

SUPPLEMENTARY DATA

SUPPLEMENTAL TABLE 1. Unique eluted peptides from HLA-DQ6.2 expressing EBV-BLCL.

HLA-DQ6.2 expressing cells (total 7.5*10⁹) were eluted and eluted peptides were detected employing mass spectrometry as described in Research design and methods. A total of 1156 unique peptides (ordered per protein) are shown with Best Mascot Ion scores > 45. The peptide sequences of these peptides have been used to obtain the peptide binding motif of HLA-DQ6.2 by molecular modelling as described in research design and methods.

| Protein name | Protein accession number | Peptide sequence | Peptide identification | Mascot ion score | Mascot identify score | Start | Stop |
|--|--------------------------|------------------------|------------------------|------------------|-----------------------|-------|------|
| AARS Alanyl-tRNA synthetase, cytoplasmic | IPI0002744Z | EALATAVIPQWQKDE | 95.00% | 62.4 | 40.7 | 800 | 814 |
| ABCA3 ATP-binding cassette sub-family A member 3 | IPI0001780C | DPSDGIAGLIEEERT | 95.00% | 99.2 | 39.1 | 883 | 897 |
| ABCA3 ATP-binding cassette sub-family A member 3 | IPI0001780C | DPSDGIAGLIEEER | 95.00% | 90.6 | 40.2 | 883 | 896 |
| ABCB6 Isoform 4 of ATP-binding cassette sub-family B member 6, mitochondrial | IPI0006548E | NDEVEAAAQAAGIHD | 95.00% | 125 | 38.2 | 152 | 166 |
| ABCB6 Isoform 4 of ATP-binding cassette sub-family B member 6, mitochondrial | IPI0006548E | DEVEAAAQAAGIHDA | 95.00% | 101 | 37.9 | 153 | 167 |
| ABCB6 Isoform 4 of ATP-binding cassette sub-family B member 6, mitochondrial | IPI0006548E | GNDEVEAAAQAAGIHDA | 95.00% | 99.8 | 37.2 | 151 | 167 |
| ABCB6 Isoform 4 of ATP-binding cassette sub-family B member 6, mitochondrial | IPI0006548E | NDEVEAAAQAAGIHDA | 95.00% | 97.4 | 38.4 | 152 | 167 |
| ABCB6 Isoform 4 of ATP-binding cassette sub-family B member 6, mitochondrial | IPI0006548E | GNDEVEAAAQAAGIHD | 95.00% | 79.6 | 36.6 | 151 | 166 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | NTVLSGGTMYPGIADR | 95.00% | 141 | 40.5 | 296 | 312 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | NTVLSGGTMYPGIADRM | 95.00% | 140 | 39.8 | 296 | 313 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | TVLSGGTMYPGIADR | 95.00% | 140 | 40.6 | 297 | 312 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | TVLSGGTMYPGIADRM | 95.00% | 137 | 40.3 | 297 | 313 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | TVLSGGTMYPGIADRMQ | 95.00% | 130 | 40.4 | 297 | 314 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | NTVLSGGTMYPGIADRMQ | 95.00% | 118 | 40.1 | 296 | 314 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | YANTVLSGGTMYPGIADR | 95.00% | 107 | 40 | 294 | 312 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | LSGGTMYPGIADR | 95.00% | 101 | 38.7 | 299 | 312 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | VLSGGTMYPGIADR | 95.00% | 97.6 | 39.3 | 298 | 312 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | LSGGTMYPGIADRM | 95.00% | 93.5 | 39.3 | 299 | 313 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | NTVLSGGTMYPGIADR | 95.00% | 88 | 39.2 | 296 | 311 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | SGGTMYPGIADR | 95.00% | 81.8 | 37.6 | 300 | 312 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | LSGGTMYPGIADRMQ | 95.00% | 53 | 38.7 | 299 | 314 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | VLSGGTMYPGIADR | 95.00% | 51.9 | 40.3 | 298 | 311 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | ANTVLSGGTMYPGIADR | 95.00% | 51.5 | 40.1 | 295 | 311 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | DFEQEMATAASSSS | 95.00% | 103 | 31.5 | 222 | 235 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | ATAASSSSLEKSYELPD | 95.00% | 66.4 | 39.2 | 228 | 244 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | ATAASSSSLEKSYELPDG | 95.00% | 58.7 | 39.3 | 228 | 245 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | DFEQEMATAASSSSLE | 95.00% | 52.4 | 34.2 | 222 | 237 |
| ACTB Actin, cytoplasmic 1 | IPI0002143E | DSGDGVTHTVPIYEGYA | 95.00% | 57.1 | 38.1 | 154 | 170 |
| ADAM10 ADAM 10 | IPI00013897 | KSLNTGIITVQNYG | 95.00% | 70.1 | 40.1 | 175 | 188 |
| ADAM10 ADAM 10 | IPI00013897 | KYQMTGVVEVTQIPQ | 95.00% | 61.6 | 40.8 | 3 | 17 |
| ADAM9 Isoform 1 of ADAM 9 | IPI0044093Z | APRPSYKQVSYVIQAEQKEH | 95.00% | 57.8 | 41.7 | 58 | 77 |
| AGRN Agrin | IPI0037456Z | TEATQGLVLWVGKAT | 95.00% | 86 | 39.9 | 1899 | 1913 |
| AGRN Agrin | IPI0037456Z | TEATQGLVLWVGKATER | 95.00% | 75.2 | 40.8 | 1899 | 1915 |
| AGRN Agrin | IPI0037456Z | TEATQGLVLWVGKATE | 95.00% | 68.1 | 40.9 | 1899 | 1914 |
| AGRN Agrin | IPI0037456Z | APDFSKLARAASVSSGFDGAIQ | 95.00% | 74.5 | 41 | 1768 | 1789 |
| AGRN Agrin | IPI0037456Z | VPEQAAVALERTFVG | 95.00% | 86.5 | 40.6 | 1498 | 1513 |
| AGRN Agrin | IPI0037456Z | GVPEQAAVALERTFVG | 95.00% | 61.3 | 40.8 | 1497 | 1513 |
| AGRN Agrin | IPI0037456Z | VPEQAAVALERTFVGA | 95.00% | 50.7 | 40.6 | 1498 | 1514 |
| ALB Uncharacterized protein ALB | IPI00022434 | LVTDLTK | 95.00% | 48.8 | 39 | 143 | 149 |
| ALDOA Fructose-bisphosphate aldolase A | IPI0046543E | TPSQGAGAAASESL | 95.00% | 94.8 | 40.4 | 398 | 411 |
| ALDOA Fructose-bisphosphate aldolase A | IPI0046543E | TPSQGAGAAASESLF | 95.00% | 69.5 | 40 | 398 | 412 |
| ALDOA Fructose-bisphosphate aldolase A | IPI0046543E | TPSQGAGAAASESLFV | 92.30% | 46.8 | 39.7 | 398 | 413 |
| APP Isoform APP770 of Amyloid beta A4 protein (Fragment) | IPI0000660E | EDVGSNKGAIIGLMVG | 95.00% | 67.8 | 41.5 | 674 | 689 |
| APP Isoform APP770 of Amyloid beta A4 protein (Fragment) | IPI0000660E | EDVGSNKGAIIGLMVGGV | 95.00% | 65.4 | 40.8 | 674 | 691 |
| APP Isoform APP770 of Amyloid beta A4 protein (Fragment) | IPI0000660E | AEDVGSNKGAIIGLMVGGV | 95.00% | 64.1 | 40.7 | 673 | 691 |
| APP Isoform APP770 of Amyloid beta A4 protein (Fragment) | IPI0000660E | EDVGSNKGAIIGLMVGG | 95.00% | 63.9 | 41.3 | 674 | 690 |
| APP Isoform APP770 of Amyloid beta A4 protein (Fragment) | IPI0000660E | DVGSNKGAIIGLMVGGV | 95.00% | 61 | 40.2 | 675 | 691 |
| APP Isoform APP770 of Amyloid beta A4 protein (Fragment) | IPI0000660E | DVGSNKGAIIGLMVGGV | 95.00% | 60 | 38.7 | 675 | 692 |
| APP Isoform APP770 of Amyloid beta A4 protein (Fragment) | IPI0000660E | DVGSNKGAIIGLMVG | 95.00% | 51.2 | 39 | 675 | 689 |
| APP Isoform APP770 of Amyloid beta A4 protein (Fragment) | IPI0000660E | AEDVGSNKGAIIGLMVG | 94.80% | 49.9 | 41.1 | 673 | 689 |
| APP Isoform APP770 of Amyloid beta A4 protein (Fragment) | IPI0000660E | DVGSNKGAIIGLMVGG | 95.00% | 48.1 | 39.1 | 675 | 690 |
| APPL1 DCC-interacting protein 13-alpha | IPI0001583E | FLANIGTSVQNV | 95.00% | 112 | 39.2 | 225 | 237 |
| ARID1B Isoform 1 of AT-rich interactive domain-containing protein 1B | IPI00015404 | GAGAVAAAAA | 95.00% | 83 | 38.6 | 335 | 349 |
| ARL8B ADP-ribosylation factor-like protein 8B | IPI00018871 | GVNAIVYMIDAADRE | 95.00% | 82.5 | 40 | 88 | 102 |
| ARL8B ADP-ribosylation factor-like protein 8B | IPI00018871 | RGVNAIVYMIDAADREK | 95.00% | 63.1 | 40.6 | 87 | 103 |
| ATP11B Probable phospholipid-transporting ATPase IF | IPI0024079Z | DGANDVSMIQEAHV | 95.00% | 99 | 36.3 | 405 | 419 |
| ATP1A1 Isoform Long of Sodium/potassium-transporting ATPase subunit alpha-1 | IPI0000648Z | IISANGCKVDNSSLT | 95.00% | 73.2 | 41.5 | 204 | 218 |
| ATP1A1 Isoform Long of Sodium/potassium-transporting ATPase subunit alpha-1 | IPI0000648Z | IISANGCKVDNSSLTG | 95.00% | 51.9 | 40.6 | 204 | 219 |
| ATP1A1 Isoform Long of Sodium/potassium-transporting ATPase subunit alpha-1 | IPI0000648Z | LDNFASIVTGVVEG | 95.00% | 60 | 39.5 | 750 | 764 |
| ATP1A1 Isoform Long of Sodium/potassium-transporting ATPase subunit alpha-1 | IPI0000648Z | LDNFASIVTGV | 95.00% | 57.2 | 40.9 | 750 | 762 |
| ATP1A1 Isoform Long of Sodium/potassium-transporting ATPase subunit alpha-1 | IPI0000648Z | NPRDAKACVVHGSDL | 95.00% | 57 | 39.7 | 655 | 669 |
| ATP1A1 Isoform Long of Sodium/potassium-transporting ATPase subunit alpha-1 | IPI0000648Z | NPRDAKACVVHGSDLK | 90.70% | 48.5 | 40.8 | 655 | 670 |

