | 11 | 0.000523 | 0.44988 | -2.09221 | 0.248628 | D3Z183 | Major facil | Mfsd6 | DDKVAILTDDEEEQK |
| S | 0.999996 | 1404 | 0.001326 | 0.001514 | 3.013807 | 2.619556 | Q8CJ19 | Protein-m | Mical3 | PPLLTPKSPSDKELR |
| S | 1 | 1406 | 0.003027 | 0.003965 | 2.490595 | 2.096343 | Q8CJ19 | Protein-m | Mical3 | LLTPKSPSDKELRSS |
| T | 1 | 785 | 0.002074 | 0.945869 | -2.01512 | 0.076384 | Q9JM52 | Misshapen | Mink1 | FVLLKERTLDEAPKP |
| S | 0.969406 | 766 | 0.027459 | 0.099549 | -3.99104 | -2.43044 | Q8VE19 | WD repeat | Mios | SQYGVSGSPTKSKVT |
| S | 1 | 237 | 3.48E-05 | 0.337076 | -1.26664 | 0.10418 | Q99KX1 | Myeloid le | Mlf2 | AIQGPEDSPSRQSRR |
| S | 0.999999 | 1719 | 0.036984 | 0.995741 | -1.99516 | 0.041688 | Q9QZQ1 | Afadin | Mllt4 | YLKTQVLSPDSLFTA |
| S | 0.999996 | 1083 | 0.003093 | 0.736781 | -1.39391 | -0.14049 | Q9QZQ1 | Afadin | Mllt4 | ELMTRTSSVVTLEVA |
| S | 1 | 85 | 0.038815 | 0.495853 | -1.4871 | 0.447031 | Q9D2P8 | Myelin-ass | Mobp | PKHQPAASPVVVRAP |
| S | 0.999917 | 38 | 0.005528 | 0.639497 | -0.74217 | 0.105384 | Q9CWE0 | Mitochond | Mtfr1l | LKPCPRASFETLPNI |
| S | 1 | 58 | 0.038103 | 0.999485 | -1.48755 | -0.01089 | Q9Z2D1 | Myotubula | Mtmr2 | STSADNFSPDLRVLR |
| S | 1 | 575 | 0.008024 | 0.768916 | -1.56296 | -0.18073 | Q6P9S0 | MTSS1-like | Mtss1l | VGPTRAGSEECVFYT |
| S | 1 | 419 | 0.039002 | 0.996692 | -1.72999 | -0.03232 | Q6P9S0 | MTSS1-like | Mtss1l | MVLTRGLSLEHQKSS |
| S | 0.993195 | 307 | 0.031593 | 0.99152 | -2.15838 | -0.06104 | Q6KAU4 | Multivesic | Mvb12b | AAARLPPSPTRCQQI |
| S | 0.964721 | 199 | 0.042597 | 0.6106 | 0.749215 | -0.1884 | Q6KAU4 | Multivesic | Mvb12b | VPRNHDSSQPTTPSQ |
| T | 1 | 3954 | 0.008154 | 0.689153 | -2.70766 | -0.38013 | Q7TPH6 | E3 ubiquiti | Mycbp2 | ISGDAEPTPEQEEKA |
| S | 1 | 214 | 0.18915 | 0.000719 | -0.78392 | -3.05561 | Q5SV64 | | Myh10 | DHNIPQESPKPVKPQ |
| S | 1 | 1973 | 0.033175 | 0.911205 | -2.55832 | 0.245538 | Q6URW6 | Myosin-14 | Myh14 | RLEEGVASDEEEAEG |
| S | 1 | 1943 | 0.046788 | 0.381233 | -1.04363 | -0.40183 | Q8VDD5 | Myosin-9 | Myh9 | RKGTGDCSDEEVDGK |
| S | 1 | 20 | 0.005793 | 0.367206 | -2.77427 | -0.64277 | Q3THE2 | Myosin reg | Myl12b;M | KRPQRATSNVFAMFD |
| S | 1 | 1460 | 0.01655 | 0.994852 | -2.5452 | 0.047298 | Q6PDN3 | Myosin lig | Mylk | PKDEVEVSDDDEKEP |
| S | 1 | 2028 | 0.003625 | 0.996788 | -1.5168 | 0.015524 | Q9JMH9-6 | Unconvent | Myo18a | KPLAPDPSDDEHDPV |
| S | 1 | 1259 | 0.002877 | 0.38678 | -1.44729 | -0.27665 | Q8C170 | Unconvent | Myo9a | IVRQRPKSLEDLHQK |
| S | 1 | 2138 | 0.002525 | 0.023548 | -5.26673 | -2.7695 | P70670 | Nascent po | Naca | TPTVQEESEEEEVDE |
| S | 1 | 284 | 0.784821 | 0.029518 | 0.26052 | -1.35751 | Q9CWZ7 | Gamma-sc | Napg | GGGIKKKSPATPQAK |
| S | 0.97915 | 999 | 0.017593 | 0.23545 | 6.708202 | 2.585529 | Q9EPN1 | Neurobeac | Nbea | EIEDLSQSQSPESET |
| T | 0.999446 | 795 | 0.9766 | 0.042093 | 0.086655 | -1.35397 | O35136 | Neural cell | Ncam2 | VNEPNETTPLTEPEK |
| S | 0.999281 | 22 | 0.017205 | 0.1796 | -3.48799 | -1.50727 | Q3UYV9 | Nuclear ca | Ncbp1 | PHKRRKTSDANETED |
| S | 0.99837 | 286 | 0.023825 | 0.788097 | -2.41655 | -0.34721 | Q9ESJ4 | NCK-intera | Nckipsd | LEAQDALSPETTEEK |
| S | 1 | 403 | 0.010271 | 0.003931 | -1.32831 | -1.4863 | P09405 | Nucleolin | Ncl | TLLAKNLSFNITEDE |
| S | 1 | 215 | 0.640362 | 0.022217 | -0.17988 | -0.72336 | Q9ERR1 | Nuclear dis | Ndel1 | SAVQASLSLPATPVG |
| T | 1 | 219 | 0.640362 | 0.022217 | -0.17988 | -0.72336 | Q9ERR1 | Nuclear dis | Ndel1 | ASLSLPATPVGKGTE |
| S | 1 | 2 | 0.027909 | 0.360504 | -1.45021 | -0.50114 | Q62433 | Protein ND | Ndrg1 | _______MSRELHDVD |
| S | 1 | 332 | 0.013383 | 0.650987 | -1.81972 | -0.31175 | Q9QYG0 | Protein ND | Ndrg2 | LSRSRTASLTSAASI |
| T | 0.999379 | 20 | 0.009822 | 0.975078 | -1.70282 | 0.061747 | Q9QYG0 | Protein ND | Ndrg2 | KPLLPGQTPETAKEA |
| S | 1 | 342 | 0.015522 | 0.196395 | -3.74235 | -1.51709 | Q9QYG0 | Protein ND | Ndrg2 | SAASIDGSRSRSRTL |
| S | 0.999296 | 334 | 0.041139 | 0.060448 | 1.76778 | 1.412431 | Q9QYF9 | Protein ND | Ndrg3 | SRTHSTSSSIGSGES |
| T | 0.809258 | 308 | 0.036548 | 0.106798 | -2.10106 | 1.350014 | Q8BTG7 | Protein ND | Ndrg4 | AVPSASMTRLARSRT |
| S | 1 | 480 | 0.025902 | 0.996011 | -0.7259 | 0.013324 | E9PXB7 | E3 ubiquiti | Nedd4l | DTLSNPQSPQPSPYN |
| S | 1 | 508 | 0.00948 | 0.762179 | -1.7355 | 0.212548 | P19246 | Neurofilam | Nefh | PPAEEAASPEKETKS |
| S | 1 | 809 | 0.006824 | 0.691582 | -2.23083 | 0.298754 | P19246 | Neurofilam | Nefh | KPPAEAKSPEKAKSP |
| S | 1 | 769 | 0.036768 | 0.906981 | -1.85617 | 0.187941 | P19246 | Neurofilam | Nefh | KSPIEVKSPEKAKTP |
| S | 1 | 631 | 4.86E-05 | 0.917159 | -6.09326 | -0.13154 | P19246 | Neurofilam | Nefh | KSPAEAKSPAEAKSP |
| S | 1 | 637 | 0.000069 | 0.918113 | -5.70623 | -0.13154 | P19246 | Neurofilam | Nefh | KSPAEAKSPATVKSP |
| S | 1 | 679 | 0.017999 | 0.988544 | -3.17332 | -0.09009 | P19246 | Neurofilam | Nefh | KSPAEVKSPGEAKSP |
| S | 1 | 619 | 0.027075 | 0.465261 | -2.2347 | 0.641288 | P19246 | Neurofilam | Nefh | KSPAEAKSPAEAKSP |
| S | 1 | 655 | 0.046455 | 0.902558 | -1.8344 | 0.203542 | P19246 | Neurofilam | Nefh | KSPSEAKSPAEAKSP |
| S | 1 | 589 | 0.008838 | 0.990027 | -3.59179 | -0.07984 | P19246 | Neurofilam | Nefh | KSPATVKSPGEAKSP |
| S | 1 | 595 | 0.034487 | 0.991194 | -2.70413 | -0.07984 | P19246 | Neurofilam | Nefh | KSPGEAKSPSEAKSP |
| S | 1 | 553 | 0.029559 | 0.981823 | -2.46091 | 0.100477 | P19246 | Neurofilam | Nefh | KSPGEAKSPGEAKSP |
| S | 1 | 605 | 0.160474 | 0.038504 | -2.10757 | 3.009043 | P08553 | Neurofilam | Nefm | EKPEKAKSPMPKSPV |
| S | 1 | 502 | 0.033522 | 0.731935 | -1.85345 | -0.33777 | P08553 | Neurofilam | Nefm | EEPEAEKSPVKSPEA |
| S | 1 | 769 | 0.003302 | 0.244436 | -2.28949 | -0.58323 | P08553 | Neurofilam | Nefm | VTNGLDVSPAEEKKG |
| S | 0.999996 | 30 | 0.044583 | 0.94541 | -2.369 | 0.190832 | P08553 | Neurofilam | Nefm | SFSRVSGSPSSGFRS |
| S | 0.999972 | 1071 | 0.032508 | 0.728758 | -1.13925 | 0.207438 | P51954 | Serine/thr | Nek1 | EQPGDEYSEEEESVL |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 904 | 0.042632 | 0.79416 | 1.077235 | 0.178281 | Q5NCX5 | Neuralized | Neurl4 | SNTATEKSFPLHSPV |
| S | 1 | 909 | 0.042632 | 0.79416 | 1.077235 | 0.178281 | Q5NCX5 | Neuralized | Neurl4 | EKSFPLHSPVAGVAH |
| S | 0.999998 | 2804 | 0.014718 | 0.995902 | -1.42958 | -0.02301 | Q04690 | Neurofibr | Nf1 | DKENVELSPTAGHCN |
| S | 0.969001 | 51 | 0.00091 | 0.785181 | -1.65152 | -0.11232 | B1AY10 | Transcripti | Nfx1 | GRRNYSSSPPCHLPR |
| S | 1 | 606 | 0.009167 | 0.656733 | -1.55372 | 0.240018 | Q8CHT1 | Ephexin-1 | Ngef | NRRTKFVSFTSRLLD |
| T | 0.998623 | 299 | 0.026316 | 0.226559 | 2.569793 | -1.11949 | Q91VE6 | MKI67 FH | Nifk | VKEDTQKTPTSASPG |
| S | 1 | 38 | 0.022794 | 0.996089 | -0.72044 | -0.01266 | O70311 | Glycylpept | Nmt2 | ETEHAKGSPGGDLGA |
| S | 1 | 563 | 0.022544 | 0.135496 | -3.62309 | -1.87575 | E9Q5C9 | | Nolc1 | NGKAAKESEEEEEEE |
| S | 1 | 513 | 0.006388 | 0.440109 | -1.06597 | 0.223252 | Q9D6Z1 | Nucleolar | Nop56 | APKEELASDLEEMAT |
| S | 1 | 509 | 0.04081 | 0.690855 | -2.24824 | 0.475145 | Q6DFW4 | Nucleolar | Nop58 | HIKEEPLSEEEPCTS |
| S | 1 | 892 | 0.015995 | 0.943065 | -1.50277 | -0.0941 | F8WGF2 | Nitric oxid | Nos1 | YSDSRKSSGDGPDLR |
| S | 1 | 125 | 0.002069 | 0.003373 | -4.10746 | -3.29581 | Q61937 | Nucleopho | Npm1 | AVEEDAESEDEDEED |
| S | 1 | 20 | 0.003262 | 0.578683 | -3.16516 | -0.44716 | Q91V36 | Nuclear re | Nrbp2 | EREREDESEDESDIL |
| S | 1 | 1178 | 0.001192 | 0.207658 | -2.2597 | -0.49622 | Q810U4 | Neuronal | Nrcam | DGTFGEYSDAEDHKP |
| S | 1 | 85 | 0.005506 | 0.371586 | -2.07399 | -0.47135 | Q8BHG1 | Nardilysin | Nrd1 | ARLGADESEEEGRSF |
| S | 1 | 207 | 0.02498 | 0.995401 | -1.82689 | -0.03567 | P46460 | Vesicle-fus | Nsf | KTKENRQSIINPDWN |
| S | 1 | 31 | 0.006186 | 0.644973 | -1.91932 | 0.276702 | Q5NCR9 | Nuclear sp | Nsrp1;Ccd | QKPSVFGSDSDDDET |
| S | 1 | 33 | 0.016654 | 0.984772 | -2.07251 | 0.066621 | Q5NCR9 | Nuclear sp | Nsrp1;Ccd | PSVFGSDSDDDETSV |
| S | 1 | 368 | 0.008684 | 0.876994 | -1.85415 | -0.15137 | Q02819 | Nucleobin | Nucb1 | NARAQRLSQETEALG |
| S | 1 | 181 | 0.009754 | 0.398169 | -1.41025 | 0.350424 | Q80XU3 | Nuclear ub | Nucks1 | LKATVTPSPVKGKAK |
| S | 1 | 113 | 0.00163 | 0.257242 | -2.00173 | -0.4255 | Q80XU3 | Nuclear ub | Nucks1 | MLLEDVGSEEEPEED |
| S | 1 | 58 | 0.416444 | 0.028366 | 1.083623 | -2.74733 | Q80XU3 | Nuclear ub | Nucks1 | GKNSQEDSEDSEEKD |
| S | 0.985484 | 244 | 0.00034 | 0.73098 | -5.40283 | -0.34336 | Q9QZS3-2 | Protein nu | Numb | PSPSSPTSPTPDGTA |
| S | 1 | 411 | 5.51E-05 | 0.176596 | -4.44858 | -0.55113 | O08919 | Numb-like | Numbl | PGHKRTPSEAERWLE |
| T | 1 | 279 | 0.016976 | 0.208011 | -1.89312 | 0.765355 | O08919 | Numb-like | Numbl | GEKGEAGTPVAAGTT |
| S | 1 | 238 | 0.026144 | 0.91488 | -1.11705 | 0.098277 | Q3B7Z2 | Oxysterol- | Osbp | TALQRSLSELESLKL |
| S | 0.844783 | 58 | 0.043099 | 0.383114 | -1.01051 | -0.37878 | S4R1M9 | Oxysterol- | Osbpl10 | LGGGGSRSSPGSVAA |
| S | 1 | 214 | 0.019084 | 0.562195 | -1.00356 | 0.22223 | Q62422 | Osteoclast | Ostf1 | DYLDDEDSD_______ |
| T | 0.999999 | 176 | 0.001384 | 0.972039 | -2.80881 | -0.06928 | Q4KMM3 | Oxidation | Oxr1 | AEFDKTTTPDVAHPK |
| T | 1 | 72 | 0.003298 | 0.528964 | -2.66241 | 0.411924 | Q4KMM3 | Oxidation | Oxr1 | SELKRFYTIDTGQKK |
| S | 0.999999 | 346 | 0.00209 | 0.108372 | -3.19454 | -1.02279 | Q4KMM3 | Oxidation | Oxr1 | AFTESELSPIREELL |
| T | 0.988976 | 175 | 0.286801 | 0.039457 | -0.92569 | -1.70994 | Q9DBN4 | Putative m | P33monox | HPASAQSTPSSTPHA |
| S | 0.879487 | 779 | 0.001036 | 0.694699 | -1.15223 | 0.100667 | Q8K212 | Phosphofu | Pacs1 | SLTVPSTSPPSSSGL |
| T | 1 | 181 | 0.036737 | 0.576533 | -1.25079 | -0.32133 | Q61644 | Protein kir | Pacsin1 | SKTEQSVTPEQQKKL |
| S | 0.999994 | 186 | 0.000823 | 0.954956 | -3.98949 | 0.112507 | Q61036 | Serine/thr | Pak3 | PPLAPPVSEEEDEEE |
| T | 1 | 141 | 0.040306 | 0.722891 | -1.3853 | 0.271488 | Q9Z0P4-2 | Paralemmi | Palm | TLVNAQQTPLGTPKE |
| T | 1 | 145 | 0.00353 | 0.794969 | -1.25256 | 0.111444 | Q9Z0P4-2 | Paralemmi | Palm | AQQTPLGTPKENRTS |
| S | 1 | 355 | 0.001288 | 0.353068 | -1.15201 | -0.19559 | Q8BR92 | Paralemmi | Palm2 | SPEGKEESLATDPAP |
| S | 1 | 42 | 0.019856 | 0.760807 | 1.336949 | 0.19734 | V9GX56 | | Pank2 | DPLRRRASSAAPSGS |
| S | 1 | 264 | 0.048495 | 0.949908 | -1.74034 | -0.13733 | P58501 | PAX3- and | Paxbp1 | REDENDASDDEDDDE |
| S | 1 | 788 | 0.022775 | 0.246495 | -1.13134 | 0.455868 | F7BJK1 | | Pcdh1 | MSDAPGDSPRIHLPL |
| S | 1 | 2288 | 0.040704 | 0.130812 | -0.74046 | -0.45589 | Q9QYX7 | Protein pic | Pclo | QTKEQPGSPHSVSGE |
| S | 0.966368 | 4598 | 0.023857 | 0.002305 | -2.58104 | -4.02027 | Q9QYX7 | Protein pic | Pclo | PSPGQPGSPSVSKKK |
| S | 1 | 3582 | 0.001375 | 0.234204 | -1.8207 | 0.390295 | Q9QYX7 | Protein pic | Pclo | KPLPDDISPQKVLHP |
| S | 0.999983 | 2502 | 0.033539 | 0.173312 | 0.993104 | 0.519121 | Q9QYX7 | Protein pic | Pclo | SPHSNKSSPRYSKSL |
| S | 1 | 1766 | 0.010609 | 0.018972 | 1.314043 | 1.017354 | Q9QYX7 | Protein pic | Pclo | KTPPSNLSPIEDASP |
| S | 0.999993 | 1772 | 0.010609 | 0.018972 | 1.314043 | 1.017354 | Q9QYX7 | Protein pic | Pclo | LSPIEDASPTEELRQ |
| T | 1 | 1760 | 0.010609 | 0.018972 | 1.314043 | 1.017354 | Q9QYX7 | Protein pic | Pclo | RRRERPKTPPSNLSP |
| S | 1 | 302 | 0.015817 | 0.202451 | -2.64852 | -1.06453 | P59913 | Protein-L-i | Pcmtd1 | LIPQPLDSEEDEKME |
| S | 1 | 362 | 0.016259 | 0.987649 | -1.9428 | -0.05584 | P49586 | Choline-ph | Pcyt1a | RAVTCDISEDEED__ |
| S | 1 | 319 | 0.539527 | 0.01912 | 0.550027 | -1.90785 | P49586 | Choline-ph | Pcyt1a | QAISPKQSPSSSPTH |
| S | 0.985195 | 323 | 0.420704 | 0.012636 | 0.550027 | -1.72757 | P49586 | Choline-ph | Pcyt1a | PKQSPSSSPTHERSP |
| S | 0.995366 | 232 | 0.003315 | 0.840521 | -2.90039 | 0.219547 | P35486 | Pyruvate d | Pdha1 | NRYGMGTSVERAAAS |
| S | 1 | 1359 | 0.020321 | 0.955191 | -3.15001 | 0.185011 | F8WHU5 | | Pds5b | AQQSRAESPETSAVE |
| S | 0.999981 | 1255 | 0.01431 | 0.279078 | -1.16487 | 0.391874 | Q4VA53 | Sister chro | Pds5b | RKRGRTASDSDEQQW |
| S | 1 | 1356 | 0.044595 | 0.980426 | -3.89233 | 0.185011 | Q4VA53 | Sister chro | Pds5b | RAQQRAESPETSAVE |
| S | 1 | 748 | 0.018578 | 0.578346 | -1.02733 | -0.21945 | Q99K01 | Pyridoxal- | Pdxdc1 | HDNLEAHSPEQPPRA |
| S | 1 | 282 | 0.016752 | 0.962787 | -2.21269 | -0.11238 | Q69Z38 | Pseudopo | Peak1 | NFRANTLSPVRFFVS |
| S | 1 | 426 | 0.001765 | 0.000138 | 2.280397 | 3.496955 | F8SLQ3 | PEX5-relat | Pex5l | LVKNKKGSPGLTRRM |
| S | 0.999733 | 175 | 0.151844 | 0.0033 | -1.16155 | -2.97011 | Q8CAA7 | Glucose 1, | Pgm2l1 | AGVMITASHNRKEDN |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 181 | 9.62E-05 | 0.525704 | -1.34045 | -0.09839 | O55022 | Membrane | Pgrmc1 | GEEPTVYSDDEEPKD |
| T | 1 | 205 | 0.005054 | 0.741665 | -2.09992 | 0.233754 | Q80UU9 | Membrane | Pgrmc2 | GEEPSEYTDEEDTKD |
| S | 0.99934 | 91 | 0.000191 | 0.799272 | -1.63143 | 0.076697 | Q501J7-2 | Phosphata | Phactr4 | IGSARSSSPVLVEEE |
| S | 1 | 207 | 0.004128 | 0.478542 | -1.41346 | 0.250894 | E9Q3L2 | | Pi4ka | VSSISQVSPERGIPP |
| S | 1 | 1204 | 0.009472 | 0.551145 | -2.00933 | 0.381655 | O35954 | Membrane | Pitpnm1 | VDFLRKQSQLLRSRG |
| T | 0.990822 | 287 | 0.040849 | 0.996459 | -3.04209 | -0.05959 | O35954 | Membrane | Pitpnm1 | PGTSTAGTPDGPEAP |
| S | 0.752697 | 397 | 0.017303 | 0.999666 | -3.02416 | 0.014457 | Q6ZPQ6 | Membrane | Pitpnm2 | SEFRVASSVEQLNII |
| S | 1 | 321 | 0.049662 | 0.829628 | -0.75389 | -0.11662 | Q3UHE1 | Membrane | Pitpnm3 | SSKRLSKSNVDVSSG |
| T | 1 | 231 | 0.015814 | 0.884065 | -1.67447 | -0.15312 | O55176 | E3 ubiquiti | Pja1 | KPKVFFDTDDDDDVP |
| S | 0.999909 | 536 | 0.015995 | 0.942906 | 1.090831 | 0.068408 | P70268 | Serine/thr | Pkn1 | AVATGTFSPNASPGA |
| S | 1 | 540 | 0.015995 | 0.942906 | 1.090831 | 0.068408 | P70268 | Serine/thr | Pkn1 | GTFSPNASPGAEIRH |
| S | 0.999999 | 220 | 0.022041 | 0.957846 | -2.32681 | 0.135214 | Q68FH0 | Plakophilir | Pkp4 | SVPSRAQSPSYVTST |
| S | 1 | 775 | 0.003845 | 0.001819 | -1.94003 | -2.04935 | Q68FH0 | Plakophilir | Pkp4 | DDLLGKESPSKDSEP |
| S | 1 | 514 | 0.017159 | 0.999971 | -2.54667 | 0.003591 | Q68FH0 | Plakophilir | Pkp4 | TRSPSIDSIQKDPRE |
| S | 1 | 394 | 0.032668 | 0.927864 | -1.13577 | -0.09713 | Q68FH0 | Plakophilir | Pkp4 | SSYASQHSQLGQELR |
| S | 0.974624 | 336 | 0.035619 | 0.774994 | -0.81711 | -0.13571 | Q68FH0 | Plakophilir | Pkp4 | QGQVGSSSPKRSGMT |
| S | 1 | 313 | 0.007594 | 0.978545 | -1.51189 | -0.04778 | Q68FH0 | Plakophilir | Pkp4 | QTTTRVGSPLTLTDA |
| S | 1 | 1197 | 0.031151 | 0.903118 | 1.392723 | 0.137735 | Q9Z1B3 | 1-phospha | Plcb1 | AAKVNLKSPSSEEIE |
| S | 1 | 1199 | 0.031151 | 0.903118 | 1.392723 | 0.137735 | Q9Z1B3 | 1-phospha | Plcb1 | KVNLKSPSSEEIERE |
| S | 1 | 676 | 0.005826 | 0.637557 | -1.07561 | 0.155184 | A2AP18-2 | 1-phospha | Plch2 | SKIKKVASVEEGDET |
| T | 1 | 557 | 0.000702 | 0.006508 | -3.55923 | -1.94607 | Q3USB7 | Inactive ph | Plcl1 | DLLEGEVTDEDEEAE |
| S | 1 | 1324 | 0.042632 | 0.5754 | -1.52018 | 0.408101 | Q9QXS1-6 | Plectin | Plec | AQLEPVASPAKKPKV |
| S | 0.999999 | 574 | 0.004215 | 0.979941 | -1.89319 | 0.050455 | E9Q6H8 | | Plekha5 | TYRSEVTSPIQRGDV |
| T | 0.999997 | 116 | 0.037155 | 0.032834 | -2.43412 | -2.25281 | P60202 | Myelin prc | Plp1 | CGKGLSATVTGGQKG |
| S | 0.999999 | 726 | 0.029345 | 0.996641 | -0.99062 | 0.017248 | A2AJT4 | Arginine/s | Pnisr | RTFCRSGSISVKVIR |
| S | 1 | 306 | 0.01186 | 0.476749 | -3.2596 | -0.74355 | Q9EQ28 | DNA polyn | Pold3 | RGKRVDLSDEEAKET |
| S | 1 | 17 | 0.032368 | 0.677724 | -1.01588 | -0.20703 | B8QI35 | Liprin-alph | Ppfia3 | SEDGRRGSALGPDEA |
| S | 1 | 683 | 0.026625 | 0.815192 | -4.47697 | -0.61051 | B8QI35 | Liprin-alph | Ppfia3 | TPRLAPPSPAREGTD |
| S | 0.999998 | 435 | 0.020673 | 0.972466 | -2.48895 | -0.11426 | Q8C8U0 | Liprin-beta | Ppfibp1 | SSLQKSSSLGNLKKE |
| S | 1 | 939 | 0.049852 | 0.729875 | -3.65878 | -0.74981 | A2ARP1 | Inositol he | Ppip5k1 | EMKTDPGSIENLCPG |
| S | 1 | 545 | 0.007788 | 0.942083 | -1.14559 | -0.06077 | Q80TL0 | Protein ph | Ppm1e | GYEGRVDSFTDRTSL |
| S | 1 | 157 | 0.035599 | 0.956052 | -2.52326 | 0.170382 | Q8R4S0 | Protein ph | Ppp1r14c | IRGMRKLSPPQKKSV |
| S | 1 | 156 | 0.014182 | 0.046271 | -0.87847 | 0.573646 | Q60829-2 | Protein ph | Ppp1r1b | GEEPQHPSPP_____ |
| S | 1 | 61 | 0.019608 | 0.021532 | -1.65076 | -1.44126 | Q60829-2 | Protein ph | Ppp1r1b | NLSENQASEEEDELG |
| S | 1 | 54 | 0.001073 | 0.084357 | 0.854679 | 0.257634 | A2AJW4 | Protein ph | Ppp1r3d | IIQRRSRSLPTSPER |
| S | 0.996712 | 58 | 0.001073 | 0.084357 | 0.854679 | 0.257634 | A2AJW4 | Protein ph | Ppp1r3d | RSRSLPTSPERRAKA |
| S | 1 | 81 | 0.014772 | 0.639123 | -1.06946 | 0.192237 | Q9CW07 | Protein ph | Ppp1r3g | RSRARSFSLPADPIL |
| S | 0.999733 | 75 | 0.033457 | 0.986606 | -3.62293 | 0.131072 | Q9CW07 | Protein ph | Ppp1r3g | ELQEYRRSRARSFSL |
| S | 1 | 497 | 0.10563 | 0.049413 | 1.097352 | 1.248908 | Q60996 | Serine/thr | Ppp2r5c | RPLVRRKSELPQDPH |
| S | 1 | 81 | 0.002643 | 0.07861 | 1.279812 | 0.480642 | Q91V89 | | Ppp2r5d | KKERRQSSFPFNLNK |
| S | 1 | 565 | 0.005393 | 0.412546 | -1.74949 | -0.36909 | Q91V89 | | Ppp2r5d | KVLLRRKSELPQDVY |
| S | 1 | 80 | 0.006533 | 0.009149 | 1.556349 | 1.285638 | Q91V89 | | Ppp2r5d | VKKERRQSSFPFNLN |
| S | 1 | 81 | 0.034166 | 0.385832 | 1.556349 | 0.54407 | Q91V89 | | Ppp2r5d | KKERRQSSFPFNLNK |
| S | 1 | 479 | 0.035138 | 0.562794 | -1.77935 | 0.462843 | P48453 | Serine/thr | Ppp3cb | SPPHRICSFEEAKGL |
| S | 0.966381 | 670 | 0.007237 | 0.725746 | -0.89797 | -0.11288 | Q8R3Q2 | Serine/thr | Ppp6r2 | PGLAAPSSPTQKEGP |
| S | 1 | 209 | 0.048235 | 0.840503 | -1.6333 | -0.24114 | Q9EQC8 | | Prcc | HAFSRKPSDISSDAK |
| S | 1 | 108 | 0.228354 | 0.046803 | -1.48827 | -2.33883 | Q9R078 | 5'-AMP-ac | Prkab1 | SKLPLTRSQNNFVAI |
| T | 0.999737 | 198 | 0.024854 | 0.510214 | -2.31967 | 0.602665 | P68181 | cAMP-dep | Prkaca;Prk | RVKGRTWTLCGTPEY |
| S | 1 | 112 | 0.0094 | 0.728333 | -0.7943 | -0.10559 | P31324 | cAMP-dep | Prkar2b | NRFTRRASVCAEAYN |
| S | 0.999996 | 319 | 0.02553 | 0.647335 | -1.27732 | 0.259918 | Q4VA93 | Protein kir | Prkca | PAGNKVISPSEDRKQ |
| S | 0.99983 | 11 | 0.003477 | 0.664761 | -1.08006 | 0.131144 | P68404-2 | Protein kir | Prkcb | PAAGPPPSEGEESTV |
| S | 0.999251 | 206 | 0.008143 | 0.942397 | -3.15989 | 0.168904 | P68404-2 | Protein kir | Prkcb | KLIPDPKSESKQKTK |
| T | 0.99992 | 642 | 0.020523 | 0.960612 | -3.44825 | 0.189931 | P68404 | Protein kir | Prkcb | TRQPVELTPTDKLFI |
| T | 1 | 641 | 0.005716 | 0.996537 | -1.30658 | -0.01541 | P68404-2 | Protein kir | Prkcb | TRHPPVLTPPDQEVI |
| S | 1 | 660 | 0.000274 | 0.076102 | -5.83658 | -1.36283 | P68404-2 | Protein kir | Prkcb | QSEFEGFSFVNSEFL |
| S | 0.999996 | 643 | 0.011131 | 0.436132 | -1.17929 | -0.28373 | P28867 | Protein kir | Prkcd | LNEKPQLSFSDKNLI |
| S | 1 | 729 | 0.002311 | 0.759777 | -1.22153 | -0.10894 | P16054 | Protein kir | Prkce | QEEFKGFSYFGEDLM |
| T | 1 | 655 | 0.0102 | 0.300503 | -1.3862 | 0.412705 | P63318 | Protein kir | Prkcg | TRAAPALTPPDRLVL |
| S | 0.999886 | 18 | 0.005956 | 0.478386 | -1.28377 | -0.24794 | Q9WTX2 | Interferon- | Prkra | PPLQREDSGTFSLGK |
| S | 1 | 619 | 0.008241 | 0.203597 | -1.64072 | -0.56125 | Q922U1 | U4/U6 sma | Prpf3 | KGDDDEESDEEAVKK |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 88 | 0.01675 | 0.966353 | -2.17566 | 0.104914 | Q61136 | Serine/thr | Prpf4b | RKEVIEASDKEGLSP |
| S | 1 | 363 | 0.047453 | 0.97908 | -1.47907 | -0.07404 | Q7TSC1 | Protein PR | Prrc2a | EGHKDSQSAAAEEPE |
| S | 0.999421 | 378 | 0.027035 | 0.999979 | -0.79863 | 0.001077 | Q7TSC1 | Protein PR | Prrc2a | TDGKKGTSPGSELPP |
| S | 1 | 799 | 0.054614 | 0.031017 | 0.734146 | 0.771054 | Q6PE13 | Proline-ric | Prrt3 | ELDLRPPSPINLSRS |
| S | 0.99766 | 44 | 0.001991 | 0.024128 | -1.52401 | -0.75563 | E9PUC5 | | Psd3 | KSMKISNSSEFSAKE |
| S | 1 | 342 | 0.023778 | 0.426758 | -4.33341 | -1.28232 | E9PUC5 | PH and SE | Psd3 | KKSHSSPSLNPDASP |
| T | 0.999921 | 273 | 0.010456 | 0.221055 | -1.02878 | 0.359044 | Q3TXS7 | 26S protea | Psmd1 | QNLRTVGTPIASVPG |
| T | 0.999623 | 20 | 0.03319 | 0.876049 | -1.1338 | 0.130621 | Q8VDM4 | 26S protea | Psmd2 | SQQPSATTPSGADEK |
| T | 1 | 250 | 0.015804 | 0.045902 | 2.786818 | 1.873956 | O35226 | 26S protea | Psmd4 | AAEAGIATPGTEDSD |
| T | 1 | 253 | 0.022231 | 0.086079 | 2.309687 | 1.396825 | O35226 | 26S protea | Psmd4 | AGIATPGTEDSDDAL |
| S | 1 | 153 | 0.011503 | 0.349893 | -1.80182 | 0.506087 | Q8BHL8 | Proteasom | Psmf1 | WEKARANSPPREFPP |
| S | 1 | 576 | 0.001253 | 0.001965 | -4.24481 | -3.44238 | B9EKR1 | Receptor-t | Ptprz1 | KEVSADVSEEENFLT |
| S | 1 | 572 | 0.094728 | 0.027716 | -1.60709 | -2.07078 | B9EKR1 | Receptor-t | Ptprz1 | ITEYKEVSADVSEEE |
| S | 1 | 576 | 0.127375 | 0.014416 | -1.52113 | -2.57378 | B9EKR1 | Receptor-t | Ptprz1 | KEVSADVSEEENFLT |
| S | 1 | 342 | 0.020647 | 0.428167 | -1.24439 | -0.35411 | Q8R4E6 | Purine-rich | Purg | RMDGRRASGEEQECL |
| S | 0.999997 | 159 | 0.025519 | 0.327374 | 1.749693 | 0.62545 | Q8R4E6 | Purine-rich | Purg | RQKHSAPSPPVSVGS |
| S | 1 | 163 | 0.025519 | 0.327374 | 1.749693 | 0.62545 | Q8R4E6 | Purine-rich | Purg | SAPSPPVSVGSEEHP |
| S | 1 | 166 | 0.025519 | 0.327374 | 1.749693 | 0.62545 | Q8R4E6 | Purine-rich | Purg | SPPVSVGSEEHPHSV |
| T | 1 | 301 | 0.031988 | 0.562348 | -1.31024 | 0.332405 | Q80V76 | | Pygo2 | SSGRGGGTPDANSLA |
| S | 0.997145 | 1007 | 0.019722 | 0.999887 | -1.09353 | -0.00314 | E9Q9Q2 | | R3hdm1 | RQAKKAASTDLGAGE |
| S | 1 | 278 | 0.038887 | 0.511704 | -1.23241 | -0.36071 | Q9DCB4 | R3H doma | R3hdm1;R | QDGRRSKSIEEREEE |
| S | 0.999972 | 381 | 0.027371 | 0.904166 | -1.19502 | -0.11346 | Q80TM6 | R3H doma | R3hdm2 | PPVTKASSFSGISIL |
| S | 0.999738 | 923 | 0.025084 | 0.439805 | -0.95523 | -0.28043 | Q80TM6 | R3H doma | R3hdm2 | RQALKSASTDLGTAD |
| S | 1 | 530 | 0.00121 | 0.218028 | -1.28067 | 0.276025 | Q8R361 | Rab11 fam | Rab11fip5 | TAAPVEASPDRKQPR |
| S | 1 | 410 | 0.00273 | 0.155048 | -1.17515 | -0.34952 | O35551 | Rab GTPas | Rabep1 | RRAQSTDSLGTSSSL |
| S | 1 | 594 | 0.002742 | 0.991935 | -2.47027 | -0.03771 | Q5U3K5 | Rab-like pr | Rabl6 | FPVREDLSDVTDEDT |
| S | 1 | 483 | 0.000632 | 0.304585 | -2.99948 | -0.47629 | Q5U3K5 | Rab-like pr | Rabl6 | SKNISLSSEEEAEGL |
| S | 1 | 594 | 0.047982 | 0.978136 | 0.846486 | 0.043474 | Q5U3K5 | Rab-like pr | Rabl6 | FPVREDLSDVTDEDT |
| T | 1 | 597 | 0.047982 | 0.978136 | 0.846486 | 0.043474 | Q5U3K5 | Rab-like pr | Rabl6 | REDLSDVTDEDTGPA |
| S | 0.999999 | 160 | 7.19E-05 | 0.341226 | -3.83108 | 0.362868 | P54728 | UV excisio | Rad23b | AQTPVLTSPAPADST |
| S | 1 | 270 | 0.037562 | 0.352474 | -1.0049 | 0.381884 | Q64012 | RNA-bindi | Raly | APQEDTASEAGTPQG |
| T | 1 | 274 | 0.004023 | 0.292698 | -1.30032 | 0.316068 | Q64012 | RNA-bindi | Raly | DTASEAGTPQGEVQT |
| S | 0.999997 | 788 | 0.031522 | 0.096129 | -0.72108 | 0.461213 | Q9ERU9 | E3 SUMO- | Ranbp2 | SPTKYSLSPSKSYKY |
| S | 1 | 148 | 0.002259 | 0.632616 | -2.47129 | -0.2907 | Q9CT10 | Ran-bindi | Ranbp3 | NLTQRSPSESAEETH |
| S | 0.995153 | 708 | 0.02307 | 0.070491 | 4.853861 | 3.160461 | Q5SVL6 | Rap1 GTPa | Rap1gap2 | DKLSHASSSAGH___ |
| S | 0.997132 | 597 | 0.013077 | 0.703192 | -4.4736 | -0.68256 | E9Q912 | | Rap1gds1 | KSVAQQASLTEQRLT |
| S | 1 | 192 | 0.027515 | 0.375265 | -3.02591 | 1.015614 | G5E867 | | Raph1 | NQHRRTASAGTVSDA |
| S | 1 | 218 | 0.000918 | 0.999961 | -2.00927 | -0.00168 | P42208 | Septin-2 | Sept2 | YHLPDAESDEDEDFK |
| S | 1 | 118 | 0.044103 | 0.936376 | -1.84395 | 0.160481 | P28661 | Septin-4 | Sept4 | KLDPYDSSEDDKEYV |
| S | 1 | 225 | 0.019377 | 0.039041 | -2.02281 | -1.49989 | Q9Z2Q6 | Septin-5 | Sept5 | YQFPECDSDEDEDFK |
| T | 1 | 13 | 0.00014 | 0.692885 | -4.77062 | 0.274783 | Q9Z2Q6 | Septin-5 | Sept5 | RYKSKLATPEDKQDI |
| T | 0.999659 | 336 | 0.005266 | 0.432629 | -1.49558 | 0.303337 | Q9Z2Q6 | Septin-5 | Sept5 | IPILPLPTPDAETEK |
| T | 0.984848 | 418 | 0.001012 | 0.931967 | -5.01443 | 0.183464 | Q9R1T4 | Septin-6 | Sept6 | SQAGGSQTLKRDKEK |
| S | 0.980126 | 422 | 5.71E-06 | 0.374366 | -5.63662 | 0.301485 | O55131 | Septin-7 | Sept7 | RILEQQNSSRTLEKN |
| T | 1 | 227 | 0.02204 | 0.489451 | -2.65258 | 0.692021 | O55131 | Septin-7 | Sept7 | KIYEFPETDDEEENK |
| S | 0.99716 | 788 | 0.000265 | 0.000977 | -2.82402 | -1.91822 | E9PW37 | | Rasal2 | SSPNVSGSLSSGLQR |
| S | 1 | 14 | 0.032391 | 0.68196 | 0.937816 | 0.189449 | Q9CW46 | Ribonucle | Raver1 | VTHRPPLSPEAEAEA |
| S | 1 | 1145 | 0.002977 | 0.974844 | -1.6687 | 0.046148 | P97868-2 | E3 ubiquiti | Rbbp6 | GTEIVKPSPKRKMEG |
| S | 1 | 723 | 0.02796 | 0.97847 | -2.19283 | 0.096131 | Q99KG3 | RNA-bindi | Rbm10 | LASDDRPSPPRGLVA |
| S | 1 | 293 | 0.023282 | 0.571111 | -1.42626 | 0.327211 | Q0VBL3 | | Rbm15 | GGGQRSLSPGGAALG |
| S | 1 | 698 | 0.006175 | 0.037911 | -2.20979 | 1.251175 | B2RY56 | RNA-bindi | Rbm25 | NKFEDEDSDDVPRKR |
| S | 1 | 578 | 0.042191 | 0.801419 | -1.52951 | -0.24702 | B2RY56 | RNA-bindi | Rbm25 | QIKQEPESEEEEEEK |
| S | 1 | 42 | 8.11E-05 | 0.020403 | -2.36495 | -0.6241 | A0A023T6 | RNA-bindi | RBM8 | RKGRGFGSEEGSRAR |
| S | 0.99999 | 56 | 0.040779 | 0.443014 | -1.01912 | -0.33979 | A0A023T6 | RNA-bindi | RBM8;Rbm | RMREDYDSVEQDGDE |
| S | 1 | 205 | 0.000831 | 0.363912 | -1.35235 | 0.205091 | Q91VM5 | RNA bindi | Rbmxl1;Rb | SRRDVYLSPRDDGYS |
| S | 1 | 108 | 0.629264 | 0.038362 | 1.011693 | 3.43585 | Q9JHG6 | Calcipressi | Rcan1;Rca | PTKQFLISPPASPPV |
| S | 0.999968 | 120 | 0.515912 | 0.000413 | -0.20777 | -1.64524 | Q3UZA1 | CapZ-inter | Rcsd1 | AIVSPFHSPPSTPSS |
| S | 0.995172 | 123 | 0.515912 | 0.000413 | -0.20777 | -1.64524 | Q3UZA1 | CapZ-inter | Rcsd1 | SPFHSPPSTPSSPGI |
| T | 0.995552 | 124 | 0.515912 | 0.000413 | -0.20777 | -1.64524 | Q3UZA1 | CapZ-inter | Rcsd1 | PFHSPPSTPSSPGIR |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.954145 | 537 | 0.026519 | 0.212798 | -6.2531 | -2.80884 | A2AFI8 | RalBP1-ass | Reps2 | PSQAAESSPTKMDAP |
| S | 1 | 68 | 0.046062 | 0.325869 | 1.009033 | -0.42567 | P35601 | Replicatio | Rfc1 | KKRIIYDSDSESEET |
| S | 0.99942 | 241 | 0.001902 | 0.013861 | -2.20818 | -1.2483 | O54829 | Regulator | Rgs7 | QNDIRSHSPTHTPTP |
| T | 0.999721 | 247 | 0.915575 | 0.000362 | -0.1776 | -4.30392 | O54829 | Regulator | Rgs7 | HSPTHTPTPETKPPT |
| S | 0.999427 | 38 | 0.000134 | 0.9787 | -4.90032 | 0.064311 | Q8BQP9 | Regulator | Rgs7bp | GDWERRGSGSESAHK |
| S | 1 | 346 | 0.04558 | 0.956389 | -2.06377 | 0.148841 | Q99NE5 | Regulating | Rims1 | RRLEKGRSQDYPDRL |
| S | 0.999993 | 563 | 0.011092 | 0.205055 | 0.986318 | 0.361182 | Q99NE5 | Regulating | Rims1 | RPSISVISPTSPGAL |
| S | 0.999978 | 566 | 0.011092 | 0.205055 | 0.986318 | 0.361182 | Q99NE5 | Regulating | Rims1 | ISVISPTSPGALKDA |
| S | 0.98015 | 719 | 0.013965 | 0.07922 | 1.078376 | 0.595503 | Q3V3V9-2 | Leucine-ric | Rltpr | PYPTEPSSPERSPPS |
| S | 0.999999 | 723 | 0.013965 | 0.07922 | 1.078376 | 0.595503 | Q3V3V9-2 | Leucine-ric | Rltpr | EPSSPERSPPSPATD |
| S | 0.999995 | 726 | 0.013965 | 0.07922 | 1.078376 | 0.595503 | Q3V3V9-2 | Leucine-ric | Rltpr | SPERSPPSPATDQRG |
| T | 1 | 13 | 0.494322 | 0.045219 | -1.80804 | -4.59519 | Q8BFU3 | RING finge | Rnf214 | VAGLGAGTPSPSESS |
| S | 0.992426 | 64 | 0.003441 | 0.01754 | -2.59688 | -1.57859 | Q9D0L8 | mRNA cap | Rnmt | NSSYVQDSPSKKRKL |
| S | 0.866098 | 1403 | 0.00358 | 0.318313 | -1.93996 | 0.438524 | G5E843 | Roundabo | Robo1 | SQCPRPTSPVSTDSN |
| S | 1 | 118 | 0.00551 | 0.204819 | -4.23587 | -1.31537 | Q9D7S7 | 60S riboso | Rpl22l1 | ISQDEDGSESED___ |
| S | 0.999955 | 863 | 0.785796 | 0.027719 | 0.514478 | 1.698791 | Q8K4Q0 | Regulatory | Rptor | LTQSAPASPTNKGMH |
| S | 1 | 1347 | 0.001753 | 0.999795 | -1.82497 | -0.00402 | E9Q4Y2 | | Rsf1 | KKPYRIESDEEEDFE |
| S | 0.999999 | 6 | 0.009794 | 0.52 | -2.20605 | -0.4461 | Q9DBU6 | Serine/Arg | Rsrc1 | __MGRRSSDTEEESR |
| S | 0.999036 | 16 | 0.011499 | 0.397271 | -1.03271 | 0.267435 | Q8K0T0 | Reticulon- | Rtn1 | DEPLSLGSPGSQWFG |
| T | 0.998251 | 332 | 0.003487 | 0.601774 | -1.50392 | 0.206685 | Q8K0T0 | Reticulon- | Rtn1 | DDSPGSVTPPSSGTE |
| S | 0.999651 | 217 | 0.003251 | 0.919439 | -2.66952 | 0.137975 | Q9ES97 | Reticulon- | Rtn3 | HICTYSLSPSELPVA |
| S | 0.999998 | 953 | 0.048675 | 0.626222 | -0.93361 | -0.2368 | Q99P72 | Reticulon- | Rtn4 | EAEEKLPSDTEKEDR |
| S | 1 | 145 | 0.031671 | 0.246467 | -1.13766 | 0.500545 | Q99P72 | Reticulon- | Rtn4 | PPAPAGASPLAEPAA |
| S | 0.999986 | 836 | 0.033199 | 0.041668 | 4.567194 | 3.834091 | Q99P72 | Reticulon- | Rtn4 | MKESETFSDSSPIEI |
| S | 0.958274 | 838 | 0.028477 | 0.104294 | 5.224 | 3.161387 | Q99P72 | Reticulon- | Rtn4 | ESETFSDSSPIEIID |
| T | 0.938899 | 834 | 0.024075 | 0.029927 | 4.781054 | 4.035474 | Q99P72 | Reticulon- | Rtn4 | DKMKESETFSDSSPI |
| T | 1 | 1864 | 0.008153 | 0.877155 | -1.99263 | 0.160131 | E9Q401 | Ryanodine | Ryr2 | VPEEEGGTPEKEISI |
| S | 0.99945 | 2807 | 0.037637 | 0.010265 | -2.34526 | -2.93224 | E9Q401 | Ryanodine | Ryr2 | YNRTRRISQTSQVSI |
| S | 0.999975 | 2813 | 0.098126 | 0.018031 | -2.34526 | -3.42067 | E9Q401 | Ryanodine | Ryr2 | ISQTSQVSIDAAHGY |
| S | 1 | 366 | 0.034982 | 0.990516 | -1.49851 | 0.046108 | D3YXK2 | Scaffold at | Safb;Safb2 | RAPTAALSPEPQDSK |
| S | 0.999999 | 241 | 0.008523 | 0.00019 | -0.47511 | -0.97383 | F8VQK5 | SAM and S | Sash1 | TCNSREQSDDETEDS |
| S | 1 | 831 | 0.033731 | 0.152193 | -1.0621 | -0.58578 | F8VQK5 | SAM and S | Sash1 | ESWPRSHSLDDLQGD |
| S | 0.999602 | 694 | 0.007976 | 0.018872 | -2.69057 | -1.94838 | F8VQK5 | SAM and S | Sash1 | LQEYDSNSDQSGSQE |
| S | 1 | 20 | 0.031002 | 0.962559 | -0.95422 | -0.0571 | Q6ZPE2 | Myotubula | Sbf1 | FGPHPRGSGEGQGQI |
| S | 1 | 493 | 0.046057 | 0.972132 | -1.73893 | -0.09989 | Q5U4C3 | Splicing fa | Scaf1 | RYRQRSASPGPPPAR |
| S | 1 | 691 | 0.111717 | 0.048642 | -1.73917 | -2.02791 | Q5U4C3 | Splicing fa | Scaf1 | KREVLYDSEGLSADE |
| S | 1 | 695 | 0.108869 | 0.044433 | -1.73917 | -2.06289 | Q5U4C3 | Splicing fa | Scaf1 | LYDSEGLSADERGGK |
| S | 1 | 617 | 0.003353 | 0.830245 | -1.11471 | -0.0877 | Q6DID3 | Protein SC | Scaf8 | EPVQTAQSPAPVEKE |
| S | 1 | 270 | 0.007796 | 0.180769 | -3.3469 | -1.18913 | Q03517 | Secretogra | Scg2 | TQEEVRDSKENTEKN |
| S | 0.999983 | 532 | 0.032757 | 0.99922 | -1.1363 | -0.00981 | Q03517 | Secretogra | Scg2 | KRVPSPVSSEDDLQE |
| S | 1 | 205 | 0.001561 | 0.166431 | -1.02724 | -0.26264 | P12961 | Neuroend | Scg5 | KKSVPHFSEEEKEAE |
| S | 0.999998 | 1939 | 0.00043 | 0.999869 | -2.84606 | 0.003708 | A2APX8 | Sodium ch | Scn1a | KRTVKQASFTYNKNK |
| S | 1 | 715 | 0.411233 | 0.033974 | 0.892071 | 2.134631 | A2APX8 | Sodium ch | Scn1a | SQRQRAMSIASILTN |
| S | 1 | 718 | 0.701167 | 0.034431 | 0.525761 | 2.134631 | A2APX8 | Sodium ch | Scn1a | QRAMSIASILTNTVE |
| S | 1 | 558 | 0.044705 | 0.865837 | 1.837635 | 0.240574 | B1AWN6 | Sodium ch | Scn2a1 | RFSSPHQSLLSIRGS |
| S | 0.864026 | 288 | 0.034088 | 0.530214 | 1.54011 | 0.420818 | Q63918 | Serum dep | Sdpr | KASSGKSSPFKVSPL |
| S | 1 | 7 | 0.012085 | 0.319587 | -1.70973 | 0.512563 | Q80ZX0 | | Sec24b | _MSAPAGSPHPAAGA |
| S | 1 | 782 | 0.006786 | 0.89671 | -2.50503 | 0.175242 | O09126 | Semaphori | Sema4d | KTPKSDFSDLEQSVK |
| T | 1 | 223 | 0.00845 | 0.680908 | -0.98467 | 0.141891 | Q99NB9 | Splicing fa | Sf3b1 | SSWDQAETPGHTPSL |
| T | 1 | 227 | 0.00845 | 0.680908 | -0.98467 | 0.141891 | Q99NB9 | Splicing fa | Sf3b1 | QAETPGHTPSLRWDE |
| S | 0.99931 | 398 | 0.026759 | 0.77273 | -0.71463 | -0.11049 | Q8VD37-8 | SH3-conta | Sgip1 | DYLETLSSPKECGLG |
| S | 1 | 300 | 0.042329 | 0.178406 | -1.77522 | -0.97857 | Q8VD37-8 | SH3-conta | Sgip1 | SIFGPVLSPKSVAVN |
| S | 0.998038 | 265 | 0.000052 | 0.823418 | -5.75355 | -0.19192 | Q8VD37-8 | SH3-conta | Sgip1 | ATPPRTGSPLTVATG |
| S | 1 | 78 | 0.003443 | 0.612355 | -1.99423 | -0.26789 | Q8VD37-8 | SH3-conta | Sgip1 | IDWERYNSPELDEEG |
| T | 1 | 180 | 0.060145 | 0.030657 | -2.96293 | -3.2137 | Q8VD37-8 | SH3-conta | Sgip1 | VARPRRSTPTPELTS |
| S | 1 | 484 | 0.007801 | 0.635407 | 1.132332 | 0.175652 | Q8VD37-8 | SH3-conta | Sgip1 | GDVSRPFSPPIHSSS |
| S | 0.999995 | 306 | 0.983255 | 0.000102 | 0.061043 | -4.44274 | Q8BJU0-2 | Small gluta | Sgta | VVRSRTPSASHEEQQ |
| S | 0.999995 | 306 | 0.003906 | 0.439873 | -1.70267 | -0.31867 | Q8BJU0-2 | Small gluta | Sgta | VVRSRTPSASHEEQQ |
| S | 0.999995 | 306 | 0.000698 | 0.788296 | -3.04925 | 0.194244 | Q8BJU0-2 | Small gluta | Sgta | VVRSRTPSASHEEQQ |
| S | 0.993792 | 219 | 0.010941 | 0.788635 | -1.63065 | -0.19233 | Q91ZM2-6 | SH2B adap | Sh2b1 | ALANDGTSPGERWTH |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.987967 | 103 | 0.000487 | 0.816498 | -5.67967 | -0.30789 | Q8BG73 | SH3 doma | Sh3bgrl2 | GLKPRPASTAEP___ |
| S | 1 | 377 | 0.039069 | 0.288574 | -2.68011 | -1.15372 | Q99LH9 | SH3 doma | Sh3bp5l | QSRGRRGSDIGVRGG |
| S | 1 | 342 | 0.00441 | 0.877082 | -2.3997 | 0.167262 | Q99LH9 | SH3 doma | Sh3bp5l | LSLRTVASDLQKCDS |
| S | 1 | 413 | 0.028994 | 0.880758 | -0.74062 | -0.0805 | D3YZU5 | | Shank1 | DVVPFQESPKYAARR |
| S | 1 | 1377 | 0.023527 | 0.060246 | -2.00401 | 1.376751 | D3YZU5 | | Shank1 | QPPPRPPSPRYDAPP |
| S | 1 | 1013 | 0.021091 | 0.128782 | -1.23572 | -0.64079 | D3Z5K8 | SH3 and m | Shank2 | KQSNVEDSPEKTCSI |
| S | 1 | 354 | 0.033448 | 0.496204 | -1.4398 | 0.415048 | Q61120 | SHC-transf | Shc3 | PMLSKAASVECISPV |
| T | 0.849693 | 3 | 0.041766 | 0.294919 | -2.4111 | -1.04547 | A2ALU4-2 | Protein Sh | Shroom2 | ______METSRSPSPQ |
| S | 1 | 493 | 0.03483 | 0.009707 | -2.2975 | -2.84941 | Q6P4S6 | Serine/thr | Sik3 | GPLGRRASDGGANIQ |
| T | 1 | 411 | 0.010371 | 0.988454 | -2.20737 | 0.054895 | Q6P4S6 | Serine/thr | Sik3 | YLSMRRHTVGVADPR |
| S | 1 | 533 | 0.028684 | 0.974624 | 0.799919 | 0.038394 | Q6P4S6 | Serine/thr | Sik3 | VTPVDEESSDGEPDQ |
| S | 1 | 534 | 0.028684 | 0.974624 | 0.799919 | 0.038394 | Q6P4S6 | Serine/thr | Sik3 | TPVDEESSDGEPDQE |
| S | 1 | 1564 | 4.65E-06 | 0.199459 | -4.59172 | 0.327281 | Q8C0T5 | Signal-ind | Sipa1l1 | RALHRTLSDESIYSS |
| S | 0.999125 | 1544 | 0.004421 | 0.641551 | 0.898531 | -0.12072 | Q8C0T5 | Signal-ind | Sipa1l1 | FKFHALSSPQSPFPT |
| S | 1 | 1547 | 0.004421 | 0.641551 | 0.898531 | -0.12072 | Q8C0T5 | Signal-ind | Sipa1l1 | HALSSPQSPFPTTPT |
| S | 0.999995 | 1538 | 0.005575 | 0.551334 | -1.63186 | 0.273553 | G3X9J0 | | Sipa1l3 | KSLQRTLSDESLCSG |
| S | 1 | 368 | 0.006855 | 0.020911 | -1.37054 | -0.93281 | Q8VDQ8 | NAD-depe | Sirt2 | PNPSTTISPGKSPPP |
| S | 0.998212 | 1905 | 0.00383 | 0.999057 | -2.60222 | 0.014601 | A2AQ25 | Sickle tail | Skt;Etl4 | SSPPSPASPTSLNQG |
| S | 0.999932 | 960 | 0.004637 | 0.005663 | -4.84626 | -4.14012 | Q91V14 | Solute carr | Slc12a5 | IQSITDESRGSIRRK |
| S | 1 | 491 | 0.049801 | 0.992486 | -1.27279 | 0.038511 | P53986 | Monocarb | Slc16a1 | GDPTEEESPV_____ |
| S | 1 | 24 | 0.00117 | 0.893575 | -4.62323 | -0.22196 | P43006 | Excitatory | Slc1a2 | RMHDSHLSSDEPKHR |
| S | 1 | 562 | 0.040899 | 0.431467 | -1.53956 | 0.523854 | P43006 | Excitatory | Slc1a2 | NGKSADCSVEEEPWK |
| S | 1 | 268 | 0.01793 | 0.632872 | -1.57926 | 0.301724 | Q80UP8 | Sodium-de | Slc20a2 | RKVQEAESPGFKELP |
| S | 0.993286 | 312 | 0.049012 | 0.62503 | -1.41866 | -0.36139 | Q8BUN9 | | Slc24a2 | VPEAQAKSPTAGDKD |
| S | 0.99523 | 149 | 0.037415 | 0.532861 | -1.62166 | -0.45259 | P48962 | ADP/ATP t | Slc25a4 | AADVGKGSSQREFNG |
| S | 1 | 634 | 0.039874 | 0.434738 | -1.1483 | -0.3858 | Q3UHK1 | Proton my | Slc2a13 | HLSDNDASDVE____ |
| S | 1 | 52 | 0.034702 | 0.168519 | -1.18557 | -0.63279 | Q8K2P7 | Sodium-co | Slc38a1 | SDRESRRSLTNSHLE |
| S | 1 | 258 | 0.013232 | 0.930727 | -1.57019 | -0.10401 | E9Q585 | | Slc4a1ap | KKMLGEDSDEEEEAN |
| S | 1 | 198 | 9.64E-05 | 0.524161 | -0.9998 | 0.073625 | P16283 | Anion exc | Slc4a3 | VGLQSDQSPQRSGSS |
| S | 1 | 22 | 0.000179 | 0.000013 | -2.15367 | -3.29422 | Q6PGE7 | Sodium-de | Slc6a7 | PDLLMTPSDQGDVDL |
| T | 1 | 20 | 0.000179 | 0.000013 | -2.15367 | -3.29422 | Q6PGE7 | Sodium-de | Slc6a7 | ITPDLLMTPSDQGDV |
| S | 1 | 600 | 0.018842 | 0.99765 | -3.33427 | 0.043214 | P28571-1 | Sodium- a | Slc6a9 | YAPTTTPSPEDGFEV |
| T | 0.806717 | 597 | 0.001994 | 0.987813 | -2.46646 | 0.043214 | P28571-1 | Sodium- a | Slc6a9 | TGRYAPTTTPSPEDG |
| T | 0.997075 | 598 | 0.022542 | 0.996823 | -2.73708 | 0.043214 | P28571-1 | Sodium- a | Slc6a9 | GRYAPTTTPSPEDGF |
| S | 1 | 527 | 0.777679 | 0.003841 | -0.09474 | -0.79582 | Q9QXW9 | Large neut | Slc7a8 | TPVKDPDSEEQP___ |
| S | 1 | 21 | 0.021044 | 0.853318 | -1.9944 | -0.22374 | Q9QXW9 | Large neut | Slc7a8 | NHPGSDTSPEAEASS |
| S | 1 | 282 | 0.596325 | 0.014487 | -0.65487 | -2.69878 | Q68FL0 | Sodium/ca | Slc8a1 | HEGDRPASKTEIEMD |
| S | 1 | 801 | 0.117373 | 0.027126 | -0.87762 | 1.225322 | Q61165 | Sodium/h | Slc9a1 | QRIQRCLSDPGPHPE |
| S | 1 | 697 | 0.042549 | 0.892779 | -3.21422 | 0.366387 | Q61165 | Sodium/h | Slc9a1 | VPAHKLDSPTLSRAR |
| S | 0.999151 | 647 | 0.001317 | 0.048554 | -3.12007 | -1.16555 | O54988 | STE20-like | Slk | EQVSESNSIEELERL |
| S | 1 | 289 | 0.013027 | 0.899374 | -1.03326 | 0.083315 | Q8CH25 | SAFB-like t | Sltm | VQDAIAQSPEKEAKD |
| S | 1 | 283 | 0.005081 | 0.229456 | -1.3496 | -0.39068 | Q3UID0 | SWI/SNF | Smarcc2 | TLTDEVNSPDSDRRD |
| S | 0.999944 | 488 | 0.04713 | 0.495197 | 1.123284 | 0.357297 | Q3UMB5 | Smith-Ma | Smcr8 | SVLSKSDSQASLTVP |
| S | 1 | 200 | 0.390325 | 0.013478 | -0.79265 | -2.32752 | Q80U23 | Syntaphili | Snph | KEEGTGESAGGSPAR |
| S | 0.999734 | 208 | 0.022942 | 0.995409 | -4.24785 | -0.08104 | Q80U23 | Syntaphili | Snph | AGGSPARSLTRSSTY |
| S | 1 | 226 | 0.023155 | 0.297041 | -2.42815 | -0.89329 | Q62376 | U1 small n | Snrnp70 | YDERPGPSPLPHRDR |
| S | 1 | 194 | 0.089062 | 0.03047 | 1.963674 | -2.41615 | Q61234 | Alpha-1-sy | Snta1 | SPLQRQPSSPGPQPR |
| S | 1 | 195 | 0.018726 | 0.822601 | 2.750666 | -0.33413 | Q61234 | Alpha-1-sy | Snta1 | PLQRQPSSPGPQPRN |
| S | 1 | 75 | 0.000686 | 0.038623 | -1.23804 | 0.429419 | Q61235 | Beta-2-syn | Sntb2 | NRGLGPPSPPAPPRG |
| S | 0.998536 | 29 | 0.013144 | 0.973665 | -1.63752 | -0.06556 | Q8C080 | Sorting ne | Snx16 | NRNQRSSSFGSVSTS |
| S | 1 | 49 | 0.015699 | 0.74591 | -1.46143 | -0.21107 | Q3UHD6 | Sorting ne | Snx27 | VRIVKSESGYGFNVR |
| S | 0.99332 | 639 | 0.035127 | 0.94491 | -2.01506 | 0.152501 | Q6NZL0 | Protein SO | Soga3 | LMREQSESLSELRQH |
| S | 1 | 1723 | 0.020849 | 0.80299 | -1.37774 | -0.18302 | Q9QX47 | Protein SO | Son | QAVAVALSPKESSED |
| S | 1 | 62 | 0.046343 | 0.034498 | -0.77446 | -0.75288 | Q62417 | Sorbin and | Sorbs1 | SPVSPQESPKHESKS |
| S | 0.999999 | 58 | 0.029204 | 0.484613 | 1.474004 | -0.4177 | Q62417 | Sorbin and | Sorbs1 | TPSSSPVSPQESPKH |
| S | 1 | 62 | 0.029204 | 0.484613 | 1.474004 | -0.4177 | Q62417 | Sorbin and | Sorbs1 | SPVSPQESPKHESKS |
| S | 0.96391 | 446 | 0.436154 | 0.006585 | -0.88386 | 3.329989 | D3Z080 | Sorbin and | Sorbs2 | FISSSPSSPSRAQDH |
| S | 0.96391 | 497 | 0.432438 | 0.017763 | -1.05794 | 3.113258 | Q3UTJ2-2 | Sorbin and | Sorbs2 | FISSSPSSPSRAQGG |
| S | 1 | 819 | 0.003108 | 0.987686 | -1.80729 | -0.03512 | Q6PHU5 | Sortilin | Sort1 | KSGYHDDSDEDLLE_ |
| S | 0.999992 | 716 | 0.030687 | 0.203081 | 1.35986 | -0.6486 | Q58A65-2 | C-Jun-ami | Spag9 | GSKQRSASQSSLDKL |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.996953 | 719 | 0.030687 | 0.203081 | 1.35986 | -0.6486 | Q58A65-2 | C-Jun-amir | Spag9 | QRSASQSSLDKLDQE |
| S | 0.999991 | 888 | 0.006509 | 0.919415 | -1.36297 | -0.08257 | Q2KN98 | Cytospin-A | Specc1l | VSPMQRHSISGPIST |
| S | 1 | 2042 | 0.014819 | 0.661523 | -0.96854 | 0.166578 | Q62407 | Striated m | Speg | RSLHKAASVELPQRR |
| S | 1 | 749 | 0.008713 | 0.027336 | -3.25948 | -2.1882 | Q62504 | Msx2-inter | Spen | RPIERSQSPVHLRRP |
| S | 1 | 1077 | 0.995532 | 0.001123 | -0.02283 | -1.95635 | Q62504 | Msx2-inter | Spen | ERLNSALSPKDCQDP |
| S | 1 | 286 | 0.000932 | 0.215159 | -2.01371 | -0.41277 | Q6P6N5 | Sprouty-re | Spred3 | TPAPAKASPEAEEAA |
| S | 1 | 1029 | 0.009795 | 0.025122 | -4.17858 | -2.95026 | A3KGU7 | Spectrin al | Sptan1 | KKLDPAQSASRENLL |
| S | 1 | 1031 | 0.001907 | 0.000445 | -3.2979 | -4.02977 | A3KGU7 | Spectrin al | Sptan1 | LDPAQSASRENLLEE |
| S | 1 | 2296 | 0.152336 | 0.046096 | 0.541119 | -0.71906 | Q91ZE6 | | Sptbn4 | RRIERQESSEQETPT |
| S | 0.99812 | 74 | 0.000809 | 0.12784 | -1.83142 | -0.45003 | P05480 | Neuronal p | Src | NSSDTVTSPQRAGPL |
| S | 1 | 1077 | 0.019449 | 0.078973 | -1.93199 | -1.16087 | B1AQX9 | | Srcin1 | VFIKKAESEELEVQK |
| S | 0.999999 | 546 | 1.91E-05 | 0.985712 | -5.16337 | -0.03718 | B1AQX9 | | Srcin1 | RQSFRKDSGSSSVFA |
| S | 0.999936 | 900 | 0.041332 | 0.563367 | -2.30962 | -0.62808 | B1AQX9 | | Srcin1 | DFEIPPPSPPLNLHE |
| S | 1 | 1037 | 0.922617 | 0.002122 | -0.07874 | 1.369044 | B1AQX9 | | Srcin1 | RTEKPSKSPPPPPPR |
| S | 0.999775 | 319 | 0.003582 | 0.871856 | -2.6944 | 0.183363 | B1AQX9 | | Srcin1 | RREMVYASRESSPTR |
| S | 0.999726 | 323 | 0.005271 | 0.908743 | -2.97278 | 0.183363 | B1AQX9 | | Srcin1 | VYASRESSPTRRLNN |
| S | 1 | 868 | 0.006028 | 0.044011 | -3.93529 | -2.1241 | Q812A2 | SLIT-ROBO | Srgap3 | AAIPRRRSGGDTHSP |