SUPPLEMENTARY DATA

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|--|-------------|-----------------------|--------|------|------|------|------|
| ATP2B1 Isoform D of Plasma membrane calcium-transporting ATPase 1 | IPI0002169E | DPLLLSGTHVMEGSGRM | 89.40% | 46.5 | 40.6 | 257 | 273 |
| ATP2C1 Isoform 2 of Calcium-transporting ATPase type 2C member 1 | IPI0022047E | ITGDSQETAVAIASR | 95.00% | 114 | 40.8 | 569 | 583 |
| ATP2C1 Isoform 2 of Calcium-transporting ATPase type 2C member 1 | IPI0022047E | ITGDSQETAVAIASRLG | 95.00% | 114 | 40.5 | 569 | 585 |
| ATP2C1 Isoform 2 of Calcium-transporting ATPase type 2C member 1 | IPI0022047E | TGDSQETAVAIASRLG | 95.00% | 78 | 40.1 | 570 | 585 |
| ATP2C1 Isoform 2 of Calcium-transporting ATPase type 2C member 1 | IPI0022047E | DGVNDAVALKAADIG | 95.00% | 91.9 | 40.8 | 644 | 658 |
| ATP2C1 Isoform 2 of Calcium-transporting ATPase type 2C member 1 | IPI0022047E | GKPTEGALIALAMK | 95.00% | 85 | 35.3 | 423 | 436 |
| ATP2C1 Isoform 2 of Calcium-transporting ATPase type 2C member 1 | IPI0022047E | KPTEGALIALAMK | 95.00% | 77.2 | 34.6 | 424 | 436 |
| ATP2C1 Isoform 2 of Calcium-transporting ATPase type 2C member 1 | IPI0022047E | YEQVIKYCTTYQSKG | 95.00% | 65.4 | 40.2 | 483 | 497 |
| ATP2C1 Isoform 2 of Calcium-transporting ATPase type 2C member 1 | IPI0022047E | GDGVNDAVALKAADIG | 95.00% | 57.3 | 40.6 | 643 | 658 |
| ATP2C1 Isoform 2 of Calcium-transporting ATPase type 2C member 1 | IPI0022047E | EQVIKYCTTYQSKG | 95.00% | 53.5 | 39.6 | 484 | 497 |
| ATP5A1 ATP synthase subunit alpha, mitochondrial | IPI0044049E | EPDNVGVVVFVGNDK | 95.00% | 112 | 39.1 | 110 | 123 |
| ATP6AP1 Vacuolar ATP synthase subunit S1 | IPI0078411E | NKQDSAFSNLENALD | 95.00% | 87.9 | 38.7 | 111 | 125 |
| ATP6AP1 Vacuolar ATP synthase subunit S1 | IPI0078411E | VPYTAALTAVRPSRVA | 91.90% | 46.8 | 37.2 | 213 | 228 |
| ATP7A Isoform 4 of Copper-transporting ATPase 1 | IPI0002861C | LSDTNEPLVVIQPSSE | 95.00% | 90.1 | 40.8 | 444 | 460 |
| ATP7A Isoform 4 of Copper-transporting ATPase 1 | IPI0002861C | DTNEPLVVIQPSSE | 95.00% | 59.1 | 40.7 | 446 | 459 |
| ATP7A Isoform 4 of Copper-transporting ATPase 1 | IPI0002861C | SDTNEPLVVIQPSSE | 95.00% | 52.1 | 40.3 | 445 | 460 |
| ATP7A Isoform 4 of Copper-transporting ATPase 1 | IPI0002861C | KPGSTVIAGSINQNGSL | 95.00% | 57 | 40.7 | 806 | 822 |
| ATP8A1 Isoform Long of Probable phospholipid-transporting ATPase IA | IPI0003240E | DGANDVSMIQTAVHG | 95.00% | 90.1 | 37.5 | 793 | 807 |
| ATP8A1 Isoform Long of Probable phospholipid-transporting ATPase IA | IPI0003240E | NGIVSQSEVIRAYDTT | 95.00% | 77.5 | 39.8 | 1134 | 1149 |
| ATP8A1 Isoform Long of Probable phospholipid-transporting ATPase IA | IPI0003240E | GIVSQSEVIRAYDTTKQRP | 95.00% | 63 | 41 | 1135 | 1153 |
| ATP8A1 Isoform Long of Probable phospholipid-transporting ATPase IA | IPI0003240E | ENDFALIDGKT | 95.00% | 76.6 | 41.6 | 729 | 740 |
| ATP8A1 Isoform Long of Probable phospholipid-transporting ATPase IA | IPI0003240E | KENDFALIDGKT | 95.00% | 71.4 | 40.6 | 728 | 740 |
| ATP8A1 Isoform Long of Probable phospholipid-transporting ATPase IA | IPI0003240E | RKENDFALIDGKT | 93.50% | 52.3 | 39.9 | 727 | 740 |
| B2M B2M protein | IPI0079637E | TPTEKDEYACRVNHVT | 95.00% | 53.3 | 39.2 | 91 | 106 |
| B4GALT1 Isoform Long of Beta-1,4-galactosyltransferase 1 | IPI00215767 | TPLQGGNSAAAIGQSSGELR | 95.00% | 144 | 40.6 | 45 | 65 |
| B4GALT1 Isoform Long of Beta-1,4-galactosyltransferase 1 | IPI00215767 | GGNSNSAAAIGQSSGEL | 95.00% | 118 | 39.1 | 49 | 64 |
| B4GALT1 Isoform Long of Beta-1,4-galactosyltransferase 1 | IPI00215767 | TPLQGGNSAAAIGQSSGEL | 95.00% | 109 | 40.2 | 45 | 64 |
| B4GALT1 Isoform Long of Beta-1,4-galactosyltransferase 1 | IPI00215767 | GGNSNSAAAIGQSSGELR | 95.00% | 90.4 | 39.9 | 49 | 65 |
| B4GALT1 Isoform Long of Beta-1,4-galactosyltransferase 1 | IPI00215767 | TPLQGGNSAAAIGQS | 95.00% | 80.4 | 39.6 | 45 | 60 |
| B4GALT1 Isoform Long of Beta-1,4-galactosyltransferase 1 | IPI00215767 | GGNSNSAAAIGQSSG | 95.00% | 74.5 | 37.1 | 49 | 62 |
| B4GALT1 Isoform Long of Beta-1,4-galactosyltransferase 1 | IPI00215767 | TPLQGGNSAAAIGQ | 95.00% | 54.7 | 39.7 | 45 | 59 |
| B4GALT5 Beta-1,4-galactosyltransferase 5 | IPI0001165E | DNVRTIGAQVYEQV | 95.00% | 85.8 | 40.6 | 55 | 68 |
| B4GALT5 Beta-1,4-galactosyltransferase 5 | IPI0001165E | DNVRTIGAQVYEQ | 95.00% | 82.9 | 40.1 | 55 | 67 |
| B4GALT5 Beta-1,4-galactosyltransferase 5 | IPI0001165E | DNVRTIGAQVYEQVL | 95.00% | 78.2 | 40.5 | 55 | 69 |
| B4GALT5 Beta-1,4-galactosyltransferase 5 | IPI0001165E | DNVRTIGAQVYEQVLR | 95.00% | 66 | 40.3 | 55 | 70 |
| BIRC6 baculoviral IAP repeat-containing 6 | IPI0029963E | QSPSANVL | 95.00% | 45.3 | 42.3 | 4202 | 4209 |
| BLMH Bleomycin hydrolase | IPI0021957E | AQNVGTTHTDL | 95.00% | 47.7 | 38.2 | 107 | 116 |
| BMPR2 Bone morphogenetic protein receptor type-2 | IPI0078315E | SVNSHAATTQYANGTV | 95.00% | 61.4 | 38.6 | 815 | 830 |
| BST2 Bone marrow stromal antigen 2 | IPI00026241 | QQELTEAQKGFQDVE | 95.00% | 70.5 | 39.4 | 71 | 85 |
| BST2 Bone marrow stromal antigen 2 | IPI00026241 | LQELTEAQKGFQDVE | 95.00% | 66.8 | 40.9 | 70 | 85 |
| BST2 Bone marrow stromal antigen 2 | IPI00026241 | LLQELTEAQKGFQDVE | 95.00% | 66.7 | 41 | 69 | 85 |
| BTN3A2 Butyrophilin subfamily 3 member A2 | IPI0009958E | EVAASVIMRGGSGEG | 95.00% | 73.3 | 40.6 | 203 | 217 |
| C14orf56 similar to FLJ00035 protein | IPI00888501 | KEAGNGVN | 95.00% | 56.7 | 41.5 | 109 | 116 |
| C19orf28 Isoform 2 of Uncharacterized MFS-type transporter C19orf28 | IPI0016664C | GPHTNSGAFVYGSMS | 95.00% | 49.9 | 35.2 | 386 | 400 |
| C1orf38 Isoform 2 of Induced by contact to basement membrane 1 protein | IPI00003922 | LEELVSATTQSSKQ | 95.00% | 105 | 40.7 | 93 | 106 |
| C21orf67 Isoform A of Uncharacterized protein C21orf67 | IPI00067917 | VENPSP1 | 95.00% | 56.5 | 39.5 | 10 | 16 |
| C3orf52 TPA-induced transmembrane protein | IPI0030304E | TPLNAGDKVFPSLD | 95.00% | 72.7 | 40.1 | 26 | 39 |
| C6orf72 Uncharacterized protein C6orf72 | IPI00026031 | QVYVNDLPVNSGVTR | 95.00% | 71.2 | 40.7 | 71 | 85 |
| CADM1 Isoform 1 of Cell adhesion molecule 1 | IPI0000381E | VPPRNLMDIQKDTAVE | 94.50% | 54.6 | 39.7 | 142 | 158 |
| CADM1 Isoform 1 of Cell adhesion molecule 1 | IPI0000381E | VPPRNLMDIQKDTAVEG | 93.40% | 52.3 | 40.1 | 142 | 159 |
| CALCOCO2 Calcium-binding and coiled-coil domain-containing protein 2 | IPI0074336C | LPIDLNNKSAKQKEVQ | 95.00% | 74.5 | 38.9 | 77 | 92 |
| CALCOCO2 Calcium-binding and coiled-coil domain-containing protein 2 | IPI0074336C | MKQNETTAMKQKQELMD | 95.00% | 55.2 | 38.9 | 289 | 305 |
| CALCOCO2 Calcium-binding and coiled-coil domain-containing protein 2 | IPI0074336C | VDEEDGVVRGASIPFQFRPEN | 92.20% | 51.7 | 41.7 | 110 | 129 |
| CALCOCO2 Calcium-binding and coiled-coil domain-containing protein 2 | IPI0074336C | VDEEDGVVRGASIPFQFRPE | 92.10% | 51.3 | 41.5 | 110 | 128 |
| CALCOCO2 Calcium-binding and coiled-coil domain-containing protein 2 | IPI0074336C | VDEEDGVVRGASIPFQ | 95.00% | 49.5 | 40.2 | 110 | 124 |
| CALCOCO2 Calcium-binding and coiled-coil domain-containing protein 2 | IPI0074336C | EDGVVRGASIPFQFRPE | 90.70% | 48.7 | 41.1 | 112 | 128 |
| CALM3;CALM2;CALM1 Calmodulin | IPI0007524E | VNYEEFVQMMTAK | 95.00% | 95.1 | 38.6 | 140 | 152 |
| CALM3;CALM2;CALM1 Calmodulin | IPI0007524E | GYISAAELRHVMT | 95.00% | 77.4 | 39.6 | 102 | 114 |
| CALM3;CALM2;CALM1 Calmodulin | IPI0007524E | GYISAAELRHVMTN | 95.00% | 73 | 40.2 | 102 | 115 |
| CALM3;CALM2;CALM1 Calmodulin | IPI0007524E | DNGYISAAELRHVMTN | 95.00% | 68.9 | 39.5 | 99 | 115 |
| CALM3;CALM2;CALM1 Calmodulin | IPI0007524E | NGYISAAELRHV | 95.00% | 66.2 | 40.1 | 101 | 112 |
| CALM3;CALM2;CALM1 Calmodulin | IPI0007524E | DNGYISAAELRHVMT | 95.00% | 65.3 | 40.2 | 99 | 114 |
| CALM3;CALM2;CALM1 Calmodulin | IPI0007524E | NGYISAAELRHVMTN | 95.00% | 63.5 | 39.8 | 101 | 115 |
| CALM3;CALM2;CALM1 Calmodulin | IPI0007524E | DKDNGYISAAELRHVMTN | 95.00% | 60.2 | 39.9 | 97 | 115 |
| CALM3;CALM2;CALM1 Calmodulin | IPI0007524E | DNGYISAAELRHVM | 95.00% | 57.4 | 39.2 | 99 | 113 |
| CALM3;CALM2;CALM1 Calmodulin | IPI0007524E | DKDGDGTITTKELGTVMRSLG | 94.80% | 56.8 | 41.2 | 21 | 41 |
| CALML5 Calmodulin-like protein 5 | IPI0002153E | FSAVDTDGNNGTIN | 95.00% | 95.7 | 37.6 | 17 | 29 |
| CALML5 Calmodulin-like protein 5 | IPI0002153E | SAVDTDGNNGTIN | 95.00% | 76.2 | 36.7 | 18 | 29 |
| CAPG gelsolin-like capping protein | IPI0084809C | APNTQVEILPQGH | 95.00% | 79.4 | 41.1 | 323 | 336 |
| CAPG gelsolin-like capping protein | IPI0084809C | TGQMNLTKVADSSPF | 95.00% | 57.3 | 40.4 | 258 | 272 |

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|--|-------------|----------------------|--------|------|------|-----|-----|
| CAPG Macrophage-capping protein | IPI00027341 | TGQMNLTKVADSSPF | 95.00% | 57.3 | 40.4 | 258 | 272 |
| CAPG Macrophage-capping protein | IPI00027341 | APNTQVEILPQGRE | 95.00% | 74.9 | 39.1 | 323 | 336 |
| CAPG Macrophage-capping protein | IPI00027341 | APNTQVEILPQGRES | 94.80% | 49.1 | 40.3 | 323 | 337 |
| CCAR1 Cell division cycle and apoptosis regulator protein 1 | IPI00217357 | LQQAAAAAAA | 95.00% | 59.4 | 39.4 | 69 | 79 |
| CCDC50 Isoform 2 of Coiled-coil domain-containing protein 50 | IPI0021705E | QVDMRAAQVAQDEEIA | 95.00% | 65.5 | 39.1 | 323 | 338 |
| CCR7 C-C chemokine receptor type 7 | IPI00027687 | NITSSTCELSKQ | 95.00% | 85 | 38.3 | 292 | 303 |
| CCT2 T-complex protein 1 subunit beta | IPI0029777E | EGNTTAGLDMREGTIGDM | 95.00% | 76.9 | 35.8 | 471 | 488 |
| CCT8 59 kDa protein | IPI0030292E | EDGAISTIVLRGSTDN | 95.00% | 88.3 | 40.7 | 368 | 383 |
| CCT8 59 kDa protein | IPI0030292E | DGAISTIVLRGSTDNL | 95.00% | 86.4 | 40 | 369 | 384 |
| CCT8 59 kDa protein | IPI0030292E | DGAISTIVLRGSTDN | 95.00% | 84.2 | 40.8 | 369 | 383 |
| CD22 Isoform CD22-alpha of B-cell receptor CD22 | IPI0021839C | QWLLEGVPMRQAAVT | 95.00% | 73 | 40.5 | 175 | 189 |
| CD22 Isoform CD22-alpha of B-cell receptor CD22 | IPI0021839C | QWLLEGVPMRQAA | 95.00% | 51.6 | 39.3 | 175 | 187 |
| CD300A Isoform 2 of CMRF35-like molecule 8 | IPI0005409E | SPREELHYASVVFDSNTN | 95.00% | 70.3 | 39.1 | 111 | 128 |
| CD320 CD320 antigen | IPI00641251 | YGVIAAAA VLSAS | 95.00% | 80.8 | 40.5 | 187 | 199 |
| CD40 Isoform 1 of Tumor necrosis factor receptor superfamily member 5 | IPI0001828E | APVQETLHGCCPVTQEDGKE | 95.00% | 72.9 | 39.2 | 249 | 268 |
| CD40 Isoform 1 of Tumor necrosis factor receptor superfamily member 5 | IPI0001828E | APVQETLHGCCPVTQEDG | 95.00% | 62.2 | 38.7 | 249 | 266 |
| CD44 Isoform 12 of CD44 antigen | IPI0029716C | DETRNLQNVDMKIGV | 95.00% | 60.7 | 40.7 | 677 | 691 |
| CD44 Isoform 12 of CD44 antigen | IPI0029716C | ADETRNLQNVDMKIGV | 94.30% | 54.8 | 40.4 | 676 | 691 |
| CD47 Isoform OA3-293 of Leukocyte surface antigen CD47 | IPI00216514 | VPTDFSSAKIEVSQ | 95.00% | 83.2 | 41.2 | 77 | 90 |
| CD47 Isoform OA3-293 of Leukocyte surface antigen CD47 | IPI00216514 | VPTDFSSAKIEVSQ | 95.00% | 61.6 | 40.9 | 77 | 91 |
| CD55 Decay-accelerating factor splicing variant 4 | IPI0015241E | LISGSSVQWSDPLPE | 95.00% | 75.1 | 40.8 | 205 | 219 |
| CD55 Decay-accelerating factor splicing variant 4 | IPI0015241E | ISGSSVQWSDPLPE | 95.00% | 51.7 | 39.2 | 206 | 219 |
| CD69 Early activation antigen CD69 | IPI00014854 | TSAGNACSEHGATL | 95.00% | 49.2 | 35.4 | 107 | 120 |
| CD70 CD70 antigen | IPI0003171E | IQRFAQAQQPLE | 91.60% | 46.8 | 40 | 38 | 51 |
| CD79A Isoform Long of B-cell antigen receptor complex-associated protein alpha | IPI0000847G | GLNLDDCSMYEDISRG | 95.00% | 85.2 | 33.9 | 152 | 167 |
| CD80 T-lymphocyte activation antigen CD80 | IPI00015914 | VEELAQTIRYWQKE | 94.60% | 55.7 | 40.5 | 56 | 69 |
| CD84 Isoform 3 of SLAM family member 5 | IPI0002203E | YDEILQSKVLPSKEEPV | 90.10% | 47.5 | 40.7 | 165 | 181 |
| CD97 Isoform 2 of CD97 antigen | IPI0029941E | APPVRLHIAQTLLSNLED | 90.60% | 46.9 | 39.4 | 318 | 335 |
| CDC42SE2 CDC42 small effector protein 2 | IPI0002497E | SGMNSVSIQIQMQ | 95.00% | 58.9 | 36.3 | 48 | 61 |
| CDSN cDNA FLJ78714, highly similar to Homo sapiens corneodesmosin, mRNA | IPI00646774 | GILNPSQPGQSSSSSQT | 95.00% | 66.2 | 39.3 | 185 | 201 |
| CHL1 Isoform 2 of Neural cell adhesion molecule L1-like protein | IPI0029905E | IPSSVQVPTIIKQSKVQ | 92.30% | 45.2 | 35.1 | 13 | 30 |
| CLCN7 Putative chloride channel protein 7 | IPI00020524 | GPMIHSGSVIAAGISQG | 95.00% | 59.5 | 40.5 | 201 | 217 |
| CMIP Isoform 1 of C-Maf-inducing protein | IPI0002843E | IDNNDTLQIIS | 94.00% | 49.5 | 41.3 | 454 | 465 |
| CMIP Isoform 1 of C-Maf-inducing protein | IPI0002843E | IDNNDTLQIIS | 85.30% | 45.7 | 41.3 | 453 | 465 |
| COCH Cochlin | IPI0001238E | EISDIGAKIAAVQ | 95.00% | 82.7 | 41.1 | 249 | 261 |
| COCH Cochlin | IPI0001238E | EISDIGAKIAAVQFT | 90.40% | 46.7 | 40.5 | 249 | 263 |
| COCH Cochlin | IPI0001238E | STKENVLAVIRNIR | 92.90% | 45.9 | 34.6 | 276 | 289 |
| CPD Carboxypeptidase D | IPI0002707E | AENGLESMLRSSSN | 95.00% | 80 | 40.2 | 911 | 925 |
| CPD Carboxypeptidase D | IPI0002707E | AENGLESMLRSSSNL | 95.00% | 67.6 | 40.7 | 911 | 926 |
| CPD Carboxypeptidase D | IPI0002707E | SGNLHGGSVVASYPFDD | 95.00% | 64.8 | 37.4 | 253 | 269 |
| CPD Carboxypeptidase D | IPI0002707E | SGNLHGGSVVASYPFDD | 95.00% | 55 | 39.1 | 253 | 268 |
| CR2 Isoform B of Complement receptor type 2 | IPI0021698E | TPIAVGTVIR | 95.00% | 84.5 | 36.9 | 39 | 48 |
| CR2 Isoform B of Complement receptor type 2 | IPI0021698E | TPIAVGTVIRYS | 95.00% | 81.2 | 39 | 39 | 50 |
| CSTF2 Isoform 1 of Cleavage stimulation factor 64 kDa subunit | IPI0001325E | ATEEQLK | 95.00% | 56 | 44.3 | 27 | 33 |
| CTNND1 Isoform 1AB of Catenin delta-1 | IPI0018246E | ASILASVKEQEAQFE | 95.00% | 83.9 | 40.9 | 10 | 24 |
| CTSA Lysosomal protective protein | IPI00021794 | KDPENSPVVLWNLGGPG | 95.00% | 81.8 | 40.8 | 71 | 87 |
| CTSD Cathepsin D | IPI0001122E | AIVDTGTSMLVGPVD | 95.00% | 52.2 | 41.1 | 163 | 177 |
| CTSH Cathepsin H | IPI00297487 | GALESAIAIATGKM | 95.00% | 98.8 | 39.8 | 148 | 161 |
| CTSH Cathepsin H | IPI00297487 | TGALESAIAIATGKM | 95.00% | 98.4 | 39.5 | 147 | 161 |
| CTSH Cathepsin H | IPI00297487 | TTGALESAIAIATGKM | 95.00% | 94.7 | 41.3 | 146 | 161 |
| CTSH Cathepsin H | IPI00297487 | GALESAIAIATGKMLS | 95.00% | 85.8 | 41 | 148 | 163 |
| CTSH Cathepsin H | IPI00297487 | GALESAIAIATGKML | 95.00% | 79.5 | 38.5 | 148 | 162 |
| CTSH Cathepsin H | IPI00297487 | TGALESAIAIATGKML | 95.00% | 78.7 | 40 | 147 | 162 |
| CTSH Cathepsin H | IPI00297487 | TPDKVNHAVLAVGYGEK | 95.00% | 65.2 | 40 | 275 | 291 |
| CTSH Cathepsin H | IPI00297487 | TPDKVNHAVLAVGYGEKN | 95.00% | 64.2 | 40.5 | 275 | 292 |
| CTSH Cathepsin H | IPI00297487 | TPDKVNHAVLAVGYGEKNG | 95.00% | 57.5 | 40.5 | 275 | 293 |
| CTSH Cathepsin H | IPI00297487 | GPQWGMNGYFLIERGKNM | 95.00% | 59.5 | 39.8 | 304 | 321 |
| CTSH Cathepsin H | IPI00297487 | WGMNGYFLIERGKNM | 94.40% | 53.8 | 39.2 | 307 | 321 |
| CTSH Cathepsin H | IPI00297487 | GPQWGMNGYFLIERGKN | 93.60% | 53.6 | 40.9 | 304 | 320 |
| CTSS Cathepsin S | IPI0029915C | QNVNHGVLVVGYGDL | 95.00% | 74.1 | 39 | 274 | 288 |
| CTSS Cathepsin S | IPI0029915C | NVNHGVLVVGYGDL | 95.00% | 52.3 | 39.5 | 275 | 288 |
| CTSS Cathepsin S | IPI0029915C | IDNKGIDSDASYPY | 95.00% | 55 | 38.8 | 193 | 206 |
| CTSS Cathepsin S | IPI0029915C | LPYGREVDLKEAVANKGPVS | 91.80% | 49.3 | 39.9 | 230 | 249 |
| CTSZ Cathepsin Z | IPI0000274E | VDGVNYASITRNQHIQ | 93.20% | 52.9 | 41 | 71 | 87 |
| CTSZ Cathepsin Z | IPI0000274E | VDGVNYASITRNQH | 91.80% | 49 | 39.6 | 71 | 84 |
| DAAM1 Isoform 1 of Disheveled-associated activator of morphogenesis 1 | IPI0033780C | IDQLNSMAARKSLL | 95.00% | 54.8 | 37.6 | 107 | 120 |
| DAG1 Dystroglycan | IPI00028911 | VQFNSNSQLMYGLPDSS | 95.00% | 64.6 | 37.9 | 552 | 568 |
| DCD Dermcidin | IPI00027547 | PGLARQ | 95.00% | 50.7 | 39.6 | 49 | 54 |
| DDX6 Probable ATP-dependent RNA helicase DDX6 | IPI0003032C | DNIAQMVVPTRE | 95.00% | 57.7 | 38.5 | 163 | 175 |
| DHCR24 24-dehydrocholesterol reductase | IPI0001670C | AVIMTGVMTDEAEPS | 95.00% | 77.6 | 38.2 | 277 | 291 |