| S | 1 | 309 | 0.04781 | 0.359076 | 1.100981 | 0.443087 | O70551 | SRSF prote | Srpk1 | RPNKQEESESPVDRP |
| S | 1 | 311 | 0.04781 | 0.359076 | 1.100981 | 0.443087 | O70551 | SRSF prote | Srpk1 | NKQEESESPVDRPLT |
| S | 1 | 260 | 0.000627 | 0.416484 | -2.27457 | 0.297178 | E9PUK6 | Serine/arg | Srrm1 | VPEPKEPSPEKNSKK |
| S | 1 | 429 | 0.011267 | 0.696834 | -1.77087 | -0.26421 | E9PUK6 | Serine/arg | Srrm1 | RKSRVSVSPGRTSGK |
| S | 1 | 635 | 0.004129 | 0.000784 | -2.76704 | -3.56251 | E9PUK6 | Serine/arg | Srrm1 | PPKRRTASPPPPPKR |
| T | 1 | 633 | 0.031756 | 0.017579 | -2.95186 | -3.08345 | E9PUK6 | Serine/arg | Srrm1 | SPPPKRRTASPPPPP |
| S | 1 | 723 | 0.042844 | 0.884201 | -3.58282 | 0.426908 | E9PUK6 | Serine/arg | Srrm1 | PPVRRGASASPQGRQ |
| S | 1 | 725 | 0.017692 | 0.669546 | -2.41363 | 0.426908 | E9PUK6 | Serine/arg | Srrm1 | VRRGASASPQGRQSP |
| S | 1 | 731 | 0.017395 | 0.597444 | -2.1049 | 0.426908 | E9PUK6 | Serine/arg | Srrm1 | ASPQGRQSPSPSTRP |
| S | 1 | 2648 | 0.005203 | 0.986352 | -1.90224 | 0.043764 | Q8BTI8 | Serine/arg | Srrm2 | DSRSLSYSPVERRQP |
| S | 1 | 2535 | 0.007132 | 0.606009 | -2.53567 | 0.407455 | Q8BTI8 | Serine/arg | Srrm2 | VALKRVPSPTPVPKE |
| S | 1 | 888 | 0.018894 | 0.176334 | -1.48014 | 0.66003 | Q8BTI8 | Serine/arg | Srrm2 | QSPSRSSSPQPKVKT |
| S | 0.999975 | 1360 | 0.014142 | 0.163902 | -1.09484 | 0.467635 | Q8BTI8 | Serine/arg | Srrm2 | FSSQKVSSPVLETVQ |
| T | 1 | 1448 | 0.002049 | 0.514816 | -2.53921 | 0.362244 | Q8BTI8 | Serine/arg | Srrm2 | EPKALPQTPRARSHS |
| S | 0.999985 | 2075 | 0.022348 | 0.535825 | -2.05771 | 0.497296 | Q8BTI8 | Serine/arg | Srrm2 | CFSRPSMSPTPLDRC |
| S | 0.999999 | 850 | 0.455786 | 0.00514 | -0.18072 | -0.74536 | Q8BTI8 | Serine/arg | Srrm2 | QRQSHSESSPDGEVK |
| S | 1 | 851 | 0.175335 | 0.033462 | -0.4844 | -0.74536 | Q8BTI8 | Serine/arg | Srrm2 | RQSHSESSPDGEVKS |
| S | 1 | 2052 | 0.000222 | 0.850251 | -3.27805 | 0.134072 | Q8BTI8 | Serine/arg | Srrm2 | PPATRNHSGSRTPPV |
| S | 1 | 2054 | 0.003856 | 0.968511 | -4.07748 | 0.134072 | Q8BTI8 | Serine/arg | Srrm2 | ATRNHSGSRTPPVAL |
| S | 1 | 1687 | 0.01816 | 0.374439 | -3.11225 | 0.938748 | Q8BTI8 | Serine/arg | Srrm2 | RRRSPSVSSPEPTEK |
| S | 1 | 777 | 0.03778 | 0.01957 | 1.456653 | 1.553234 | Q8BTI8 | Serine/arg | Srrm2 | LRRSLSGSSPCPKQK |
| S | 1 | 757 | 0.043946 | 0.636672 | -2.72261 | -0.65696 | Q8BTI8 | Serine/arg | Srrm2 | SHVSSRRSRSLSSPR |
| T | 1 | 2056 | 0.000831 | 0.923004 | -3.57882 | 0.134072 | Q8BTI8 | Serine/arg | Srrm2 | RNHSGSRTPPVALSS |
| S | 1 | 4 | 0.018932 | 0.982033 | -1.21922 | -0.04403 | Q99MR6 | Serrate RN | Srrt | ____MGDSDDEYDRR |
| S | 1 | 67 | 0.047657 | 0.655901 | -0.88743 | -0.21096 | Q99MR6 | Serrate RN | Srrt | RNRRERFSPPRHELS |
| S | 1 | 74 | 0.047657 | 0.655901 | -0.88743 | -0.21096 | Q99MR6 | Serrate RN | Srrt | SPPRHELSPPQKRMR |
| S | 1 | 477 | 0.007314 | 0.209679 | -2.13649 | -0.70134 | E9Q6E5 | | Srsf11 | KRPTEAVSPKTKECS |
| S | 1 | 291 | 0.024459 | 0.854666 | -3.76689 | -0.4372 | Q8VE97 | Serine/arg | Srsf4 | AGKAKSHSPSRHDSK |
| S | 1 | 303 | 0.002963 | 0.106989 | -1.39529 | -0.48482 | Q3TWW8 | Serine/arg | Srsf6 | RSQSRSHSPLPAPPS |
| S | 1 | 260 | 0.040059 | 0.734123 | -1.17364 | 0.223583 | Q8BL97 | Serine/arg | Srsf7 | PSGSPHRSASPERMD |
| S | 1 | 262 | 0.040059 | 0.734123 | -1.17364 | 0.223583 | Q8BL97 | Serine/arg | Srsf7 | GSPHRSASPERMD__ |
| S | 1 | 221 | 0.845579 | 0.004069 | -0.18897 | -1.94239 | Q8BL97 | Serine/arg | Srsf7 | IGSRYFQSRSRSRSR |
| S | 1 | 219 | 0.040059 | 0.734123 | -1.17364 | 0.223583 | Q8BL97-4 | Serine/arg | Srsf7 | PSGSPHRSASPERMD |
| S | 1 | 221 | 0.040059 | 0.734123 | -1.17364 | 0.223583 | Q8BL97-4 | Serine/arg | Srsf7 | GSPHRSASPERMD__ |
| S | 1 | 320 | 0.026395 | 0.172938 | -0.75693 | 0.371211 | Q3U4B1 | | Ssbp4 | MDGLPKNSPGAVGGL |
| S | 1 | 16 | 0.023723 | 0.012153 | -1.95581 | -2.07168 | P54227 | Stathmin | Stmn1 | KELEKRASGQAFELI |
| S | 1 | 63 | 0.010708 | 0.770575 | -1.22712 | -0.15136 | P54227 | Stathmin | Stmn1 | AAEERRKSHEAEVLK |
| S | 1 | 16 | 0.912631 | 0.006109 | 0.11575 | -1.48541 | P54227 | Stathmin | Stmn1 | KELEKRASGQAFELI |
| S | 1 | 25 | 0.912631 | 0.006109 | 0.11575 | -1.48541 | P54227 | Stathmin | Stmn1 | QAFELILSPRSKESV |
| S | 1 | 50 | 0.848074 | 0.043533 | -0.38523 | -2.21086 | P55821 | Stathmin-2 | Stmn2 | KQINKRASGQAFELI |
| S | 0.99962 | 62 | 0.848074 | 0.043533 | -0.38523 | -2.21086 | P55821 | Stathmin-2 | Stmn2 | ELILKPPSPISEAPR |
| S | 1 | 81 | 0.00261 | 0.927363 | -1.50598 | 0.070134 | O70166 | Stathmin-3 | Stmn3 | PPKRKDASLEELQKR |
| S | 1 | 223 | 0.005949 | 0.017291 | -1.55649 | -1.07602 | P58404 | Striatin-4 | Strn4 | VEGAPRASPGPGGLS |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.999979 | 598 | 0.033898 | 0.391717 | -1.54039 | -0.53198 | Q5DQR4 | Syntaxin-b | Stxbp5l | GSTNTVSSEGVTKDS |
| S | 0.992883 | 733 | 0.014563 | 0.089622 | -0.75356 | 0.403838 | Q8CH09 | SURP and | Sugp2 | KPCPQPSSPGALGPS |
| T | 1 | 11 | 0.016501 | 0.377965 | -1.37812 | 0.403287 | P63046 | Sulfotrans | Sult4a1 | SEAETPGTPGEFESK |
| S | 1 | 642 | 0.005035 | 0.018993 | 1.269088 | 0.824282 | O88935-1 | Synapsin-1 | Syn1 | PQLAQKPSQDVPPPI |
| S | 0.999996 | 67 | 0.04978 | 0.357759 | 0.871215 | 0.355581 | O88935 | Synapsin-1 | Syn1 | VASPAAPSPGSSGGG |
| T | 0.961084 | 512 | 0.033574 | 0.200416 | 1.635583 | 0.804138 | O88935 | Synapsin-1 | Syn1 | PQRLPSPTAAPQQSA |
| S | 1 | 426 | 0.038732 | 0.696439 | -2.7037 | 0.556238 | Q64332 | Synapsin-2 | Syn2 | LSRTPALSPQRPLTT |
| S | 0.999997 | 540 | 0.018934 | 0.040473 | -1.43576 | -1.04763 | Q8JZP2 | Synapsin-3 | Syn3 | PHLNKSQSLTNSLST |
| S | 1 | 8306 | 0.002238 | 0.243319 | -1.75654 | 0.411298 | Q6ZWR6-4 | Nesprin-1 | Syne1 | SASRTLPSEDEEGEE |
| S | 1 | 1070 | 0.000569 | 0.047761 | -1.35634 | -0.42545 | F6SEU4 | Ras/Rap G | Syngap1 | PPLQRGKSQQLTVSA |
| S | 0.999997 | 87 | 0.024375 | 0.140055 | -0.84037 | 0.438554 | F6SEU4 | Ras/Rap G | Syngap1 | KLLRRTVSVPVEGRP |
| S | 1 | 258 | 0.031477 | 0.966583 | -3.79362 | 0.214991 | E9Q3E2 | Synaptopo | Synpo | RHLEKVASEEEEVPL |
| T | 1 | 128 | 0.010656 | 0.920589 | -3.14088 | 0.212223 | P46097 | Synaptota | Syt2 | DDAETGLTEGEGEGE |
| S | 1 | 163 | 0.007268 | 0.449715 | -1.31242 | 0.278738 | Q9R1Q8 | Transgelin | Tagln3 | QQNRRGFSEEQLRQG |
| S | 1 | 1446 | 0.035058 | 0.742379 | 0.76519 | -0.13765 | A2A690 | Protein TA | Tanc2 | QGLPVIQSPPSSPAH |
| S | 1 | 965 | 0.007723 | 0.157467 | -0.85184 | -0.31941 | Q5F2E8 | Serine/thr | Taok1 | SSMGVRNSPQALRRT |
| S | 1 | 22 | 0.000647 | 0.293646 | -1.71716 | 0.279528 | Q8BHL3 | TBC1 dom | Tbc1d10b | HGAPAAPSPPPRGSR |
| S | 0.994745 | 58 | 3.09E-05 | 0.004588 | -1.70507 | -0.52938 | Q80VE5 | | Tbc1d22b | LKNKKASSFHEFARN |
| S | 0.998709 | 751 | 0.036874 | 0.014784 | 0.644414 | 0.73262 | Q8BYJ6-2 | TBC1 dom | Tbc1d4 | RTELLPLSPLSPTME |
| S | 0.986813 | 754 | 0.119322 | 0.015417 | 0.481772 | 0.78279 | Q8BYJ6-2 | TBC1 dom | Tbc1d4 | LLPLSPLSPTMEEEP |
| S | 0.999958 | 565 | 0.540588 | 0.001031 | 0.427393 | -2.9098 | Q80XQ2 | TBC1 dom | Tbc1d5 | KTISSSPSIESLPGG |
| S | 0.998669 | 561 | 0.980297 | 0.041491 | 0.095684 | 1.638481 | Q80XQ2 | TBC1 dom | Tbc1d5 | GQSSKTISSSPSIES |
| S | 0.999999 | 210 | 0.01277 | 0.016506 | -2.45096 | -2.0567 | Q62313 | Trans-Golg | Tgoln1;Tg | TLTSKTESGETLAGD |
| S | 1 | 243 | 0.005895 | 0.816011 | -1.60745 | 0.150765 | Q569Z6 | Thyroid ho | Thrap3 | RASVSDLSPRERSPA |
| S | 1 | 248 | 0.006363 | 0.252748 | -1.58294 | -0.46087 | Q569Z6 | Thyroid ho | Thrap3 | DLSPRERSPALKSPL |
| S | 1 | 253 | 0.009883 | 0.827591 | -0.87141 | -0.08888 | Q569Z6 | Thyroid ho | Thrap3 | ERSPALKSPLQSVVV |
| S | 1 | 935 | 2.47E-05 | 0.025196 | -3.02011 | -0.59153 | Q569Z6 | Thyroid ho | Thrap3 | GEIEDDESGTENREE |
| S | 1 | 669 | 0.007726 | 0.11084 | -3.71987 | -1.5901 | Q569Z6 | Thyroid ho | Thrap3 | EAAKNKKSPEIHRRI |
| S | 1 | 912 | 0.005545 | 0.255035 | -1.37958 | 0.387328 | B9EHJ3 | | Tjp1 | QAIHRIDSPGLKPAS |
| S | 1 | 912 | 0.005545 | 0.255035 | -1.37958 | 0.387328 | P39447 | Tight junct | Tjp1 | QAIHRIDSPGLKPAS |
| S | 1 | 175 | 0.020083 | 0.002819 | -2.21515 | -3.15551 | P39447 | Tight junct | Tjp1 | SPRSDRRSVASSQPA |
| S | 0.98158 | 467 | 0.255336 | 0.036757 | -0.5065 | -0.89936 | Q80W04 | Transmem | Tmcc2 | GSATLVSSPKYGSDD |
| S | 1 | 60 | 0.012933 | 0.132145 | -2.36601 | -1.07434 | Q8C996 | Transmem | Tmem163 | ISESGQFSDGLEDRG |
| S | 1 | 56 | 0.006292 | 0.01686 | -1.02137 | -0.71992 | Q8C996 | Transmem | Tmem163 | RQPRISESGQFSDGL |
| S | 1 | 60 | 0.006292 | 0.01686 | -1.02137 | -0.71992 | Q8C996 | Transmem | Tmem163 | ISESGQFSDGLEDRG |
| S | 0.999906 | 327 | 0.018567 | 0.866038 | -1.2259 | -0.12653 | B1AZA5 | Transmem | Tmem245 | SSRSSPSSPSPTLGR |
| S | 0.999999 | 114 | 0.02552 | 0.361003 | -1.67901 | -0.56606 | Q99LG1 | Transmem | Tmem51 | PHSQEEDSQEEEEDV |
| S | 0.860163 | 151 | 0.02616 | 0.034021 | 1.309725 | 1.091165 | Q99LG1 | Transmem | Tmem51 | QEQNPRLSISLPSYE |
| T | 0.99945 | 159 | 0.018805 | 0.999102 | -1.11224 | -0.0089 | Q61029 | Lamina-as | Tmpo | GTESRSSTPLPTVSS |
| T | 0.99945 | 159 | 0.018805 | 0.999102 | -1.11224 | -0.0089 | Q61033 | Lamina-as | Tmpo | GTESRSSTPLPTVSS |
| S | 1 | 245 | 0.016333 | 0.412886 | -6.01891 | -1.65572 | Q8VBT0 | Thioredoxi | Tmx1 | EADEEDVSEEEAEDR |
| S | 1 | 72 | 0.002063 | 0.756037 | -1.44188 | 0.126628 | Q80YX1 | Tenascin | Tnc | SVDLESASGEKDLTP |
| S | 1 | 740 | 0.028752 | 0.996691 | -1.20001 | -0.02062 | E9PUL9 | Traf2 and | Tnik | ANSKSEGSPVLPHEP |
| S | 0.999961 | 581 | 0.027121 | 0.247719 | -3.07804 | -1.29565 | E9PUL9 | Traf2 and | Tnik | PALTASQSVHEQPTK |
| S | 1 | 1612 | 0.049604 | 0.562059 | -1.6138 | 0.463625 | P58871 | 182 kDa ta | Tnks1bp1 | RASRVPSSDEEVVEE |
| S | 1 | 429 | 0.000404 | 0.762294 | -3.57819 | -0.21798 | P58871 | 182 kDa ta | Tnks1bp1 | SLAQRRFSEGVLQPP |
| S | 1 | 911 | 0.005203 | 0.820622 | -1.83146 | 0.164424 | P58871 | 182 kDa ta | Tnks1bp1 | KNLSRGYSSQDAEEQ |
| S | 0.999998 | 1373 | 0.004665 | 0.016874 | 2.332822 | 1.534355 | P58871 | 182 kDa ta | Tnks1bp1 | LDPKSSGSLSPGLET |
| S | 0.998992 | 724 | 0.101345 | 0.027714 | -0.53354 | 0.703474 | Q8BYI9 | Tenascin- | Tnr | RITFTPSSGISSEVT |
| S | 0.996921 | 1313 | 0.042803 | 0.299287 | -1.11421 | -0.48266 | Q8BKI2 | Trinucleoti | Tnrc6b | RQPSMKHSPSHPVGP |
| S | 0.999976 | 462 | 0.037357 | 0.356961 | 1.190591 | 0.448271 | O88746 | Target of | Tom1 | DRLPNLASPSAEGPP |
| S | 0.999997 | 472 | 0.037357 | 0.356961 | 1.190591 | 0.448271 | O88746 | Target of | Tom1 | AEGPPRPSPGTAPRR |
| S | 1 | 138 | 0.000835 | 0.986262 | -3.19418 | -0.04925 | Q9DCC8 | Mitochon | Tomm20 | QRIVSAQSLAEDDVE |
| S | 1 | 15 | 0.002833 | 0.993887 | -2.11238 | 0.028257 | Q9CPQ3 | Mitochon | Tomm22 | AGAGEPLSPEELLPK |
| S | 0.999755 | 479 | 0.146688 | 0.017287 | 0.898883 | 1.532551 | Q8CG79 | Apoptosis- | Tp53bp2;T | GTLRKNQSSEDILRD |
| S | 0.997304 | 168 | 0.043416 | 0.997977 | 1.273643 | 0.019171 | A2AUD5 | | Tpd52l2 | HPLSQSFSSYSIRHS |
| S | 0.999872 | 159 | 0.040783 | 0.871192 | -1.20688 | 0.150443 | Q7TQD2 | Tubulin po | Tppp | GVTKAVSSPTVSRLT |
| S | 1 | 2141 | 0.000109 | 0.27769 | -4.79086 | -0.55387 | F6ZDS4 | Nucleopro | Tpr | QTPQAPQSPRRPPHP |
| S | 0.997229 | 14 | 0.042908 | 0.004145 | 1.397502 | 2.240913 | Q9DBS2 | Tumor pro | Tprg1l;Tpr | TVDSAGTSPTAVLAA |
| S | 1 | 440 | 0.026605 | 0.996482 | -2.41021 | -0.04184 | Q9ESN6 | Tripartite | Trim2 | GVKRRVKSPGSGHVK |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 473 | 0.153886 | 0.011854 | -0.40846 | -0.77923 | Q62318 | Transcripti | Trim28 | SGMKRSRSGEGEVSG |
| S | 1 | 427 | 0.003379 | 0.997647 | -2.65327 | -0.02287 | Q9R1R2 | Tripartite | Trim3 | RPGDLPPSPDDVKRR |
| S | 1 | 7 | 0.012575 | 0.910444 | -1.53972 | 0.115544 | Q9R1R2 | Tripartite | Trim3 | _MAKREDSPGPEVQP |
| T | 1 | 41 | 0.013445 | 0.091848 | -3.88333 | -2.0237 | Q8C7M3 | E3 ubiquiti | Trim9 | ARNILVQTPESESPQ |
| S | 1 | 822 | 0.0312 | 0.734034 | -1.70796 | 0.303682 | A2AU91 | Tumor sup | Trp53bp1; | KDAVTEDSPQPPLPS |
| S | 0.982093 | 268 | 0.043544 | 0.730977 | -3.17768 | -0.62456 | A2AU91 | Tumor sup | Trp53bp1; | RSEDRPSSPQVSVAA |
| S | 1 | 533 | 0.00279 | 0.000209 | -1.85433 | -2.88691 | A2AU91 | Tumor sup | Trp53bp1; | SKMESLGSPRTEEDR |
| S | 1 | 1096 | 0.000373 | 0.899066 | -4.12865 | -0.15109 | A2AU91 | Tumor sup | Trp53bp1; | AAPEDSASPVSQQRA |
| S | 0.999886 | 15 | 0.000341 | 0.153547 | -1.76563 | -0.33709 | Q9WTR1 | Transient | Trpv2 | PAFRLETSDGDEEGS |
| S | 0.999177 | 1797 | 0.0276 | 0.884404 | -1.04929 | -0.11063 | F7CGG2 | Transform | Trrap | AVFGRSQSLPGADSL |
| S | 0.995463 | 1366 | 0.958594 | 0.027829 | -0.20702 | -1.26089 | Q61037-6 | Tuberin | Tsc2 | QPLSKSSSSPELQTL |
| S | 0.99981 | 38 | 0.946985 | 0.037167 | -0.18508 | 1.965049 | D3YZZ4 | | Tsc22d4 | GCVSSPCSPRGSSPI |
| S | 1 | 3 | 0.271407 | 0.007589 | -1.25139 | -3.41933 | O88852 | Testis-spe | Tspyl1 | _____MSSPERDEGT |
| S | 1 | 1222 | 0.031035 | 0.965633 | -1.03349 | 0.059192 | Q6PCN3 | Tau-tubuli | Ttbk1 | SKPAAPRSPGLPAST |
| T | 1 | 41 | 0.001051 | 0.018865 | -1.91525 | -0.881 | P05213 | Tubulin al | Tuba1b;Tu | GQMPSDKTIGGGDDS |
| S | 1 | 340 | 0.010394 | 0.280242 | -1.38514 | 0.429961 | P05213 | Tubulin al | Tuba1b;Tu | AAIKTKRSIQFVDWC |
| T | 1 | 55 | 0.04016 | 0.909226 | -1.12362 | -0.11509 | P68372 | Tubulin be | Tubb4b | NVYYNEATGGKYVPR |
| S | 1 | 79 | 0.015444 | 0.872911 | -1.62891 | 0.15582 | P26369 | Splicing fa | U2af2 | EHGGLIRSPRHEKKK |
| S | 1 | 202 | 0.013697 | 0.941856 | -1.3987 | 0.085201 | Q6NV83 | U2 snRNP- | U2surp | GEKEKKKSNLELFKE |
| S | 1 | 146 | 0.026033 | 0.765468 | -1.91192 | -0.29921 | Q8BH48 | Ubiquitin- | Ubap1 | ATKQKVLSPPHTKAD |
| S | 0.999943 | 1761 | 0.021225 | 0.993624 | -2.62469 | 0.057871 | A2AN08-5 | E3 ubiquiti | Ubr4 | LVRHASTSPADKAKV |
| S | 0.999999 | 952 | 0.115278 | 0.016327 | -0.53598 | -0.8479 | A2RSJ4 | UHRF1-bin | Uhrf1bp1l | PLLFKSASDTNLQKG |
| S | 1 | 668 | 0.031077 | 0.771618 | -1.24955 | -0.20174 | Q7TMI3 | E3 ubiquiti | Uhrf2 | EATKRPASDDECPGD |
| S | 0.999999 | 450 | 0.715064 | 0.026736 | 0.280635 | -0.96461 | O70405 | Serine/thr | Ulk1 | RIEQNLQSPTQQQTA |
| S | 1 | 2044 | 0.007095 | 0.261055 | -0.8714 | 0.256114 | B1AY13 | Ubiquitin | Usp24 | QRVSDQNSPVLPKKS |
| S | 0.936641 | 796 | 0.838544 | 0.040763 | -0.12513 | -0.7066 | E9Q6Y8 | Ubiquitin | Usp31 | SKQASVTSAASSRRT |
| S | 1 | 929 | 0.002931 | 0.967294 | -1.23647 | 0.038977 | M0QWN7 | Ubiquitin | Usp35 | DPAAEPGSPRVRAEP |
| S | 1 | 675 | 0.012727 | 0.668571 | -2.12246 | -0.34649 | P35123 | Ubiquitin | Usp4 | EEGKEQLSEVEGSGE |
| S | 1 | 779 | 0.002272 | 0.763144 | -2.12788 | -0.18741 | P56399 | Ubiquitin | Usp5 | MDISEGRSAAESISE |
| T | 1 | 623 | 0.000597 | 0.902229 | -2.16094 | 0.085791 | P56399 | Ubiquitin | Usp5 | DIAPPLVTPDEPKGS |
| S | 1 | 775 | 0.019574 | 0.007613 | -2.15539 | -2.43008 | P56399 | Ubiquitin | Usp5 | AEAAMDISEGRSAAE |
| S | 0.999988 | 2547 | 0.004565 | 0.999732 | -1.03226 | -0.00321 | P70398 | Probable u | Usp9x | YEGGEEVSPPQTKGS |
| S | 1 | 63 | 0.385708 | 0.016394 | 0.308853 | -0.85695 | Q62442 | Vesicle-ass | Vamp1 | LERDQKLSELDDRAD |
| S | 1 | 61 | 0.385708 | 0.016394 | 0.308853 | -0.85695 | P63044 | Vesicle-ass | Vamp2;Va | LERDQKLSELDDRAD |
| S | 1 | 30 | 0.003399 | 0.560862 | -1.88315 | -0.27729 | O70480 | Vesicle-ass | Vamp4 | RNLLEDDSDEEEDFF |
| S | 0.999791 | 756 | 0.020107 | 0.473249 | -5.07348 | -1.32869 | Q8CDG3 | Deubiquiti | Vcpip1 | TIRDGPSSAPATPTK |
| T | 0.985187 | 760 | 1.99E-06 | 0.180356 | -5.45453 | -0.34194 | Q8CDG3 | Deubiquiti | Vcpip1 | GPSSAPATPTKAPYS |
| T | 0.978683 | 1397 | 0.003064 | 0.976885 | -5.3298 | 0.142081 | Q8BX70-2 | Vacuolar p | Vps13c | KACREVSTPQDVHTT |
| S | 1 | 871 | 0.133775 | 0.022826 | -1.19006 | -1.82421 | Q8BX70-2 | Vacuolar p | Vps13c | LLLDGVESESDEEFF |
| S | 1 | 873 | 0.133775 | 0.022826 | -1.19006 | -1.82421 | Q8BX70-2 | Vacuolar p | Vps13c | LDGVESESDEEFFDA |
| S | 0.99988 | 223 | 0.00643 | 0.790451 | -3.66268 | -0.37878 | Q8VHI6 | Wiskott-Al | Wasf3 | PDNRLSQSVHHGASS |
| S | 0.999983 | 233 | 0.026369 | 0.593162 | -2.2519 | -0.51278 | Q8VHI6 | Wiskott-Al | Wasf3 | HGASSEGSLSPDTRS |
| S | 0.999996 | 1942 | 0.00481 | 0.677196 | -4.33143 | 0.551671 | Q6VNB8 | WD repeat | Wdfy3 | TGMNRSQSEYCNVGT |
| S | 0.919614 | 208 | 0.034987 | 0.061723 | -2.95152 | -2.23942 | Q8K1X1 | WD repeat | Wdr11 | VYISSPHSSPAHNKL |
| S | 0.999261 | 347 | 0.001155 | 0.269505 | -2.89278 | 0.557457 | Q3UWE6 | WD repeat | Wdr20 | FGRDRANSTQSRLSK |
| S | 0.999468 | 175 | 0.2395 | 0.004425 | -0.69055 | -2.00996 | Q6PEV3 | WAS/WAS | Wipf2 | TGMKHSSSAPPPPPP |
| S | 1 | 211 | 0.022237 | 0.863386 | -0.90067 | 0.098457 | P0C7L0 | WAS/WAS | Wipf3 | PIKAQLVSPPAPPTK |
| S | 1 | 665 | 0.045797 | 0.350827 | -1.23879 | -0.49944 | Q9Z0U0 | Xenotropi | Xpr1 | RSWKYNQSISLRRPR |
| S | 0.965002 | 1105 | 0.017662 | 0.60344 | -2.6207 | 0.527637 | B2RR83 | Probable | Ythdc2 | DGIPNDSSDSEMEDR |
| S | 0.997606 | 210 | 0.016698 | 0.177661 | -2.48854 | -1.07211 | P62259 | 14-3-3 pro | Ywhae | IAELDTLSEESYKDS |
| S | 0.998912 | 207 | 0.005109 | 0.024741 | -2.78527 | -1.69474 | P63101 | 14-3-3 pro | Ywhaz | IAELDTLSEESYKDS |
| S | 0.998513 | 64 | 0.000156 | 0.932526 | -3.6776 | 0.090399 | P63101 | 14-3-3 pro | Ywhaz | SSWRVVSSIEQKTEG |
| S | 1 | 198 | 0.002153 | 0.847091 | -2.03505 | 0.136617 | E9Q784 | | Zc3h13 | IIIQKEVSPEVVRSK |
| S | 1 | 77 | 0.03833 | 0.457244 | -0.76807 | -0.24568 | E9Q784 | | Zc3h13 | YSSNYRRSPERPTGD |
| S | 0.999693 | 1059 | 0.086545 | 0.000851 | -0.76612 | -2.15436 | B0V2M3 | Zinc finger | Zfp318;Zn | NEKSCIKSPSSTESL |
| S | 0.999958 | 465 | 0.003715 | 0.440671 | -1.99069 | -0.36786 | A2A482 | | Zmynd8 | QAGSLSGSPKPFSPQ |
| S | 0.999968 | 461 | 0.691987 | 0.048712 | -0.21177 | -0.76374 | A2A482 | | Zmynd8 | TKTGQAGSLSGSPKP |
| S | 0.999958 | 465 | 0.691987 | 0.048712 | -0.21177 | -0.76374 | A2A482 | | Zmynd8 | QAGSLSGSPKPFSPQ |
| S | 0.999996 | 559 | 0.009756 | 0.472086 | -4.46747 | -0.97975 | Q8BZ47 | Zinc finger | Znf609 | VPQKGSLSPARSATP |
| S | 1 | 606 | 0.017467 | 0.853412 | -1.58729 | -0.16972 | Q61464 | Zinc finger | Znf638;Zf | ETVDKGLSPAQKPKL |

|  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.999926 | 18 | 0.021949 | 0.996967 | -2.96949 | -0.04549 | Q71FD5 | E3 ubiquiti | Znrf2 | NGRTRAYSGSDLPSG |
| S | 1 | 130 | 0.017962 | 0.032935 | -2.96901 | -2.26365 | D3Z4U0 | Zinc finger | Zranb2 | EYIEREESDGEYDEF |
| S | 1 | 163 | 0.01041 | 0.492004 | -3.79055 | -0.81624 | D3Z4U0 | Zinc finger | Zranb2 | KEVEDKESEGEEEDE |
| S | 1 | 198 | 0.006481 | 0.120758 | -1.9643 | -0.78147 | D3Z4U0 | Zinc finger | Zranb2 | SKYNLDASEEEDSNK |
| S | 1 | 28 | 0.003738 | 0.893054 | -1.31013 | -0.08145 | P0C913 | Overexpressed in colo |  | VKDTTEDSITEDDKR |

# STR

| Amino acid | Localizatio | Position | nalf_pvalu | U50_pval | log2_nalf_ | log2_U50_ | Protein | Protein na | Gene nam | Short sequence window |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.999994 | 936 | 0.086645 | 0.008287 | 2.674727 | 4.527307 | Q3UHJ0 | AP2-associ | Aak1 | GGHSRNSSGSSESSL |
| S | 0.986558 | 676 | 0.611634 | 1.13E-06 | -0.164506 | -5.152286 | Q3UHJ0 | AP2-associ | Aak1 | ATTTPSGSPRTSQQN |
| S | 0.999999 | 88 | 0.038873 | 0.001102 | 0.516048 | 1.077737 | Q3THG9 | Alanyl-tRN | Aarsd1;Gm | HFTESPLSPGSQVQV |
| S | 0.888056 | 516 | 0.649994 | 0.047996 | 0.497134 | 1.649796 | Q80YE4 | Serine/thr | Aatk | ELCAPDSSPPGVVPV |
| S | 0.999993 | 502 | 0.698207 | 0.04719 | -0.303492 | -1.119821 | Q8K4G5 | Actin-bindi | Ablim1 | TSQGSINSPVYSRHS |
| S | 1 | 387 | 0.507379 | 0.041232 | 0.450384 | -1.201881 | Q9R1V6-11 | Disintegrin | Adam22 | SDKRKLASGECKCED |
| S | 0.998242 | 934 | 0.225408 | 0.025151 | -0.467767 | -0.867327 | Q9R1V6-11 | Disintegrin | Adam22 | PAKSPSSSTGSIASS |
| S | 0.998242 | 868 | 0.225408 | 0.025151 | -0.467767 | -0.867327 | Q9R1V6 | Disintegrin | Adam22 | PAKSPSSSTGSIASS |
| T | 1 | 62 | 0.142252 | 0.021326 | 0.810697 | 1.294543 | P84309 | Adenylate | Adcy5 | KRSGGAVTPQQQQRL |
| S | 0.998507 | 555 | 0.116365 | 0.015181 | 0.771372 | 1.246914 | E9Q1K3 |  | Add1 | GLAEQTFSPAKSVSF |
| S | 1 | 614 | 0.0158 | 0.096398 | -0.731762 | -0.390554 | Q9QYB8 | Beta-addu | Add2 | PSKAGTKSPAVSPSK |
| S | 1 | 618 | 0.0158 | 0.096398 | -0.731762 | -0.390554 | Q9QYB8 | Beta-addu | Add2 | GTKSPAVSPSKTSED |
| S | 1 | 614 | 0.258995 | 0.02721 | -0.375427 | -0.72867 | Q9QYB8 | Beta-addu | Add2 | PSKAGTKSPAVSPSK |
| S | 1 | 618 | 0.258995 | 0.02721 | -0.375427 | -0.72867 | Q9QYB8 | Beta-addu | Add2 | GTKSPAVSPSKTSED |
| S | 0.996724 | 532 | 0.032146 | 0.061962 | -0.957789 | -0.709157 | Q9QYB8 | Beta-addu | Add2 | AEKSRSPSTESQLMS |
| S | 1 | 423 | 0.761383 | 0.032144 | -0.718916 | 3.435436 | Q9QYB5 | Gamma-ad | Add3 | EDDSAPLSPLKFMAQ |
| S | 1 | 42 | 0.007078 | 0.006044 | 2.34166 | 2.173073 | Q9QYB5 | Gamma-ad | Add3 | YLRERNMSPDLRQDF |
| S | 1 | 210 | 0.985498 | 0.027348 | -0.0681 | 1.52765 | Q3UPL5 | Uncharact | Ag2 | AKKSFLQSLECLRRS |
| S | 0.999795 | 802 | 0.747284 | 0.046569 | 0.190783 | 0.79255 | Q3UHD9 | Arf-GAP wi | Agap2 | RNLARALSTDCTPSG |
| S | 0.997369 | 281 | 0.044409 | 0.056825 | 1.639311 | 1.363903 | O88845 | A-kinase ar | Akap10 | GSRNSCSSPLRELSE |
| S | 1 | 467 | 0.000616 | 0.000021 | 0.55804 | 1.002106 | Q9WTQ5 | A-kinase ar | Akap12 | HTQLTDLSPEEKMLP |
| S | 0.99999 | 36 | 0.005264 | 0.454668 | -0.93088 | -0.18189 | A2API8 |  | Akap2;Pak | EPAASSLSPDHKNME |
| S | 0.997296 | 480 | 0.126206 | 0.012932 | 0.504205 | 0.873376 | E9Q9K8 |  | Akap6 | HIKEISSSLGRLTDC |
| S | 0.996543 | 124 | 0.567922 | 0.0373525 | -0.297894 | 0.830759 | P31750 | RAC-alpha | Akt1 | TMDFRSGSPSDNSGA |
| T | 0.999987 | 247 | 0.991041 | 0.00911 | 0.071322 | -2.689839 | Q9D1F4 | Proline-ric | Akt1s1 | LPRPRLNTSDFQKLK |
| S | 1 | 244 | 0.726658 | 0.001426 | 0.216364 | 1.9878 | Q7TQF7 | Amphiphy | Amph | QHADKAFSIQGAPSD |
| S | 0.999374 | 1722 | 0.999672 | 0.037863 | 0.010344 | 1.421027 | S4R291 | Ankyrin-2 | Ank2 | LPTAKATSPLIEETP |
| S | 1 | 1925 | 0.46863 | 0.046135 | 0.354086 | 0.856443 | S4R291 | Ankyrin-2 | Ank2 | HEKHLPVSPGKTEKQ |
| S | 1 | 2085 | 0.566778 | 0.005324 | 0.164173 | 0.814015 | S4R291 | Ankyrin-2 | Ank2 | GDMDFQISPDRKTST |
| S | 1 | 2359 | 0.34402 | 0.024435 | 0.463196 | 1.079596 | S4R291 | Ankyrin-2 | Ank2 | KPQGAIRSPQGLELP |
| S | 1 | 3231 | 0.801573 | 0.012623 | 0.151876 | 1.033293 | S4R291 | Ankyrin-2 | Ank2 | SSPEEQKSVIEIPTA |
| T | 1 | 2494 | 0.008227 | 0.00364 | -1.420577 | -1.533823 | S4R291 | Ankyrin-2 | Ank2 | KSPLSPDTPSSEEVS |
| S | 0.996647 | 1526 | 0.036041 | 0.364534 | 3.248228 | 1.195155 | S4R2K9 |  | Ank3 | KSGSLSSSPSNTPSA |
| S | 1 | 486 | 0.003411 | 0.998772 | -0.937302 | -0.005847 | B2RW11 |  | Ankrd34a | RLLGGFQSLGGPGEP |
| S | 1 | 260 | 0.211864 | 0.018406 | 0.75373 | 1.473237 | Q3UUF8 | Ankyrin re | Ankrd34b | KHQARVASLQEELQD |
| S | 1 | 653 | 0.821216 | 0.018038 | -0.202321 | -1.33912 | Q8K298 | Actin-bindi | Anln | TRVPRAESADSLGSE |
| S | 1 | 656 | 0.821216 | 0.018038 | -0.202321 | -1.33912 | Q8K298 | Actin-bindi | Anln | PRAESADSLGSEDRD |
| S | 1 | 659 | 0.821216 | 0.018038 | -0.202321 | -1.33912 | Q8K298 | Actin-bindi | Anln | ESADSLGSEDRDLLY |
| S | 1 | 754 | 0.030855 | 0.140572 | 1.855978 | 1.030083 | O54774 | AP-3 comp | Ap3d1 | EKGKRRHSSLPTESD |
| S | 0.999999 | 851 | 0.027035 | 0.541433 | -0.774786 | -0.194949 | Q80V94 | AP-4 comp | Ap4e1 | SELFRSESLSGPPSA |
| S | 1 | 330 | 0.033018 | 0.947063 | -1.498596 | -0.109197 | V9GWV1 | ADP-ribosy | Arfgap1 | AEPPKAKSPSSDSWT |
| S | 0.999987 | 240 | 0.010002 | 0.076294 | -1.831611 | 0.943653 | A2A5R2 | Brefeldin A | Arfgef2 | LKQSQAQSKPTTPEK |
| S | 1 | 856 | 0.169413 | 0.006854 | -0.378442 | -0.855106 | Q811P8 | Rho GTPas | Arhgap32 | TASSEPVSPVQEKLS |
| S | 0.997274 | 871 | 0.484681 | 0.031092 | 0.323952 | 0.899277 | Q811P8 | Rho GTPas | Arhgap32 | PFFTLDLSPTDDKSS |
| S | 0.999982 | 1328 | 0.04893 | 0.924027 | -2.41478 | 0.237929 | F8VQN6 | Rho guani | Arhgef12 | GDIATCDSPRTSTES |
| S | 0.999721 | 1485 | 0.039712 | 0.525325 | 2.371424 | -0.68191 | Q3UPH7 | Rho guani | Arhgef40 | SPSLQPPSPGSSTPA |
| S | 1 | 269 | 0.030514 | 0.067733 | 1.715834 | 1.218619 | P98203 | Armadillo | Arvcf | GLEDDTRSLAADDEG |
| S | 1 | 712 | 0.978278 | 0.02755 | 0.04214 | 0.768577 | Q6PIC6 | Sodium/po | Atp1a2;At | TGDGVNDSPALKKAD |
| S | 0.945867 | 1160 | 0.000344 | 0.632423 | -3.196505 | -0.25143 | Q9R0K7 | Plasma me | Atp2b2 | QNSSPPSSLNKNNSA |
| S | 1 | 1116 | 0.002989 | 0.724027 | -2.112845 | -0.217839 | S4R1C4 | Calcium-tr | Atp2b2 | QGALRRQSSVTSQSQ |
| S | 0.999991 | 1117 | 0.004558 | 0.726564 | -1.932379 | -0.217839 | S4R1C4 | Calcium-tr | Atp2b2 | GALRRQSSVTSQSQD |
| T | 1 | 36 | 0.331332 | 0.007814 | 0.298961 | 0.904459 | Q91XV3 | Brain acid | Basp1 | AGTEEEGTPKESEPQ |
| S | 0.999953 | 495 | 0.021692 | 0.89157 | -1.049232 | 0.100237 | Q3UTZ3 | Uncharact | BC037034 | RPLSRKSSPSSPAVR |
| S | 1 | 615 | 0.184861 | 0.048515 | 0.682298 | 0.96633 | Q80YN3 | Breast carc | Bcas1 | GLGPKRMSDAQVQTD |
| S | 0.985049 | 498 | 0.181908 | 0.041425 | 0.524242 | 0.77175 | Q80YN3 | Breast carc | Bcas1 | RQMSVRSSEGIPRSE |
| S | 1 | 601 | 0.236139 | 0.023259 | 0.633073 | 1.224571 | Q80YN3 | Breast carc | Bcas1 | KSEKRRQSLGGFLKG |
| S | 1 | 559 | 0.705179 | 0.012589 | -0.14675 | -0.780136 | F8WIG2 | Brain-enric | Begain | VQLCGAGSSPEPEHG |
| S | 1 | 560 | 0.705179 | 0.012589 | -0.14675 | -0.780136 | F8WIG2 | Brain-enric | Begain | QLCGAGSSPEPEHGS |
| S | 0.999774 | 324 | 0.575671 | 0.007745 | 0.221294 | 1.0217 | O08539 | Myc box-d | Bin1 | PEPASGASPGATIPK |
| S | 1 | 399 | 0.022298 | 0.001307 | 0.529331 | 0.916959 | Q5RJI5 | Serine/thr | Brsk1 | KRRPERKSMEVLSIT |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 383 | 0.465913 | 0.007629 | 0.242559 | 0.92838 | G3UWV4 | Serine/thre | Brsk2 | KRRPERKSMEVLSVT |
| S | 1 | 383 | 0.465913 | 0.007629 | 0.242559 | 0.92838 | Q69Z98 | Serine/thre | Brsk2 | KRRPERKSMEVLSVT |
| S | 0.999998 | 394 | 0.545119 | 0.009688 | 0.25236 | 1.045934 | Q69Z98 | Serine/thre | Brsk2 | LSVTDGGSPVPARRA |
| S | 0.999613 | 446 | 0.893338 | 0.023393 | -0.089807 | -0.744071 | G3UWV4 | Serine/thre | Brsk2 | ASSGLSTSPLSSPRV |
| S | 1 | 235 | 0.028456 | 0.018505 | 0.737678 | 0.738333 | O88737 | Protein bas | Bsn | TTAPRSKSQQQLHSP |
| S | 0.999973 | 2645 | 0.393382 | 0.002617 | -1.088344 | -4.704623 | O88737 | Protein bas | Bsn | RSRLSRHSDSGSDSK |
| S | 0.999999 | 2647 | 0.455021 | 0.004199 | -1.088344 | -4.695032 | O88737 | Protein bas | Bsn | RLSRHSDSGSDSKHD |
| S | 1 | 148 | 0.154699 | 0.023104 | 1.710304 | 2.763115 | Q8R149 | BUD13 hor | Bud13 | RHDTPDPSPPRKARH |
| S | 0.999995 | 396 | 0.88574 | 0.042429 | 0.118443 | 0.803347 | Q80X80 | C2 domain- | C2cd2l | PGPGKSLSPAATVTA |
| S | 1 | 411 | 0.88574 | 0.042429 | 0.118443 | 0.803347 | Q80X80 | C2 domain- | C2cd2l | ELHYEQGSPRNLGTP |
| S | 0.675234 | 832 | 0.004175 | 0.155657 | -3.383475 | 1.105468 | D3YXF5 | | C7 | RCRGQSISITAIKPC |
| S | 0.961326 | 2028 | 0.079113 | 0.048846 | 1.242703 | 1.288352 | P97445 | Voltage-de | Cacna1a | EMGTDGYSDSEHYLP |
| S | 1 | 450 | 0.024813 | 0.45217 | 3.228834 | 0.925655 | P97445 | Voltage-de | Cacna1a | DQLADIASVGSPFAR |
| S | 1 | 453 | 0.038022 | 0.724646 | 3.232498 | 0.620638 | P97445 | Voltage-de | Cacna1a | ADIASVGSPFARASI |
| S | 0.999964 | 1038 | 0.416714 | 0.023517 | -0.465447 | -1.240747 | P97445 | Voltage-de | Cacna1a | LATGEPASPHDSLGH |
| S | 0.994504 | 1042 | 0.062421 | 0.027448 | -1.679395 | -1.897912 | P97445 | Voltage-de | Cacna1a | EPASPHDSLGHSGLP |
| S | 0.999992 | 1051 | 0.526476 | 0.00583 | -0.49762 | -2.249969 | P97445 | Voltage-de | Cacna1a | GHSGLPPSPAKIGNS |
| S | 0.994452 | 477 | 0.013356 | 1.55E-05 | 0.418969 | -1.599154 | Q8R0S4 | Voltage-de | Cacnb4 | RNRLSSSSQHSRDHY |
| S | 1 | 253 | 0.141491 | 0.008264 | -0.369188 | -0.743614 | O88602 | Voltage-de | Cacng2 | PSHSRDASPVGVKGF |
| T | 1 | 376 | 0.009252 | 0.007473 | 1.208335 | 1.136946 | Q99N28 | Cell adhesi | Cadm3 | DDAPDADTAIINAEG |
| S | 0.999012 | 358 | 0.085519 | 0.049531 | 2.004049 | 2.122324 | Q5SVJ0 | Calcium/ca | Camk2b | GVKPQTNSTKNSSAI |
| S | 1 | 1259 | 0.507993 | 0.01812 | 0.247601 | 0.824246 | Q6P9K8 | Caskin-1 | Caskin1 | VPLPGPGSPEVKRAH |
| S | 1 | 1818 | 0.022231 | 0.084692 | -1.27553 | -0.775527 | Q9WUF3 | CASP8-assc | Casp8ap2 | GHKKRKNSPGVSHSS |
| S | 0.999996 | 253 | 0.031341 | 0.001536 | 0.453691 | 0.8308 | A2AEV7 | | Ccdc120 | FRAVSGGSPERRAPW |
| S | 1 | 15 | 0.160213 | 0.022307 | 0.426327 | 0.704796 | Q8CI71 | Coiled-coil | Ccdc132 | MTRQGLKSPPESLND |
| S | 1 | 559 | 0.040197 | 0.034044 | -0.826173 | -0.773983 | Q8CI71 | Coiled-coil | Ccdc132 | SAYQDYDSDSDVPEE |
| S | 1 | 561 | 0.040197 | 0.034044 | -0.826173 | -0.773983 | Q8CI71 | Coiled-coil | Ccdc132 | YQDYDSDSDVPEELK |
| S | 1 | 50 | 0.077709 | 0.005428 | 0.773183 | 1.394527 | Q3TVA9 | Coiled-coil | Ccdc136 | MGKHRGLSLTETELE |
| S | 1 | 261 | 0.030201 | 0.060777 | 0.918608 | 0.672657 | Q8VDN4 | Coiled-coil | Ccdc92 | RSATGQHSPARDKPH |
| S | 1 | 211 | 0.965847 | 0.006333 | -0.076207 | -1.587073 | Q9D6J3 | Coiled-coil | Ccdc94 | HRRLLEDSESEDEAP |
| S | 1 | 213 | 0.972976 | 0.008891 | -0.076207 | -1.652028 | Q9D6J3 | Coiled-coil | Ccdc94 | RLLEDSESEDEAPPS |
| S | 1 | 83 | 0.016064 | 0.006712 | 1.079733 | 1.192583 | Q8BGU5 | Cyclin-Y | Ccny | DVREKRKSLFINHHP |
| S | 0.999973 | 440 | 0.950835 | 0.034065 | -0.137781 | -1.558761 | Q69ZA1 | Cyclin-depe | Cdk13 | RSRHSSISPSTLTLK |
| S | 1 | 326 | 0.818771 | 0.039936 | -0.297966 | -1.582497 | Q69ZA1 | Cyclin-depe | Cdk13 | PLGGRDESPVSHRAS |
| S | 1 | 316 | 0.791104 | 0.020361 | -0.297966 | -1.743171 | Q69ZA1 | Cyclin-depe | Cdk13 | AYRRRQRSLSPLGGR |
| S | 1 | 318 | 0.916971 | 0.032304 | -0.297966 | -2.593792 | Q69ZA1 | Cyclin-depe | Cdk13 | RRRQRSLSPLGGRDE |
| S | 0.999999 | 829 | 0.091643 | 0.012496 | 0.488078 | 0.762323 | Q6A065 | Centrosom | Cep170 | KSLVRQGSFTIDKPS |
| S | 0.99882 | 24 | 0.009402 | 0.084277 | -2.260681 | -1.111183 | P18760 | Cofilin-1 | Cfl1 | DMKVRKSSTPEEVKK |
| S | 1 | 1194 | 0.139575 | 0.009327 | 0.654824 | 1.274803 | E9QKH0 | CLIP-associ | Clasp1 | IEKFSFRSQEDLNEP |
| S | 1 | 535 | 0.04667 | 0.077961 | 1.645227 | 1.258766 | F7DCH5 | CLIP-associ | Clasp2 | PSVSQGCSREASRES |
| S | 0.999999 | 461 | 0.30856 | 0.037053 | 1.061106 | 2.075458 | F7DCH5 | CLIP-associ | Clasp2 | RTKMVSQSQPGSRSG |
| S | 1 | 531 | 0.039559 | 0.158455 | 3.044842 | 1.727807 | F7DCH5 | CLIP-associ | Clasp2 | RIPRPSVSQGCSREA |
| S | 1 | 535 | 0.03411 | 0.079181 | 4.344215 | 3.02718 | F7DCH5 | CLIP-associ | Clasp2 | PSVSQGCSREASRES |
| S | 0.999847 | 401 | 0.502437 | 0.025112 | 0.363207 | -1.100523 | B9EHT4 | CAP-Gly do | Clip3 | KGKKKSPSSPSLGSL |
| S | 1 | 100 | 0.428776 | 0.027779 | 0.442569 | 1.152093 | Q923F1 | | Clns1a | EESKEPLSDEDEEDN |
| S | 1 | 169 | 0.009909 | 0.005092 | 0.861357 | 0.900786 | P16330 | 2',3'-cyclic- | Cnp | EKNQWQLSADDLKKL |
| S | 1 | 556 | 0.999127 | 0.034933 | -0.014583 | -1.254427 | Q9Z140 | Copine-6 | Cpne6 | PAMTPSPSP______ |
| S | 1 | 656 | 0.811207 | 0.000761 | 0.288322 | 3.806587 | Q6P1J1 | Dihydropyr | Crmp1 | HQSNFSLSGAQIDDN |
| S | 1 | 638 | 0.264571 | 0.02371 | -1.609255 | -3.274015 | Q6P1J1 | Dihydropyr | Crmp1 | PSAKSSPSKHQPPPI |
| T | 1 | 683 | 0.414096 | 0.019471 | -2.375735 | -6.621152 | Q6P1J1 | Dihydropyr | Crmp1 | PGGRSNITSLG____ |
| S | 1 | 346 | 0.866835 | 0.036694 | -0.250116 | -1.622997 | P30999 | Catenin de | Ctnnd1 | LAQHERGSLASLDSL |
| S | 1 | 349 | 0.866835 | 0.036694 | -0.250116 | -1.622997 | P30999 | Catenin de | Ctnnd1 | HERGSLASLDSLRKG |
| S | 1 | 352 | 0.866835 | 0.036694 | -0.250116 | -1.622997 | P30999 | Catenin de | Ctnnd1 | GSLASLDSLRKGMPP |
| S | 0.960205 | 356 | 0.093092 | 0.0175 | 0.668425 | 0.965016 | E9QKH8 | Catenin de | Ctnnd2 | IGTYATLSPTKRLVH |
| S | 0.999513 | 456 | 0.995491 | 0.021349 | -0.022685 | 0.97812 | E9QKH8 | Catenin de | Ctnnd2 | FRTSTAPSSPGVDSV |
| S | 0.998618 | 457 | 0.995491 | 0.021349 | -0.022685 | 0.97812 | E9QKH8 | Catenin de | Ctnnd2 | RTSTAPSSPGVDSVP |
| S | 0.960205 | 356 | 0.263642 | 0.034488 | 2.064484 | 3.791091 | E9QKH8 | Catenin de | Ctnnd2 | IGTYATLSPTKRLVH |
| T | 0.998749 | 453 | 0.995056 | 0.023213 | -0.022685 | 0.913737 | E9QKH8 | Catenin de | Ctnnd2 | TGTFRTSTAPSSPGV |
| S | 1 | 407 | 0.343282 | 2.88E-05 | 0.379948 | -3.880773 | Q60598 | Src substra | Cttn | QTPPASPSPQPIEDR |
| S | 1 | 392 | 0.245759 | 0.045004 | 0.504284 | 0.829927 | Q9JLM8 | Serine/thre | Dclk1 | RGWRREESEEGFQIP |
| S | 0.999076 | 337 | 0.997787 | 0.014017 | -0.037441 | -2.565778 | Q9JLM8 | Serine/thre | Dclk1 | SPSPSPTSPGSLRKQ |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.994594 | 359 | 0.011062 | 0.010011 | -2.068016 | -1.894821 | Q6PGN3-5 | Serine/thre | Dclk2 | SSSSSPTSPGSFRGL |
| S | 1 | 25 | 0.000591 | 0.999778 | -1.922772 | 0.003483 | Q921N6 | Probable A | Ddx27 | PVEPESDSGDEEEEG |
| S | 0.999697 | 473 | 0.050275 | 0.010023 | 1.111651 | 1.518659 | Q8K382 | DENN dom | Dennd1a | PLPKTMPSPQAETQD |
| S | 0.999941 | 418 | 0.939359 | 0.026628 | -0.474847 | 5.14514 | Q6NS52 | Diacylglyce | Dgkb | NKMQRANSVTMDGQG |
| S | 0.999331 | 137 | 0.067907 | 0.047322 | 1.675006 | 1.66984 | E9QNN1 | ATP-depen | Dhx9 | VESSGYGSPGPTWDR |
| S | 1 | 248 | 0.068879 | 0.024552 | 2.572939 | 3.087533 | Q8BJ42 | Disks large- | Dlgap2 | KLFTKSHSLEGSSKS |
| S | 0.999664 | 269 | 0.388174 | 0.004104 | -1.396295 | -5.407952 | Q9WV69 | Dematin | Dmtn | PIRRKTRSLPDRTPF |
| S | 1 | 451 | 0.306326 | 0.039731 | -0.689285 | 1.316779 | Q8BPN8 | DmX-like p | Dmxl2 | MKLDHELSLDRESEA |
| S | 0.999953 | 10 | 0.113299 | 0.047217 | 1.125593 | 1.33047 | P60904 | DnaJ homo | Dnajc5 | DQRQRSLSTSGESLY |
| S | 0.981065 | 764 | 0.216127 | 0.004781 | 0.416151 | 1.134603 | Q80TZ3-3 | Putative ty | Dnajc6 | GGFPPLSSPQKASPQ |
| S | 0.999493 | 512 | 0.321833 | 0.038089 | 0.677822 | 1.347135 | P39053-4 | Dynamin-1 | Dnm1 | QMNKKKTSGNQDEIL |
| S | 0.999883 | 851 | 0.314331 | 0.004699 | 0.350302 | 1.15729 | P39053-4 | Dynamin-1 | Dnm1 | PSRSGQASPSRPESP |
| S | 1 | 522 | 0.193911 | 0.01663 | -3.119026 | -6.016383 | O08553 | Dihydropyr | Dpysl2 | PASSAKTSPAKQQAP |
| S | 1 | 537 | 0.39385 | 0.024735 | -0.670638 | -1.697183 | O08553 | Dihydropyr | Dpysl2 | PVRNLHQSGFSLSGA |
| S | 1 | 540 | 0.39385 | 0.024735 | -0.670638 | -1.697183 | O08553 | Dihydropyr | Dpysl2 | NLHQSGFSLSGAQID |
| S | 1 | 542 | 0.39385 | 0.024735 | -0.670638 | -1.697183 | O08553 | Dihydropyr | Dpysl2 | HQSGFSLSGAQIDDN |
| S | 0.736273 | 7475 | 0.000948 | 0.333709 | -3.508487 | -0.576834 | S4R1P5 | Dystonin | Dst | MLRSESNSSITATQP |
| S | 1 | 405 | 0.07237 | 0.017476 | 0.639008 | 0.85026 | Q8R1Q8 | Cytoplasmi | Dync1li1 | SPRVPGGSPRTPNRS |
| S | 0.9966 | 516 | 6.86E-06 | 0.013357 | -6.100284 | -1.084169 | Q8R1Q8 | Cytoplasmi | Dync1li1 | VSPTTPTSPTEGEAS |
| S | 1 | 405 | 0.058234 | 0.037709 | 1.709801 | 1.734732 | Q8R1Q8 | Cytoplasmi | Dync1li1 | SPRVPGGSPRTPNRS |
| T | 0.998775 | 513 | 0.075901 | 0.044317 | -0.906969 | -0.954367 | Q8R1Q8 | Cytoplasmi | Dync1li1 | PASVSPTTPTSPTEG |
| T | 1 | 408 | 0.058542 | 0.037791 | 1.600151 | 1.625081 | Q8R1Q8 | Cytoplasmi | Dync1li1 | VPGGSPRTPNRSVSS |
| S | 0.989463 | 244 | 0.688747 | 0.014121 | -0.205135 | -1.022479 | Q69ZW3 | EH domain | Ehbp1 | PSAKSASSSEELINT |
| S | 1 | 446 | 0.131216 | 0.028028 | 0.722685 | 1.041734 | Q69ZW3 | EH domain | Ehbp1 | PKPSPIPSPVLGQKP |
| S | 0.989463 | 241 | 0.139842 | 0.011526 | -1.617391 | -2.99408 | Q69ZW3 | EH domain | Ehbp1 | ANVPSAKSASSSEEL |
| S | 0.989463 | 244 | 0.233833 | 0.03799 | -1.617391 | -2.727382 | Q69ZW3 | EH domain | Ehbp1 | PSAKSASSSEELINT |
| S | 1 | 120 | 0.996319 | 0.031841 | 0.023763 | -1.020024 | Q8JZQ9 | Eukaryotic | Eif3b | GAEEEGGSDGSAAEA |
| S | 0.999992 | 79 | 0.901597 | 0.039416 | -0.368176 | -2.767131 | Q8JZQ9 | Eukaryotic | Eif3b | TATSPAASPTPQSAE |
| S | 0.999955 | 108 | 0.262691 | 0.001338 | -0.203843 | -0.809197 | Q05D44 | Eukaryotic | Eif5b | GQKGKKTSFDENDSE |
| S | 1 | 114 | 0.262691 | 0.001338 | -0.203843 | -0.809197 | Q05D44 | Eukaryotic | Eif5b | TSFDENDSEELEDKD |
| S | 1 | 544 | 0.998897 | 0.018336 | -0.048436 | -4.396486 | A2AUK5 | Band 4.1-li | Epb4.1l1;E | RLPSSPASPSPKGTP |
| S | 1 | 96 | 0.199329 | 0.043636 | 0.712814 | 1.075147 | Q9WV92 | Band 4.1-li | Epb41l3 | QFEDDKLSQRSSSSK |
| S | 0.993316 | 416 | 0.000127 | 0.124236 | 4.525254 | 0.762755 | Q80VP1 | Epsin-1 | Epn1 | LRTALPTSGSSTGEL |
| S | 0.937526 | 340 | 0.479096 | 0.034479 | -0.880316 | -2.353055 | Q925F2 | Endothelia | Esam | GTFTPTPSVSSQALS |
| S | 0.833114 | 661 | 0.037576 | 0.043841 | -2.266913 | -1.941044 | Q3TZZ7 | Extended s | Esyt2 | HRDLGRSSSSLLASP |
| S | 0.997641 | 662 | 0.040234 | 0.049069 | -2.100516 | -1.774647 | Q3TZZ7 | Extended s | Esyt2 | RDLGRSSSSLLASPS |
| S | 0.99972 | 663 | 0.037576 | 0.043841 | -2.266913 | -1.941044 | Q3TZZ7 | Extended s | Esyt2 | DLGRSSSSLLASPSH |
| S | 1 | 367 | 0.7059 | 0.02656 | 0.184263 | 0.81109 | P70429 | Ena/VASP- | Evl | SRVKPAGSVNDVGLD |
| S | 0.999999 | 257 | 0.032642 | 0.009725 | 1.38384 | 1.685196 | Q8C739 | Protein FA | Fam110b | PSLQRSKSDLSDRYF |
| S | 0.989253 | 267 | 0.010207 | 0.962132 | -0.85808 | 0.038923 | Q9DB52 | Protein FA | Fam122a | TTTDSPVSPAQAASP |
| S | 1 | 630 | 0.247233 | 0.009949 | -0.598876 | -1.464587 | Q5XG69 | Soluble la | Fam169a | SAEKAVDSSSEEIEV |
| S | 1 | 631 | 0.247233 | 0.009949 | -0.598876 | -1.464587 | Q5XG69 | Soluble la | Fam169a | AEKAVDSSSEEIEVE |
| S | 1 | 632 | 0.247233 | 0.009949 | -0.598876 | -1.464587 | Q5XG69 | Soluble la | Fam169a | EKAVDSSSEEIEVEV |
| S | 1 | 849 | 0.061806 | 0.030579 | 1.161753 | 1.271454 | A2ATK9 | | Fam171a1 | VPLEPLASPNQRRSA |
| T | 0.999667 | 196 | 0.983675 | 0.013972 | 0.049384 | -1.239665 | Q8K4Z2 | Fibronecti | Fndc5 | KSASETSTPEHQGGG |
| S | 1 | 402 | 0.934595 | 0.000192 | -0.115077 | -3.645613 | P42128 | Forkhead b | Foxk1 | FGPLSSRSAPASPTH |
| S | 0.999926 | 406 | 0.877461 | 6.77E-05 | -0.115077 | -3.219221 | P42128 | Forkhead b | Foxk1 | SSRSAPASPTHPGLM |
| S | 1 | 402 | 0.047233 | 0.087292 | -1.426953 | -1.055964 | P42128 | Forkhead b | Foxk1 | FGPLSSRSAPASPTH |
| S | 0.999926 | 406 | 0.047233 | 0.087292 | -1.426953 | -1.055964 | P42128 | Forkhead b | Foxk1 | SSRSAPASPTHPGLM |
| S | 1 | 414 | 0.047233 | 0.087292 | -1.426953 | -1.055964 | P42128 | Forkhead b | Foxk1 | PTHPGLMSPRSSGLQ |
| S | 0.999948 | 24 | 0.000914 | 0.976313 | -3.452612 | 0.07156 | Q3UFK8 | FERM dom | Frmd8 | SHRSSVSSVGARAAD |
| S | 0.999999 | 1936 | 0.13109 | 0.00617 | 0.587252 | 1.230938 | E9Q8I9 | Protein fu | Fry | SDLFTVLSRSSSPDL |
| S | 0.994605 | 143 | 0.294828 | 0.017552 | 0.402247 | 0.935584 | Q9Z1S8 | GRB2-asso | Gab2 | ASHGPRSSPAEFSSS |
| S | 0.998676 | 803 | 0.311686 | 0.02885 | -0.374875 | -0.789633 | Q3V0G7-2 | GTPase-act | Garnl3 | KGASAHTSPQTPPAR |
| T | 1 | 806 | 0.311686 | 0.02885 | -0.374875 | -0.789633 | Q3V0G7-2 | GTPase-act | Garnl3 | SAHTSPQTPPARDTP |
| S | 1 | 96 | 0.017334 | 0.143989 | 2.422548 | 1.145647 | Q8CHY6 | Transcripti | Gatad2a | KSEKRPPSPDVIVLS |
| S | 1 | 130 | 0.341009 | 0.007194 | -0.324003 | -1.01656 | Q8VHR5 | Transcripti | Gatad2b | SPDIIVLSDNEASSP |
| S | 0.999987 | 567 | 0.391235 | 0.011066 | 0.829027 | -2.558687 | Q8BMI3 | ADP-ribosy | Gga3 | PLFQSQGSPQKGPEL |
| S | 1 | 372 | 0.005689 | 0.001858 | 0.798494 | 0.91822 | P23242 | Gap juncti | Gja1 | SRASSRASSRPRPDD |
| S | 0.999849 | 257 | 0.293915 | 0.027546 | -0.588293 | -1.214954 | P23242 | Gap juncti | Gja1 | TTGPLSPSKDCGSPK |
| S | 0.980125 | 325 | 0.047901 | 0.603107 | -3.076079 | 0.811476 | P23242 | Gap juncti | Gja1 | NRMGQAGSTISNSHA |

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|---|---|---|---|---|---|---|---|---|---|---|
| T | 0.999986 | 50 | 0.04715 | 0.783448 | 2.66814 | 0.468701 | P36916 | Guanine nu | Gnl1 | RREEQTDTSDGESVT |
| S | 1 | 35 | 0.075297 | 0.022289 | 0.992411 | 1.256253 | Q9CRA5 | Golgi phos | Golph3 | AAGGGGGSGEDEAQS |
| S | 0.990797 | 200 | 4.17E-05 | 1.19E-05 | -6.846918 | -7.900142 | Q8BUV3 | Gephyrin;M | Gphn | LSPPPTTSPHKQTED |
| S | 0.999869 | 691 | 0.213103 | 0.039697 | -3.650361 | -5.825729 | Q3UNH4 | G protein-r | Gprin1 | AAAAAQKSPSAEAAA |
| S | 1 | 491 | 0.045771 | 0.001119 | 0.544626 | 1.18746 | Q6IR34 | G-protein-s | Gpsm1 | GIPRAPSSDEECFFD |
| S | 1 | 1059 | 0.94454 | 0.012875 | 0.156109 | -2.133982 | P35436 | Glutamate | Grin2a | LPEEVAHSDISETSS |
| S | 0.999983 | 1062 | 0.96708 | 0.008056 | 0.156109 | -3.131109 | P35436 | Glutamate | Grin2a | EVAHSDISETSSRAT |
| S | 1 | 645 | 0.105676 | 0.01963 | -0.647271 | -0.947678 | Q9Z1E4 | Glycogen [s | Gys1 | RPASVPPSPSLSRHS |
| S | 1 | 647 | 0.103196 | 0.019801 | 1.306552 | 1.893046 | Q9Z1E4 | Glycogen [s | Gys1 | ASVPPSPSLSRHSSP |
| S | 1 | 921 | 0.08053 | 0.029731 | 0.950755 | 1.139387 | O70507 | Potassium/ | Hcn4 | PLQPGARSPQAAQPP |
| S | 1 | 132 | 0.071945 | 0.013842 | -1.333419 | -1.877384 | P51859 | Hepatoma- | Hdgf | KKGSAEGSSDEEGKL |
| S | 1 | 133 | 0.071945 | 0.013842 | -1.333419 | -1.877384 | P51859 | Hepatoma- | Hdgf | KGSAEGSSDEEGKLV |
| S | 1 | 231 | 0.755668 | 0.002102 | -0.36775 | -3.33302 | Q3UMU9 | Hepatoma- | Hdgfrp2 | KKKVPSASDSDSKAD |