SUPPLEMENTARY DATA

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|--|-------------|---------------------------|--------|------|------|------|------|
| DHCR24 24-dehydrocholesterol reductase | IPI00016703 | GGLIMGTGIESSSHK | 95.00% | 64.7 | 40.3 | 165 | 179 |
| DHRS7 Isoform 1 of Dehydrogenase/reductase SDR family member 7 | IPI00006957 | DILVNNNGMSQRSL | 95.00% | 72 | 38.8 | 133 | 146 |
| DNAJC5 Isoform 1 of DnaJ homolog subfamily C member 5 | IPI00402231 | DEREATDTPVIQPASAT | 95.00% | 84.6 | 40.4 | 162 | 179 |
| DNAJC5 Isoform 1 of DnaJ homolog subfamily C member 5 | IPI00402231 | EATDTPVIQPASAT | 95.00% | 73.4 | 40.9 | 165 | 179 |
| DNAJC5 Isoform 1 of DnaJ homolog subfamily C member 5 | IPI00402231 | EATDTPVIQPASA | 95.00% | 50.7 | 40.7 | 165 | 178 |
| DSP Isoform DPI of Desmoplakin | IPI00013933 | SEILSDPSDDTKG | 95.00% | 76.1 | 38.5 | 1802 | 1814 |
| DSP Isoform DPI of Desmoplakin | IPI00013933 | ILSDPSDDTKG | 95.00% | 59.9 | 41.1 | 1804 | 1814 |
| DSP Isoform DPI of Desmoplakin | IPI00013933 | IVDPVSNLR | 95.00% | 53.1 | 39.3 | 1701 | 1709 |
| EEF1A1 Elongation factor 1-alpha | IPI00025447 | VIIINHPPQISAGYA | 95.00% | 70.8 | 40 | 344 | 358 |
| EEF1A1 Elongation factor 1-alpha | IPI00025447 | IILNHPGQISAGYA | 95.00% | 70 | 40.5 | 345 | 358 |
| EEF1A1 Elongation factor 1-alpha | IPI00025447 | VIIINHPPQISAGYAPV | 95.00% | 66.3 | 39.1 | 344 | 360 |
| EEF1A1 Elongation factor 1-alpha | IPI00025447 | VIIINHPPQISAGYAP | 95.00% | 55 | 37.5 | 344 | 359 |
| EEF1A1 Elongation factor 1-alpha | IPI00025447 | IILNHPGQISAGYAPV | 95.00% | 54.3 | 37.1 | 345 | 360 |
| EEF1A1 Elongation factor 1-alpha | IPI00025447 | IILNHPGQISAGYAP | 94.20% | 48.6 | 40.3 | 345 | 359 |
| EEF1A1 Elongation factor 1-alpha | IPI00025447 | KDGNASGTTLLEALD | 95.00% | 57.4 | 41.1 | 219 | 233 |
| EEF1A1 Elongation factor 1-alpha | IPI00025447 | DGNASGTTLLEALD | 89.90% | 46.7 | 40.7 | 220 | 233 |
| EFHD2 EF-hand domain-containing protein D2 | IPI00060181 | TPEQPGLNGAAAAAAGAPDEA | 95.00% | 79.2 | 39.4 | 24 | 44 |
| EFHD2 EF-hand domain-containing protein D2 | IPI00060181 | QPGLNGAAAAAAGAPD | 95.00% | 49.5 | 39.3 | 27 | 42 |
| EHD4 EH domain-containing protein 4 | IPI0000557E | SDFESEAIAFRGQDDK | 90.10% | 46.7 | 39.9 | 200 | 216 |
| EIF4B Eukaryotic translation initiation factor 4B | IPI0001207E | SPTSGGGKVAQAQPS | 95.00% | 70.1 | 39.6 | 504 | 518 |
| EIF6 Eukaryotic translation initiation factor 6 | IPI0001010E | GTVNRGSEVIAAGMV | 95.00% | 55.1 | 41 | 165 | 179 |
| ENG Isoform Long of Endoglin | IPI00017567 | EPGQQSFVQVRVSPSVS | 95.00% | 71.1 | 40.6 | 468 | 484 |
| ENG Isoform Long of Endoglin | IPI00017567 | EPGQQSFVQVRVSPS | 95.00% | 69.3 | 40.9 | 468 | 482 |
| ENG Isoform Long of Endoglin | IPI00017567 | EPGQQSFVQVRVSPSV | 95.00% | 60.8 | 41 | 468 | 483 |
| ENG Isoform Long of Endoglin | IPI00017567 | DANHNMQIWTTEYS | 95.00% | 62.2 | 33.5 | 264 | 278 |
| ENG Isoform Long of Endoglin | IPI00017567 | GPEGGTVELIQGRAAKGN | 95.00% | 56 | 39.1 | 498 | 515 |
| ENG Isoform Long of Endoglin | IPI00017567 | GPEGGTVELIQGRAAKG | 94.70% | 54 | 38.6 | 498 | 514 |
| ENG Isoform Long of Endoglin | IPI00017567 | IDANHNMQIWTTEYS | 95.00% | 52.9 | 36.7 | 263 | 277 |
| ENG Isoform Long of Endoglin | IPI00017567 | IDANHNMQIWTTEYS | 95.00% | 51.5 | 36.6 | 263 | 278 |
| ENG Isoform Long of Endoglin | IPI00017567 | LIDANHNMQIWTTEYS | 95.00% | 50.3 | 39 | 262 | 277 |
| ENG Isoform Long of Endoglin | IPI00017567 | IDANHNMQIWTTEYS | 95.00% | 48.4 | 37.3 | 263 | 276 |
| ENO1 Isoform alpha-enolase of Alpha-enolase | IPI0046524E | TDKVVIGMDVAASE | 95.00% | 87.8 | 40.4 | 144 | 157 |
| ENO1 Isoform alpha-enolase of Alpha-enolase | IPI0046524E | TDKVVIGMDVAASEFF | 95.00% | 74.8 | 40.5 | 144 | 159 |
| ENO1 Isoform alpha-enolase of Alpha-enolase | IPI0046524E | TDKVVIGMDVAASEF | 95.00% | 71.9 | 39.1 | 144 | 158 |
| ENPP5 Ectonucleotide pyrophosphatase/phosphodiesterase family member 5 | IPI00011994 | AGHTSGAAMWPGTDVK | 95.00% | 89.4 | 38.8 | 130 | 145 |
| ENTPD1 Isoform Placental I of Ectonucleoside triphosphate diphosphohydrolase | IPI00220852 | YPFDFQGARITGQEEG | 95.00% | 83.4 | 39.9 | 159 | 175 |
| ENTPD1 Isoform Placental I of Ectonucleoside triphosphate diphosphohydrolase | IPI00220852 | DFQGARITGQEEG | 95.00% | 79.5 | 40.2 | 162 | 175 |
| ENTPD1 Isoform Placental I of Ectonucleoside triphosphate diphosphohydrolase | IPI00220852 | YPFDFQGARITGQEEGA | 95.00% | 67.6 | 39.7 | 159 | 176 |
| ENTPD1 Isoform Placental I of Ectonucleoside triphosphate diphosphohydrolase | IPI00220852 | YPFDFQGARITGQEE | 95.00% | 60.1 | 39.6 | 159 | 174 |
| ENTPD1 Isoform Placental I of Ectonucleoside triphosphate diphosphohydrolase | IPI00220852 | DFQGARITGQEEGA | 95.00% | 59.4 | 40.3 | 162 | 176 |
| ESAM Endothelial cell-selective adhesion molecule | IPI00303161 | GPGAADVAVAGVVTLVG | 95.00% | 49.8 | 37.2 | 244 | 260 |
| ESAM Endothelial cell-selective adhesion molecule | IPI00303161 | AVPVMVPAQSQAGSLV | 93.80% | 48 | 39.9 | 375 | 390 |
| F11R Junctional adhesion molecule A | IPI00001754 | SDTGEYSCEARNYGY | 95.00% | 64.5 | 28.7 | 205 | 219 |
| F11R Junctional adhesion molecule A | IPI00001754 | DTGEYSCEARNYGY | 95.00% | 57.7 | 28 | 206 | 219 |
| FAM38A family with sequence similarity 38, member A | IPI00006093 | DPGEREAGASLYQGLM | 95.00% | 67.5 | 38.7 | 1667 | 1682 |
| FAM3C Protein FAM3C | IPI00334282 | DNVLMGSKVKNVGRGIN | 95.00% | 64.2 | 41.1 | 89 | 105 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | DQMAQKSQSTQISQEELE | 95.00% | 126 | 38.2 | 76 | 93 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | DQMAQKSQSTQISQEELE | 95.00% | 98.1 | 39.4 | 76 | 92 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | MAQKSQSTQISQEELE | 95.00% | 97.4 | 39.6 | 78 | 93 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | DQMAQKSQSTQISQEELEEL | 95.00% | 91.9 | 39.9 | 76 | 94 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | MAQKSQSTQISQEELEEL | 95.00% | 88.2 | 40.6 | 78 | 94 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | GDQMAQKSQSTQISQEELE | 95.00% | 85.6 | 38.2 | 75 | 93 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | AQKSQSTQISQEELEEL | 95.00% | 85 | 40.6 | 79 | 94 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | AQKSQSTQISQEELE | 95.00% | 84.1 | 40.5 | 79 | 93 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | MAQKSQSTQISQEELEELR | 95.00% | 81.7 | 41.6 | 78 | 95 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | AQKSQSTQISQEELE | 95.00% | 74.9 | 40.6 | 79 | 92 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | GDQMAQKSQSTQISQEELEELR | 95.00% | 71.2 | 40.7 | 75 | 95 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | GDQMAQKSQSTQISQEELEELRAEQ | 95.00% | 65.6 | 41.9 | 73 | 101 |
| FCER2 Isoform A of Low affinity immunoglobulin epsilon Fc receptor | IPI00027491 | DQMAQKSQSTQISQEELEELR | 93.80% | 53.8 | 40.7 | 76 | 95 |
| FLOT1 Flotillin-1 | IPI0002743E | SQMLMQAEAAASVR | 95.00% | 109 | 39.5 | 62 | 76 |
| FLT1 Isoform Flt1 of Vascular endothelial growth factor receptor 1 | IPI0001833E | DADSNMGNRIESITQ | 95.00% | 59.6 | 37.4 | 493 | 507 |
| FLT1 Isoform Flt1 of Vascular endothelial growth factor receptor 1 | IPI0001833E | IDQSNSHANIFYSVLT | 93.70% | 48.3 | 40.3 | 282 | 297 |
| FLVCR1 Feline leukemia virus subgroup C receptor-related protein 1 | IPI00022344 | RPDDEEGAAVAPGHP | 95.00% | 98.9 | 38.9 | 3 | 17 |
| FLVCR1 Feline leukemia virus subgroup C receptor-related protein 1 | IPI00022344 | DDEEGAAVAPGHP | 95.00% | 84.8 | 34.7 | 5 | 17 |
| FLVCR1 Feline leukemia virus subgroup C receptor-related protein 1 | IPI00022344 | TPLAPEEETQARLLPAGAG | 95.00% | 83.6 | 40.9 | 69 | 87 |
| FLVCR1 Feline leukemia virus subgroup C receptor-related protein 1 | IPI00022344 | TPLAPEEETQARLLPAG | 95.00% | 66.9 | 40.3 | 69 | 85 |
| FLVCR1 Feline leukemia virus subgroup C receptor-related protein 1 | IPI00022344 | APEEETQARLLPAGAG | 95.00% | 65.2 | 39.9 | 72 | 87 |
| FTL Ferritin light polypeptide variant | IPI0037567E | IRQNYSTDVEAAVN | 95.00% | 92.8 | 40.7 | 5 | 18 |
| FTL Ferritin light polypeptide variant | IPI0037567E | IRQNYSTDVEAAVNSL | 95.00% | 88.6 | 40.6 | 5 | 20 |
| FTL Ferritin light polypeptide variant | IPI0037567E | IRQNYSTDVEAAVNS | 95.00% | 80.4 | 40.3 | 5 | 19 |

SUPPLEMENTARY DATA

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|--|-------------|-------------------------|--------|------|------|------|------|
| FTMT Ferritin, mitochondrial | IPI0016668E | DSEAAINRQINLE | 95.00% | 76.1 | 39.9 | 75 | 87 |
| GALNT10 Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 10 | IPI0037520E | QPDGTPGGSGAAVAPAAGQGS | 95.00% | 118 | 38.3 | 35 | 57 |
| GALNT10 Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 10 | IPI0037520E | TPGGSGAAVAPAAGQGS | 95.00% | 117 | 39 | 39 | 57 |
| GALNT10 Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 10 | IPI0037520E | TPGGSGAAVAPAAGQGS | 95.00% | 116 | 40.4 | 39 | 59 |
| GALNT10 Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 10 | IPI0037520E | TPGGSGAAVAPAAGQGS | 95.00% | 110 | 39.3 | 39 | 56 |
| GALNT10 Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 10 | IPI0037520E | TPGGSGAAVAPAAGQGS | 95.00% | 89.7 | 38.7 | 39 | 54 |
| GALNT10 Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 10 | IPI0037520E | QPDGTPGGSGAAVAPAAGQGS | 95.00% | 64.8 | 39.9 | 35 | 54 |
| GALNT10 Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 10 | IPI0037520E | GTPGGSGAAVAPAAGQGS | 95.00% | 61.7 | 38.9 | 38 | 57 |
| GALNT10 Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 10 | IPI0037520E | TPGGSGAAVAPAAGQGS | 95.00% | 55.2 | 38.3 | 39 | 53 |
| GALNT10 Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 10 | IPI0037520E | GTPGGSGAAVAPAAGQGS | 94.10% | 54.3 | 40.4 | 38 | 59 |
| GALNT2 Polypeptide N-acetylgalactosaminyltransferase 2 | IPI0000466E | EAYVGGTMVRSQDPY | 95.00% | 110 | 36.7 | 84 | 99 |
| GALNT2 Polypeptide N-acetylgalactosaminyltransferase 2 | IPI0000466E | EAYVGGTMVRSQDPYA | 95.00% | 94.6 | 37.8 | 84 | 100 |
| GALNT2 Polypeptide N-acetylgalactosaminyltransferase 2 | IPI0000466E | AYVGGTMVRSQDPY | 95.00% | 83.4 | 38.9 | 85 | 99 |
| GALNT2 Polypeptide N-acetylgalactosaminyltransferase 2 | IPI0000466E | EAYVGGTMVRSQDP | 95.00% | 79.9 | 37.7 | 84 | 98 |
| GAPDH Glyceraldehyde-3-phosphate dehydrogenase | IPI0021901E | FRVPTANVS | 95.00% | 61.7 | 39.8 | 233 | 241 |
| GAPDH Glyceraldehyde-3-phosphate dehydrogenase | IPI0021901E | EGLMTTVHAIATQ | 95.00% | 59.8 | 41 | 172 | 185 |
| GAPDH Glyceraldehyde-3-phosphate dehydrogenase | IPI0021901E | MAHMASKE | 95.00% | 49.6 | 38.5 | 328 | 335 |
| GART Isoform Long of Trifunctional purine biosynthetic protein adenosine-3 | IPI0002527E | EAWVIGSVVAREG | 95.00% | 77 | 38.8 | 759 | 772 |
| GART Isoform Long of Trifunctional purine biosynthetic protein adenosine-3 | IPI0002527E | DIQQHKEEAWVIGSVVAREGSPR | 95.00% | 76.9 | 41.9 | 752 | 775 |
| GART Isoform Long of Trifunctional purine biosynthetic protein adenosine-3 | IPI0002527E | EAWVIGSVVAREGSPR | 95.00% | 73.1 | 41.5 | 758 | 775 |
| GART Isoform Long of Trifunctional purine biosynthetic protein adenosine-3 | IPI0002527E | EAWVIGSVVAREGSPR | 95.00% | 60.5 | 39.8 | 759 | 775 |
| GLG1 golgi apparatus protein 1 | IPI0041471I | IEMWSYAAKVAPAD | 95.00% | 93.7 | 40.6 | 1116 | 1129 |
| GLG1 golgi apparatus protein 1 | IPI0041471I | IEMWSYAAKVAPADG | 95.00% | 88.1 | 39.8 | 1116 | 1130 |
| GLG1 golgi apparatus protein 1 | IPI0041471I | GEKGNLGMNCQQALQ | 95.00% | 72.1 | 38.6 | 471 | 485 |
| GOLIM4 Golgi integral membrane protein 4 | IPI0000496E | MALQRQAEELEGRPOHQ | 88.00% | 45.2 | 40.9 | 458 | 474 |
| GOT1 Aspartate aminotransferase, cytoplasmic | IPI0021902E | NLDYVATSIHEAVTK | 95.00% | 104 | 40.9 | 397 | 411 |
| GOT1 Aspartate aminotransferase, cytoplasmic | IPI0021902E | NLDYVATSIHEAVT | 95.00% | 87.1 | 40.1 | 397 | 410 |
| HGFAC Hepatocyte growth factor activator | IPI0002919E | SPEVYGDISPNN | 95.00% | 80.6 | 37 | 569 | 581 |
| HLA-DMB HLA class II histocompatibility antigen, DM beta chain | IPI0000079E | GVLNSLANVLSQH | 95.00% | 67.2 | 38.8 | 67 | 79 |
| HLA-DMB HLA class II histocompatibility antigen, DM beta chain | IPI0000079E | GVLNSLANVLSQHLN | 95.00% | 65 | 39.5 | 67 | 81 |
| HLA-DPA1 HLA class II histocompatibility antigen, DP alpha chain | IPI0002171I | IKADHVSTYAAFVQTHRPT | 95.00% | 82.2 | 41.4 | 32 | 50 |
| HLA-DPA1 HLA class II histocompatibility antigen, DP alpha chain | IPI0002171I | IKADHVSTYAAFVQTHRPTG | 95.00% | 65.9 | 41.4 | 32 | 51 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | SFEAQGALANIAVDK | 95.00% | 145 | 40.4 | 94 | 108 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | ASFEAQGALANIAVDK | 95.00% | 131 | 40.1 | 93 | 108 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | SFEAQGALANIAVDKAN | 95.00% | 127 | 40.9 | 94 | 110 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | ASFEAQGALANIAVDKA | 95.00% | 125 | 40.8 | 93 | 109 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | ASFEAQGALANIAVDKAN | 95.00% | 124 | 40.6 | 93 | 110 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | FEAQGALANIAVDK | 95.00% | 123 | 41.6 | 95 | 108 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | SFEAQGALANIAVDKA | 95.00% | 119 | 40.7 | 94 | 109 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | FEAQGALANIAVDKAN | 95.00% | 117 | 40.8 | 95 | 110 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | FEAQGALANIAVDKA | 95.00% | 104 | 39.9 | 95 | 109 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | ASFEAQGALANIAVD | 95.00% | 95 | 40.2 | 93 | 107 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | EAQGALANIAVDKA | 95.00% | 93.2 | 40.2 | 96 | 109 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | EAQGALANIAVDK | 95.00% | 92.7 | 40.3 | 96 | 108 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | EAQGALANIAVDKAN | 95.00% | 90.5 | 39.7 | 96 | 110 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | SFEAQGALANIAVD | 95.00% | 83.9 | 40.2 | 94 | 107 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | TVLTNSPVELREPNV | 95.00% | 86.6 | 38.5 | 131 | 145 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | TVLTNSPVELREPNVL | 95.00% | 71.9 | 38.3 | 131 | 146 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | VLTNPSVLEPNV | 95.00% | 68.7 | 39.1 | 132 | 145 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | VLTNPSVLEPNVL | 95.00% | 66.6 | 38.2 | 132 | 146 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | TNSPVELREPNVL | 95.00% | 60.8 | 39.5 | 134 | 146 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | TVLTNSPVELREPNVLI | 95.00% | 60 | 37.1 | 131 | 147 |
| HLA-DRA HLA class II histocompatibility antigen, DR alpha chain | IPI0000517I | VLTNPSVLEPNVLI | 95.00% | 53.5 | 36.6 | 132 | 147 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | WTAVDTAAQISEQKSND | 95.00% | 141 | 38.9 | 154 | 170 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | TAVDTAAQISEQKSND | 95.00% | 139 | 39.6 | 155 | 170 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | WTAVDTAAQISEQKSND | 95.00% | 136 | 39.9 | 154 | 169 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | WTAVDTAAQISEQK | 95.00% | 126 | 39.5 | 154 | 167 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | SWTAVDTAAQISEQK | 95.00% | 125 | 40.1 | 153 | 167 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | TAVDTAAQISEQK | 95.00% | 125 | 39.5 | 155 | 167 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | TAVDTAAQISEQKSND | 95.00% | 116 | 40.4 | 155 | 169 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | TAVDTAAQISEQKSNDASEAE | 95.00% | 116 | 37.9 | 155 | 175 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | AVDTAAQISEQKSND | 95.00% | 115 | 39.8 | 156 | 170 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | AVDTAAQISEQK | 95.00% | 113 | 40 | 156 | 167 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | AVDTAAQISEQKSND | 95.00% | 113 | 39.9 | 156 | 171 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | WTAVDTAAQISEQKSNDAS | 95.00% | 112 | 38.8 | 154 | 172 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | TAVDTAAQISEQKSNDASEA | 95.00% | 111 | 39.3 | 155 | 174 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | WTAVDTAAQISEQKSND | 95.00% | 110 | 39.2 | 154 | 171 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | AVDTAAQISEQKSND | 95.00% | 109 | 40.4 | 156 | 169 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | TAVDTAAQISEQKSND | 95.00% | 109 | 40.9 | 155 | 168 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI0001036E | TAVDTAAQISEQKSND | 95.00% | 105 | 39.7 | 155 | 171 |

SUPPLEMENTARY DATA

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|--|-------------|------------------------|--------|------|------|-----|-----|
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TAVDTAAQISEQKSNDAEAEHC | 95.00% | 105 | 38.2 | 155 | 177 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | WTAVDTAAQISEQKSNDAEAE | 95.00% | 101 | 37.9 | 154 | 177 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | SWTAVDTAAQISEQKSN | 95.00% | 100 | 39.8 | 153 | 169 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TAVDTAAQISEQKSNDAEAEI | 95.00% | 99.8 | 38.1 | 155 | 176 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | WTAVDTAAQISEQKSN | 95.00% | 94.2 | 40.1 | 154 | 168 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | DTAAQISEQKSN | 95.00% | 97.3 | 40 | 158 | 169 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TAVDTAAQISEQKSNDAEAEI | 95.00% | 93.7 | 39.4 | 155 | 178 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | VDTAAQISEQK | 95.00% | 93.3 | 41.6 | 157 | 167 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | DTAAQISEQKSNDA | 95.00% | 90.3 | 38.6 | 158 | 171 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | WTAVDTAAQISEQ | 95.00% | 90.3 | 39.2 | 154 | 166 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TAVDTAAQISEQKSNDA | 95.00% | 89.2 | 39.4 | 155 | 172 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | AVDTAAQISEQKSNDAEAEI | 95.00% | 84.9 | 39.8 | 156 | 178 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | DTAAQISEQK | 95.00% | 80.7 | 40.3 | 158 | 167 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TAAQISEQKSN | 95.00% | 79.3 | 40.4 | 159 | 169 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | AVDTAAQISEQKSN | 95.00% | 78.4 | 41 | 156 | 168 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | AVDTAAQISEQKSNDAEAE | 95.00% | 77.2 | 38.2 | 156 | 177 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | VDTAAQISEQKSNDA | 95.00% | 73.3 | 39.7 | 157 | 170 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | DTAAQISEQKSNDA | 95.00% | 71.8 | 38.8 | 158 | 170 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TAAQISEQKSNDA | 95.00% | 70.1 | 37.7 | 159 | 170 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | WTAVDTAAQISEQKSNDAEAEI | 95.00% | 70 | 39.2 | 154 | 178 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | DTAAQISEQKSNDAEAE | 95.00% | 67.8 | 35.7 | 158 | 177 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | VDTAAQISEQKSN | 95.00% | 65.2 | 40.4 | 157 | 169 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | WTAVDTAAQISEQKSNDAEAEI | 95.00% | 64.7 | 37.7 | 154 | 176 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TAAQISEQKSNDA | 95.00% | 64 | 37.3 | 159 | 171 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | DLRSWTAVDTAAQISEQK | 95.00% | 63.3 | 41.3 | 150 | 167 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | EDLRSWTAVDTAAQISEQKSN | 95.00% | 63 | 41.1 | 149 | 169 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TAAQISEQK | 95.00% | 56.6 | 41.4 | 159 | 167 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TAVDTAAQISEQKSNDAEAEI | 95.00% | 51.7 | 39.7 | 155 | 179 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TAVDTAAQISEQ | 95.00% | 51.5 | 39.4 | 155 | 166 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | WTAVDTAAQISEQKSNDAEAEI | 95.00% | 51.3 | 39.4 | 154 | 179 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | EDLRSWTAVDTAAQISEQK | 92.20% | 51.2 | 41.2 | 149 | 167 |
| HLA-E major histocompatibility complex, class I, E precursor | IPI00010362 | TQDTELVEVTRPAGDG | 95.00% | 69.2 | 39.4 | 246 | 260 |
| HLA-F major histocompatibility complex, class I, F isoform 1 precursor | IPI00294547 | EWTTGYAKANAQTDR | 95.00% | 73.2 | 39.3 | 82 | 96 |
| HLA-F major histocompatibility complex, class I, F isoform 1 precursor | IPI00294547 | TQDTELVEVTRPAGDG | 95.00% | 69.2 | 39.4 | 246 | 260 |
| HLA-G HLA class I histocompatibility antigen, alpha chain G | IPI0001598E | LALNEDLRSWTAADTAAQ | 95.00% | 106 | 41.1 | 148 | 165 |
| HLA-G HLA class I histocompatibility antigen, alpha chain G | IPI0001598E | LALNEDLRSWTAADT | 95.00% | 86.6 | 40.4 | 148 | 162 |
| HLA-G HLA class I histocompatibility antigen, alpha chain G | IPI0001598E | LALNEDLRSWTAADTA | 95.00% | 74.8 | 40.2 | 148 | 163 |
| HLA-G HLA class I histocompatibility antigen, alpha chain G | IPI0001598E | LALNEDLRSWTAAD | 95.00% | 61.9 | 39.3 | 148 | 161 |
| HLA-G HLA class I histocompatibility antigen, alpha chain G | IPI0001598E | LALNEDLRSWTAADTAA | 95.00% | 59.6 | 40.3 | 148 | 164 |
| HSP90AA2 Putative heat shock protein HSP 90-alpha A2 | IPI00031522 | DLINNLGTIAKSGTK | 95.00% | 84.7 | 38.5 | 102 | 116 |
| HSP90AA2 Putative heat shock protein HSP 90-alpha A2 | IPI00031522 | DLINNLGTIAKSGTKA | 95.00% | 80.5 | 38.1 | 102 | 117 |
| HSP90B1 Endoplasmic | IPI0002723C | DSNEFSVIADPRG | 95.00% | 78.3 | 37.7 | 226 | 238 |
| HSP90B1 Endoplasmic | IPI0002723C | ESDSNEFSVIADPRGN | 95.00% | 69.2 | 37 | 224 | 239 |
| HSP90B1 Endoplasmic | IPI0002723C | ESDSNEFSVIADPRGNT | 95.00% | 67.7 | 36.9 | 224 | 240 |
| HSP90B1 Endoplasmic | IPI0002723C | SDSNEFSVIADPRG | 95.00% | 65.8 | 38.5 | 225 | 238 |
| HSPA13 Stress 70 protein chaperone microsome-associated 60 kDa protein | IPI0029929E | AVVTGVAIQAGIDGG | 95.00% | 111 | 39.1 | 435 | 449 |
| HSPA13 Stress 70 protein chaperone microsome-associated 60 kDa protein | IPI0029929E | VINEPTAAAMAYGLH | 95.00% | 107 | 38.7 | 200 | 214 |
| HSPA13 Stress 70 protein chaperone microsome-associated 60 kDa protein | IPI0029929E | RVINEPTAAAMAYGLH | 95.00% | 73.6 | 40.1 | 199 | 214 |
| HSPA13 Stress 70 protein chaperone microsome-associated 60 kDa protein | IPI0029929E | LRVINEPTAAAMAYGLH | 95.00% | 64.4 | 40.8 | 198 | 214 |
| HSPA13 Stress 70 protein chaperone microsome-associated 60 kDa protein | IPI0029929E | RVINEPTAAAMAYG | 95.00% | 62.9 | 39.8 | 199 | 212 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | INEPTAAAIYGLDRTG | 95.00% | 123 | 41.1 | 173 | 189 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | INEPTAAAIYGLDRT | 95.00% | 113 | 40.2 | 173 | 188 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | INEPTAAAIYGLDR | 95.00% | 110 | 39.8 | 173 | 187 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | IINEPTAAAIYGLDRTG | 95.00% | 108 | 40.4 | 172 | 189 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | IINEPTAAAIYGLD | 95.00% | 96.2 | 40.1 | 172 | 186 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | IINEPTAAAIYGL | 95.00% | 90.5 | 39.5 | 172 | 185 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | LRIINEPTAAAIYGLD | 95.00% | 81 | 39.7 | 170 | 186 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | RIINEPTAAAIYGL | 95.00% | 72 | 39.6 | 171 | 185 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | ALESYAFNMKSAVEDEG | 95.00% | 68.4 | 37.1 | 541 | 557 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | RIINEPTAAAIYGLD | 95.00% | 64.8 | 40.5 | 171 | 186 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | LRIINEPTAAAIYGL | 95.00% | 61.3 | 39.3 | 170 | 184 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | RIINEPTAAAIYGL | 95.00% | 61.2 | 38.8 | 171 | 184 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | EPTAAAIYGLD | 95.00% | 52.9 | 40.9 | 175 | 186 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | INEPTAAAIYGLDRTGKGE | 91.70% | 50.4 | 41.3 | 173 | 192 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | INEPTAAAIYGL | 86.80% | 45 | 40.2 | 173 | 185 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | AKRTLSSSTQASLEIDS | 90.80% | 49 | 41.3 | 270 | 286 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | AKRTLSSSTQASLEID | 89.60% | 46.3 | 40.1 | 270 | 285 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | GAAVQAAILMGDKSEN | 95.00% | 94.7 | 41 | 372 | 387 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | EAVYGAAVQAA | 90.30% | 46 | 39.9 | 367 | 378 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | NPDEAVYGAAVQAA | 95.00% | 57.8 | 39 | 364 | 378 |