| S | 1 | 233 | 0.764534 | 0.000873 | -0.36775 | -4.125957 | Q3UMU9 | Hepatoma- | Hdgfrp2 | KVPSASDSDSKADSD |
| S | 1 | 229 | 0.252094 | 0.04276 | -1.592344 | -2.692455 | Q3UMU9 | Hepatoma- | Hdgfrp2 | GRKKKVPSASDSDSK |
| S | 1 | 352 | 0.013477 | 0.253452 | -1.660509 | 0.57784 | Q640R3 | Hepatocyte | Hepacam | SPPVPGRSPGLPIRS |
| S | 1 | 301 | 0.376459 | 0.047256 | 1.016511 | -2.088893 | Q640R3 | Hepatocyte | Hepacam | EADTLPRSGEQERKN |
| S | 1 | 7 | 0.438519 | 0.018528 | 0.541618 | 1.593113 | P18608 | Non-histon | Hmgn1 | _MPKRKVSADGAAKA |
| S | 1 | 88 | 0.024995 | 0.013676 | 2.277415 | 2.375736 | Q9CX86 | Heterogene | Hnrnpa0 | RAVSREDSARPGAHA |
| S | 0.999944 | 182 | 0.885884 | 0.046725 | -0.312261 | -2.061497 | Q8R081 | Heterogene | Hnrnpl | KISRPGDSDDSRSVN |
| S | 1 | 943 | 0.036565 | 0.001715 | -1.923581 | -3.588083 | Q8CDA1 | Phosphatid | Inpp5f | SPLKKSPSADSIHTR |
| S | 0.999998 | 946 | 0.013705 | 0.001399 | -1.303391 | -1.966521 | Q8CDA1 | Phosphatid | Inpp5f | KKSPSADSIHTRTGF |
| S | 1 | 132 | 0.031411 | 0.014188 | 1.082605 | 1.18975 | Q3TES0 | IQ motif an | Iqsec3 | SRVQTPQSPHQHPVA |
| T | 1 | 517 | 0.137318 | 0.006012 | 0.624992 | 1.341081 | P81122 | Insulin rece | Irs2 | FSSHRSNTPESIAET |
| S | 1 | 185 | 0.863105 | 0.011336 | -0.28217 | -2.442892 | Q8C1D8 | Protein IWS | Iws1 | PKPRISDSESEELPK |
| S | 1 | 187 | 0.694962 | 0.009423 | 0.354377 | -1.975764 | Q8C1D8 | Protein IWS | Iws1 | PRISDSESEELPKPR |
| S | 1 | 70 | 0.902427 | 0.047135 | -0.450537 | -3.232325 | Q8BNW9 | Kelch repea | Kbtbd11 | AAEGSEASPPSLRSD |
| S | 0.992395 | 434 | 0.024825 | 0.014897 | 0.752438 | 0.767056 | P63141 | Potassium | Kcna2 | AQYLQVTSCPKIPSS |
| S | 1 | 447 | 0.195197 | 0.011877 | -0.933495 | -1.962971 | P63141 | Potassium | Kcna2 | SSPDLKKSRSASTIS |
| T | 1 | 452 | 0.15095 | 0.013269 | -1.180504 | -2.174184 | P63141 | Potassium | Kcna2 | KKSRSASTISKSDYM |
| S | 1 | 552 | 0.342591 | 0.015383 | 0.857661 | 2.245143 | Q9Z0V2 | Potassium | Kcnd2 | VSGSHRGSVQELSTI |
| S | 1 | 546 | 0.341489 | 0.004958 | 0.570081 | 1.951582 | Q9Z0V2 | Potassium | Kcnd2 | RIPNANVSGSHRGSV |
| S | 1 | 548 | 0.342591 | 0.015383 | 0.857661 | 2.245143 | Q9Z0V2 | Potassium | Kcnd2 | PNANVSGSHRGSVQE |
| S | 1 | 938 | 0.217143 | 0.034518 | 0.836207 | 1.399402 | Q08460 | Calcium-ac | Kcnma1 | HGMLRQPSITTGVNI |
| S | 0.935653 | 200 | 0.170043 | 0.033437 | 2.766654 | 4.204835 | Q6WVG3 | BTB/POZ d | Kctd12 | AGPLLTPSQSLDGSR |
| S | 1 | 221 | 0.116776 | 0.042571 | 0.846272 | 1.04171 | Q7TSH8 | Uncharacte | Kiaa0195 | GDLFPPFSPPPSPRG |
| S | 1 | 225 | 0.116776 | 0.042571 | 0.846272 | 1.04171 | Q7TSH8 | Uncharacte | Kiaa0195 | PPFSPPPSPRGEVKR |
| S | 1 | 1301 | 0.005712 | 0.005559 | 3.262328 | 2.936223 | A2AAE1 | Uncharacte | Kiaa1109 | QDKSVGQSPLRSPLK |
| S | 1 | 180 | 0.215788 | 0.014467 | 0.431231 | 0.90296 | Q148V7 | LisH domai | Kiaa1468;2 | GQLNRAGSISTLDSL |
| S | 1 | 180 | 0.967256 | 0.034561 | -0.06329 | 0.879986 | Q148V7 | LisH domai | Kiaa1468;2 | GQLNRAGSISTLDSL |
| S | 1 | 186 | 0.967256 | 0.034561 | -0.06329 | 0.879986 | Q148V7 | LisH domai | Kiaa1468;2 | GSISTLDSLDFARYS |
| S | 0.999763 | 933 | 0.373503 | 0.020592 | 0.453584 | 1.163049 | Q61768 | Kinesin-1 h | Kif5b | PGQHPAASPTHPGTV |
| S | 1 | 579 | 0.097791 | 0.043828 | 0.687892 | 0.789349 | Q91YS4 | Kinesin ligh | Klc2 | SRMKRASSLNFLNKS |
| S | 0.991117 | 13 | 0.884503 | 0.004691 | -0.240049 | -2.811984 | Q8BGY4 | Kelch-like p | Klhl26 | GSSGSSQSPERPSSL |
| S | 1 | 494 | 0.002053 | 0.001269 | 3.179723 | 3.158437 | Q6ZQ58 | La-related | Larp1 | HYQKETESAPGSPRA |
| T | 0.998112 | 842 | 0.967295 | 0.030114 | -0.123909 | -1.789984 | Q6ZQ58 | La-related | Larp1 | AVGSYGCTPQSLPKF |
| S | 1 | 169 | 0.229959 | 0.04459 | -0.999134 | -1.597454 | D3YU59 | LIM and ca | Limch1 | KETDDIDSPKRSIRD |
| S | 0.988995 | 608 | 0.00051 | 0.000202 | 3.653871 | 3.967516 | Q7TME0 | Lipid phosp | Lppr4 | STVTCTGSIRYKTLT |
| S | 0.999996 | 90 | 0.914974 | 0.037271 | -0.250105 | -2.066349 | Q3UZ39-2 | Leucine-ric | Lrrfip1 | FRRNTSASDEDERLS |
| S | 0.999538 | 192 | 0.328921 | 0.033108 | 0.369371 | 0.772786 | Q8K2F8 | Protein LSM | Lsm14a | QLDPLRKSPTMEQAV |
| S | 1 | 1052 | 0.002433 | 0.476464 | -2.746345 | -0.434566 | Q9QYR6 | Microtubul | Map1a | PGPEEAMSEEGKVPL |
| S | 1 | 2230 | 0.948168 | 0.004965 | 0.057206 | 1.015356 | Q9QYR6 | Microtubul | Map1a | RPASPALSEGSSSEA |
| S | 1 | 1062 | 0.207446 | 0.017739 | 0.384863 | 0.752229 | Q9QYR6 | Microtubul | Map1a | GKVPLSRSPQAQDTL |
| T | 0.981373 | 2182 | 0.859641 | 0.010836 | 0.130672 | 1.127743 | Q9QYR6 | Microtubul | Map1a | ALALVPGTPTRTRHD |
| S | 0.999999 | 2234 | 0.20144 | 0.016702 | 2.637205 | 5.166222 | Q9QYR6 | Microtubul | Map1a | PALSEGSSSEATTPV |
| S | 0.997469 | 1139 | 0.854627 | 0.04367 | 0.329578 | 1.937803 | Q9QYR6 | Microtubul | Map1a | FSPEDAESLSVLSVV |
| S | 1 | 541 | 0.544564 | 0.0244 | 1.468889 | -4.825388 | P14873 | Microtubul | Map1b | KLKQRADSRESLKPA |
| S | 0.98415 | 1851 | 0.138569 | 0.030621 | 1.236205 | 1.775892 | P14873 | Microtubul | Map1b | NRDLTTSSVEKDSGG |
| S | 1 | 1438 | 0.517583 | 0.046674 | 0.434231 | 1.13821 | P14873 | Microtubul | Map1b | QGFPDRESPVSDLTS |
| S | 1 | 1293 | 0.012803 | 0.008878 | 0.857764 | 0.838283 | P14873 | Microtubul | Map1b | EGEARSVSPGVTQAV |
| S | 1 | 1508 | 0.027049 | 0.005688 | 0.786315 | 1.032674 | P14873 | Microtubul | Map1b | IDVSQFGSFKEDTKM |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.99867 | 1321 | 0.000498 | 0.389678 | -3.458575 | 0.450299 | P14873 | Microtubul | Map1b | EVVSPSQSVTGSAGH |
| S | 1 | 825 | 0.563305 | 0.035747 | -0.357403 | -1.094977 | P14873 | Microtubul | Map1b | KELEAERSLMSSPED |
| S | 1 | 828 | 0.563305 | 0.035747 | -0.357403 | -1.094977 | P14873 | Microtubul | Map1b | EAERSLMSSPEDLTK |
| S | 1 | 829 | 0.563305 | 0.035747 | -0.357403 | -1.094977 | P14873 | Microtubul | Map1b | AERSLMSSPEDLTKD |
| S | 0.999991 | 1317 | 0.010328 | 0.494871 | -2.228876 | -0.476697 | P14873 | Microtubul | Map1b | EKTLEVVSPSQSVTG |
| S | 0.99867 | 1321 | 0.567854 | 0.048153 | -2.156493 | -6.120738 | P14873 | Microtubul | Map1b | EVVSPSQSVTGSAGH |
| S | 0.997711 | 1334 | 0.010593 | 0.18514 | -6.210243 | -2.350404 | P14873 | Microtubul | Map1b | GHTPYYQSPTDEKSS |
| S | 1 | 1161 | 0.264196 | 0.04406 | 0.500877 | 0.859487 | P20357 | Microtubul | Map2 | DEGKKETSPETSLIQ |
| S | 1 | 1743 | 0.010687 | 0.166546 | 0.951919 | 0.377187 | P20357 | Microtubul | Map2 | KAQAKVGSLDNAHHV |
| T | 0.999458 | 1260 | 0.937532 | 0.019967 | -0.109177 | 1.255646 | P20357 | Microtubul | Map2 | KLLFRSDTLQISDLL |
| S | 0.999945 | 726 | 0.06354 | 0.019372 | 2.644074 | 3.291006 | P20357 | Microtubul | Map2 | FGRGHDLSPLASDIL |
| S | 0.999395 | 1796 | 0.038963 | 0.910559 | 5.081798 | -0.511992 | P20357 | Microtubul | Map2 | VASPRRLSNVSSSGS |
| S | 1 | 449 | 0.998755 | 0.040337 | 0.021463 | -1.484952 | O08648 | Mitogen-ac | Map3k4 | VELRELESGTEESDE |
| S | 1 | 454 | 0.99868 | 0.044467 | 0.021463 | -1.40249 | O08648 | Mitogen-ac | Map3k4 | LESGTEESDEEPTPS |
| S | 1 | 832 | 0.212182 | 0.008715 | 0.300748 | 0.706916 | Q7TSJ2 | Microtubul | Map6 | PEPPKNQSPVVLGPI |
| S | 0.999961 | 905 | 0.510976 | 0.044632 | 0.983619 | 2.58211 | Q7TSJ2 | Microtubul | Map6 | HTEYIEGSP_______ |
| S | 0.995086 | 415 | 0.011352 | 0.016458 | 3.213079 | 2.621642 | Q80W82 | Mitogen-ac | Mapk10 | GVVKGQPSPSAQVQQ |
| S | 1 | 28 | 0.012038 | 0.364833 | -2.691426 | 0.744918 | Q9WVI9 | C-Jun-amin | Mapk8ip1 | FLGLHIASPPNFRLT |
| S | 1 | 732 | 0.059209 | 0.039162 | 1.123754 | 1.133789 | Q9ESN9-3 | C-Jun-amin | Mapk8ip3 | EPKSTHPSPEKKKAK |
| S | 1 | 499 | 0.687074 | 0.039168 | -0.282636 | -1.073552 | A2A5Y6 | Microtubul | Mapt | GSGEPPKSGERSGYS |
| Y | 0.999893 | 702 | 0.163412 | 0.005898 | -1.959212 | -4.51822 | A2A5Y6 | Microtubul | Mapt | DHGAEIVYKSPVVSG |
| S | 0.980171 | 721 | 0.109642 | 0.014866 | -0.851163 | -1.354247 | A2A5Y6 | Microtubul | Mapt | RHLSNVSSTGSIDMV |
| S | 1 | 163 | 0.095373 | 0.001631 | 0.49843 | 1.258437 | P26645 | Myristoylat | Marcks | SFKLSGFSFKKSKKE |
| S | 1 | 104 | 0.96532 | 0.016872 | 0.060688 | 0.989463 | P28667 | MARCKS-re | Marcksl1 | PFKLSGLSFKRNRKE |
| S | 1 | 468 | 0.093145 | 0.024862 | 0.763823 | 1.007296 | Q8VHJ5 | Serine/thre | Mark1 | LGSTTVGSKSEVTAS |
| S | 1 | 412 | 0.0465 | 0.561725 | -2.331929 | 0.657847 | Q8VHJ5 | Serine/thre | Mark1 | AHLKVQRSISANQKQ |
| T | 1 | 208 | 0.021366 | 0.000437 | 0.436241 | 0.94379 | Q05512 | Serine/thre | Mark2;Mar | TFGNKLDTFCGSPPY |
| S | 1 | 598 | 0.016387 | 0.009519 | 2.819915 | 2.881837 | Q8K310 | Matrin-3 | Matr3 | KSRKRSYSPDGKESP |
| S | 1 | 131 | 0.06619 | 0.003708 | 2.691135 | 5.033554 | Q6PCP5 | Mitochond | Mff | LKRERSMSENAVRQN |
| T | 1 | 1653 | 0.106109 | 0.019754 | 1.026656 | 1.502853 | Q8CJ19 | Protein-me | Mical3 | LRGTQEPTLKHEATS |
| S | 1 | 1450 | 0.069109 | 0.01445 | 1.236472 | 1.700796 | Q99104 | Unconvent | Myo5a | VGQMENISPGQIIDE |
| S | 0.999983 | 946 | 0.501494 | 0.008454 | -0.247441 | 0.982093 | P13595 | Neural cell | Ncam1 | APPASKASPAPTPTP |
| T | 1 | 788 | 0.022402 | 0.026431 | 3.948915 | 3.381644 | P13595 | Neural cell | Ncam1 | VRTEEERTPNHDGGK |
| S | 0.999983 | 946 | 0.591991 | 0.001581 | 0.219037 | 1.491486 | P13595 | Neural cell | Ncam1 | APPASKASPAPTPTP |
| T | 0.681346 | 21 | 0.022985 | 0.069028 | -1.964243 | -1.286155 | Q3UYV9 | Nuclear ca | Ncbp1 | QPHKRRKTSDANETE |
| S | 0.998686 | 472 | 0.680332 | 0.037111 | 0.402586 | 1.530262 | Q6DFV7 | Nuclear re | Ncoa7 | QEVMGPESDTELKGA |
| S | 0.99998 | 231 | 0.485732 | 0.00192 | -0.374298 | -2.025466 | Q9ERR1 | Nuclear dis | Ndel1 | GTENSFPSPKAIPNG |
| S | 0.748925 | 346 | 0.001723 | 0.00318 | -5.095398 | -3.980239 | Q9QYG0 | Protein ND | Ndrg2 | IDGSRSRSRTLSQSS |
| S | 0.999706 | 350 | 0.385935 | 0.017882 | -1.959478 | -5.32074 | Q9QYG0 | Protein ND | Ndrg2 | RSRSRTLSQSSESGT |
| S | 1 | 332 | 0.419636 | 0.048685 | -0.484694 | -1.062479 | Q9QYG0 | Protein ND | Ndrg2 | LSRSRTASLTSAASI |
| S | 0.999998 | 476 | 0.946936 | 0.024327 | 0.089423 | -1.064316 | E9PXB7 | E3 ubiquiti | Nedd4l | RAVKDTLSNPQSPQP |
| S | 0.999917 | 488 | 0.872332 | 0.038411 | 0.155015 | -1.016827 | E9PXB7 | E3 ubiquiti | Nedd4l | PQPSPYNSPKPQHKV |
| S | 1 | 745 | 0.001369 | 0.622107 | -6.680839 | -0.718833 | P19246 | Neurofilam | Nefh | KSPGEAKSPGEAKSP |
| T | 1 | 586 | 0.918949 | 0.023737 | 0.198563 | -1.901446 | P19246 | Neurofilam | Nefh | AEPKSPATVKSPGEA |
| S | 1 | 605 | 0.097873 | 0.026399 | 0.768475 | 1.014295 | P08553 | Neurofilam | Nefm | EKPEKAKSPMPKSPV |
| S | 1 | 904 | 0.943865 | 0.047893 | -0.146257 | -1.402117 | Q5NCX5 | Neuralized | Neurl4 | SNTATEKSFPLHSPV |
| S | 1 | 909 | 0.943865 | 0.047893 | -0.146257 | -1.402117 | Q5NCX5 | Neuralized | Neurl4 | EKSFPLHSPVAGVAH |
| S | 1 | 79 | 0.81514 | 0.023624 | -0.24607 | -1.489647 | O09130 | NFATC2-int | Nfatc2ip | PAKPEQDSDSDSEGA |
| S | 1 | 81 | 0.81514 | 0.023624 | -0.24607 | -1.489647 | O09130 | NFATC2-int | Nfatc2ip | KPEQDSDSDSEGAAE |
| S | 1 | 83 | 0.81514 | 0.023624 | -0.24607 | -1.489647 | O09130 | NFATC2-int | Nfatc2ip | EQDSDSDSEGAAEGP |
| S | 0.999972 | 304 | 0.20245 | 0.042384 | -0.944321 | -1.446018 | Q91VE6 | MKI67 FHA | Nifk | QKTPTSASPGGKRPR |
| S | 1 | 891 | 0.06802 | 0.029903 | -1.175828 | -1.33349 | F8WGF2 | Nitric oxide | Nos1 | SYSDSRKSSGDGPDL |
| S | 1 | 243 | 0.034839 | 0.296156 | -3.906597 | -1.606402 | Q64322 | Neural prol | Npdc1 | SPSTPRISPGDQRLA |
| S | 1 | 19 | 0.83638 | 0.047637 | 0.149918 | 0.803406 | Q80XU3 | Nuclear ub | Nucks1 | DYSQFQESDDADEDY |
| S | 0.996682 | 726 | 0.025584 | 0.032346 | 1.066341 | 0.895486 | Q6PFX7 | Neuronal t | Nyap1 | YRLGRSASTSGVRQA |
| S | 0.998948 | 15 | 0.888859 | 0.042481 | 0.112192 | 0.772363 | Q4KMM3 | Oxidation r | Oxr1 | WLKKKSQSVDITAPG |
| S | 1 | 361 | 0.023741 | 0.345201 | 0.886546 | 0.30138 | Q9DCE5 | p21-activat | Pak1ip1 | KQPTKGNSPVTAKKR |
| S | 1 | 247 | 0.035762 | 0.128992 | -1.900997 | -1.134618 | Q3ULB5 | Serine/thre | Pak6 | GRPGGEGSPSPKNQE |
| S | 0.950201 | 161 | 0.297312 | 0.048925 | 1.067687 | 1.89036 | Q9Z0P4-2 | Paralemmi | Palm | PVRSPGGSTMMKAVV |
| S | 0.989919 | 164 | 0.123388 | 0.01283 | 0.637544 | 1.097412 | Q3TVI8 | Pre-B-cell l | Pbxip1 | RRRGREPSSSQPVVP |
| S | 1 | 173 | 0.39146 | 0.040269 | 0.396793 | 0.875699 | P60335 | Poly(rC)-bi | Pcbp1 | MLETLSQSPQGRVMT |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 1185 | 0.087568 | 0.035895 | 1.416071 | 1.656529 | E9Q2S0 | | Pcdh7 | MPVDERGSQEKLANG |
| S | 0.999872 | 1292 | 0.163081 | 0.024 | 0.552083 | 0.90178 | Q9QYX7 | Protein pic | Pclo | SSSQQPKSPQGLSDT |
| T | 0.997663 | 1552 | 0.002619 | 0.941892 | -3.411151 | 0.1413 | Q9QYX7 | Protein pic | Pclo | RLTRKSSTSFDDDAG |
| S | 0.991809 | 50 | 0.02407 | 0.132722 | 1.477899 | 0.784418 | Q8VBU5 | | Pde4b | PKISPRSSPRNSPCF |
| S | 1 | 119 | 0.847936 | 0.015811 | -0.57321 | -4.306899 | Q8CI51-3 | PDZ and LII | Pdlim5 | AEGQRRGSQGDIKQQ |
| S | 1 | 228 | 0.84461 | 0.011781 | -0.57321 | -4.574997 | Q8CI51 | PDZ and LII | Pdlim5 | AEGQRRGSQGDIKQQ |
| S | 1 | 125 | 0.039346 | 0.004768 | 1.785973 | 2.706643 | Q3UWL8 | Prefoldin sı | Pfdn4 | QLYAKFGSNINLEAD |
| S | 0.999999 | 522 | 0.853 | 0.014378 | -0.157103 | -1.232288 | Q6PDH0 | Pleckstrin h | Phldb1 | GRRTRSPSPTLGESL |
| S | 0.999991 | 5 | 0.902416 | 1.5E-06 | -0.059575 | -4.085484 | Q2TBE6 | Phosphatid | Pi4k2a | ___MDETSPLVSPER |
| S | 0.999968 | 23 | 0.148143 | 0.038446 | 1.10828 | 1.534033 | Q9Z1T6 | 1-phosphat | Pikfyve | DLPRSPASPSHLTHF |
| S | 0.999557 | 1713 | 0.004226 | 0.001483 | 0.639099 | 0.721067 | Q9Z1T6 | 1-phosphat | Pikfyve | DNRPKSSSPIRLPEI |
| S | 0.998409 | 4274 | 5.88E-05 | 0.921317 | -6.207673 | 0.135563 | Q9QXS1-6 | Plectin | Plec | GFRSRSSSVGSSSSY |
| S | 0.999488 | 1020 | 0.876158 | 0.039768 | 0.111758 | 0.738366 | E9Q6H8 | | Plekha5 | GVPLRTKSPTPESST |
| S | 0.9826 | 868 | 0.014898 | 0.014701 | -1.772784 | -1.590915 | Q3UIL6 | Pleckstrin h | Plekha7 | LQPSPPTSPVRTPLE |
| S | 1 | 242 | 0.605394 | 0.032899 | 0.411558 | 1.393533 | O35621 | Phosphoma | Pmm1 | TVGHSVVSPQDTVQR |
| S | 0.999999 | 33 | 0.037678 | 0.078132 | -0.862198 | 0.620277 | Q8R4S0 | Protein pho | Ppp1r14c | PRGGTGGSPGSSSSS |
| T | 1 | 497 | 0.040476 | 0.004575 | 0.486564 | 0.750329 | Q4VA93 | Protein kin | Prkca | MDGVTTRTFCGTPDY |
| T | 1 | NaN | 0.040476 | 0.004575 | 0.486564 | 0.750329 | | Protein kin | Prkcb | WDGVTTKTFCGTPDY |
| T | 1 | 514 | 0.040476 | 0.004575 | 0.486564 | 0.750329 | P63318 | Protein kin | Prkcg | FPGSTTRTFCGTPDY |
| S | 1 | 303 | 0.974241 | 0.043946 | -0.130582 | -1.918993 | Q02111 | Protein kin | Prkcq | ESTQQARSLRDSEHI |
| T | 0.957752 | 609 | 0.194504 | 0.039314 | 0.564368 | 0.867545 | Q7TSC1 | Protein PRI | Prrc2a | EEVPPPTTPPAPKME |
| S | 1 | 845 | 0.951886 | 0.029589 | 0.075873 | 0.902059 | Q6PE13 | Proline-rich | Prrt3 | ALRPRRGSQPDAELD |
| S | 0.999984 | 832 | 0.047734 | 0.130798 | -3.222549 | -2.076916 | Q6PE13 | Proline-rich | Prrt3 | CGLRGLASSPTGGAL |
| S | 1 | 791 | 0.229201 | 0.043575 | -0.450517 | -0.72396 | Q6PE13 | Proline-rich | Prrt3 | VGPAPSLSELDLRPP |
| S | 1 | 342 | 0.000111 | 0.906323 | -4.348246 | -0.118879 | E9PUC5 | PH and SEC | Psd3 | KKSHSSPSLNPDASP |
| T | 1 | 253 | 0.017211 | 0.912545 | -1.215225 | -0.097353 | O35226 | 26S protea | Psmd4 | AGIATPGTEDSDDAL |
| S | 1 | 748 | 0.038055 | 0.154869 | 2.632819 | 1.491263 | P35831 | Tyrosine-pı | Ptpn12 | KKDQITKSPAEVTDI |
| S | 0.999804 | 176 | 0.052019 | 0.007342 | -0.753489 | -1.119645 | P18052 | Receptor-ty | Ptpra | KKYKQAGSHSNSFRL |
| S | 0.999997 | 159 | 0.828785 | 0.007354 | -0.177805 | -1.502174 | Q8R4E6 | Purine-rich | Purg | RQKHSAPSPPVSVGS |
| S | 1 | 163 | 0.828785 | 0.007354 | -0.177805 | -1.502174 | Q8R4E6 | Purine-rich | Purg | SAPSPPVSVGSEEHP |
| S | 1 | 166 | 0.828785 | 0.007354 | -0.177805 | -1.502174 | Q8R4E6 | Purine-rich | Purg | SPPVSVGSEEHPHSV |
| S | 0.999959 | 515 | 0.020991 | 0.015111 | -0.965974 | -0.939191 | Q8R361 | Rab11 fami | Rab11fip5 | KEPTQKPSPHPVKPL |
| S | 1 | 480 | 0.617637 | 0.007536 | -0.450111 | -2.26131 | Q5U3K5 | Rab-like pr | Rabl6 | PMPSKNISLSSEEEA |
| S | 1 | 482 | 0.617637 | 0.007536 | -0.450111 | -2.26131 | Q5U3K5 | Rab-like pr | Rabl6 | PSKNISLSSEEEAEG |
| S | 1 | 483 | 0.617637 | 0.007536 | -0.450111 | -2.26131 | Q5U3K5 | Rab-like pr | Rabl6 | SKNISLSSEEEAEGL |
| S | 1 | 2729 | 0.962458 | 0.031854 | 0.316719 | 4.197201 | Q9ERU9 | E3 SUMO-p | Ranbp2 | GGEDEDGSDEDVVHN |
| S | 0.999997 | 788 | 0.067041 | 0.016921 | -1.211602 | -1.586889 | Q9ERU9 | E3 SUMO-p | Ranbp2 | SPTKYSLSPSKSYKY |
| S | 0.990471 | 1119 | 0.984053 | 0.014171 | 0.1681 | -4.255206 | Q8CHG7 | Rap guanin | Rapgef2 | QLSSPPTSPQSSPRK |
| S | 0.992155 | 133 | 0.442156 | 0.039572 | 0.305416 | 0.737987 | E9PW37 | | Rasal2 | RCLRRTVSVPSEGQF |
| S | 1 | 646 | 0.036212 | 0.247475 | -2.555354 | -1.164206 | Q9ESK9 | RB1-inducil | Rb1cc1 | KVSTSQASPQSAASP |
| S | 1 | 42 | 0.57563 | 0.008903 | -0.203669 | 0.909684 | A0A023T67 | RNA-bindir | RBM8 | RKGRGFGSEEGSRAR |
| S | 0.999997 | 451 | 0.039001 | 0.099915 | -2.621108 | -1.754951 | Q8CFE3 | REST corep | Rcor1 | ANQKPVKSPESSIKI |
| S | 0.999999 | 561 | 0.150502 | 0.018051 | 1.329664 | 2.264701 | O54916 | RalBP1-ass | Reps1 | PSHSRSSSLDMNRTF |
| S | 1 | 675 | 0.026467 | 0.599235 | 1.179071 | -0.265739 | Q80TZ9 | Arginine-gl | Rere | KTKTQEISRPNSPSE |
| S | 0.999989 | 679 | 0.048567 | 0.377931 | 1.129643 | -0.442174 | Q80TZ9 | Arginine-gl | Rere | QEISRPNSPSEGEGE |
| S | 1 | 271 | 0.044083 | 0.011515 | 0.902197 | 1.14724 | P47708 | Rabphilin-3 | Rph3a | AGLRRANSVQAARPA |
| S | 0.999034 | 240 | 0.69339 | 0.008517 | -0.11674 | -1.00721 | P62754 | 40S riboson | Rps6 | RLSSLRASTSKSESS |
| S | 0.99962 | 244 | 0.69339 | 0.008517 | -0.11674 | -1.00721 | P62754 | 40S riboson | Rps6 | LRASTSKSESSQK__ |
| S | 1 | 434 | 0.113187 | 0.024143 | -0.576795 | -0.819845 | P56183 | Ribosomal | Rrp1 | PQNKEAGSEAESSSA |
| S | 0.999651 | 217 | 0.188099 | 0.011292 | 0.469607 | 0.983974 | Q9ES97 | Reticulon-3 | Rtn3 | HICTYSLSPSELPVA |
| S | 1 | 145 | 0.969412 | 0.021149 | 0.048328 | 0.793303 | Q99P72 | Reticulon-4 | Rtn4 | PPAPAGASPLAEPAA |
| S | 0.999932 | 839 | 0.089501 | 0.026668 | -4.065129 | -5.19254 | Q99P72 | Reticulon-4 | Rtn4 | SETFSDSSPIEIIDE |
| T | 0.999886 | 568 | 0.905879 | 0.023558 | -0.093099 | -0.824194 | Q61909 | Protein CBI | Runx1t1 | PRSTTPGTPSTIETT |
| S | 1 | 20 | 0.033877 | 0.885888 | -3.37514 | -0.373527 | Q6ZPE2 | Myotubula | Sbf1 | FGPHPRGSGEGQGQI |
| S | 0.999983 | 532 | 0.618723 | 0.002286 | 0.188766 | 1.246579 | Q03517 | Secretogra | Scg2 | KRVPSPVSSEDDLQE |
| S | 1 | 141 | 0.051935 | 0.019886 | 1.76949 | 2.058841 | P12961 | Neuroendo | Scg5 | APDTAEFSREFQLDQ |
| S | 1 | 137 | 0.883993 | 0.00681 | -0.393058 | -4.213781 | O08547 | Vesicle-tra | Sec22b | RARRNLGSINTELQD |
| S | 0.999998 | 735 | 0.026823 | 0.222889 | 2.874669 | 1.268205 | G3X928 | SEC23-inte | Sec23ip | PKTKEMASPSSESNE |
| S | 1 | 28 | 0.398266 | 0.011534 | -0.28499 | -0.881231 | P28661 | Septin-4 | Sept4 | IKHFLEDSSDDAELS |
| S | 1 | 29 | 0.398266 | 0.011534 | -0.28499 | -0.881231 | P28661 | Septin-4 | Sept4 | KHFLEDSSDDAELSK |
| S | 1 | 287 | 1.07E-08 | 0.032423 | 7.473548 | 0.288583 | Q8VD37-8 | SH3-contai | Sgip1 | AKIEKLPSISDLDSI |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 300 | 1.07E-08 | 0.032423 | 7.473548 | 0.288583 | Q8VD37-8 | SH3-contai | Sgip1 | SIFGPVLSPKSVAVN |
| S | 0.999699 | 633 | 0.01484 | 0.020999 | 1.122447 | 0.919307 | Q8BPQ7 | Small G prc | Sgsm1 | AKCSSGASLDSHLHR |
| T | 0.999824 | 647 | 0.046262 | 0.099267 | 1.302444 | 0.917567 | Q8BPQ7 | Small G prc | Sgsm1 | RMLHRDSTISNESSQ |
| S | 0.999389 | 1094 | 0.283523 | 0.021681 | 0.447969 | 0.966686 | D3Z5K8 | SH3 and m | Shank2 | RNSPAFLSTDLGDED |
| S | 1 | 533 | 0.024376 | 0.040479 | -0.743234 | -0.578994 | Q6P4S6 | Serine/thre | Sik3 | VTPVDEESSDGEPDQ |
| S | 1 | 534 | 0.024376 | 0.040479 | -0.743234 | -0.578994 | Q6P4S6 | Serine/thre | Sik3 | TPVDEESSDGEPDQE |
| S | 1 | 1249 | 0.359962 | 0.046809 | 0.382759 | 0.76672 | Q8C0T5 | Signal-indu | Sipa1l1 | QDPVVHLSPNKQGHS |
| S | 0.998212 | 1905 | 0.013326 | 0.10387 | -2.5577 | -1.275462 | A2AQ25 | Sickle tail p | Skt;Etl4 | SSPPSPASPTSLNQG |
| S | 1 | 1044 | 0.986882 | 0.02703 | -0.048653 | -1.151783 | Q91V14 | Solute carr | Slc12a5 | AEKNKGPSPVSSEGI |
| S | 1 | 1047 | 0.986882 | 0.02703 | -0.048653 | -1.151783 | Q91V14 | Solute carr | Slc12a5 | NKGPSPVSSEGIKDF |
| S | 1 | 1048 | 0.986882 | 0.02703 | -0.048653 | -1.151783 | Q91V14 | Solute carr | Slc12a5 | KGPSPVSSEGIKDFF |