SUPPLEMENTARY DATA

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|--|-------------|-------------------------|--------|------|------|-----|-----|
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | NPDEAVAYGAAVQAAI | 95.00% | 51.3 | 40.5 | 364 | 379 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | SDNQPGLVLIQVYEGER | 95.00% | 105 | 40.3 | 432 | 447 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | NALESYAFNMKSAVEDEG | 95.00% | 98.7 | 36.6 | 540 | 557 |
| HSPA1B;HSPA1A Heat shock 70 kDa protein 1 | IPI0030492E | DLNKSINPDEAVA | 95.00% | 52.8 | 40.7 | 358 | 370 |
| HSPA5 HSPA5 protein | IPI0000336E | TASDNQPTVTIKVYEGERP | 93.80% | 54.5 | 41.4 | 454 | 472 |
| HSPA5 HSPA5 protein | IPI0000336E | EAVAYGAAVQAGVLS | 95.00% | 78.1 | 40.4 | 393 | 407 |
| HSPA5 HSPA5 protein | IPI0000336E | IINEPTAAAIYGLDK | 95.00% | 128 | 40.6 | 199 | 214 |
| HSPA5 HSPA5 protein | IPI0000336E | INEPTAAAIYGLDK | 95.00% | 112 | 40.5 | 200 | 214 |
| HSPA5 HSPA5 protein | IPI0000336E | NEPTAAAIYGLDK | 95.00% | 104 | 39.9 | 201 | 214 |
| HSPA5 HSPA5 protein | IPI0000336E | IINEPTAAAIYGLD | 95.00% | 96.2 | 40.1 | 199 | 213 |
| HSPA5 HSPA5 protein | IPI0000336E | IINEPTAAAIYGL | 95.00% | 90.5 | 39.5 | 199 | 212 |
| HSPA5 HSPA5 protein | IPI0000336E | EPTAAAIYGLDK | 95.00% | 77.1 | 40.7 | 202 | 214 |
| HSPA5 HSPA5 protein | IPI0000336E | RIINEPTAAAIYGL | 95.00% | 72 | 39.6 | 198 | 212 |
| HSPA5 HSPA5 protein | IPI0000336E | RIINEPTAAAIYGLD | 95.00% | 64.8 | 40.5 | 198 | 213 |
| HSPA5 HSPA5 protein | IPI0000336E | RIINEPTAAAIYGL | 95.00% | 61.2 | 38.8 | 198 | 211 |
| HSPA5 HSPA5 protein | IPI0000336E | EPTAAAIYGLD | 95.00% | 52.9 | 40.9 | 202 | 213 |
| HSPA5 HSPA5 protein | IPI0000336E | IINEPTAAAIYGLDKREGEKN | 95.00% | 45.5 | 41.3 | 199 | 220 |
| HSPA5 HSPA5 protein | IPI0000336E | INEPTAAAIYGL | 86.80% | 45 | 40.2 | 200 | 212 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | IINEPTAAAIYGLDK | 95.00% | 128 | 40.6 | 172 | 187 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | INEPTAAAIYGLDK | 95.00% | 112 | 40.5 | 173 | 187 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | IINEPTAAAIYGLDKK | 95.00% | 110 | 39.1 | 172 | 188 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | INEPTAAAIYGLDKK | 95.00% | 107 | 39.5 | 173 | 188 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | NEPTAAAIYGLDK | 95.00% | 104 | 39.9 | 174 | 187 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | IINEPTAAAIYGLD | 95.00% | 96.2 | 40.1 | 172 | 186 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | IINEPTAAAIYGL | 95.00% | 90.5 | 39.5 | 172 | 185 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | RIINEPTAAAIYGLDKK | 95.00% | 88.8 | 37.8 | 171 | 188 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | INEPTAAAIYGLDKKVG | 95.00% | 88.5 | 39.7 | 173 | 190 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | NEPTAAAIYGLDKK | 95.00% | 85.1 | 39.9 | 174 | 188 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | INEPTAAAIYGLDKKV | 95.00% | 82.8 | 38.9 | 173 | 189 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | LRIINEPTAAAIYGLD | 95.00% | 81 | 39.7 | 170 | 186 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | EPTAAAIYGLDK | 95.00% | 77.1 | 40.7 | 175 | 187 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | EPTAAAIYGLDKK | 95.00% | 74.3 | 40.5 | 175 | 188 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | RIINEPTAAAIYGL | 95.00% | 72 | 39.6 | 171 | 185 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | EPTAAAIYGLDKKVG | 95.00% | 69.1 | 39.7 | 175 | 190 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | RIINEPTAAAIYGLD | 95.00% | 64.8 | 40.5 | 171 | 186 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | INEPTAAAIYGL | 86.80% | 45 | 40.2 | 173 | 185 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | LRIINEPTAAAIYGL | 95.00% | 61.3 | 39.3 | 170 | 184 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | RIINEPTAAAIYGL | 95.00% | 61.2 | 38.8 | 171 | 184 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | EPTAAAIYGLD | 95.00% | 52.9 | 40.9 | 175 | 186 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | GKELNKSINPDEAVAYG | 95.00% | 60.7 | 41.2 | 356 | 372 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | KELNKSINPDEAVAYG | 95.00% | 59.1 | 40.8 | 357 | 372 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | ELNKSINPDEAVA | 95.00% | 52.5 | 40.7 | 358 | 370 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | GKELNKSINPDEAVA | 95.00% | 50.8 | 40.4 | 356 | 370 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | KELNKSINPDEAVA | 95.00% | 64.7 | 40.3 | 357 | 370 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | ELNKSINPDEAVAYG | 95.00% | 72.2 | 40.5 | 358 | 372 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | AKRTLSSSTQASIEIDS | 90.80% | 49 | 41.3 | 270 | 286 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | AKRTLSSSTQASIEID | 89.60% | 46.3 | 40.1 | 270 | 285 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | NPDEAVAYGAAVQAAIILSGDKS | 95.00% | 125 | 41.7 | 364 | 385 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | NPDEAVAYGAAVQAA | 95.00% | 57.8 | 39 | 364 | 378 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | EAVAYGAAVQAAIILSG | 95.00% | 86 | 40.2 | 367 | 382 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | NPDEAVAYGAAVQAAI | 95.00% | 51.3 | 40.5 | 364 | 379 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | EAVAYGAAVQAA | 90.30% | 46 | 39.9 | 367 | 378 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | DKSQIHDIIVLGGSTR | 89.50% | 45.5 | 39.5 | 327 | 342 |
| HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein | IPI0000386E | SDNQPGLVLIQVYEGER | 95.00% | 105 | 40.3 | 432 | 447 |
| HSPB1 Heat shock protein beta-1 | IPI0002551I | TVEAMPKPLATQSNE | 95.00% | 66.9 | 40.9 | 34 | 48 |
| ICAM1 Intercellular adhesion molecule 1 | IPI0000849A | LFPVSEAQVHLALGDQ | 95.00% | 105 | 40.1 | 242 | 257 |
| ICAM3 Intercellular adhesion molecule 3 | IPI0003162C | EPAEVTATVLASRDD | 95.00% | 90.1 | 41.1 | 169 | 183 |
| ICAM3 Intercellular adhesion molecule 3 | IPI0003162C | GDTLTATATATARADQ | 95.00% | 125 | 39.8 | 271 | 286 |
| ICAM3 Intercellular adhesion molecule 3 | IPI0003162C | GDTLTATATATARADQE | 95.00% | 103 | 40 | 271 | 287 |
| ICAM3 Intercellular adhesion molecule 3 | IPI0003162C | HGDTLTATATATARADQ | 95.00% | 84.4 | 39.4 | 270 | 286 |
| ICAM3 Intercellular adhesion molecule 3 | IPI0003162C | HGDTLTATATATARADQEG | 95.00% | 68.8 | 39.7 | 270 | 288 |
| IFITM2 Interferon-induced transmembrane protein 2 | IPI0000892Z | MVGDTVGAQAYASTAK | 95.00% | 135 | 39.2 | 89 | 104 |
| IFITM2 Interferon-induced transmembrane protein 2 | IPI0000892Z | VGDVTGAQAYASTAK | 95.00% | 117 | 39 | 90 | 104 |
| IFITM2 Interferon-induced transmembrane protein 2 | IPI0000892Z | GDVTGAQAYASTAK | 95.00% | 104 | 39.9 | 91 | 104 |
| IFITM2 Interferon-induced transmembrane protein 2 | IPI0000892Z | VGDVTGAQAYAST | 95.00% | 90.5 | 39.6 | 90 | 102 |
| IFITM2 Interferon-induced transmembrane protein 2 | IPI0000892Z | DRKMGVDVTGAQAYASTAK | 95.00% | 87.8 | 40.5 | 86 | 104 |
| IFITM2 Interferon-induced transmembrane protein 2 | IPI0000892Z | DVTGAQAYASTA | 95.00% | 74.4 | 38.1 | 92 | 103 |
| IFITM2 Interferon-induced transmembrane protein 2 | IPI0000892Z | DVTGAQAYASTAK | 95.00% | 70.3 | 39.3 | 92 | 104 |
| IFITM2 Interferon-induced transmembrane protein 2 | IPI0000892Z | VTGAQAYASTAK | 95.00% | 62.5 | 39.9 | 93 | 104 |
| IFITM2 Interferon-induced transmembrane protein 2 | IPI0000892Z | DVTGAQAYAS | 95.00% | 45.1 | 38.3 | 92 | 101 |