| S | 0.996488 | 548 | 0.046583 | 0.202452 | -1.979494 | -1.062594 | Q9Z0E8 | Solute carr | Slc22a5 | MQKDGEESPTVLKST |
| S | 0.996307 | 297 | 0.417468 | 0.030753 | 0.502984 | 1.24989 | Q8CGA3 | Large neut | Slc43a2 | EGHKLCLSTVDLEVK |
| S | 0.9996 | 297 | 0.012913 | 0.030779 | 0.861777 | 0.61631 | Q5DTL9 | Sodium-dri | Slc4a10 | GQQKGHTSPCGMKQR |
| S | 1 | 600 | 0.129539 | 0.047244 | -0.70392 | -0.873254 | P28571-1 | Sodium- ar | Slc6a9 | YAPTTTPSPEDGFEV |
| T | 0.806717 | 597 | 0.129539 | 0.047244 | -0.70392 | -0.873254 | P28571-1 | Sodium- ar | Slc6a9 | TGRYAPTTTPSPEDG |
| T | 0.997075 | 598 | 0.129539 | 0.047244 | -0.70392 | -0.873254 | P28571-1 | Sodium- ar | Slc6a9 | GRYAPTTTPSPEDGF |
| T | 0.872036 | 607 | 0.037168 | 0.021293 | 1.618544 | 1.681055 | Q61165 | Sodium/hy | Slc9a1 | KIPSAVSTVSMQNIH |
| S | 1 | 117 | 0.996603 | 0.043938 | -0.021403 | -0.874207 | P70441 | Na(+)/H(+) | Slc9a3r1 | LLRPQEKSEQAEPPA |
| S | 1 | 465 | 0.351784 | 0.010683 | -0.469106 | -1.364807 | Q3URD3 | Sarcolemm | Slmap | KAKESDLSDTLSPSK |
| S | 1 | 469 | 0.351784 | 0.010683 | -0.469106 | -1.364807 | Q3URD3 | Sarcolemm | Slmap | SDLSDTLSPSKEKSS |
| T | 0.999998 | 467 | 0.351784 | 0.010683 | -0.469106 | -1.364807 | Q3URD3 | Sarcolemm | Slmap | KESDLSDTLSPSKEK |
| S | 0.999996 | 999 | 0.125516 | 0.021415 | 0.794074 | 1.208753 | Q8CH25 | SAFB-like tı | Sltm | TQHSSTASPVNRIVQ |
| T | 0.998003 | 315 | 0.913464 | 0.000331 | -0.235345 | -5.733885 | E9Q9A3 | | Snap91 | TVTSPNSTPAKTIDT |
| T | 0.998003 | 317 | 0.761679 | 3.18E-05 | -0.235345 | -5.209688 | Q61548 | Clathrin co | Snap91 | TVTSPNSTPAKTIDT |
| S | 1 | 204 | 0.112368 | 0.011922 | 2.841628 | 4.815623 | Q80U23 | Syntaphilin | Snph | TGESAGGSPARSLTR |
| S | 0.982977 | 49 | 0.762828 | 0.012765 | 0.124158 | 0.755819 | Q80U23 | Syntaphilin | Snph | SCKGSDSSPTPRRSM |
| S | 1 | 97 | 0.158499 | 0.009753 | 0.358143 | 0.72468 | Q9CWK8 | Sorting nex | Snx2 | LILSSEPSPAVTPVT |
| S | 1 | 745 | 0.046091 | 0.354602 | 2.331155 | 0.935459 | Q3UTJ2-2 | Sorbin and | Sorbs2 | LCPKRRFSIESLLEE |
| S | 1 | 748 | 0.046091 | 0.354602 | 2.331155 | 0.935459 | Q3UTJ2-2 | Sorbin and | Sorbs2 | KRRFSIESLLEEETQ |
| S | 0.999998 | 1120 | 0.875058 | 0.016301 | 0.219976 | -1.832231 | Q62245 | Son of seve | Sos1 | PFHSRSASVSSISLS |
| S | 1 | 565 | 0.168292 | 0.00994 | 0.454612 | -0.938004 | D3YTL8 | Protein spiı | Spire1 | RFSTKSRSVDKSDEE |
| S | 1 | 563 | 0.582765 | 0.02743 | -0.314033 | -1.071047 | D3YTL8 | Protein spiı | Spire1 | IARFSTKSRSVDKSD |
| S | 1 | 565 | 0.582765 | 0.02743 | -0.314033 | -1.071047 | D3YTL8 | Protein spiı | Spire1 | RFSTKSRSVDKSDEE |
| S | 1 | 569 | 0.582765 | 0.02743 | -0.314033 | -1.071047 | D3YTL8 | Protein spiı | Spire1 | KSRSVDKSDEELQFP |
| S | 1 | 2162 | 0.004966 | 0.130862 | -1.119149 | -0.40651 | Q3UGX2 | | Sptb | KVLDTPLSEGDEPTT |
| T | 1 | 2159 | 0.046797 | 0.701104 | -1.891525 | -0.40651 | Q3UGX2 | | Sptb | PLFKVLDTPLSEGDE |
| S | 0.991008 | 2339 | 0.357539 | 0.017548 | 0.337139 | 0.876193 | Q62261 | Spectrin be | Sptbn1 | VVTITSESSPGKREK |
| S | 0.999696 | 2340 | 0.196545 | 0.004205 | 0.295451 | 0.795277 | Q62261 | Spectrin be | Sptbn1 | VTITSESSPGKREKD |
| T | 0.999999 | 2319 | 0.040994 | 0.669958 | -1.701303 | 0.376327 | Q62261 | Spectrin be | Sptbn1 | TSASTQSTPASSRAQ |
| S | 0.999999 | 546 | 0.05173 | 0.004674 | -0.529091 | -0.871503 | B1AQX9 | | Srcin1 | RQSFRKDSGSSSVFA |
| S | 1 | 555 | 0.05173 | 0.004674 | -0.529091 | -0.871503 | B1AQX9 | | Srcin1 | SSSVFAESPGGKARS |
| S | 1 | 858 | 0.881874 | 0.040234 | -0.230001 | -1.554826 | Q812A2 | SLIT-ROBO | Srgap3 | MGRVRLRSDGAAIPR |
| S | 1 | 919 | 0.248019 | 0.026164 | 0.628653 | 1.206971 | Q812A2 | SLIT-ROBO | Srgap3 | RRMATFGSAGSINYP |
| S | 1 | 868 | 0.998547 | 0.020414 | -0.023242 | -1.788076 | Q812A2 | SLIT-ROBO | Srgap3 | AAIPRRRSGGDTHSP |
| S | 0.973273 | 1007 | 0.063492 | 0.009375 | 0.720467 | 1.072723 | Q812A2 | SLIT-ROBO | Srgap3 | NPPGPISSEPASPLH |
| S | 0.999999 | 487 | 0.986666 | 0.001599 | 0.016372 | -0.749704 | O54781 | SRSF prote | Srpk2 | HDRSRTVSASSTGDL |
| S | 0.995436 | 490 | 0.986666 | 0.001599 | 0.016372 | -0.749704 | O54781 | SRSF prote | Srpk2 | SRTVSASSTGDLPKT |
| S | 1 | 387 | 0.58295 | 0.023595 | -0.424391 | -1.506797 | E9PUK6 | Serine/argi | Srrm1 | PRKTRRLSPSASPPR |
| S | 1 | 389 | 0.58295 | 0.023595 | -0.424391 | -1.506797 | E9PUK6 | Serine/argi | Srrm1 | KTRRLSPSASPPRRR |
| S | 1 | 391 | 0.58295 | 0.023595 | -0.424391 | -1.506797 | E9PUK6 | Serine/argi | Srrm1 | RRLSPSASPPRRRHR |
| S | 0.999999 | 2404 | 0.132163 | 0.024231 | 0.619485 | 0.930625 | Q8BTI8 | Serine/argi | Srrm2 | PAQDRPRSPVPSAFS |
| S | 1 | 1097 | 0.042947 | 0.529392 | -1.994173 | -0.582171 | Q8BTI8 | Serine/argi | Srrm2 | PKLKSGMSPEQSKTK |
| S | 1 | 1849 | 0.468473 | 0.003378 | -0.752387 | -3.487945 | Q8BTI8 | Serine/argi | Srrm2 | RRSRSRTSPVSRRRS |
| S | 1 | 349 | 0.069624 | 0.000455 | -0.353475 | -1.058691 | Q8BTI8 | Serine/argi | Srrm2 | EKSAVRPSPSPERSS |
| S | 1 | 351 | 0.069624 | 0.000455 | -0.353475 | -1.058691 | Q8BTI8 | Serine/argi | Srrm2 | SAVRPSPSPERSSTG |
| S | 1 | 2644 | 0.627467 | 0.029261 | -0.756146 | -2.756696 | Q8BTI8 | Serine/argi | Srrm2 | DSLRDSRSLSYSPVE |
| S | 1 | 2646 | 0.627467 | 0.029261 | -0.756146 | -2.756696 | Q8BTI8 | Serine/argi | Srrm2 | LRDSRSLSYSPVERR |
| S | 1 | 2648 | 0.627467 | 0.029261 | -0.756146 | -2.756696 | Q8BTI8 | Serine/argi | Srrm2 | DSRSLSYSPVERRQP |
| S | 1 | 2019 | 0.987698 | 0.027094 | 0.045039 | -1.100719 | Q8BTI8 | Serine/argi | Srrm2 | RAARGKRSLTRSPPA |
| S | 1 | 2023 | 0.987698 | 0.027094 | 0.045039 | -1.100719 | Q8BTI8 | Serine/argi | Srrm2 | GKRSLTRSPPAIRRR |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 433 | 0.886738 | 0.02712 | -0.228605 | -1.762379 | Q8BTI8 | Serine/argi | Srrm2 | TKGSRHASSSPESLK |
| S | 1 | 434 | 0.879325 | 0.024433 | -0.239487 | -1.832664 | Q8BTI8 | Serine/argi | Srrm2 | KGSRHASSSPESLKP |
| S | 1 | 435 | 0.87085 | 0.026834 | -0.247862 | -1.781636 | Q8BTI8 | Serine/argi | Srrm2 | GSRHASSSPESLKPT |
| S | 1 | 438 | 0.550068 | 0.020482 | -0.821976 | -2.853804 | Q8BTI8 | Serine/argi | Srrm2 | HASSSPESLKPTPAP |
| T | 1 | 2021 | 0.987698 | 0.027094 | 0.045039 | -1.100719 | Q8BTI8 | Serine/argi | Srrm2 | ARGKRSLTRSPPAIR |
| S | 1 | 738 | 0.19466 | 0.006086 | 0.824614 | 2.030467 | Q922B9 | Sperm-spe | Ssfa2 | YPLRRSQSLPTTLLS |
| S | 1 | 383 | 0.047974 | 0.757173 | 0.959407 | 0.181753 | Q9Z1W9 | STE20/SPS | Stk39 | VRRVPGSSGHLHKTE |
| S | 0.999934 | 328 | 0.036537 | 0.179094 | -3.868768 | -2.04282 | Q8C9H6 | Striatin-int | Strip2 | VKSMRAASPPSYTLD |
| S | 1 | 339 | 0.036978 | 0.179778 | -4.551043 | -2.407294 | Q8C9H6 | Striatin-int | Strip2 | YTLDLGESQLAPPPS |
| S | 0.999653 | 782 | 0.523938 | 0.013654 | -1.056709 | -3.881923 | Q8K400 | Syntaxin-bi | Stxbp5 | SFSRSRSSSVTSIDK |
| S | 0.992883 | 733 | 0.047344 | 0.034204 | 0.980268 | 0.96114 | Q8CH09 | SURP and ( | Sugp2 | KPCPQPSSPGALGPS |
| S | 0.999704 | 510 | 0.153367 | 0.047086 | -3.985542 | -5.277621 | O88935 | Synapsin-1 | Syn1 | PLPQRLPSPTAAPQQ |
| S | 1 | 427 | 0.337897 | 0.046666 | -0.389659 | -0.751887 | O88935 | Synapsin-1 | Syn1 | RQPQRDASPGRGSHS |
| S | 1 | 426 | 0.017808 | 0.20068 | 0.888394 | 0.369343 | Q64332 | Synapsin-2 | Syn2 | LSRTPALSPQRPLTT |
| T | 1 | 422 | 0.025059 | 0.567785 | 1.121427 | 0.263877 | Q64332 | Synapsin-2 | Syn2 | MNQLLSRTPALSPQR |
| S | 1 | 461 | 0.002743 | 0.096373 | -4.637376 | -1.641812 | Q8JZP2 | Synapsin-3 | Syn3 | SPSQQRLSPQGQQPV |
| S | 0.999498 | 544 | 0.004533 | 0.866269 | -2.432484 | 0.178838 | Q8JZP2 | Synapsin-3 | Syn3 | KSQSLTNSLSTSDTS |
| S | 0.999443 | 205 | 0.023504 | 0.555461 | 0.798449 | 0.188861 | Q9CXF4 | TBC1 doma | Tbc1d15 | QNKSLSQSFENLLDE |
| S | 1 | 19 | 0.047271 | 0.205072 | -2.453907 | 1.315399 | P24529 | Tyrosine 3- | Th | KGFRRAVSEQDTKQA |
| S | 0.998026 | 1417 | 0.15765 | 0.009819 | -1.695545 | -3.41796 | B1AZI6 | THO compl | Thoc2 | RKIDSHPSPSHSSTV |
| S | 0.999999 | 679 | 0.061736 | 0.020507 | 0.585379 | 0.711713 | Q569Z6 | Thyroid ho | Thrap3 | IHRRIDISPSTFRKH |
| S | 1 | 378 | 0.035198 | 0.108063 | -4.953066 | -3.136538 | Q9Z0U1 | Tight juncti | Tjp2 | NIPALNDSDSEVEDI |
| S | 0.998773 | 206 | 0.000768 | 0.028642 | -2.159645 | -0.832663 | Q62441 | Transducin | Tle4 | RDSIKSSSVSPSASF |
| S | 0.999969 | 208 | 0.00008 | 0.018477 | -3.085321 | -0.832663 | Q62441 | Transducin | Tle4 | SIKSSSVSPSASFRG |
| S | 1 | 21 | 0.689912 | 0.03193 | 0.345499 | 1.39722 | Q3UHI4 | Protein TM | Tmed8 | SPAARRGSAGGVGDR |
| S | 0.999999 | 1437 | 0.102703 | 0.037915 | 1.114128 | 1.354536 | P58871 | 182 kDa ta | Tnks1bp1 | PSSCLTRSPPSGSQS |
| S | 0.999976 | 462 | 0.045952 | 0.335736 | 1.010494 | 0.418659 | O88746 | Target of M | Tom1 | DRLPNLASPSAEGPP |
| S | 0.99999 | 1460 | 0.047028 | 0.020973 | 1.000233 | 1.115103 | Q64511 | DNA topois | Top2b | SNEEDTASVFAPSFG |
| S | 1 | 1509 | 0.366951 | 0.010837 | -0.415823 | -1.237536 | Q64511 | DNA topois | Top2b | KIVETINSDSDSEFG |
| S | 1 | 1511 | 0.366951 | 0.010837 | -0.415823 | -1.237536 | Q64511 | DNA topois | Top2b | VETINSDSDSEFGIP |
| S | 1 | 1513 | 0.366951 | 0.010837 | -0.415823 | -1.237536 | Q64511 | DNA topois | Top2b | TINSDSDSEFGIPKK |
| S | 0.999968 | 140 | 0.015977 | 0.797889 | -0.915349 | -0.115377 | Q921T2 | Torsin-1A-i | Tor1aip1 | HSQQPQLSPATSGRG |
| S | 0.997563 | 697 | 0.827662 | 0.006655 | 0.175929 | 1.51575 | Q8CG79 | Apoptosis- | Tp53bp2;T | ERIPRPLSPTKLLPF |
| S | 0.999989 | 166 | 0.889987 | 0.046436 | 0.12112 | -0.817357 | A2AUD5 | | Tpd52l2 | RAHPLSQSFSSYSIR |
| S | 0.997304 | 168 | 0.564777 | 0.02122 | 0.214893 | -0.758947 | A2AUD5 | | Tpd52l2 | HPLSQSFSSYSIRHS |
| S | 1 | 31 | 1.71E-06 | 0.000001 | 7.589765 | 7.56014 | Q7TQD2 | Tubulin pol | Tppp | ARAAKRLSLESEGAN |
| S | 1 | 34 | 1.71E-06 | 0.000001 | 7.589765 | 7.56014 | Q7TQD2 | Tubulin pol | Tppp | AKRLSLESEGANEGA |
| S | 0.968381 | 708 | 0.048706 | 0.019689 | 2.711464 | 3.103892 | Q3TLI0 | Trafficking | Trappc10 | MLLRRQESGSSLEPP |
| S | 1 | 440 | 6.97E-05 | 0.329362 | -4.890488 | -0.46994 | Q9ESN6 | Tripartite n | Trim2 | GVKRRVKSPGSGHVK |
| S | 1 | 443 | 3.89E-05 | 0.409723 | -6.323593 | -0.46994 | Q9ESN6 | Tripartite n | Trim2 | RRVKSPGSGHVKQKA |
| S | 0.999982 | 512 | 0.833633 | 0.007337 | 0.338394 | 1.51029 | Q9EP53 | Hamartin | Tsc1 | YRDSLSGSQRKTHSA |
| S | 0.998021 | 519 | 0.485779 | 0.012437 | -0.200951 | -0.707397 | Q6P5F7 | Protein twe | Ttyh3 | TSQPRPDSSGSGH__ |
| S | 0.96764 | 66 | 0.2765 | 0.02056 | 0.880198 | 1.900669 | E9QMD2 | | Ube2ql1 | PGGSGDASPGPGKGK |
| S | 1 | 36 | 0.159154 | 0.025227 | 0.54227 | 0.86573 | Q99PL6 | UBX domai | Ubxn6 | EKTTKGKSPQLALRQ |
| S | 1 | 668 | 0.083342 | 0.044022 | 0.96663 | 1.050327 | Q7TMI3 | E3 ubiquiti | Uhrf2 | EATKRPASDDECPGD |
| S | 0.99999 | 1151 | 0.020366 | 0.013538 | 1.057293 | 1.048217 | E9Q6Y8 | Ubiquitin c | Usp31 | RSLSREGSRQSLGSD |
| S | 0.936641 | 796 | 0.034421 | 0.964351 | -2.32391 | -0.139531 | E9Q6Y8 | Ubiquitin c | Usp31 | SKQASVTSAASSRRT |
| S | 1 | 751 | 0.018965 | 0.027735 | -0.85043 | -0.688737 | P56399 | Ubiquitin c | Usp5 | ALRATNNSLERAVDW |
| S | 0.997669 | 253 | 0.601617 | 0.013865 | 0.171559 | 0.72183 | Q60932 | Voltage-de | Vdac1 | FSAKVNNSSLIGLGY |
| S | 1 | 310 | 0.01993 | 0.017248 | 5.21533 | 4.839778 | Q8R5H6 | Wiskott-Al | Wasf1 | LIENRPQSPAAGRTP |
| S | 1 | 312 | 0.856589 | 0.039958 | 0.152028 | 0.92381 | Q8CGF6 | WD repeat | Wdr47 | ADAYMTRSLNPALDG |
| T | 1 | 689 | 0.10385 | 0.037322 | 1.86826 | 2.290177 | Q9Z0U0 | Xenotropic | Xpr1 | TKVLIEDTDDEANT_ |
| S | 1 | 907 | 0.524909 | 0.037858 | -1.159316 | -3.266578 | E9Q784 | | Zc3h13 | KRYRNEGSPSPRQSP |
| S | 1 | 515 | 0.083592 | 0.008659 | -0.519121 | -0.859377 | Q8BJ05 | Zinc finger | Zc3h14 | VQPDKPASPKFIVTL |
| S | 1 | 336 | 0.529125 | 0.024031 | 0.259026 | 0.831513 | Q62523 | Zyxin | Zyx | QNQNQVRSPGGPGPL |

# HIPPO

| Amino acid | Localizatio | Position | nalf_pvalu | U50_pval | log2_nalf_ | log2_U50_ | Protein | Protein na | Gene name | Short sequence window |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 507 | 0.023551 | 0.058599 | 1.071703 | 0.742661 | E9Q3M9 | | 2010300C0 | APPERDMSPPEGDVA |
| S | 1 | 4 | 0.023551 | 0.058599 | 1.071703 | 0.742661 | F7B0R9 | | 2010300C0 | ____XDMSPPEGDVA |
| S | 0.99993 | 211 | 0.052399 | 0.00265 | 0.625564 | 1.175416 | Q8R2R3 | Alpha- and | Aagab | HSEQQEPSPTAERTE |
| S | 0.959734 | 13 | 0.998675 | 0.020111 | 0.034752 | -2.810459 | Q3UHJ0 | AP2-associ | Aak1 | DSRREQGSSGLGSGS |
| S | 0.952726 | 795 | 0.327731 | 0.018134 | 1.198427 | 2.932335 | Q3UHJ0 | AP2-associ | Aak1 | KLIEGLKSPDTSLLL |
| S | 0.986558 | 676 | 0.009228 | 0.980719 | -5.667344 | 0.17766 | Q3UHJ0 | AP2-associ | Aak1 | ATTTPSGSPRTSQQN |
| S | 0.999944 | 411 | 0.031443 | 0.543146 | 1.177062 | -0.307536 | Q8K4G5 | Actin-bindi | Ablim1 | PGSSIPGSPGHTIYA |
| T | 0.99853 | 378 | 0.006104 | 0.341777 | -3.30833 | 0.810726 | Q8BL65 | Actin-bindi | Ablim2 | SVSLGHYTPTSRSPQ |
| S | 0.999999 | 444 | 0.257879 | 0.025647 | 2.156517 | 4.242831 | Q7TQI7 | Ankyrin re | Abtb2 | RRSPTVDSGDIRQAA |
| S | 1 | 79 | 0.004378 | 0.000201 | -0.721857 | -1.2534 | Q5SWU9 | Acetyl-CoA | Acaca | FHMRSSMSGLHLVKQ |
| S | 1 | 413 | 0.012723 | 0.065013 | -2.32527 | -1.335597 | Q9JIX8 | Apoptotic | Acin1 | LQPEQIVSEEETPPP |
| S | 1 | 455 | 0.044405 | 0.011029 | 0.615433 | 0.792484 | Q3V117 | ATP-citrate | Acly | PAPSRTASFSESRAD |
| S | 1 | 355 | 0.017798 | 0.00459 | 0.763544 | 0.944843 | Q9QYC0 | Alpha-add | Add1 | KYKAKSRSPGTPAGE |
| T | 1 | 358 | 0.096041 | 0.026926 | 0.589589 | 0.76916 | Q9QYC0 | Alpha-add | Add1 | AKSRSPGTPAGEGSG |
| S | 0.999629 | 688 | 0.049322 | 0.245845 | -4.13552 | 2.06406 | Q9QYB8 | Beta-addu | Add2 | DKTESVTSGPLSPEG |
| T | 0.996084 | 668 | 0.054053 | 0.049133 | 2.831837 | 2.605137 | Q9QYB5 | Gamma-ad | Add3 | TIKSPERTEEVLSPD |
| S | 1 | 1052 | 0.030635 | 0.036966 | 1.04944 | 0.891416 | Q9ESC8 | AF4/FMR2 | Aff4 | SKAVGMPSPVSPKLS |
| S | 1 | 1351 | 0.00099 | 0.963857 | -1.941494 | -0.050827 | Q9WTQ5 | A-kinase a | Akap12 | ERGKALGSLEGSPSL |
| S | 1 | 87 | 0.084643 | 0.043857 | -3.713123 | -4.05951 | Q9DBT5 | AMP deam | Ampd2 | QRLERQISQDVKLEP |
| S | 1 | 1839 | 0.391923 | 0.037003 | 2.127355 | 4.811512 | S4R291 | Ankyrin-2 | Ank2 | SGKPEKHSPGSPSTK |
| S | 0.999991 | 1842 | 0.279301 | 0.024114 | -1.060146 | -2.207697 | S4R291 | Ankyrin-2 | Ank2 | PEKHSPGSPSTKNER |
| S | 0.999997 | 3338 | 0.036172 | 0.167253 | 0.701527 | 0.37992 | S4R291 | Ankyrin-2 | Ank2 | APDGRSKSESDASSL |
| S | 1 | 2491 | 0.034768 | 0.297514 | -1.659965 | -0.680511 | S4R291 | Ankyrin-2 | Ank2 | SSGKSPLSPDTPSSE |
| T | 1 | 2772 | 0.034178 | 0.022113 | 1.160325 | 1.16597 | S4R291 | Ankyrin-2 | Ank2 | DSLAHQDTCENDREE |
| S | 0.999988 | 460 | 0.146417 | 0.021868 | -0.915137 | -1.468006 | B2RW11 | | Ankrd34a | PPSGAPGSPRTKRKL |
| S | 0.999958 | 665 | 0.018508 | 0.453584 | -1.889969 | -0.500984 | Q6PB70 | Anoctamin | Ano8 | EPEGPPGSPGPEPQT |
| S | 0.5 | 518 | 0.049953 | 0.025221 | -0.71204 | -0.769878 | P17426 | AP-2 comp | Ap2a1 | IAGDPRSSPPVQFSL |
| S | 0.999753 | 481 | 0.046697 | 0.026207 | 0.841238 | 0.882877 | P98084 | Amyloid b | Apba2 | RRMPRSASQDCIETT |
| S | 1 | 276 | 0.009347 | 0.005301 | 0.966607 | 0.98757 | P55088 | Aquaporin- | Aqp4 | AAQQTKGSYMEVEDN |
| S | 1 | 276 | 0.054287 | 0.016915 | -3.763118 | -4.622976 | A2A5R2 | Brefeldin A | Arfgef2 | EAPRERGSPVSGRAE |
| S | 0.999998 | 199 | 0.034233 | 0.008076 | 0.743199 | 0.958467 | Q8C0D4 | Rho GTPas | Arhgap12 | SQEQSCDSAGEGSER |
| S | 0.999993 | 1089 | 0.540368 | 0.023785 | 1.071429 | 3.517325 | Q6DFV3 | Rho GTPas | Arhgap21 | KSEPKTQSPHSPKEE |
| S | 1 | 1092 | 0.212794 | 0.017479 | 2.095154 | 4.157474 | Q6DFV3 | Rho GTPas | Arhgap21 | PKTQSPHSPKEESER |
| S | 1 | 968 | 0.016204 | 0.981027 | -1.92092 | 0.068558 | E9PYT0 | Rho GTPas | Arhgap5 | SEDVFLPSPRDCFPY |
| S | 1 | 931 | 0.018471 | 0.006701 | 0.751854 | 0.860599 | Q60875 | Rho guanin | Arhgef2 | REAQELGSPEDRLQD |
| S | 1 | 639 | 0.022061 | 0.010775 | 3.098273 | 3.3159 | Q8K4I3 | Rho guanin | Arhgef6 | RKTERKASEEEYVIR |
| S | 0.999426 | 408 | 0.062379 | 0.018072 | 1.067205 | 1.34445 | Q9DCB4 | cAMP-regu | Arpp21 | GKLSKTGSESSSSAG |
| S | 0.994467 | 46 | 0.015507 | 0.132835 | 6.57646 | 3.117704 | Q8BHE3 | Caytaxin | Atcay | GAVEDSSSPPSTLNL |
| S | 1 | 561 | 0.060382 | 0.008609 | -0.55929 | -0.836916 | P50516 | V-type pro | Atp6v1a | AVETTAQSDNKITWS |
| S | 0.999895 | 1223 | 0.031499 | 0.03998 | 0.83171 | 0.696356 | Q61687 | Transcripti | Atrx | SHTGFCQSSGDEALS |
| S | 0.999885 | 1224 | 0.031499 | 0.03998 | 0.83171 | 0.696356 | Q61687 | Transcripti | Atrx | HTGFCQSSGDEALSK |
| S | 1 | 128 | 0.982217 | 0.019373 | -0.042061 | -0.931133 | Q3U9H3 | Bcl2-associ | Bad | KGLPRPKSAGTATQM |
| S | 1 | 1269 | 0.028386 | 0.075396 | 0.72087 | 0.485426 | Q8CGM1 | Brain-speci | Bai2;Adgrb | TGTLSRLSLDEDEEP |
| S | 0.999834 | 546 | 0.039723 | 0.185048 | 2.413107 | 1.286599 | Q61361 | Brevican c | Bcan | EVGGETGSPELSGVP |
| S | 0.941461 | 414 | 0.009554 | 0.617384 | -3.983883 | -0.67152 | Q61361 | Brevican c | Bcan | EDGGGGSSTPEDPAE |
| S | 0.991641 | 497 | 0.03744 | 0.48974 | 1.082805 | 0.325613 | Q80YN3 | Breast carc | Bcas1 | LRQMSVRSSEGIPRS |
| S | 0.985049 | 498 | 0.031303 | 0.299531 | 0.820446 | 0.325613 | Q80YN3 | Breast carc | Bcas1 | RQMSVRSSEGIPRSE |
| S | 0.98754 | 686 | 0.021081 | 0.013171 | -2.342819 | -2.359435 | Q9D219 | B-cell CLL/l | Bcl9 | IPVEGPLSPSRGDFP |
| S | 1 | 267 | 0.158655 | 0.044762 | 0.621396 | 0.846204 | Q8K019 | Bcl-2-assoc | Bclaf1 | HSHSIQHSPERSGSG |
| S | 1 | 135 | 0.089344 | 0.026065 | -0.887194 | -0.929527 | P28028 | Serine/thre | Braf | ASRNNPKSPQKPIVR |
| S | 1 | 552 | 0.608058 | 0.021437 | 0.310541 | -1.184387 | Q8CFK2 | Transcripti | Brf1 | LNSKGGGSPPRDDSQ |
| S | 1 | 384 | 0.356509 | 0.04755 | 0.483486 | 0.958363 | Q5RJI5 | Serine/thre | Brsk1 | PPRKRVDSPMLSRHG |
| S | 0.999798 | 432 | 0.592882 | 0.014412 | 0.519034 | -2.128147 | Q5RJI5 | Serine/thre | Brsk1 | QHSQRSRSVSGASTG |
| S | 0.762797 | 499 | 0.123091 | 0.030249 | 0.598505 | 0.825566 | Q5RJI5 | Serine/thre | Brsk1 | PPPPSARSTPLPGPP |
| S | 1 | 450 | 0.092076 | 0.008221 | -0.524227 | -0.907153 | Q5RJI5 | Serine/thre | Brsk1 | SPLSSPRSPVFSFSP |
| S | 0.999892 | 301 | 0.021717 | 0.00925 | 2.225422 | 2.460762 | O88737 | Protein bas | Bsn | PPEVGRVSPQPPLST |
| S | 0.999999 | 2578 | 0.056648 | 0.040216 | 0.759068 | 0.750076 | O88737 | Protein bas | Bsn | RDACEPESGPDPSTV |
| S | 0.717082 | 259 | 0.548291 | 0.019801 | 0.472686 | 1.650247 | Q7TPS5 | C2 domain- | C2cd5 | AAFLPACSSPSRELK |
| S | 0.999939 | 1742 | 0.009595 | 0.013405 | 2.890672 | 2.383558 | Q01815 | Voltage-de | Cacna1c | NNQADTESPSHEKLV |
| S | 0.983258 | 43 | 0.065186 | 0.026323 | 1.645447 | 1.905609 | Q8R0S4 | Voltage-de | Cacnb4 | DGSTTSTSFILRQGS |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 96 | 0.007281 | 0.083837 | 1.140867 | 0.52868 | Q80TJ1 | Calcium-de | Cadps | SPSPSVVSEKEKEEL |
| S | 0.999012 | 358 | 0.185108 | 0.026078 | 1.974028 | 3.323353 | Q5SVJ0 | Calcium/ca | Camk2b | GVKPQTNSTKNSSAI |
| S | 0.998992 | 371 | 0.809526 | 0.000976 | -0.47616 | -5.930677 | Q5SVI3 | | Camk2b | VDGIKESSDSTNTTI |
| S | 0.998992 | 332 | 0.846313 | 0.001348 | -0.47616 | -6.266922 | Q5SVI9 | | Camk2b | ADGVKESSDSTNTTI |
| S | 0.998992 | 395 | 0.82138 | 0.001045 | -0.47616 | -6.069335 | Q5SVJ0 | Calcium/ca | Camk2b | VDGIKESSDSTNTTI |
| T | 0.99992 | 370 | 0.034717 | 0.22122 | -2.061826 | -0.97886 | E9Q1T1 | Calcium/ca | Camk2d | ESTESSNTTIEDEDV |
| S | 0.837042 | 41 | 0.0091 | 0.004223 | 2.030858 | 2.171838 | F7A856 | | Camk2d | ALESTESSNTTIEDE |
| S | 0.808458 | 560 | 0.046956 | 0.466305 | -0.706751 | -0.235883 | A2AHC3 | Calmodulir | Camsap1 | SPQMPRTSPQAPGLV |
| S | 0.999951 | 1285 | 0.330568 | 0.038448 | -1.823339 | -3.670443 | Q8C1B1 | Calmodulir | Camsap2 | KRTPRSESVEGFLSP |
| S | 0.996915 | 1291 | 0.380781 | 0.005704 | -1.133948 | -4.021826 | Q8C1B1 | Calmodulir | Camsap2 | ESVEGFLSPSRCGSR |
| S | 1 | 334 | 0.049412 | 0.048451 | 1.426536 | 1.283268 | Q80VC9 | Calmodulir | Camsap3 | LPDGHAVSPRNTETV |
| S | 0.999982 | 1077 | 0.018821 | 0.244949 | -2.023403 | 0.778525 | Q80VC9 | Calmodulir | Camsap3 | RPTSRAPSPSGLMSP |
| S | 1 | 553 | 0.006274 | 0.574906 | -4.434162 | 0.732327 | P35564 | Calnexin | Canx | KLEEKQKSDAEEDGV |
| S | 1 | 563 | 0.006274 | 0.574906 | -4.434162 | 0.732327 | P35564 | Calnexin | Canx | EEDGVTGSQDEEDSK |
| S | 1 | 31 | 0.08531 | 0.018457 | 0.534838 | 0.740024 | Q9CR86 | Calcium-re | Carhsp1 | TPRTRDRSPSPLRGN |
| S | 1 | 33 | 0.08531 | 0.018457 | 0.534838 | 0.740024 | Q9CR86 | Calcium-re | Carhsp1 | RTRDRSPSPLRGNVV |
| S | 1 | 728 | 0.061361 | 0.032904 | 1.047071 | 1.12081 | Q6P9K8 | Caskin-1 | Caskin1 | PGSPMSRSQEYLLDE |
| S | 1 | 559 | 0.038598 | 0.088565 | 0.712413 | 0.495314 | Q8CI71 | Coiled-coil | Ccdc132 | SAYQDYDSDSDVPEE |
| S | 1 | 250 | 0.028185 | 0.141571 | -2.242117 | 1.211111 | Q5SP85 | Coiled-coil | Ccdc85a | HTKHRSTSPEHLHKP |
| S | 1 | 330 | 0.007446 | 0.054612 | 1.105898 | 0.588803 | Q5SP85 | Coiled-coil | Ccdc85a | HTRHSGGSPEHLQKH |
| S | 1 | 129 | 0.025118 | 0.017346 | 1.229759 | 1.210365 | Q8QZT2 | Centriole, c | Ccsap | KETDGAPSGPGPRQQ |
| S | 1 | 136 | 3.49E-05 | 0.068488 | -4.43249 | 0.700307 | Q9JM96 | Cdc42 effe | Cdc42ep4 | DSSKLPKSLSSSPVK |
| S | 0.999619 | 140 | 4.65E-06 | 0.024544 | -4.975846 | 0.700307 | Q9JM96 | Cdc42 effe | Cdc42ep4 | LPKSLSSSPVKKADA |
| S | 1 | 300 | 0.003678 | 0.001686 | 3.368344 | 3.581501 | Q14AX6-3 | Cyclin-depe | Cdk12 | PYSRRQRSVSPYSRR |
| S | 0.999994 | 302 | 0.010844 | 0.005033 | 2.974704 | 3.187861 | Q14AX6-3 | Cyclin-depe | Cdk12 | SRRQRSVSPYSRRRS |
| T | 1 | 871 | 0.15176 | 0.000867 | 0.482177 | 1.650986 | Q69ZA1 | Cyclin-depe | Cdk13 | SEESRPYTNKVITLW |
| S | 1 | 112 | 0.140791 | 0.017982 | 2.761641 | 4.58898 | O35495 | Cyclin-depe | Cdk14 | SSSAGKESPKVRRHS |
| S | 1 | 66 | 0.071408 | 0.01714 | 1.453141 | 1.934897 | Q04899 | Cyclin-depe | Cdk18 | RQNQRRFSMEDLNKR |
| S | 1 | 56 | 0.031923 | 0.05567 | 2.384585 | 1.820197 | P98191 | Phosphatid | Cds1 | DLDARGDSDVPEVPP |
| S | 1 | 1102 | 0.178173 | 0.02512 | 0.494068 | 0.82673 | Q6A065 | Centrosom | Cep170 | RARLGEASDSELADA |
| S | 0.999999 | 829 | 0.027339 | 0.317248 | 0.729871 | 0.270536 | Q6A065 | Centrosom | Cep170 | KSLVRQGSFTIDKPS |
| S | 1 | 33 | 0.002601 | 0.095874 | -1.919768 | -0.672855 | Q91VN4 | MICOS con | Chchd6 | QGIRLSESVVNRMKD |
| S | 1 | 342 | 0.030268 | 0.004045 | 0.645562 | 0.944791 | P16014 | Secretogra | Chgb | HLAHYRASEEEPEYG |
| S | 0.999716 | 194 | 0.040548 | 0.124265 | -5.699132 | -3.571921 | Q8CJ61 | CKLF-like M | Cmtm4 | YIRARTESRDVDSRP |
| S | 0.999998 | 27 | 0.25812 | 0.026023 | -1.366086 | -2.678583 | Q9DBC3 | Cap-specifi | Cmtr1 | GELARHLSSTSDDEP |
| S | 0.9996 | 22 | 0.131031 | 0.001929 | -1.877984 | 5.114119 | P16330 | 2',3'-cyclic- | Cnp | KLFFRKMSSSGAKEK |
| S | 0.999982 | 123 | 0.037566 | 0.038404 | 2.690849 | 2.391966 | Q9EQG9 | Collagen ty | Col4a3bp | KTESGYGSESSLRRH |
| S | 0.968484 | 261 | 0.020685 | 0.353271 | -6.30165 | -2.038086 | O88587 | Catechol O | Comt | VYQGPGSSPVKS___ |
| S | 1 | 62 | 0.03274 | 0.063433 | 1.919215 | 1.417915 | Q91X84 | CREB-regul | Crtc3 | LTQYHGGSLPNVSQL |
| S | 1 | 528 | 0.93497 | 0.000954 | 0.102585 | -2.326902 | E9QKH8 | Catenin de | Ctnnd2 | PEGTLARSPSIDSIQ |
| S | 1 | 970 | 0.064017 | 0.037619 | 1.747975 | 1.826577 | Q62018 | RNA polym | Ctr9 | PPKGEEGSEEEETEN |
| T | 0.99989 | 47 | 0.077819 | 0.008101 | 0.703127 | 1.155449 | Q9JHS9 | Spliceosom | Cwc15 | KIKYRQTTQDAPEEV |
| S | 1 | 116 | 0.007831 | 0.002844 | 1.020139 | 1.15066 | Q8R4T1 | Cystin-1 | Cys1 | ASEAPGNSPKRPEGQ |
| S | 1 | 978 | 0.030495 | 0.078169 | 0.854976 | 0.580219 | Q3UHC7 | Disabled h | Dab2ip | SSSSKGDSPELKPRA |
| S | 0.999331 | 137 | 0.088562 | 0.017561 | -2.359279 | -3.346957 | E9QNN1 | ATP-depen | Dhx9 | VESSGYGSPGPTWDR |
| S | 1 | 185 | 0.161747 | 0.040669 | 0.602574 | 0.849833 | Q6PFD5 | Disks large- | Dlgap3 | KLFAKSHSLEAPGKR |
| S | 0.999999 | 970 | 0.009041 | 0.122554 | -3.780975 | -1.61843 | B1AZP2-2 | Disks large- | Dlgap4 | AASVRQNSATESADS |
| S | 0.998603 | 92 | 0.16237 | 0.031784 | 0.577862 | 0.87405 | Q9WV69 | Dematin | Dmtn | SLSPKSTSPPPSPEV |
| S | 0.999999 | 96 | 0.140303 | 0.019067 | 0.466525 | 0.762713 | Q9WV69 | Dematin | Dmtn | KSTSPPPSPEVWAES |
| S | 1 | 473 | 0.004903 | 0.029051 | 0.890074 | 0.514021 | Q8BPN8 | DmX-like p | Dmxl2 | EDGEREGSPRTHPRP |
| S | 0.999883 | 851 | 0.000771 | 0.728306 | -4.135458 | 0.314247 | P39053-4 | Dynamin-1 | Dnm1 | PSRSGQASPSRPESP |
| S | 1 | 591 | 0.107619 | 0.029499 | 3.089475 | 4.090008 | Q66L44 | Protein Do | Dos | QQRGRQHSDPGGARA |
| S | 1 | 297 | 0.097545 | 0.021088 | 1.290369 | 1.804359 | Q66L44 | Protein Do | Dos | TRLRRHASLDGASPY |
| S | 1 | 537 | 0.031244 | 0.059824 | -4.502644 | -3.343619 | O08553 | Dihydropyr | Dpysl2 | PVRNLHQSGFSLSGA |
| T | 1 | 521 | 3.3E-06 | 0.372349 | -6.807012 | 0.327087 | O08553 | Dihydropyr | Dpysl2 | TPASSAKTSPAKQQA |
| S | 0.999992 | 534 | 0.033266 | 0.036369 | -1.192519 | -1.040673 | Q9EQF6 | Dihydropyr | Dpysl5 | DLHESSFSLSGSQID |
| S | 0.999875 | 538 | 0.996548 | 0.037686 | -0.064718 | -2.738684 | Q9EQF6 | Dihydropyr | Dpysl5 | SSFSLSGSQIDDHVP |
| S | 0.9966 | 516 | 0.011796 | 0.392553 | -1.331211 | -0.34968 | Q8R1Q8 | Cytoplasmi | Dync1li1 | VSPTTPTSPTEGEAS |
| S | 1 | 128 | 0.002914 | 0.001471 | 1.344159 | 1.397377 | Q91VK2 | Elongation | Eef1d | APQTQHVSPMRQVEP |
| S | 0.987009 | 220 | 0.017597 | 0.036586 | 1.089923 | 0.803017 | Q8BG67 | Protein EFF | Efr3a | SRLGPPSSPSAADKE |
| S | 1 | 262 | 0.640964 | 0.001023 | 0.26261 | 2.156653 | Q9DCH4 | Eukaryotic | Eif3f | LIMKTCFSPNRVIGL |

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|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 38 | 0.344327 | 0.046442 | 0.424062 | 0.828657 | Q61701 | ELAV-like p | Elavl4 | SNNRNCPSPMQTGAA |
| S | 1 | 737 | 0.011156 | 0.037729 | -0.938133 | 0.612063 | E9PV14 | | Epb4.1l1 | QTEARADSSDETDTS |
| S | 1 | 75 | 0.031098 | 0.087834 | 0.723056 | 0.474909 | A2AUK5 | Band 4.1-li | Epb4.1l1;E | YSEADGLSERTTPSK |
| S | 1 | 543 | 0.000988 | 0.361169 | -1.749927 | -0.276706 | O70318 | Band 4.1-li | Epb41l2 | SSKRVSRSLDGAPIG |
| S | 0.99719 | 302 | 0.005647 | 0.864747 | -2.314634 | 0.180125 | P70429 | Ena/VASP-l | Evl | QTEDPSTSPSPGTRA |
| S | 0.99986 | 278 | 0.904031 | 0.03251 | 0.248779 | -1.999417 | Q6NS82 | Protein FA | Fam134a | LAETESESEAELAGF |
| S | 0.99998 | 405 | 0.092557 | 0.012059 | 3.228845 | 5.104128 | Q9DBR2 | Protein FA | Fam13c | AVGPEPGSSGEETSD |
| S | 0.999908 | 406 | 0.305121 | 0.036449 | 1.949698 | 3.807331 | Q9DBR2 | Protein FA | Fam13c | VGPEPGSSGEETSDA |
| S | 1 | 630 | 0.000346 | 0.000727 | -0.96955 | -0.741526 | Q5XG69 | Soluble la | Fam169a | SAEKAVDSSSEEIEV |
| S | 1 | 631 | 0.000346 | 0.000727 | -0.96955 | -0.741526 | Q5XG69 | Soluble la | Fam169a | AEKAVDSSSEEIEVE |
| S | 1 | 785 | 0.089301 | 0.021056 | -0.646997 | -0.878607 | A2A699 | Protein FA | Fam171a2 | ASELRRDSLTSPEDE |
| S | 1 | 788 | 0.089301 | 0.021056 | -0.646997 | -0.878607 | A2A699 | Protein FA | Fam171a2 | LRRDSLTSPEDELGA |
| T | 1 | 787 | 0.089301 | 0.021056 | -0.646997 | -0.878607 | A2A699 | Protein FA | Fam171a2 | ELRRDSLTSPEDELG |
| S | 1 | 723 | 0.030417 | 0.162466 | -3.084577 | -1.611703 | Q6PGL7 | WASH com | Fam21 | PKVPLLFSDEEDSEV |
| T | 1 | 24 | 0.031539 | 0.054558 | 0.78434 | 0.600334 | F8VPU2 | FERM, Rho | Farp1 | PENSGISTLERGQKP |
| S | 1 | 171 | 0.000186 | 0.981919 | -5.199535 | 0.067227 | A2APV2 | Formin-like | Fmnl2 | KSKPWSRSIEDLHRG |
| S | 0.999974 | 270 | 0.573157 | 0.041197 | 0.496024 | 1.486557 | F6XM46 | FERM dom | Frmd5 | AGMVPSRSCPSITHG |
| S | 0.999999 | 2815 | 0.020748 | 0.398288 | -2.661656 | 0.797668 | E9Q8I9 | Protein fur | Fry | KATFAGGSRDGVITC |
| S | 0.999999 | 192 | 0.792906 | 0.031627 | -0.644098 | -3.371165 | P06837 | Neuromod | Gap43 | PPTETAESSQAEEEK |
| S | 0.999999 | 86 | 0.015227 | 0.714623 | -5.051829 | -0.78007 | P06837 | Neuromod | Gap43 | EKKEGDGSATTDAAP |
| S | 0.997092 | 110 | 0.006723 | 0.001552 | 1.85584 | 2.307354 | Q8CHY6 | Transcripti | Gatad2a | SDSEQPSSPRVNGLT |
| S | 0.999989 | 1786 | 0.648208 | 0.041876 | 0.536675 | 1.845662 | Q6DFZ1 | | Gbf1 | PSSSSPGSPMASSPS |
| S | 0.999202 | 1414 | 0.119186 | 0.04152 | 1.137751 | 1.420878 | E9PUU4 | | Gemin5 | RAPSQPPSPTREERN |
| S | 1 | 83 | 0.944662 | 0.043189 | 0.187948 | 1.87027 | Q99JP7 | Gamma-gl | Ggt7 | EMGSQDGSPLRETRK |
| S | 1 | 365 | 0.931438 | 0.016801 | -0.392493 | -4.490607 | P23242 | Gap juncti | Gja1 | IVDQRPSSRASSRAS |
| S | 0.999449 | 96 | 0.815887 | 0.040565 | -0.354604 | -1.85769 | Q8K3I9 | Glucocorti | Glcci1 | PGGARGPSPSSPTPP |
| S | 0.999998 | 8 | 0.046285 | 0.032613 | 3.278355 | 3.23541 | P63213 | Guanine n | Gng2 | MASNNTASIAQARKL |
| S | 0.999819 | 51 | 0.338031 | 0.049623 | -1.144683 | -2.170138 | P36916 | Guanine n | Gnl1 | REEQTDTSDGESVTH |
| S | 0.999999 | 338 | 0.014955 | 0.758684 | -4.052225 | 0.559799 | Q8BUV3 | Gephyrin; | Gphn | NILRASHSAVDITKV |
| S | 1 | 267 | 0.015025 | 0.051929 | -0.778065 | -0.49835 | P35802 | Neuronal n | Gpm6a | QELHDIHSTRSKERL |
| T | 1 | 268 | 0.015025 | 0.051929 | -0.778065 | -0.49835 | P35802 | Neuronal n | Gpm6a | ELHDIHSTRSKERLN |
| S | 1 | 622 | 0.03447 | 0.076796 | -3.35006 | -2.36432 | Q3UNH4 | G protein-r | Gprin1 | KADSASPSPRKAESQ |
| S | 0.997959 | 174 | 0.065733 | 0.015663 | 0.650067 | 0.862843 | Q80TI0-4 | GRAM dom | Gramd1b | ILRKRSRSPTPQNQD |
| T | 0.999962 | 200 | 0.010539 | 0.010497 | 0.717178 | 0.642084 | Q80TI0-4 | GRAM dom | Gramd1b | SSDKSPSTPEQGVQR |
| S | 1 | 2 | 0.044588 | 0.006521 | 1.606254 | 2.34638 | Q2NL51 | Glycogen s | Gsk3a | ______MSGGGPSGG |
| S | 1 | 580 | 0.105716 | 0.020761 | 0.548978 | 0.792363 | O08582 | GTP-bindin | Gtpbp1 | LLQTTNNSPMNSKPQ |
| S | 1 | 647 | 0.009193 | 0.004839 | 1.888618 | 1.962681 | Q9Z1E4 | Glycogen [ | Gys1 | ASVPPSPSLSRHSSP |
| S | 0.998862 | 5 | 0.035218 | 0.968604 | 2.842296 | -0.160881 | P10922 | Histone H1 | H1f0 | ___MTENSTSAPAAK |
| S | 1 | 81 | 0.022859 | 0.544626 | -1.959877 | -0.469139 | A8DUK4 | Hemoglobi | Hbbt1;Hbb | DGLNHLDSLKGTFAS |
| S | 1 | 842 | 0.01003 | 0.035066 | -0.736241 | -0.477772 | O88703 | Potassium/ | Hcn2 | PDRRDSASPGAASGL |
| S | 1 | 847 | 0.01003 | 0.035066 | -0.736241 | -0.477772 | O88703 | Potassium/ | Hcn2 | SASPGAASGLDPLDS |
| S | 1 | 394 | 0.037069 | 0.832899 | -3.016815 | -0.42447 | P70288 | Histone de | Hdac2 | EDAVHEDSGDEDGED |
| S | 0.999898 | 68 | 0.116053 | 0.023963 | 3.092815 | 4.444126 | Q8K4P8 | E3 ubiquiti | Hecw1 | ITIPRSTSDTDLVTS |
| S | 1 | 321 | 0.058578 | 0.024191 | 0.97875 | 1.121874 | Q640R3 | Hepatocyte | Hepacam | ILKDKDSSEPDENPA |
| S | 1 | 302 | 0.000111 | 0.000124 | 2.21475 | 1.934174 | Q8R1M0 | Embryonic | Hmces | PKKEVPDSPKKDASG |
| S | 0.998617 | 233 | 0.023356 | 0.337652 | -0.798957 | -0.274027 | Q9Z204-2 | Heterogen | Hnrnpc | EKSEEEQSSASVKKD |
| S | 0.99999 | 236 | 0.023356 | 0.337652 | -0.798957 | -0.274027 | Q9Z204-2 | Heterogen | Hnrnpc | EEEQSSASVKKDETN |
| S | 1 | 159 | 0.004232 | 0.001454 | 0.976594 | 1.107015 | Q99JP6-2 | Homer pro | Homer3 | EKLFRSQSADTPGPT |
| S | 1 | 112 | 0.051843 | 0.00043 | 1.357604 | 3.762679 | Q3TEA8 | Heterochr | Hp1bp3 | KEENNNKSAEEPKKD |
| T | 1 | 540 | 0.068508 | 0.024126 | 0.717548 | 0.863584 | Q61316 | Heat shock | Hspa4 | EQQQQPQTPAENKAE |
| S | 1 | 254 | 0.039187 | 0.185421 | -4.012726 | -2.129483 | P63017 | Heat shock | Hspa8 | RKHKKDISENKRAVR |
| S | 1 | 1853 | 0.772374 | 0.046519 | 0.17916 | 0.794526 | P42859 | Huntingtin | Htt | KSLNPQKSGEEEDSG |
| S | 0.999985 | 636 | 0.003928 | 0.00607 | -0.740924 | -0.59979 | Q8K3X4 | Interferon | Irf2bpl | TASARRNSSSPVSPA |
| S | 0.998238 | 638 | 0.003928 | 0.00607 | -0.740924 | -0.59979 | Q8K3X4 | Interferon | Irf2bpl | SARRNSSSPVSPASV |
| S | 1 | 641 | 0.003928 | 0.00607 | -0.740924 | -0.59979 | Q8K3X4 | Interferon | Irf2bpl | RNSSSPVSPASVPGQ |
| S | 0.999933 | 343 | 0.870215 | 0.005775 | -0.246469 | -2.579661 | P35569 | Insulin rece | Irs1 | SVDGSPVSPSTNRTH |
| S | 0.999963 | 303 | 0.000327 | 0.69024 | -5.518072 | -0.381477 | P81122 | Insulin rece | Irs2 | EFRPRSKSQSSGSSA |
| S | 0.999686 | 756 | 0.002 | 0.456971 | -3.008861 | -0.471289 | Q5DTX6 | Junctional | Jcad | LQGQTSLSPSRNSAF |
| S | 0.997127 | 172 | 0.003939 | 0.807341 | -1.535185 | 0.134906 | Q8K0T4 | Katanin p6 | Katnal1 | KNVQDGASDSEIPKF |
| S | 1 | 440 | 0.016029 | 0.022467 | -0.97697 | -0.801563 | P63141 | Potassium | Kcna2 | TSCPKIPSSPDLKKS |
| S | 1 | 441 | 0.016029 | 0.022467 | -0.97697 | -0.801563 | P63141 | Potassium | Kcna2 | SCPKIPSSPDLKKSR |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.999443 | 9 | 0.109993 | 0.031574 | 0.61053 | 0.799583 | P62482 | Voltage-ga | Kcnab2 | YPESTTGSPARLSLR |
| S | 0.999995 | 2603 | 0.408646 | 0.011995 | 0.460438 | -1.435202 | A2AAE1 | Uncharacte | Kiaa1109 | RYTAGSASPTPTFKT |
| S | 0.970831 | 607 | 0.065543 | 0.004132 | 0.561761 | 1.022146 | Q91YS4 | | Klc2 | DSRTLSSSSMDLSRR |
| S | 1 | 445 | 0.102358 | 0.007093 | 0.959357 | 1.781816 | Q91YS4 | Kinesin ligh | Klc2 | YKACKVDSPTVNTTL |
| S | 1 | 1160 | 0.187424 | 0.017073 | 0.444484 | 0.839394 | A2AFG7 | | L1cam | KEDTQVDSEARPMKD |
| S | 1 | 1166 | 0.187424 | 0.017073 | 0.444484 | 0.839394 | P11627 | Neural cell | L1cam | KEDTQVDSEARPMKD |
| S | 1 | 1522 | 0.84716 | 0.007493 | -0.12597 | -1.131197 | Q80TS3 | Latrophilin- | Lphn3;Adg | PPNKDGASPEGTSKG |
| S | 0.999465 | 1536 | 0.073447 | 0.006065 | -0.839038 | -1.448659 | Q80TS3 | Latrophilin- | Lphn3;Adg | GPAHLVTSL_______ |
| S | 0.995257 | 343 | 0.422738 | 0.043443 | -0.513613 | -1.169644 | Q7TPB0 | Lipid phosp | Lppr3 | PVAREKTSLGSLKRA |
| S | 0.997145 | 4452 | 0.029129 | 0.004731 | 0.579667 | 0.810154 | E9QA63 | Microtubul | Macf1 | KAMDATLSPTKTETV |
| T | 1 | 1045 | 0.131184 | 0.015322 | 0.566143 | 0.953801 | A2AGQ7 | | Madd | SPTENVNTPVGKDPG |
| S | 1 | 322 | 0.621223 | 0.047274 | 0.790875 | 2.491646 | Q9QYR6 | Microtubul | Map1a | HRADSKESLKAAPKT |
| S | 0.999698 | 2212 | 0.495388 | 0.008816 | 1.607631 | 6.251569 | Q9QYR6 | Microtubul | Map1a | PQLPSPSSPGAPLLS |
| S | 0.980162 | 852 | 0.006197 | 0.56667 | -3.03799 | -0.50781 | Q9QYR6 | Microtubul | Map1a | AEDQSVASLTAPQTE |
| S | 1 | 2267 | 0.02819 | 0.02086 | 0.85346 | 0.826287 | P14873 | Microtubul | Map1b | KSKPLAASPKPGALK |
| S | 1 | 2122 | 0.107332 | 0.036875 | 0.627079 | 0.780173 | P14873 | Microtubul | Map1b | SEKPLTQSGGAPPPS |
| S | 1 | 1497 | 0.024343 | 0.002865 | 0.664743 | 0.991887 | P14873 | Microtubul | Map1b | RKLGGDVSPTQIDVS |
| S | 1 | 1508 | 0.024343 | 0.002865 | 0.664743 | 0.991887 | P14873 | Microtubul | Map1b | IDVSQFGSFKEDTKM |
| S | 1 | 1768 | 0.003664 | 0.762229 | -3.448493 | -0.33869 | P14873 | Microtubul | Map1b | LASEKVQSLEGEKLS |
| S | 1 | 1352 | 0.021927 | 0.005012 | 0.677673 | 0.867076 | P20357 | Microtubul | Map2 | QAEPKDGSPDAPATP |
| S | 0.989397 | 476 | 0.035921 | 0.074035 | 0.863591 | 0.623712 | P20357 | Microtubul | Map2 | IQTSTEQSFSKEDQK |
| S | 1 | 1352 | 0.090164 | 0.020975 | -0.537002 | -0.7323 | P20357 | Microtubul | Map2 | QAEPKDGSPDAPATP |
| S | 0.999937 | 136 | 0.06415 | 0.02359 | -0.913287 | -1.08336 | P20357 | Microtubul | Map2 | ETANLPPSPPPSPAS |
| T | 1 | 1620 | 0.141072 | 0.035502 | 0.560634 | 0.77867 | P20357 | Microtubul | Map2 | YSSRTPGTPGTPSYP |
| T | 1 | 1623 | 0.141072 | 0.035502 | 0.560634 | 0.77867 | P20357 | Microtubul | Map2 | RTPGTPGTPSYPRTP |
| T | 1 | 1358 | 0.090164 | 0.020975 | -0.537002 | -0.7323 | P20357 | Microtubul | Map2 | GSPDAPATPEKEEVA |
| T | 0.687039 | 1594 | 0.992254 | 0.001554 | -0.096538 | 5.849223 | P20357 | Microtubul | Map2 | RRAGKSGTSTPTTPG |
| T | 0.987626 | 1164 | 0.013429 | 0.019002 | 2.755707 | 2.259056 | P20357 | Microtubul | Map2 | KKETSPETSLIQDEV |
| S | 0.888631 | 391 | 0.012768 | 0.016157 | -2.847166 | -2.401934 | P47809 | Dual specif | Map2k4 | DQMPATPSSPMYVD_ |
| S | 0.994743 | 900 | 0.017457 | 0.367394 | -1.492288 | -0.451045 | Q1HKZ5 | Mitogen-ac | Map3k13 | SSHSDGLSDKECAVR |
| S | 0.568219 | 540 | 0.043443 | 0.999619 | 1.375165 | -0.00898 | Q3U1V8 | Mitogen-ac | Map3k9 | KSLISNRSSPPASPT |
| S | 1 | 667 | 0.017215 | 0.078731 | -0.981239 | -0.572133 | P27546-3 | Microtubul | Map4 | PNKEPPPSPEKKAKP |
| T | 0.999582 | 658 | 0.017215 | 0.078731 | -0.981239 | -0.572133 | P27546-3 | Microtubul | Map4 | VTGNDITTPPNKEPP |
| S | 0.999985 | 611 | 0.241628 | 0.026798 | 0.516981 | 0.973927 | E9PVG7 | Mitogen-ac | Map4k4 | SPVSRSHSFSDPSPK |
| S | 0.999986 | 616 | 0.241628 | 0.026798 | 0.516981 | 0.973927 | E9PVG7 | Mitogen-ac | Map4k4 | SHSFSDPSPKFAHHH |
| S | 1 | 86 | 0.007022 | 0.006978 | 4.121856 | 3.692181 | Q7TSJ2 | Microtubul | Map6 | TGPAPGPSVDRETVA |
| T | 1 | 91 | 0.003819 | 0.003649 | 4.461083 | 4.031408 | Q7TSJ2 | Microtubul | Map6 | GPSVDRETVAAPGRS |
| S | 1 | 401 | 0.052416 | 0.041158 | 1.411954 | 1.35443 | A2AJI0 | MAP7 dom | Map7d1 | RKPGAGGSPALARRR |
| S | 1 | 315 | 0.004066 | 0.005397 | 2.108751 | 1.767916 | A2AG50 | MAP7 dom | Map7d2 | AASGGHGSPLRRCEP |
| S | 1 | 704 | 0.152961 | 0.024487 | -0.883124 | -1.398934 | A2A5Y6 | Microtubul | Mapt | GAEIVYKSPVVSGDT |
| S | 0.998794 | 50 | 3.14E-06 | 0.135636 | -3.536259 | 0.272043 | A2A5Y6 | Microtubul | Mapt | DGAEEPGSETSDAKS |
| S | 0.998794 | 50 | 0.000705 | 0.574937 | -2.669441 | 0.272043 | B1AQW6 | | Mapt | DGAEEPGSETSDAKS |
| S | 1 | 507 | 0.152042 | 0.033262 | 0.816818 | 1.188897 | A2A5Y6 | Microtubul | Mapt | GERSGYSSPGSPGTP |
| T | 1 | 513 | 0.025188 | 0.020683 | 1.006843 | 0.94809 | A2A5Y6 | Microtubul | Mapt | SSPGSPGTPGSRSRT |
| S | 1 | 619 | 0.188721 | 0.009988 | -0.522156 | -1.128624 | Q8K310 | Matrin-3 | Matr3 | TDAQKTESPAEGKEQ |
| S | 0.999669 | 154 | 0.013858 | 0.007763 | 1.08482 | 1.116061 | Q8R3C0 | Mini-chron | Mcmbp | NANQARVSPSTSYTP |
| S | 1 | 438 | 0.074572 | 0.013574 | 2.951135 | 4.222857 | Q9Z2D6-2 | Methyl-Cp | Mecp2 | EKMPRGGSLESDGCP |
| S | 0.999911 | 87 | 0.46516 | 0.049143 | 0.637052 | 1.503971 | Q9Z2D6-2 | Methyl-Cp | Mecp2 | ETSESSGSAPAVPEA |
| T | 1 | 188 | 0.022285 | 0.100735 | -1.940894 | -1.114117 | Q8K3A9 | 7SK snRNA | Mepce | SRALNAETPKSSPLP |
| S | 1 | 131 | 0.355117 | 0.02788 | 1.76211 | 4.042824 | Q6PCP5 | Mitochond | Mff | LKRERSMSENAVRQN |
| S | 0.920945 | 5 | 0.082405 | 0.032213 | 3.602316 | 4.255742 | O35678 | Monoglyce | Mgll | ___MPEASSPRRTPQ |
| S | 1 | 777 | 0.006753 | 0.006929 | 2.345376 | 2.085163 | Q8VDP3 | Protein-me | Mical1 | SPPVTRVSPVPSPSQ |
| S | 0.999203 | 781 | 0.005419 | 0.005859 | 2.140835 | 1.880622 | Q8VDP3 | Protein-me | Mical1 | TRVSPVPSPSQPARR |
| S | 0.999421 | 1150 | 0.474553 | 0.030336 | 0.368418 | 1.011984 | Q8CJ19 | Protein-me | Mical3 | KQEERGTSQVSSPSQ |
| S | 1 | 699 | 0.012576 | 0.704077 | -5.584414 | -0.842249 | Q9JM52 | Misshapen | Mink1 | PAQAVRASNPDLRRS |
| S | 0.943319 | 606 | 0.005306 | 0.003348 | 0.971943 | 0.96526 | Q8K4J6 | MKL/myoc | Mkl1 | QQPAPASSPVKRESG |
| S | 0.999885 | 139 | 0.064678 | 0.016893 | 0.906123 | 1.174176 | Q9ERV1 | Probable E | Mkrn2 | GCSDPQTSPEMKPHS |
| S | 1 | 256 | 0.005921 | 0.00396 | 1.696103 | 1.663471 | P54276 | DNA misma | Msh6 | RVISDSESDIGGSDV |
| T | 0.999997 | 298 | 0.031149 | 0.245443 | -1.763133 | -0.773796 | D3YTP3 | | Mtx3 | KLPTLKLTPAEEESN |
| S | 0.961437 | 1968 | 0.005398 | 0.003426 | 4.338083 | 4.303144 | Q5SV64 | Myosin-10 | Myh10 | RGGPISFSSSRSGRR |
| S | 1 | 1983 | 0.496412 | 0.003859 | -0.165316 | -0.779936 | Q5SV64 | Myosin-10 | Myh10 | QLHIEGASLELSDDD |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 1 | 1987 | 0.496412 | 0.003859 | -0.165316 | -0.779936 | Q5SV64 | Myosin-10 | Myh10 | EGASLELSDDDTESK |
| S | 1 | 472 | 0.050608 | 0.01294 | 1.053843 | 1.355567 | E9Q411 | | Nbas | EDEGEVDSDSDPETS |
| S | 1 | 770 | 0.045446 | 0.060347 | -2.880085 | -2.368774 | P13595 | Neural cell | Ncam1 | EEGKAAFSKDESKEP |
| S | 1 | 774 | 0.045446 | 0.060347 | -2.880085 | -2.368774 | P13595 | Neural cell | Ncam1 | AAFSKDESKEPIVEV |
| S | 0.99437 | 887 | 0.020389 | 0.548981 | -1.463132 | -0.337393 | P13595 | Neural cell | Ncam1 | GVTASSSSPASAPKV |
| S | 0.999706 | 350 | 0.092542 | 0.020014 | 0.538008 | 0.749086 | Q9QYG0 | Protein ND | Ndrg2 | RSRSRTLSQSSESGT |
| S | 1 | 789 | 0.156112 | 0.049236 | -1.475735 | -1.942426 | P19246 | Neurofilam | Nefh | KSPAEAKSPEKAKSP |
| S | 1 | 523 | 0.630799 | 0.023268 | -0.791729 | -3.087347 | P19246 | Neurofilam | Nefh | RVKEEAKSPGEAKSP |
| S | 0.999936 | 419 | 0.040839 | 0.978941 | -1.54545 | 0.074352 | P19246 | Neurofilam | Nefh | GFGPSPFSLTEGLPK |
| S | 1 | 757 | 0.027431 | 0.236771 | -0.903628 | -0.389884 | P19246 | Neurofilam | Nefh | KSPAEAKSPAEAKSP |
| S | 1 | 625 | 0.005145 | 0.349786 | -4.352593 | -1.011133 | P19246 | Neurofilam | Nefh | KSPAEAKSPAEAKSP |
| S | 1 | 631 | 0.007985 | 0.456086 | -4.706833 | -1.011133 | P19246 | Neurofilam | Nefh | KSPAEAKSPAEAKSP |
| S | 1 | 637 | 0.009568 | 0.44366 | -4.4147 | -1.011133 | P19246 | Neurofilam | Nefh | KSPAEAKSPATVKSP |
| S | 1 | 723 | 0.011095 | 0.107097 | -5.31066 | -2.505447 | P08553 | Neurofilam | Nefm | EEEGSDRSPQESKKE |