SUPPLEMENTARY DATA

| | | | | | | | |
|--|-------------|------------------------|--------|------|------|-----|-----|
| IFNGR1 Interferon-gamma receptor alpha chain | IPI0001080E | VLHVWGVVTEKSKE | 94.40% | 53.2 | 38.6 | 186 | 199 |
| IFNGR1 Interferon-gamma receptor alpha chain | IPI0001080E | GVLHVWGVVTEKSKE | 91.10% | 47.1 | 38.8 | 185 | 199 |
| Ig kappa chain V-III region NG9 (Fragment) | IPI0038711E | KPGQAPRLLIYGATSRATG | 94.50% | 52.8 | 37.9 | 44 | 62 |
| Ig kappa chain V-III region NG9 (Fragment) | IPI0038711E | KPGQAPRLLIYGATSRATGIP | 94.30% | 51 | 36.7 | 44 | 64 |
| Ig lambda chain V-II region BUR | IPI00003947 | KSGNTASLTISGLQ | 95.00% | 87.7 | 39.3 | 87 | 100 |
| IGF2R Cation-independent mannose-6-phosphate receptor | IPI0028981E | TDTDAQACSIRDPSNG | 95.00% | 80 | 33.8 | 928 | 942 |
| IGF2R Cation-independent mannose-6-phosphate receptor | IPI0028981E | KPASGCEAETQTEEL | 95.00% | 47.7 | 37.7 | 982 | 996 |
| IGHG1 Putative uncharacterized protein DKFZp686H20196 | IPI0042346E | NWYVDGVEVHNAK | 95.00% | 87.5 | 39.7 | 309 | 321 |
| IGHG1 Putative uncharacterized protein DKFZp686H20196 | IPI0042346E | GALTSGVHTFPAVLQ | 95.00% | 69.6 | 38.4 | 194 | 208 |
| IGHG1 Putative uncharacterized protein DKFZp686H20196 | IPI0042346E | GALTSGVHTFPAVL | 95.00% | 57.3 | 37.8 | 194 | 207 |
| IGHG1 Putative uncharacterized protein DKFZp686H20196 | IPI0042346E | GALTSGVHTFPAVLQS | 93.40% | 48.6 | 40.9 | 194 | 209 |
| IGHG1 Putative uncharacterized protein DKFZp686P15220 | IPI0064536E | NWYVDGVEVHNAK | 95.00% | 87.5 | 39.7 | 301 | 313 |
| IGHG1 Putative uncharacterized protein DKFZp686P15220 | IPI0064536E | LVESGGGLVQPGRS | 95.00% | 68.7 | 38.4 | 23 | 37 |
| IGHG1 Putative uncharacterized protein DKFZp686P15220 | IPI0064536E | LVESGGGLVQPGRS | 95.00% | 84.9 | 39.3 | 23 | 36 |
| IGHG1 Putative uncharacterized protein DKFZp686P15220 | IPI0064536E | GALTSGVHTFPAVLQ | 95.00% | 69.6 | 38.4 | 186 | 200 |
| IGHG1 Putative uncharacterized protein DKFZp686P15220 | IPI0064536E | GALTSGVHTFPAVL | 95.00% | 57.3 | 37.8 | 186 | 199 |
| IGHG1 Putative uncharacterized protein DKFZp686P15220 | IPI0064536E | GALTSGVHTFPAVLQS | 93.40% | 48.6 | 40.9 | 186 | 201 |
| IGHM IGHM protein | IPI0047709C | LVESGGGVVQPGRS | 95.00% | 86.6 | 38.3 | 23 | 36 |
| IGHM IGHM protein | IPI0047709C | LVESGGGVVQPGRS | 95.00% | 85.1 | 39.3 | 23 | 37 |
| IGHM IGHM protein | IPI0047709C | ESGGGVVQPGRS | 95.00% | 78.5 | 38.8 | 25 | 36 |
| IGHM IGHM protein | IPI0047709C | TGETYTCVVAHEALPNR | 95.00% | 97.8 | 40.2 | 546 | 562 |
| IGHM IGHM protein | IPI0047709C | GETYTCVVAHEALPN | 95.00% | 63.5 | 39.1 | 547 | 561 |
| IGHM IGHM protein | IPI0047709C | TGETYTCVVAHEALP | 95.00% | 50.8 | 39.4 | 546 | 560 |
| IGHM IGHM protein | IPI0047709C | SPRQIQVSWLREGKQ | 91.50% | 48.2 | 39.3 | 279 | 293 |
| IGHM IGHM protein | IPI0047709C | TDVQAEAKESGPT | 95.00% | 69.9 | 40.1 | 300 | 313 |
| IGHM IGHM protein | IPI0047709C | SDISSTRGFPSVL | 85.80% | 45.2 | 40.6 | 187 | 199 |
| IGHV4-31 Anti-RhD monoclonal T125 gamma1 heavy chain | IPI00784817 | NWYVDGVEVHNAK | 95.00% | 87.5 | 39.7 | 304 | 316 |
| IGHV4-31 Anti-RhD monoclonal T125 gamma1 heavy chain | IPI00784817 | LVESGGGVVQPGRS | 95.00% | 86.6 | 38.3 | 23 | 36 |
| IGHV4-31 Anti-RhD monoclonal T125 gamma1 heavy chain | IPI00784817 | LVESGGGVVQPGRS | 95.00% | 85.1 | 39.3 | 23 | 37 |
| IGHV4-31 Anti-RhD monoclonal T125 gamma1 heavy chain | IPI00784817 | ESGGGVVQPGRS | 95.00% | 78.5 | 38.8 | 25 | 36 |
| IGHV4-31 Anti-RhD monoclonal T125 gamma1 heavy chain | IPI00784817 | GALTSGVHTFPAVLQ | 95.00% | 69.6 | 38.4 | 189 | 203 |
| IGHV4-31 Anti-RhD monoclonal T125 gamma1 heavy chain | IPI00784817 | GALTSGVHTFPAVL | 95.00% | 57.3 | 37.8 | 189 | 202 |
| IGHV4-31 Anti-RhD monoclonal T125 gamma1 heavy chain | IPI00784817 | GALTSGVHTFPAVLQS | 93.40% | 48.6 | 40.9 | 189 | 204 |
| IGKV1-5 IGKV1-5 protein | IPI00419424 | GNSQESVTEQDSKDS | 95.00% | 105 | 34.8 | 179 | 194 |
| IGKV1-5 IGKV1-5 protein | IPI00419424 | SGNSQESVTEQDSKDS | 95.00% | 101 | 33.3 | 178 | 193 |
| IGKV1-5 IGKV1-5 protein | IPI00419424 | NSQESVTEQDSKDS | 95.00% | 92.3 | 34.7 | 180 | 194 |
| IGKV1-5 IGKV1-5 protein | IPI00419424 | NSQESVTEQDSKDS | 95.00% | 87.7 | 35.6 | 180 | 192 |
| IGKV1-5 IGKV1-5 protein | IPI00419424 | NSQESVTEQDSKDS | 95.00% | 83.2 | 35.3 | 180 | 193 |
| IGKV1-5 IGKV1-5 protein | IPI00419424 | SGNSQESVTEQDSKDS | 95.00% | 81.6 | 34.2 | 178 | 194 |
| IGKV1-5 IGKV1-5 protein | IPI00419424 | GNSQESVTEQDSKDS | 95.00% | 81 | 34.4 | 179 | 193 |
| IGKV3D-15 Myosin-reactive immunoglobulin light chain variable region | IPI0054933C | KPGQAPRLLIYGASTRATGIPA | 95.00% | 82.1 | 36.4 | 59 | 80 |
| IGKV3D-15 Myosin-reactive immunoglobulin light chain variable region | IPI0054933C | LLIYGASTRATG | 95.00% | 63.1 | 39 | 66 | 77 |
| IGKV3D-15 Myosin-reactive immunoglobulin light chain variable region | IPI0054933C | APRLLIYGASTRATG | 95.00% | 55.6 | 38.5 | 63 | 77 |
| IGKV3D-15 Myosin-reactive immunoglobulin light chain variable region | IPI0054933C | LLIYGASTRATGIP | 95.00% | 55 | 38.1 | 66 | 79 |
| IGSF8 Isoform 1 of Immunoglobulin superfamily member 8 | IPI0005647E | APYAERLAAGELRLGEGTD | 90.60% | 48.4 | 40.8 | 101 | 120 |
| IL21R Interleukin-21 receptor | IPI0003424E | ELQPEALVESDG | 95.00% | 68.9 | 37.4 | 355 | 367 |
| IL4R Isoform 1 of Interleukin-4 receptor alpha chain | IPI0044438E | NVLQHGA AAPVSAPT | 95.00% | 52.4 | 39.5 | 557 | 572 |
| IL6ST Isoform 1 of Interleukin-6 receptor subunit beta | IPI00297124 | SSQNTSSTVQYSTVVH | 95.00% | 135 | 39 | 688 | 703 |
| IL6ST Isoform 1 of Interleukin-6 receptor subunit beta | IPI00297124 | ESSQNTSSTVQYSTVVH | 95.00% | 71.5 | 39 | 687 | 703 |
| IL6ST Isoform 1 of Interleukin-6 receptor subunit beta | IPI00297124 | SSQNTSSTVQYSTVV | 95.00% | 68 | 39.8 | 688 | 702 |
| IL6ST Isoform 1 of Interleukin-6 receptor subunit beta | IPI00297124 | VGKNEAVLEWDQLPVD | 95.00% | 68.6 | 40.8 | 469 | 484 |
| IL6ST Isoform 1 of Interleukin-6 receptor subunit beta | IPI00297124 | KNEAVLEWDQLPVD | 95.00% | 61.3 | 39.7 | 471 | 484 |
| IRGQ Immunity-related GTPase family Q protein | IPI0010392E | RPGDSQTAQAARDQTA | 95.00% | 76 | 39.5 | 117 | 132 |
| IRGQ Immunity-related GTPase family Q protein | IPI0010392E | RPGDSQTAQAARDQTAA | 95.00% | 66.9 | 40 | 117 | 133 |
| IRGQ Immunity-related GTPase family Q protein | IPI0010392E | RPGDSQTAQAARDQ | 95.00% | 59.7 | 38.3 | 117 | 130 |
| ITCH Isoform 1 of E3 ubiquitin-protein ligase Itchy homolog | IPI0006178C | LPPTNTNTNTSEGATSG | 95.00% | 79.6 | 38.6 | 288 | 304 |
| ITFG3 Isoform 2 of Protein ITFG3 | IPI0039665E | VPGNAGADVLLVGSE | 95.00% | 49.7 | 40.5 | 334 | 348 |
| ITGA4 Integrin alpha-4 | IPI0000980C | SDVITGSIQVSSREAN | 95.00% | 84.7 | 40.9 | 546 | 561 |
| ITGA4 Integrin alpha-4 | IPI0000980C | SDVITGSIQVSSRE | 95.00% | 76.4 | 40.4 | 546 | 559 |
| ITGA4 Integrin alpha-4 | IPI0000980C | EDDLQGAIYIYNGRADG | 95.00% | 71.2 | 38.4 | 398 | 414 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | YEDSLSSQVRTQME | 95.00% | 111 | 37.6 | 53 | 66 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | YEDSLSSQVRTQMELE | 95.00% | 108 | 38.4 | 53 | 68 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | EDSLSSQVRTQMELE | 95.00% | 92.7 | 38.3 | 54 | 68 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | LYEDSLSSQVRTQME | 95.00% | 81.6 | 39.1 | 52 | 66 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | EDSLSSQVRTQME | 95.00% | 76.5 | 37.9 | 54 | 66 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | DSLSSQVRTQMELE | 95.00% | 76.2 | 39.1 | 55 | 68 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | EDSLSSQVRTQMELEE | 95.00% | 71.9 | 38.3 | 54 | 69 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | DSLSSQVRTQME | 95.00% | 69.7 | 38.6 | 55 | 66 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | YEDSLSSQVRTQMEL | 95.00% | 61.2 | 38.4 | 53 | 67 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | EDSLSSQVRTQ | 95.00% | 61 | 39.5 | 54 | 64 |