| S | 1 | 1164 | 0.069789 | 0.029913 | -1.794505 | -2.051323 | Q810U3 | Neurofasci | Nfasc | EDGSFDYSDEDNKPL |
| S | 1 | 1174 | 0.016591 | 0.028306 | 1.325003 | 1.031617 | Q810U3 | Neurofasci | Nfasc | DNKPLQGSQTSLDGT |
| S | 1 | 1177 | 0.002073 | 0.002323 | 2.156337 | 1.880891 | Q810U3 | Neurofasci | Nfasc | PLQGSQTSLDGTIKQ |
| T | 1 | 1181 | 0.048843 | 0.085436 | 1.21646 | 0.915473 | Q810U3 | Neurofasci | Nfasc | SQTSLDGTIKQQESD |
| S | 1 | 343 | 0.025251 | 0.105005 | 1.68893 | 0.98754 | P70255 | Nuclear fac | Nfic | NSPSPQDSPRLSSFT |
| S | 1 | 696 | 0.086336 | 0.027261 | -4.78294 | -6.00179 | Q8CHT1 | Ephexin-1 | Ngef | KMEDPQRSQNKDRRK |
| S | 1 | 2369 | 0.564955 | 0.046102 | 0.402441 | 1.150743 | O88491 | Histone-lys | Nsd1 | RQKERAASPQEVTPQ |
| S | 0.984807 | 241 | 0.949395 | 0.027887 | 0.220527 | -2.594794 | Q9QZS3-2 | Protein nu | Numb | NTAPSPSSPTSPTPD |
| S | 0.999729 | 263 | 0.058525 | 0.036879 | -0.953634 | -0.975037 | O08919 | Numb-like | Numbl | PAQPGHVSPTPATTS |
| S | 1 | 191 | 0.026095 | 0.032024 | 1.616194 | 1.368102 | Q3B7Z2 | Oxysterol- | Osbp | MLAESDDSGDEESVS |
| S | 0.999695 | 44 | 0.158756 | 0.04626 | 0.65864 | 0.888673 | F8WIZ7 | Oxysterol- | Osbpl6 | HVLERTASSSTEPSV |
| S | 0.998309 | 207 | 0.12614 | 0.030872 | 1.685089 | 2.33232 | F8WIZ7 | Oxysterol- | Osbpl6 | PATSTAESSPAANVS |
| S | 0.998101 | 208 | 0.073361 | 0.045596 | 1.713464 | 1.769048 | F8WIZ7 | Oxysterol- | Osbpl6 | ATSTAESSPAANVSV |
| S | 1 | 952 | 0.027693 | 0.001769 | 0.682896 | 1.172846 | P97467 | Peptidyl-gl | Pam | DRVSTEGSDQEKDED |
| S | 1 | 43 | 0.903517 | 0.01796 | 0.144985 | 1.358205 | V9GX56 | | Pank2 | PLRRRASSAAPSGSG |
| S | 1 | 63 | 0.080581 | 0.04434 | -2.081727 | -2.232727 | Q80YV4 | Pantothen | Pank4 | HKVAKVRSFDHPGKD |
| S | 1 | 1010 | 0.000126 | 9.59E-06 | 0.7197 | 1.08732 | F7BJK1 | | Pcdh1 | QEPAGAGSPSPPEDR |
| S | 1 | 1012 | 0.19476 | 0.023383 | 0.526303 | 0.931897 | F7BJK1 | | Pcdh1 | PAGAGSPSPPEDRNT |
| S | 1 | 1481 | 0.025583 | 0.127363 | 0.724953 | 0.397027 | Q9QYX7 | Protein pic | Pclo | EEYKQEDSQGSGEDE |
| S | 1 | 1484 | 0.025583 | 0.127363 | 0.724953 | 0.397027 | Q9QYX7 | Protein pic | Pclo | KQEDSQGSGEDEDFI |
| S | 0.999993 | 1772 | 0.032884 | 0.00673 | -0.739935 | -0.985157 | Q9QYX7 | Protein pic | Pclo | LSPIEDASPTEELRQ |
| T | 1 | 1760 | 0.032884 | 0.00673 | -0.739935 | -0.985157 | Q9QYX7 | Protein pic | Pclo | RRRERPKTPPSNLSP |
| S | 0.995366 | 232 | 0.032862 | 0.008516 | 0.892954 | 1.12451 | P35486 | Pyruvate d | Pdha1 | NRYGMGTSVERAAAS |
| S | 0.85274 | 204 | 0.075425 | 0.031271 | 1.611545 | 1.865368 | Q8R1G6 | PDZ and LI | Pdlim2 | LHSPGRPSSPRFSSL |
| S | 0.999194 | 1166 | 0.27456 | 0.045918 | 0.633171 | 1.094905 | Q4VA53 | Sister chro | Pds5b | SSSSNPSSPGRIKGR |
| S | 1 | 1257 | 0.032751 | 0.095166 | 1.304911 | 0.846285 | Q4VA53 | Sister chro | Pds5b | RGRTASDSDEQQWPE |
| T | 1 | 205 | 0.052389 | 0.007905 | 0.716439 | 1.048427 | Q80UU9 | Membrane | Pgrmc2 | GEEPSEYTDEEDTKD |
| S | 1 | 1378 | 0.093676 | 0.032731 | 0.773373 | 0.949089 | E9Q3L2 | | Pi4ka | PDNQDTRSNLDITVG |
| S | 1 | 495 | 0.113741 | 0.028818 | 0.975469 | 1.325097 | O70161-2 | Phosphatid | Pip5k1c | YRRRTQSSGQDGRPQ |
| S | 1 | 946 | 0.010376 | 0.000907 | -0.999017 | -1.546033 | Q3UHE1 | Membrane | Pitpnm3 | PKPERAQSQPESDKD |
| S | 0.999998 | 24 | 0.001606 | 0.000757 | 4.431207 | 4.659751 | Q9D4F2 | Presqualen | Ppapdc2 | GGSSVPGSPAHGGGS |
| S | 0.999884 | 750 | 0.118864 | 0.04958 | 0.803059 | 0.951985 | B2RXW8 | | Ppfia1 | TTIKCETSPPSSPRP |
| S | 0.999997 | 788 | 0.00909 | 0.792331 | -1.74957 | 0.195262 | B8QI35 | Liprin-alph | Ppfia3 | PPGRESVSLAGTPSD |
| S | 0.999884 | 701 | 0.004511 | 0.005331 | 1.301647 | 1.120473 | B8QI36 | | Ppfia4 | ATIKCETSPPSSPRT |
| S | 0.999676 | 445 | 0.041006 | 0.366739 | 0.726542 | 0.27613 | Q9DBR7 | Protein ph | Ppp1r12a | LGLRKTGSYGALAEI |
| S | 1 | 6 | 0.250592 | 0.022983 | 0.529474 | 1.057161 | Q9ERT9 | Protein ph | Ppp1r1a | __MEPDNSPRKIQFT |
| S | 0.999855 | 746 | 0.115001 | 0.042059 | 0.749105 | 0.920242 | Q8R3Q2 | Serine/thre | Ppp6r2 | ETGPRCSSPVDMDHS |
| S | 1 | 329 | 0.011228 | 0.136093 | 0.908583 | 0.39418 | P16054 | Protein kin | Prkce | KLAAGAESPQPASGN |
| T | 1 | 455 | 0.823611 | 0.018481 | -0.16111 | -1.068173 | Q8CCF0 | U4/U6 sma | Prpf31 | TASSVAFTPLQGLEI |
| S | 1 | 292 | 0.004628 | 0.00433 | -0.962443 | -0.873997 | Q61136 | Serine/thre | Prpf4b | SRDRSKKSKSPVDLR |
| S | 1 | 294 | 0.004628 | 0.00433 | -0.962443 | -0.873997 | Q61136 | Serine/thre | Prpf4b | DRSKKSKSPVDLRDK |
| S | 1 | 387 | 0.239031 | 0.033336 | 0.645217 | 1.139956 | F8WHT3 | Protein PR | Prrc2b | YSEKLKFSDDEDEED |
| S | 1 | 254 | 0.043893 | 0.20124 | 0.936815 | 0.495648 | E9PUL5 | Proline-ric | Prrt2 | GSLSRHPSSQLAGPG |
| S | 1 | 129 | 0.017258 | 0.872168 | 1.019035 | 0.100568 | Q99JF8 | PC4 and SF | Psip1 | TDQEEKASNEDVTKA |
| S | 1 | 250 | 0.047666 | 0.835969 | -2.941286 | -0.439797 | O70435 | Proteasom | Psma3 | SLKEEDESDDDNM__ |
| S | 1 | 256 | 0.047176 | 0.873019 | -1.466184 | -0.189039 | O35226 | 26S protea | Psmd4 | ATPGTEDSDDALLKM |
| S | 0.999979 | 645 | 0.169785 | 0.03073 | 0.776914 | 1.207544 | B9EKR1 | Receptor-t | Ptprz1 | APEDSAPSGSEESLK |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.999876 | 647 | 0.169785 | 0.03073 | 0.776914 | 1.207544 | B9EKR1 | Receptor-t | Ptprz1 | EDSAPSGSEESLKDP |
| S | 0.999999 | 393 | 0.549884 | 0.014241 | -0.379248 | -1.442947 | Q80TM6 | R3H domai | R3hdm2 | SILTRGDSIGSSKGG |
| S | 1 | 29 | 0.017828 | 0.089086 | -1.367574 | -0.77264 | Q62172 | RalA-bindir | Ralbp1 | SGLTRTPSSEEISPT |
| T | 1 | 27 | 0.00497 | 0.441369 | -2.798217 | -0.551836 | Q62172 | RalA-bindir | Ralbp1 | HGSGLTRTPSSEEIS |
| S | 0.995153 | 708 | 0.215005 | 0.046673 | 2.52766 | 3.867172 | Q5SVL6 | Rap1 GTPa | Rap1gap2 | DKLSHASSSAGH___ |
| S | 0.999983 | 1022 | 0.016304 | 0.019621 | 0.995346 | 0.849367 | Q8CHG7 | Rap guanin | Rapgef2 | KPVKSETSPVAPRAG |
| S | 0.990471 | 1119 | 0.040245 | 0.032373 | 5.015159 | 4.765237 | Q8CHG7 | Rap guanin | Rapgef2 | QLSSPPTSPQSSPRK |
| S | 1 | 1295 | 0.127542 | 0.047993 | 1.419581 | 1.743021 | P97868-2 | E3 ubiquiti | Rbbp6 | WDKDDFESEEEDVKT |
| S | 1 | 672 | 0.123947 | 0.010766 | 3.013862 | 5.423513 | B2RY56 | RNA-bindir | Rbm25 | LKLGASNSPGQPNSV |
| S | 1 | 42 | 0.098363 | 0.013194 | 0.531291 | 0.838593 | A0A023T67 | RNA-bindir | RBM8 | RKGRGFGSEEGSRAR |
| S | 0.999963 | 506 | 0.069973 | 0.038264 | 1.330172 | 1.422129 | Q3UYI5 | Ral guanine | Rgl3 | VIEPPAASCPSSPRI |
| S | 0.997274 | 1133 | 0.078515 | 0.045948 | 1.770653 | 1.86401 | D9HP81 | Regulating | Rims2 | RSHPRTGSVQTSPSS |
| S | 0.999721 | 1137 | 0.063097 | 0.035732 | 1.686957 | 1.780314 | D9HP81 | Regulating | Rims2 | RTGSVQTSPSSTPGT |
| S | 1 | 321 | 1.17E-05 | 9.4E-06 | 4.11275 | 3.848602 | Q3V3V9-2 | Leucine-ric | Rltpr | AGPSARGSPSPAAPG |
| S | 0.999996 | 23 | 0.210179 | 0.031566 | 0.62484 | 1.05599 | P62858 | 40S ribosor | Rps28;Gm1 | KVLGRTGSQGQCTQV |
| S | 0.999834 | 360 | 0.048608 | 0.906976 | 2.063966 | -0.226284 | Q9WUT3 | Ribosomal | Rps6ka2 | TARTPTDSPGVPPSA |
| S | 1 | 434 | 0.080533 | 0.037301 | 1.124553 | 1.266344 | P56183 | Ribosomal | Rrp1 | PQNKEAGSEAESSSA |
| S | 0.999999 | 6 | 0.010052 | 0.002004 | 1.886953 | 2.440746 | Q9DBU6 | Serine/Argi | Rsrc1 | __MGRRSSDTEEESR |
| S | 1 | 350 | 0.002946 | 0.000973 | -3.408174 | -3.883392 | Q8K0T0 | Reticulon-1 | Rtn1 | AESQGKGSVSEDELI |
| S | 0.999986 | 836 | 0.919761 | 0.021052 | -0.380705 | 3.781743 | Q99P72 | Reticulon-4 | Rtn4 | MKESETFSDSSPIEI |
| S | 0.958274 | 838 | 0.446041 | 0.004712 | 0.913695 | 3.781743 | Q99P72 | Reticulon-4 | Rtn4 | ESETFSDSSPIEIID |
| T | 0.938899 | 834 | 0.000693 | 3.91E-06 | 1.807582 | 4.67563 | Q99P72 | Reticulon-4 | Rtn4 | DKMKESETFSDSSPI |
| T | 0.999945 | 5 | 0.024316 | 0.457178 | 1.71399 | 0.484642 | Q9D394 | Protein RU | Rufy3 | ___MSALTPPTDMPT |
| S | 1 | 799 | 0.037121 | 0.019164 | 1.024143 | -1.09255 | Q9QX96 | Sal-like pro | Sall2 | AISVRGDSEEVSGAE |
| S | 0.999998 | 555 | 0.52106 | 0.04909 | -0.298474 | -0.77562 | A2APX8 | Sodium cha | Scn1a | RYSSPHQSLLSIRGS |
| S | 1 | 554 | 0.032187 | 0.095884 | -3.741801 | -2.409074 | B1AWN6 | Sodium cha | Scn2a1 | TYEKRFSSPHQSLLS |
| T | 1 | 193 | 0.325707 | 0.007541 | -1.64453 | -4.967679 | Q56A07 | Sodium cha | Scn2b | KKEQKLSTDDLKTEE |
| S | 0.864026 | 288 | 0.264499 | 0.005305 | -0.61499 | 1.802794 | Q63918 | Serum dep | Sdpr | KASSGKSSPFKVSPL |
| S | 0.884937 | 1238 | 0.046221 | 0.024011 | 0.821175 | 0.879353 | A2AIX1 | | Sec16a | YSEPERPSSRASHYS |
| S | 0.998603 | 17 | 0.009252 | 0.046394 | 1.722061 | 1.012656 | Q9CQS8 | Protein tra | Sec61b;Gm | NVGSSGRSPSKAVAA |
| T | 1 | 158 | 0.010519 | 0.126718 | 0.708967 | 0.31089 | Q8BU14 | Translocati | Sec62 | KKEETPGTPKKKETK |
| T | 1 | 816 | 0.01904 | 0.555761 | 1.915985 | 0.428929 | O09126 | Semaphori | Sema4d | ALDTGYETEQDTITS |
| S | 0.5 | 126 | 0.016237 | 0.004522 | 1.417563 | 1.7198 | Q91ZM2-6 | SH2B adap | Sh2b1 | AVLGPSRSSEDLAGP |
| S | 0.5 | 127 | 0.066829 | 0.021789 | 1.334603 | 1.63684 | Q91ZM2-6 | SH2B adap | Sh2b1 | VLGPSRSSEDLAGPL |
| S | 1 | 400 | 0.034811 | 0.297542 | -2.637194 | -1.081447 | Q8R3V5 | Endophilin | Sh3glb2 | VTYLELLS_______ |
| S | 1 | 8 | 0.028591 | 0.97304 | -3.281628 | -0.162317 | A2ALU4-2 | Protein Shr | Shroom2 | METSRSPSPQFAPQK |
| S | 1 | 258 | 0.023145 | 0.905707 | -1.447778 | 0.130354 | Q8C0T5 | Signal-indu | Sipa1l1 | GGKGSGFSLDVIDGP |
| S | 1 | 1249 | 0.156512 | 0.03852 | -0.713661 | -1.008733 | Q8C0T5 | Signal-indu | Sipa1l1 | QDPVVHLSPNKQGHS |
| S | 1 | 392 | 0.000536 | 0.001512 | -1.336358 | -0.957471 | Q8CI08 | SLAIN moti | Slain2 | RLQQPRLSLQGHPTD |
| S | 0.997694 | 74 | 0.006613 | 0.003585 | -4.527584 | -4.65963 | P55012 | Solute carr | Slc12a2 | RPLGPTPSQSRFQVD |
| S | 0.916064 | 76 | 0.01078 | 0.003205 | 3.217182 | 3.813557 | P55012 | Solute carr | Slc12a2 | LGPTPSQSRFQVDPV |
| S | 0.99424 | 291 | 0.016141 | 0.018318 | -1.824174 | -1.580217 | E9Q2R3 | | Slc19a2 | KQEDPSSSPQASTS_ |
| S | 1 | 21 | 0.027573 | 0.044231 | 1.974984 | 1.550043 | P43006 | Excitatory a | Slc1a2 | VEVRMHDSHLSSDEP |
| S | 1 | 24 | 0.015287 | 0.029336 | 1.055554 | 0.797421 | P43006 | Excitatory a | Slc1a2 | RMHDSHLSSDEPKHR |
| S | 0.993286 | 312 | 0.019792 | 0.084464 | 0.978804 | 0.578016 | Q8BUN9 | | Slc24a2 | VPEAQAKSPTAGDKD |
| S | 1 | 429 | 0.043867 | 0.941648 | -2.852725 | -0.236864 | Q921R7 | Probable U | Slc35a5 | ERLTKLKSDDSDDDT |
| S | 0.999997 | 89 | 0.034517 | 0.035385 | 1.295621 | 1.150911 | F8VQC9 | Anion exch | Slc4a7 | DKEDGRESPSYDTPS |
| S | 1 | 682 | 0.004653 | 0.001858 | 3.079379 | 3.38113 | Q8BJI1 | Sodium-de | Slc6a17 | FILSKVPSEAPSPMP |
| S | 1 | 686 | 0.089075 | 0.037881 | 1.825024 | 2.115048 | Q8BJI1 | Sodium-de | Slc6a17 | KVPSEAPSPMPTHRS |
| S | 0.995378 | 790 | 0.006966 | 0.954481 | -1.588809 | -0.072394 | Q61165 | Sodium/hy | Slc9a1 | FTPGSSDSPSSQRIQ |
| S | 0.999996 | 609 | 0.061868 | 0.024465 | 3.075957 | 3.574156 | Q61165 | Sodium/hy | Slc9a1 | PSAVSTVSMQNIHPK |
| S | 1 | 603 | 0.273724 | 0.009755 | 0.441051 | 1.14021 | Q61165 | Sodium/hy | Slc9a1 | GGMGKIPSAVSTVSM |
| S | 0.999559 | 700 | 3.52E-06 | 2.05E-06 | 2.955 | 2.947144 | A1L3P4 | Sodium/hy | Slc9a6 | SLDDTRHSPA_____ |
| S | 1 | 32 | 0.303594 | 0.031817 | 0.363688 | 0.735254 | Q9DB90 | Protein SM | Smg9 | SSGPQNLSGPGGRER |
| S | 1 | 28 | 0.048617 | 0.385271 | -1.107329 | -0.428177 | P97801 | Survival mc | Smn1 | GTGQSDDSDIWDDTA |
| S | 1 | 289 | 0.078795 | 0.014602 | 0.707611 | 1.012067 | Q9JJY3 | Sphingomy | Smpd3 | QRDGDSGSLGSPSAS |
| S | 0.9999 | 292 | 0.078795 | 0.014602 | 0.707611 | 1.012067 | Q9JJY3 | Sphingomy | Smpd3 | GDSGSLGSPSASRES |
| S | 0.667127 | 304 | 0.17935 | 0.017123 | -1.044748 | -1.93535 | E9Q9A3 | | Snap91 | PSPLSKSSPATTVTS |
| S | 0.635853 | 306 | 0.17935 | 0.017123 | -1.044748 | -1.93535 | Q61548 | Clathrin co | Snap91 | PSPLSKSSPATTVTS |
| S | 1 | 75 | 0.042052 | 0.325039 | -0.738142 | -0.30381 | Q61235 | Beta-2-synt | Sntb2 | NRGLGPPSPPAPPRG |
| S | 0.963381 | 1155 | 0.043611 | 0.36749 | -1.244163 | -0.480605 | Q9JLC4 | VPS10 dom | Sorcs1 | RPATPPSSPKRGSAG |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.999913 | 360 | 0.040187 | 0.085491 | -1.087534 | -0.773723 | Q5SXY1 | Cytospin-B | Specc1 | KGSPTGSSPNNASEL |
| S | 1 | 126 | 0.167426 | 0.041635 | 0.611033 | 0.868027 | Q8R1X6 | Spartin | Spg20 | PKDACKKSPEQESVS |
| S | 0.996575 | 379 | 0.011075 | 0.451186 | -2.592594 | -0.607367 | Q9JIA7 | Sphingosin | Sphk2 | PAPAATHSPLHRSVS |
| S | 0.853856 | 100 | 0.038925 | 0.209846 | 2.282332 | 1.145655 | D3YTL8 | Protein spi | Spire1 | MEKGDESSTDLEDLK |
| S | 0.991008 | 2339 | 0.001697 | 0.001664 | -0.980902 | -0.881144 | Q62261 | Spectrin be | Sptbn1 | VVTITSESSPGKREK |
| T | 1 | 2354 | 0.205079 | 0.01564 | 0.815401 | 1.636793 | Q68FG2 | | Sptbn2 | RGLTRAMTMPPVSQP |
| T | 0.993611 | 658 | 0.794486 | 0.011286 | 0.733228 | -5.020148 | B1AQX9 | | Srcin1 | GSKSSGATPVSGPPP |
| S | 1 | 858 | 0.001982 | 0.673268 | -3.613575 | 0.380513 | Q812A2 | SLIT-ROBO | Srgap3 | MGRVRLRSDGAAIPR |
| S | 0.999276 | 560 | 0.003467 | 0.747522 | 3.320903 | 0.334446 | E9Q740 | Signal reco | Srp72 | DASKAVSSPPTSPRP |
| S | 1 | 412 | 0.528498 | 0.03308 | -1.337144 | -3.935564 | E9PUK6 | Serine/argi | Srrm1 | PPPKTRHSPTPQQSN |
| T | 0.999995 | 414 | 0.695047 | 0.049377 | -1.337144 | -4.835455 | E9PUK6 | Serine/argi | Srrm1 | PKTRHSPTPQQSNRT |
| S | 0.995074 | 766 | 0.023692 | 0.024199 | -3.351341 | -2.980889 | E9PUK6 | Serine/argi | Srrm1 | PQSVRRVSSSRSVSG |
| S | 0.999408 | 454 | 0.012846 | 0.061235 | 1.290354 | 0.756674 | Q8BTI8 | Serine/argi | Srrm2 | SRREISSSPTSKNRS |
| S | 1 | 1305 | 0.049604 | 0.111491 | 4.102524 | 2.832893 | Q8BTI8 | Serine/argi | Srrm2 | SEVNTGFSPEVKEEL |
| S | 1 | 1813 | 0.001863 | 0.491528 | -3.511005 | 0.510574 | Q8BTI8 | Serine/argi | Srrm2 | KRSRSRTSPAPWKRS |
| S | 0.999786 | 3 | 0.026627 | 0.04795 | -0.705758 | -0.536123 | E9Q6E5 | | Srsf11 | _____MSSPPAPGTA |
| S | 1 | 224 | 0.007615 | 0.002403 | 1.326018 | 1.542467 | Q8C8K3 | Serine/argi | Srsf12 | PHGRHCDSIARSPCK |
| S | 1 | 228 | 0.007615 | 0.002403 | 1.326018 | 1.542467 | Q8C8K3 | Serine/argi | Srsf12 | HCDSIARSPCKSPRA |
| S | 1 | 212 | 0.055037 | 0.012378 | 0.557669 | 0.74344 | Q62093 | Serine/argi | Srsf2 | RSKSPPKSPEEEGAV |
| S | 1 | 291 | 0.023346 | 0.784013 | -1.673795 | -0.242 | Q8VE97 | Serine/argi | Srsf4 | AGKAKSHSPSRHDSK |
| S | 1 | 297 | 0.023346 | 0.784013 | -1.673795 | -0.242 | Q8VE97 | Serine/argi | Srsf4 | HSPSRHDSKSRSRSQ |
| S | 0.948957 | 17 | 0.040257 | 0.671881 | -3.389034 | -0.742834 | Q8QZV4 | Serine/thre | Stk32c | SSAAAPPSSPPPGRA |
| S | 1 | 139 | 0.091323 | 0.043942 | 1.468931 | 1.645921 | Q9ER00 | Syntaxin-1 | Stx12 | IARARAGSRLSAEDR |
| S | 1 | 792 | 0.005125 | 0.003176 | 3.233757 | 3.223814 | Q5DQR4 | Syntaxin-bi | Stxbp5l | PPFRKAQSAACMEIS |
| S | 0.990946 | 770 | 0.287338 | 0.025388 | 1.189612 | 2.480573 | Q5DQR4 | Syntaxin-bi | Stxbp5l | CSSGKRLSSADVSKV |
| S | 0.999982 | 597 | 0.890163 | 0.004213 | 0.239292 | -2.953151 | Q5DQR4 | Syntaxin-bi | Stxbp5l | SGSTNTVSSEGVTKD |
| S | 0.992883 | 733 | 0.017344 | 0.016877 | 1.168694 | 1.052553 | Q8CH09 | SURP and | Sugp2 | KPCPQPSSPGALGPS |
| S | 1 | 461 | 0.031875 | 0.023862 | 3.854897 | 3.725494 | Q8JZP2 | Synapsin-3 | Syn3 | SPSQQRLSPQGQQPV |
| S | 1 | 461 | 0.037249 | 0.057265 | 2.370246 | 1.871993 | Q8JZP2 | Synapsin-3 | Syn3 | SPSQQRLSPQGQQPV |
| S | 1 | 22 | 0.016337 | 0.016811 | 0.867265 | 0.770127 | Q8BHL3 | TBC1 doma | Tbc1d10b | HGAPAAPSPPPRGSR |
| S | 1 | 952 | 0.014562 | 0.003849 | 4.124404 | 5.050947 | A3KGB4 | TBC1 doma | Tbc1d8b | ETESGRNSPEKGKGK |
| S | 1 | 100 | 0.120572 | 0.031839 | 0.527424 | 0.71211 | P10711 | Transcripti | Tcea1 | PAISSQNSPEAREES |
| S | 0.997481 | 23 | 6.04E-06 | 4.04E-06 | -1.6967 | -1.645883 | Q8CCT4 | Transcripti | Tceal5 | GRAEDEGSTEEGGKA |
| S | 1 | 794 | 0.66961 | 0.045531 | -0.609679 | -2.138292 | H3BL37 | Treacle pr | Tcof1 | ASAPAKESPKKGAHP |
| S | 1 | 320 | 0.073847 | 0.0303 | 0.908155 | 1.05312 | Q569Z6 | Thyroid ho | Thrap3 | KKSPVGKSPPATGSA |
| S | 1 | 86 | 0.01992 | 0.145759 | -3.382282 | -1.64947 | Q99J36 | THUMP do | Thumpd1 | IDKDQQPSGSEGEDD |
| S | 1 | 88 | 0.01992 | 0.145759 | -3.382282 | -1.64947 | Q99J36 | THUMP do | Thumpd1 | KDQQPSGSEGEDDDA |
| S | 1 | 175 | 0.004908 | 0.00246 | 3.577764 | 3.738442 | P39447 | Tight juncti | Tjp1 | SPRSDRRSVASSQPA |
| S | 1 | 178 | 0.003641 | 0.001813 | 3.6378 | 3.798478 | P39447 | Tight juncti | Tjp1 | SDRRSVASSQPAKPT |
| S | 1 | 378 | 0.05166 | 0.045633 | 1.557311 | 1.444215 | Q9Z0U1 | Tight juncti | Tjp2 | NIPALNDSDSEVEDI |
| S | 1 | 56 | 0.248148 | 0.012279 | -1.072995 | -2.497901 | Q8C996 | Transmem | Tmem163 | RQPRISESGQFSDGL |
| S | 1 | 56 | 0.014732 | 0.048647 | -1.202137 | -0.781017 | Q8C996 | Transmem | Tmem163 | RQPRISESGQFSDGL |
| S | 1 | 60 | 0.014732 | 0.048647 | -1.202137 | -0.781017 | Q8C996 | Transmem | Tmem163 | ISESGQFSDGLEDRG |
| S | 0.999543 | 101 | 0.017269 | 0.055604 | 1.489684 | 0.968224 | D3Z2D8 | CSC1-like p | Tmem63b | ERLTSVSSSVDFDQR |
| S | 1 | 678 | 0.331707 | 0.049769 | 0.49704 | 0.931124 | E9PUL9 | Traf2 and | Tnik | GSQPIRASNPDLRRT |
| S | 0.999976 | 462 | 0.037223 | 0.237426 | 2.7525 | 1.289074 | O88746 | Target of | Tom1 | DRLPNLASPSAEGPP |
| S | 1 | 1539 | 0.003418 | 0.002313 | 2.557122 | 2.495086 | Q64511 | DNA topois | Top2b | KKRKASGSENEGDYN |
| S | 1 | 1453 | 0.012003 | 0.931834 | -0.892535 | 0.057235 | Q64511 | DNA topois | Top2b | DDSAKFDSNEEDTAS |
| T | 0.978984 | 176 | 0.667519 | 0.036602 | -0.4414 | -1.639685 | Q8BU11 | TOX high m | Tox4 | PEDRLSTTPSPTNSL |
| S | 0.999755 | 479 | 0.01362 | 0.408634 | -2.673114 | -0.707839 | Q8CG79 | Apoptosis- | Tp53bp2;T | GTLRKNQSSEDILRD |
| S | 1 | 14 | 0.019192 | 0.005746 | 1.009073 | 1.208827 | P62996 | Transforme | Tra2b | QNYGERESRSASRSG |
| S | 0.999206 | 23 | 0.019105 | 0.148421 | -1.312583 | -0.628899 | Q62318 | Transcripti | Trim28 | AASAASGSPGSGEGS |
| S | 1 | 323 | 0.100491 | 0.019082 | 3.352622 | 4.859245 | Q8C1Z8 | tRNA meth | Trmt10a | KDEQGQQSSPVLQ__ |
| S | 1 | 324 | 0.106642 | 0.015899 | 2.742114 | 4.248738 | Q8C1Z8 | tRNA meth | Trmt10a | DEQGQQSSPVLQ___ |
| S | 1 | 1794 | 0.529298 | 0.025234 | -0.314787 | 0.997897 | O88196 | E3 ubiquiti | Ttc3 | LKGASQVSPSEQSPE |
| S | 1 | 678 | 0.014235 | 0.064957 | -1.213417 | -0.716753 | E9Q6P5 | | Ttc7b | ALSEVASSLQSSAPK |
| S | 0.998285 | 449 | 0.043371 | 0.394147 | -0.780482 | -0.287633 | Q9D3A9 | Protein tw | Ttyh1 | RFVQWQSSI______ |
| S | 0.999981 | 167 | 0.271132 | 0.006459 | 0.492458 | 1.396674 | Q9Z0P5 | Twinfilin-2 | Twf2 | NEVKTEISVESKHQT |
| S | 1 | 835 | 0.019343 | 0.075416 | 0.819088 | 0.498791 | Q02053 | Ubiquitin-li | Uba1 | ELKATLPSPDKLPGF |
| S | 0.980783 | 622 | 0.427471 | 0.00275 | -0.184071 | -0.833658 | O70405 | Serine/thre | Ulk1 | PLPPILGSPTKAGPS |
| S | 0.980281 | 715 | 0.0101 | 0.003765 | 1.658435 | 1.866338 | O70405 | Serine/thre | Ulk1 | TQASDSGSTDSLQEK |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| S | 0.999997 | 255 | 0.122554 | 0.029918 | 0.856377 | 1.182907 | Q4KUS2 | Protein un | Unc13a | FSEPRALSPTGSSRY |
| S | 0.998234 | 259 | 0.122554 | 0.029918 | 0.856377 | 1.182907 | Q4KUS2 | Protein un | Unc13a | RALSPTGSSRYASSG |
| S | 0.999959 | 260 | 0.13882 | 0.039935 | 0.856377 | 1.14394 | Q4KUS2 | Protein un | Unc13a | ALSPTGSSRYASSGE |
| S | 0.97941 | 49 | 0.038718 | 0.002488 | 0.657245 | 1.147852 | E9Q6Y8 | Ubiquitin c | Usp31 | PGPAAPSSPSSARSV |
| S | 0.999937 | 1103 | 0.026113 | 0.070392 | 1.292843 | 0.870111 | E9Q6Y8 | Ubiquitin c | Usp31 | QESMSSPSPQKQKSA |
| S | 0.936641 | 796 | 0.007131 | 0.015277 | 0.969396 | 0.721203 | E9Q6Y8 | Ubiquitin c | Usp31 | SKQASVTSAASSRRT |
| S | 0.982593 | 997 | 0.532237 | 0.029636 | -0.601302 | -1.835443 | Q8CDG3 | Deubiquiti | Vcpip1 | TTRSRESSPSHGLLK |
| S | 0.999341 | 783 | 0.383321 | 0.005407 | 0.275546 | -0.993709 | Q9EQH3 | Vacuolar p | Vps35 | HLRSRRESPESEGPI |
| S | 0.999998 | 235 | 0.028912 | 0.510162 | -1.614553 | 0.436754 | Q8VHI6 | Wiskott-Al | Wasf3 | ASSEGSLSPDTRSHT |
| S | 0.998169 | 205 | 0.012697 | 0.667699 | -4.275311 | -0.69879 | Q8K1X1 | WD repeat | Wdr11 | GKKVYISSPHSSPAH |
| S | 0.919614 | 208 | 0.044933 | 0.60461 | -4.718889 | -1.218596 | Q8K1X1 | WD repeat | Wdr11 | VYISSPHSSPAHNKL |
| S | 0.996606 | 346 | 0.998913 | 0.046684 | 0.0563 | 3.998395 | P0C7L0 | WAS/WAS | Wipf3 | PPPLPPKSPSFQTQK |
| S | 1 | 1090 | 0.045367 | 0.694538 | -3.518856 | -0.760393 | E9Q784 | | Zc3h13 | RKRSKGDSDVSDEEA |