SUPPLEMENTARY DATA

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|---|-------------|----------------------|--------|------|------|------|------|
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | EDLSQQVQTQEMEL | 95.00% | 55.1 | 40.1 | 54 | 67 |
| ITM2C Isoform 1 of Integral membrane protein 2C | IPI00016014 | GDKADKASASAPASATE | 94.20% | 53.8 | 39.7 | 15 | 33 |
| KCNN3 Small-conductance calcium-activated potassium channel SK3 | IPI0003246E | APPSNSTAILHPSSRQ | 95.00% | 67.7 | 40.5 | 116 | 132 |
| KCNN3 Small-conductance calcium-activated potassium channel SK3 | IPI0003246E | APPSNSTAILHPSSR | 95.00% | 66.8 | 39.9 | 116 | 131 |
| KCNN3 Small-conductance calcium-activated potassium channel SK3 | IPI0003246E | APPSNSTAILHPSSRQG | 95.00% | 64.8 | 40.5 | 116 | 133 |
| KIAA0174 Isoform 1 of Uncharacterized protein KIAA0174 | IPI0002466C | LPTASAGASTSASEDID | 95.00% | 93.1 | 38.7 | 304 | 320 |
| KIAA0174 Isoform 1 of Uncharacterized protein KIAA0174 | IPI0002466C | ADNISSAQIVGPGP | 95.00% | 60.1 | 40.2 | 259 | 273 |
| KIAA0494 Uncharacterized calcium-binding protein KIAA0494 | IPI0000613C | LEEVNSALVGYQRQND | 95.00% | 99.5 | 40.4 | 274 | 289 |
| KIAA0494 Uncharacterized calcium-binding protein KIAA0494 | IPI0000613C | SLEEVNSALVGYQRQNDL | 95.00% | 83.7 | 41.4 | 273 | 290 |
| KIAA0494 Uncharacterized calcium-binding protein KIAA0494 | IPI0000613C | ASIGNTLNSVHLAVE | 95.00% | 57.8 | 40.1 | 196 | 210 |
| KIAA0494 Uncharacterized calcium-binding protein KIAA0494 | IPI0000613C | ASIGNTLNSVHLAVEALQ | 91.10% | 46.2 | 39.7 | 196 | 213 |
| KIAA1109 Isoform 1 of Uncharacterized protein KIAA1109 | IPI0085264E | DGIAIGAALLPSLK | 95.00% | 72.1 | 33.9 | 2984 | 2997 |
| KIAA1109 Isoform 1 of Uncharacterized protein KIAA1109 | IPI0085264E | SKGGVVGGTIDVN | 95.00% | 52.5 | 41.7 | 4461 | 4473 |
| KIAA1618 Isoform 1 of Protein ALO17 | IPI0064212E | TEQQAGASASMAVDAV | 95.00% | 57.8 | 38.1 | 260 | 275 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | DLDNWTALISASKE | 95.00% | 114 | 40.3 | 68 | 81 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | EDLDNWTALISASKE | 95.00% | 95.8 | 40.2 | 67 | 81 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | LDNWTALISASKE | 95.00% | 95 | 41.4 | 69 | 81 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | DNWTALISASKEGH | 95.00% | 86 | 38.4 | 70 | 83 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | DNWTALISASKE | 95.00% | 75 | 39.9 | 70 | 81 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | EDLDNWTALISASKEGH | 95.00% | 71.8 | 40 | 67 | 83 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | DLDNWTALISASK | 95.00% | 60.9 | 40.6 | 68 | 80 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | LDNWTALISASKEGH | 95.00% | 59 | 39.1 | 69 | 83 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | EDLDNWTALISASKEGHVH | 95.00% | 57.4 | 40.2 | 67 | 85 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | EDLDNWTALISASK | 95.00% | 57.3 | 40.5 | 67 | 80 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | EGANSMTALIVAVK | 95.00% | 83.8 | 39.4 | 199 | 212 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | DPPELHAAASSESTGFG | 95.00% | 64.3 | 36.2 | 1748 | 1764 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | KSDQSGSKLLPGK | 95.00% | 60.2 | 39.1 | 1482 | 1494 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | EDEKSDQSGSKLLPGK | 90.90% | 48 | 40.1 | 1479 | 1494 |
| KIDINS220 Isoform 2 of Ankyrin repeat-rich membrane spanning protein | IPI0038490E | EDEKSDQSGSKLLPGKK | 89.90% | 47.2 | 40.7 | 1479 | 1495 |
| KRT10 Keratin, type I cytoskeletal 10 | IPI0000986E | SSGVSVESSSKGP | 95.00% | 75.1 | 37.3 | 547 | 559 |
| KRT10 Keratin, type I cytoskeletal 10 | IPI0000986E | SVGESSSKGP | 95.00% | 63.4 | 40.4 | 550 | 559 |
| KRT9 Keratin, type I cytoskeletal 9 | IPI0001935E | SRSGGGGGGGLSGGSISSY | 95.00% | 76.9 | 39.7 | 12 | 32 |
| KRT9 Keratin, type I cytoskeletal 9 | IPI0001935E | LSRSGGGGGGLSGGSISS | 95.00% | 69.1 | 40.6 | 11 | 31 |
| LAMP3 Lysosome-associated membrane glycoprotein 3 | IPI00004307 | YQGIKHAVVMFQTAVG | 95.00% | 75.6 | 40.1 | 319 | 334 |
| LAPTM5 Lysosomal-associated transmembrane protein 5 | IPI00013827 | IEHSVEVAHGKAS | 93.60% | 52.8 | 40.1 | 37 | 49 |
| LASP1 Isoform 1 of LIM and SH3 domain protein 1 | IPI00000861 | DDGWMYGTVERTGDTG | 95.00% | 85.3 | 31.8 | 236 | 251 |
| LASP1 Isoform 1 of LIM and SH3 domain protein 1 | IPI00000861 | IDDGWMYGTVERTGDTG | 95.00% | 65.6 | 35.1 | 235 | 251 |
| LDHB L-lactate dehydrogenase B chain | IPI00219217 | ADELALVDVLEDK | 95.00% | 73 | 41.1 | 46 | 58 |
| LDHB L-lactate dehydrogenase B chain | IPI00219217 | GVNVAGVSLQELNPE | 95.00% | 71.7 | 40.4 | 204 | 218 |
| LDLR Low-density lipoprotein receptor | IPI0000007C | DTEVASNRIYSDLS | 95.00% | 51 | 38.9 | 433 | 447 |
| LFNG Isoform 1 of Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe | IPI0045573E | APAPGLGAAAAAPGALVR | 95.00% | 95.2 | 36.6 | 52 | 69 |
| LFNG Isoform 1 of Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe | IPI0045573E | APAPGLGAAAAAPGALV | 95.00% | 88.3 | 38.6 | 52 | 68 |
| LGALS9 Isoform Long of Galectin-9 | IPI00010477 | ITVNGTVLSSSGTR | 95.00% | 115 | 38.4 | 31 | 44 |
| LGALS9 Isoform Long of Galectin-9 | IPI00010477 | QITVNGTVLSSSGTR | 95.00% | 95 | 39.7 | 30 | 44 |
| LGALS9 Isoform Long of Galectin-9 | IPI00010477 | SILLSGTVLPASQR | 95.00% | 103 | 37.9 | 208 | 221 |
| LGALS9 Isoform Long of Galectin-9 | IPI00010477 | SILLSGTVLPASQRFH | 95.00% | 94.2 | 38 | 208 | 223 |
| LGMN Legumain | IPI0029330C | VTPQNFLAVLRGDAEA | 95.00% | 90.8 | 40.4 | 108 | 123 |
| LGMN Legumain | IPI0029330C | TPQNFLAVLRGDAE | 95.00% | 84.1 | 39.3 | 109 | 122 |
| LGMN Legumain | IPI0029330C | VTPQNFLAVLRGDAE | 95.00% | 77.3 | 40.9 | 108 | 122 |
| LGMN Legumain | IPI0029330C | TPQNFLAVLRGDAEA | 95.00% | 75.2 | 40.8 | 109 | 123 |
| LGMN Legumain | IPI0029330C | VTPQNFLAVLRGDAEAV | 95.00% | 68.6 | 40.2 | 108 | 124 |
| LGMN Legumain | IPI0029330C | DHGSTGILVFPNEDL | 95.00% | 79.1 | 40.2 | 147 | 161 |
| LGMN Legumain | IPI0029330C | DHGSTGILVFPNED | 95.00% | 51.7 | 38.2 | 147 | 160 |
| LGMN Legumain | IPI0029330C | TDHGSTGILVFPNED | 95.00% | 46.3 | 37.3 | 146 | 160 |
| LILRB1 Uncharacterized protein LILRB1 | IPI00020967 | FLQLAGAQPOAGLSQ | 95.00% | 109 | 38.7 | 265 | 279 |
| LIPA Isoform 1 of Lysosomal acid lipase/cholesterol ester hydrolase | IPI00007207 | DMLVPTAVVWGGHD | 95.00% | 85.1 | 36.8 | 334 | 347 |
| LMAN2 Vesicular integral-membrane protein VIP36 | IPI0000995C | TPDEESIDWTKIEPSVN | 95.00% | 98.9 | 39.3 | 281 | 297 |
| LMAN2 Vesicular integral-membrane protein VIP36 | IPI0000995C | EESIDWTKIEPSVN | 95.00% | 63.9 | 39.7 | 284 | 297 |
| LNPEP Isoform 2 of Leucyl-cystinyl aminopeptidase | IPI0022124C | AKLLGMSFMNRRSSG | 95.00% | 61.2 | 37.9 | 74 | 87 |
| LNPEP Isoform 2 of Leucyl-cystinyl aminopeptidase | IPI0022124C | SFMNRRSSGLRNSATG | 90.80% | 47.1 | 39.3 | 80 | 94 |
| LOC100133661;HLA-DRB4 | IPI00107714 | AQSESAQSKMLSGVGGFV | 95.00% | 104 | 40.3 | 219 | 236 |
| LOC100133661;HLA-DRB4 | IPI00107714 | SESAQSKMLSGVGGFV | 95.00% | 101 | 40.7 | 221 | 236 |
| LOC100133661;HLA-DRB4 | IPI00107714 | QSESAQSKMLSGVGGFV | 95.00% | 93 | 40.4 | 220 | 236 |
| LOC100133661;HLA-DRB4 | IPI00107714 | QSESAQSKMLSGVGGF | 95.00% | 92.5 | 39.6 | 220 | 235 |
| LOC100133661;HLA-DRB4 | IPI00107714 | SESAQSKMLSGVGGF | 95.00% | 86.9 | 40.1 | 221 | 235 |
| LOC100133661;HLA-DRB4 | IPI00107714 | AQSESAQSKMLSGVGGF | 95.00% | 85.8 | 39.5 | 219 | 235 |
| LOC100133661;HLA-DRB4 | IPI00107714 | QSESAQSKMLSGVGG | 95.00% | 77.2 | 37.8 | 220 | 234 |
| LOC100133661;HLA-DRB4 | IPI00107714 | AQSESAQSKMLSGVGG | 95.00% | 71.8 | 39.4 | 219 | 234 |
| LOC100133661;HLA-DRB4 | IPI00107714 | AQSESAQSKMLSGVGGFVL | 95.00% | 71.7 | 40.6 | 219 | 237 |
| LOC100133661;HLA-DRB4 | IPI00107714 | WRAQSESAQSKMLSGVGGFV | 92.10% | 51.2 | 41.3 | 217 | 236 |

SUPPLEMENTARY DATA

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|---|-------------|-----------------------|--------|------|------|-----|-----|
| LOC100133661;HLA-DRB4 | IPI00107714 | QSESAQSKMLSGVG | 95.00% | 48 | 38.9 | 220 | 233 |
| LOC100133661;HLA-DRB4 | IPI00107714 | SGEVYTCQVEHPSVT | 95.00% | 70.8 | 36.8 | 196 | 210 |
| LOC100133661;HLA-DRB4 | IPI00107714 | VPRSGEVYTCQVEHPS | 95.00% | 65.7 | 39.3 | 193 | 208 |
| LOC100133661;HLA-DRB4 | IPI00107714 | VPRSGEVYTCQVEHPSVT | 95.00% | 56.5 | 40.4 | 193 | 210 |
| LOC100133661;HLA-DRB4;LOC100133583;RNASE2;HLA-DRB5;HLA-DRB3;HLI | IPI00895783 | SGEVYTCQVEHPSVT | 95.00% | 70.8 | 36.8 | 196 | 210 |
| LOC100133661;HLA-DRB4;LOC100133583;RNASE2;HLA-DRB5;HLA-DRB3;HLI | IPI00895783 | VPRSGEVYTCQVEHPS | 95.00% | 65.7 | 39.3 | 193 | 208 |
| LOC100133661;HLA-DRB4;LOC100133583;RNASE2;HLA-DRB5;HLA-DRB3;HLI | IPI00895783 | VPRSGEVYTCQVEHPSVT | 95.00% | 56.5 | 40.4 | 193 | 210 |
| LOC100133661;HLA-DRB4;LOC100133583;RNASE2;HLA-DRB5;HLA-DRB3;HLI | IPI00895783 | SESAQSKMLSGVGGFV | 95.00% | 101 | 40.7 | 221 | 236 |
| LOC100133661;HLA-DRB4;LOC100133583;RNASE2;HLA-DRB5;HLA-DRB3;HLI | IPI00895783 | SESAQSKMLSGVGGF | 95.00% | 86.9 | 40.1 | 221 | 235 |
| LOC100133661;HLA-DRB4;LOC100133583;RNASE2;HLA-DRB5;HLA-DRB3;HLI | IPI00895783 | RSESAQSKMLSGVG | 94.80% | 54.1 | 38.4 | 220 | 233 |
| LOC100133661;HLA-DRB4;LOC100133583;RNASE2;HLA-DRB5;HLA-DRB3;HLI | IPI00895783 | ARSESAQSKMLSGVGGF | 94.20% | 53.9 | 39.9 | 219 | 235 |
| LOC284194 galectin-9 like | IPI00472523 | SIILSGTVLPSAQR | 95.00% | 103 | 37.9 | 241 | 254 |
| LOC284194 galectin-9 like | IPI00472523 | SIILSGTVLPSAQRFH | 95.00% | 94.2 | 38 | 241 | 256 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | IALNEDLRSWTAADTAAQ | 95.00% | 106 | 41.1 | 148 | 165 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | DLRSWTAADTAAQITQ | 95.00% | 100 | 40.4 | 153 | 168 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | EDLRSWTAADTAAQITQ | 95.00% | 91.9 | 39.9 | 152 | 168 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | IALNEDLRSWTAADT | 95.00% | 86.6 | 40.4 | 148 | 162 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | DLRSWTAADTAAQIT | 95.00% | 76.7 | 40.6 | 153 | 167 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | IALNEDLRSWTAADTA | 95.00% | 74.8 | 40.2 | 148 | 163 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | EDLRSWTAADTAAQIT | 95.00% | 73 | 39.9 | 152 | 167 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | IALNEDLRSWTAAD | 95.00% | 61.9 | 39.3 | 148 | 161 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | EDLRSWTAADTAAQITQR | 95.00% | 60.7 | 40.5 | 152 | 169 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | IALNEDLRSWTAADTAA | 95.00% | 59.6 | 40.3 | 148 | 164 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | EDLRSWTAADTAAQITQRK | 95.00% | 58.7 | 40.9 | 152 | 170 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | DGEDQTDTELVEVTRPAGDR | 95.00% | 79.6 | 37.4 | 244 | 263 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | DGEDQTDTELVEVTRPAGDRT | 95.00% | 79 | 37.8 | 244 | 264 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | DGEDQTDTELVEVTRPAGD | 95.00% | 92.6 | 35.4 | 244 | 262 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | NTQIYKAQAQTDRS | 95.00% | 56.4 | 40.2 | 87 | 101 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | GPEYWRNTQIYKAQA | 94.80% | 55.6 | 39.9 | 80 | 95 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | YWRNTQIYKAQAQT | 94.70% | 55.4 | 40.2 | 83 | 97 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | EGPEYWRNTQIYKAQAQT | 94.30% | 54.4 | 39.9 | 79 | 97 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | RNTQIYKAQAQT | 93.20% | 51.6 | 39.8 | 86 | 96 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | TQIYKAQAQT | 91.10% | 47.2 | 40.7 | 88 | 97 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | GPEYWRNTQIYKAQAQTDRS | 95.00% | 45.7 | 40.8 | 80 | 102 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | DRNTQIYKAQAQTDRS | 95.00% | 58.4 | 40.6 | 85 | 101 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | EGPEYWRNTQIYKAQAQT | 95.00% | 57.4 | 38.7 | 79 | 98 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | GPEYWRNTQIYKAQAQT | 95.00% | 61.3 | 40.4 | 80 | 96 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | GPEYWRNTQIYKAQAQT | 95.00% | 65.4 | 39.3 | 80 | 98 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | GPEYWRNTQIYKAQAQT | 95.00% | 63.8 | 39.9 | 80 | 97 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00004657 | TQIYKAQAQTDRS | 88.10% | 45.3 | 40.8 | 88 | 101 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | IALNEDLRSWTAADTAAQ | 95.00% | 106 | 41.1 | 148 | 165 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | DLRSWTAADTAAQITQ | 95.00% | 100 | 40.4 | 153 | 168 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | EDLRSWTAADTAAQITQ | 95.00% | 91.9 | 39.9 | 152 | 168 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | IALNEDLRSWTAADT | 95.00% | 86.6 | 40.4 | 148 | 162 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | DLRSWTAADTAAQIT | 95.00% | 76.7 | 40.6 | 153 | 167 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | IALNEDLRSWTAADTA | 95.00% | 74.8 | 40.2 | 148 | 163 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | EDLRSWTAADTAAQIT | 95.00% | 73 | 39.9 | 152 | 167 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | TAADTAAQITQRKLEAAR# | 95.00% | 66.1 | 41.4 | 158 | 179 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | TAADTAAQITQRKLEAARA | 95.00% | 62.7 | 40 | 158 | 180 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | IALNEDLRSWTAAD | 95.00% | 61.9 | 39.3 | 148 | 161 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | EDLRSWTAADTAAQITQR | 95.00% | 60.7 | 40.5 | 152 | 169 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | IALNEDLRSWTAADTAA | 95.00% | 59.6 | 40.3 | 148 | 164 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | EDLRSWTAADTAAQITQRK | 95.00% | 58.7 | 40.9 | 152 | 170 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | ADTAAQITQRKLEAARAAEQ | 95.00% | 58 | 40.2 | 160 | 180 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | DTAAQITQRKLEAARAAEQ | 95.00% | 57.1 | 39.8 | 161 | 180 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | AADTAAQITQRKLEAARAAEQ | 92.00% | 51 | 41.3 | 159 | 179 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | KLEAARAAEQLR | 95.00% | 50 | 36 | 170 | 181 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | KLEAARAAEQ | 95.00% | 65.1 | 40.3 | 170 | 179 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | DGEDQTDTELVEVTRPAGDG | 95.00% | 94.5 | 34.8 | 244 | 263 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | DGEDQTDTELVEVTRPAGD | 95.00% | 92.6 | 35.4 | 244 | 262 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | DQTDTELVEVTRPAGDG | 95.00% | 83 | 37.7 | 247 | 263 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00642409 | TQTDTELVEVTRPAGDG | 95.00% | 69.2 | 39.4 | 249 | 263 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00647457 | TQTDTELVEVTRPAGDG | 95.00% | 69.2 | 39.4 | 249 | 263 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00647457 | DQTDTELVEVTRPAGDG | 95.00% | 83 | 37.7 | 247 | 263 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00647457 | DGEDQTDTELVEVTRPAGDG | 95.00% | 94.5 | 34.8 | 244 | 263 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00647457 | DGEDQTDTELVEVTRPAGD | 95.00% | 92.6 | 35.4 | 244 | 262 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00647457 | NEDLRSWTAADMAAQITKR | 95.00% | 88.3 | 41.2 | 151 | 169 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00647457 | EDLRSWTAADMAAQITKR | 95.00% | 102 | 41.3 | 152 | 169 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00647457 | DLRSWTAADMAAQ | 95.00% | 80.9 | 37.2 | 153 | 165 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;I | IPI00647457 | EDLRSWTAADMAAQ | 95.00% | 75.6 | 37.3 | 152 | 165 |

SUPPLEMENTARY DATA

| | | | | | | |
|--|--------------------------|--------|------|------|-----|-----|
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | DLRSWTAADMAAQITK | 95.00% | 75.2 | 40.8 | 153 | 168 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | EDLRSWTAADMAAQITK | 95.00% | 74.9 | 40.7 | 152 | 168 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | LRSWTAADMAAQIT | 95.00% | 64.2 | 39.8 | 154 | 167 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | DLRSWTAADMAAQIT | 95.00% | 64.1 | 40.1 | 153 | 167 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | DLRSWTAADMAAQITKR | 95.00% | 63.8 | 40.8 | 153 | 169 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | IALNEDLRSWTAAD | 95.00% | 61.9 | 39.3 | 148 | 161 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | EDLRSWTAADMAAQIT | 95.00% | 61.5 | 39.4 | 152 | 167 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | EDLRSWTAADMAAQITKRK | 95.00% | 57.5 | 41.3 | 152 | 170 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | WDQETRNVKAQSQTDTRVD | 94.90% | 56.5 | 40.7 | 84 | 101 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | GPEYWDQETRNVKAQSQTDTR | 95.00% | 55.4 | 39.1 | 80 | 99 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | GPEYWDQETRNVKAQSQTDTRVD | 94.70% | 54.7 | 39.4 | 80 | 101 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | EGPEYWDQETRNVKAQSQTDTR | 94.00% | 52.2 | 38.5 | 79 | 99 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | DQETRNVKAQSQTD | 93.00% | 50.4 | 38.8 | 85 | 98 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | DQETRNVKAQSQTDTR | 92.30% | 50.4 | 40.3 | 85 | 99 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | EGPEYWDQETRNVKAQSQTDTRVD | 95.00% | 57.7 | 38.6 | 79 | 101 |
| LOC441528;XXbac-BPG181B23.1;MICA;LOC100133382;HLA-A;HLA-B;HLA-C;L IPI00647457 | DQETRNVKAQSQTDTRVD | 88.50% | 45.2 | 40.4 | 85 | 101 |
| LOC442497;SLC3A2 4F2 cell-surface antigen heavy chain | IPI0002749E | 95.00% | 86.8 | 37.7 | 123 | 139 |
| LOC442497;SLC3A2 4F2 cell-surface antigen heavy chain | IPI0002749E | 95.00% | 80.6 | 38.7 | 119 | 139 |
| LOC442497;SLC3A2 4F2 cell-surface antigen heavy chain | IPI0002749E | 95.00% | 72.4 | 37.6 | 123 | 137 |
| LOC442497;SLC3A2 4F2 cell-surface antigen heavy chain | IPI0002749E | 95.00% | 65.4 | 37 | 119 | 134 |
| LOC442497;SLC3A2 4F2 cell-surface antigen heavy chain | IPI0002749E | 95.00% | 48.3 | 39 | 119 | 137 |
| LOC729708;LOC388642 Triosephosphate isomerase (Fragment) | IPI0038307I | 95.00% | 52.7 | 38.6 | 190 | 204 |
| LRIG3 Isoform 1 of Leucine-rich repeats and immunoglobulin-like domains protei | IPI0018426E | 95.00% | 67 | 37 | 483 | 499 |
| LRP6 Low-density lipoprotein receptor-related protein 6 | IPI0000020E | 95.00% | 90.8 | 40.6 | 655 | 670 |
| LSR Isoform 1 of Lipolysis-stimulated lipoprotein receptor | IPI0040964C | 88.20% | 45.3 | 39.9 | 359 | 375 |
| LYN Isoform LYN A of Tyrosine-protein kinase Lyn | IPI0029862E | 95.00% | 89 | 40.1 | 215 | 232 |
| LYN Isoform LYN A of Tyrosine-protein kinase Lyn | IPI0029862E | 95.00% | 86.3 | 39.6 | 215 | 229 |
| LYN Isoform LYN A of Tyrosine-protein kinase Lyn | IPI0029862E | 95.00% | 77.2 | 40.6 | 215 | 231 |
| LYN Isoform LYN A of Tyrosine-protein kinase Lyn | IPI0029862E | 95.00% | 75.2 | 40.5 | 215 | 230 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 92.7 | 38.9 | 235 | 248 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 87.2 | 41.3 | 235 | 247 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 80 | 39.1 | 236 | 248 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 78.5 | 39.8 | 233 | 248 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 78.2 | 40.9 | 235 | 246 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 72.3 | 40.1 | 234 | 248 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 68.3 | 40.3 | 233 | 247 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 63.2 | 40 | 236 | 247 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 57.4 | 41 | 234 | 247 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 54.2 | 41.3 | 234 | 246 |
| MAN1A1 MAN1A1 protein | IPI0043944E | 95.00% | 53.1 | 40.2 | 233 | 246 |
| MAN2B1 Lysosomal alpha-mannosidase | IPI0001298E | 95.00% | 65.1 | 36.7 | 155 | 171 |
| MAN2B1 Lysosomal alpha-mannosidase | IPI0001298E | 95.00% | 64.8 | 37 | 155 | 170 |
| MAN2B1 Lysosomal alpha-mannosidase | IPI0001298E | 95.00% | 57.2 | 38.9 | 796 | 810 |
| MAN2B1 Lysosomal alpha-mannosidase | IPI0001298E | 95.00% | 79.5 | 39.3 | 797 | 810 |
| MAN2B1 Lysosomal alpha-mannosidase | IPI0001298E | 95.00% | 64.7 | 39.1 | 795 | 810 |
| MAN2B1 Lysosomal alpha-mannosidase | IPI0001298E | 95.00% | 60 | 39.5 | 434 | 448 |
| MAN2B1 Lysosomal alpha-mannosidase | IPI0001298E | 95.00% | 58.4 | 33.3 | 332 | 346 |
| MAN2B1 Lysosomal alpha-mannosidase | IPI0001298E | 95.00% | 54.6 | 35.2 | 332 | 348 |
| MAN2B1 Lysosomal alpha-mannosidase | IPI0001298E | 93.40% | 50.4 | 38 | 953 | 969 |
| MAP1LC3B2 Microtubule-associated proteins 1A/1B light chain 3B-like protein | IPI0015146E | 95.00% | 53.6 | 39.4 | 82 | 97 |
| MARCKSL1 MARCKS-related protein | IPI0064118I | 95.00% | 97.4 | 37.8 | 153 | 172 |
| MARCKSL1 MARCKS-related protein | IPI0064118I | 95.00% | 90.5 | 37.5 | 153 | 169 |
| MARCKSL1 MARCKS-related protein | IPI0064118I | 95.00% | 87.4 | 36.6 | 153 | 167 |
| MARCKSL1 MARCKS-related protein | IPI0064118I | 95.00% | 82.7 | 37.1 | 153 | 168 |
| MARCKSL1 MARCKS-related protein | IPI0064118I | 95.00% | 75.3 | 36.6 | 15 | 30 |
| MDH1 Malate dehydrogenase, cytoplasmic | IPI0029100E | 95.00% | 73.5 | 39.3 | 221 | 235 |
| MDH1 Malate dehydrogenase, cytoplasmic | IPI0029100E | 95.00% | 51.8 | 39.3 | 182 | 196 |
| MFGE8 Lactadherin | IPI0000223E | 95.00% | 107 | 39.4 | 78 | 92 |
| MFGE8 Lactadherin | IPI0000223E | 95.00% | 54 | 39.8 | 298 | 309 |
| MFGE8 Lactadherin | IPI0000223E | 95.00% | 84.5 | 40.5 | 295 | 311 |
| MFGE8 Lactadherin | IPI0000223E | 93.20% | 52.2 | 40.2 | 295 | 312 |
| MFSD2 Isoform 1 of Major facilitator superfamily domain-containing protein 2 | IPI0041039I | 95.00% | 63.2 | 37.9 | 190 | 204 |
| MFSD2 Isoform 1 of Major facilitator superfamily domain-containing protein 2 | IPI0041039I | 95.00% | 50.1 | 39.9 | 191 | 204 |
| MFSD2 Isoform 1 of Major facilitator superfamily domain-containing protein 2 | IPI0041039I | 95.00% | 45.8 | 36.4 | 190 | 203 |
| MICAL3 Isoform 1 of Protein MICAL-3 | IPI00177937 | 90.40% | 47.5 | 41.4 | 733 | 745 |
| MITD1 MIT domain-containing protein 1 | IPI0010306E | 95.00% | 65.7 | 39.9 | 9 | 24 |
| MREG Isoform 1 of Melanoregulin | IPI00010751E | 90.10% | 46.9 | 40 | 35 | 51 |
| MRPL4 Isoform 1 of 39S ribosomal protein L4, mitochondrial | IPI0002333A | 95.00% | 48.4 | 38.8 | 118 | 129 |
| MS4A1 B-lymphocyte antigen CD20 | IPI0000788C | 95.00% | 75.1 | 39.1 | 49 | 62 |
| MS4A1 B-lymphocyte antigen CD20 | IPI0000788C | 93.20% | 53 | 41.1 | 48 | 63 |

SUPPLEMENTARY DATA

| | | | | | | | |
|---|-------------|---------------------------|--------|------|------|------|------|
| MTHFD1 C-1-tetrahydrofolate synthase, cytoplasmic | IPI0021834Z | EEVINAIPEKVDVG | 95.00% | 56.8 | 40.4 | 151 | 165 |
| MVP Major vault protein | IPI0000010E | VVEIIQATIIRQNQ | 95.00% | 86.1 | 36 | 159 | 172 |
| MVP Major vault protein | IPI0000010E | VVEIIQATIIRQN | 95.00% | 76.6 | 35.5 | 159 | 171 |
| MVP Major vault protein | IPI0000010E | IQATIIRQNQ | 95.00% | 72.6 | 36.4 | 162 | 172 |
| MVP Major vault protein | IPI0000010E | VVEIIQATIIRQNQA | 95.00% | 66.9 | 36.3 | 159 | 173 |
| MVP Major vault protein | IPI0000010E | VVEIIQATIIRQNQAL | 95.00% | 62.7 | 34.6 | 159 | 174 |
| MVP Major vault protein | IPI0000010E | VEIIQATIIRQNQ | 95.00% | 60.1 | 37 | 160 | 172 |
| MVP Major vault protein | IPI0000010E | IPLDENEGIVQDVKTG | 95.00% | 107 | 40.9 | 380 | 396 |
| MVP Major vault protein | IPI0000010E | DENEGIVQDVK | 95.00% | 71.6 | 39.1 | 383 | 394 |
| MVP Major vault protein | IPI0000010E | IPLDENEGIVQDVKTGK | 95.00% | 60 | 41.2 | 380 | 397 |
| MYH9 Myosin-9 | IPI0001950Z | DPLNDNIATLLHQSSDK | 95.00% | 62.9 | 40.6 | 590 | 606 |
| MYH9 Myosin-9 | IPI0001950Z | QAQIAELKMLAKKEE | 91.20% | 49.5 | 41 | 1068 | 1084 |
| NAPA Alpha-soluble NSF attachment protein | IPI0000925Z | EQYQKAIIDYEQVGTN | 95.00% | 68.4 | 40 | 176 | 191 |
| NAPA Alpha-soluble NSF attachment protein | IPI0000925Z | EQYQKAIIDYEQVG | 95.00% | 56.1 | 40 | 176 | 189 |
| NBR1 neighbor of BRCA1 gene 1 | IPI0078385E | LDEENEEVSINSQGEYE | 95.00% | 121 | 33.2 | 49 | 65 |
| NBR1 neighbor of BRCA1 gene 1 | IPI0078385E | LDEENEEVSINSQGEY | 95.00% | 96.5 | 34.8 | 49 | 64 |
| NBR1 neighbor of BRCA1 gene 1 | IPI0078385E | EDQTAALMAHLFE | 95.00% | 73.3 | 38 | 914 | 926 |
| NDFIP2 NEDD4 family-interacting protein 2 | IPI0038503E | LNEEDNNESSAIEQPP | 95.00% | 94 | 36.2 | 109 | 124 |
| NDFIP2 NEDD4 family-interacting protein 2 | IPI0038503E | EEDNNESSAIEQPP | 95.00% | 91.6 | 34.3 | 111 | 124 |
| NDFIP2 NEDD4 family-interacting protein 2 | IPI0038503E | EDNNESSAIEQPP | 95.00% | 56.5 | 34.5 | 112 | 124 |
| NDFIP2 NEDD4 family-interacting protein 2 | IPI0038503E | NPAPQIVQAASSAPALETD | 95.00% | 65.8 | 40.8 | 127 | 145 |
| NDFIP2 NEDD4 family-interacting protein 2 | IPI0038503E | NPAPQIVQAASSAPALE | 95.00% | 64.1 | 40.9 | 127 | 143 |
| NECAP2 Isoform 1 of Adaptin ear-binding coat-associated protein 2 | IPI0001818E | STGSTSSQTQPGTGWVQ | 95.00% | 92.6 | 38.1 | 246 | 262 |
| NECAP2 Isoform 1 of Adaptin ear-binding coat-associated protein 2 | IPI0001818E | STGSTSSQTQPGTGWV | 95.00% | 74.9 | 38.2 | 246 | 261 |
| NECAP2 Isoform 1 of Adaptin ear-binding coat-associated protein 2 | IPI0001818E | LAVGGSLVQPAVAPS | 95.00% | 47.9 | 38.5 | 206 | 221 |
| NECAP2 Isoform 1 of Adaptin ear-binding coat-associated protein 2 | IPI0001818E | LAVGGSLVQPAVAPS | 94.90% | 47.1 | 38.2 | 207 | 221 |
| NEDD1 Protein NEDD1 | IPI0016934E | DAVNVKGSDESIGKGDG | 95.00% | 56 | 39.6 | 60 | 76 |
| NEDD4L Isoform 4 of E3 ubiquitin-protein ligase NEDD4-like protein | IPI0002328T | VPMNGFAELVYSGNGPQ | 95.00% | 70 | 38.5 | 880 | 895 |
| NEU1 Sialidase-1 | IPI0002981T | SDEGAKFIALRRSMDQG | 91.40% | 49.4 | 40.7 | 102 | 118 |
| NID1 Isoform 1 of Nidogen-1 | IPI00026944 | ENNQVPAVAVFASQGSV | 95.00% | 73.3 | 40.5 | 211 | 226 |
| NID1 Isoform 1 of Nidogen-1 | IPI00026944 | ENNQVPAVAVFASQGSV | 95.00% | 53.3 | 40.4 | 211 | 227 |
| NID1 Isoform 1 of Nidogen-1 | IPI00026944 | EDLSPSITQRAAE | 95.00% | 65.4 | 40.7 | 124 | 136 |
| NID1 Isoform 1 of Nidogen-1 | IPI00026944 | ENTDLHSYVMNHGRSY | 95.00% | 64.8 | 38.1 | 454 | 470 |
| NID1 Isoform 1 of Nidogen-1 | IPI00026944 | NTDLHSYVMNHGRSY | 94.90% | 54.8 | 38.9 | 455 | 470 |
| NID1 Isoform 1 of Nidogen-1 | IPI00026944 | TDLHSYVMNHGRS | 93.60% | 52.3 | 39.5 | 456 | 469 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | DALLGQVKASLLPGGSEGG | 95.00% | 92.1 | 39.8 | 1643 | 1662 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | LGQVKASLLPGGSEG | 95.00% | 84.6 | 39.6 | 1646 | 1660 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | LGQVKASLLPGGSE | 95.00% | 72.4 | 39.8 | 1646 | 1659 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | LGQVKASLLPGGSEGG | 95.00% | 69.2 | 39.6 | 1646 | 1661 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | DPMDVRGSIVY | 95.00% | 69.9 | 38.6 | 1668 | 1678 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | VDDLKGSALHWAAAVN | 95.00% | 74.6 | 40.6 | 2025 | 2040 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | AVDDLKGSALHWAAAVN | 95.00% | 68.5 | 40.8 | 2024 | 2040 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | DDLKGSALHWAAAVN | 95.00% | 53.6 | 40.9 | 2026 | 2040 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | VGPLHSSLAALSQ | 95.00% | 81.4 | 39.2 | 2348 | 2362 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | GPHLSSLAALSQ | 95.00% | 68.4 | 40.5 | 2349 | 2363 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | APAVISDFIYQGASLHNQDTRTG | 95.00% | 92.4 | 41.2 | 1907 | 1929 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | SDFIYQGASLHNQDTR | 95.00% | 86.8 | 37.6 | 1912 | 1926 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | APAVISDFIYQGASLHNQDTR | 95.00% | 63.2 | 40.8 | 1907 | 1927 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | SDFIYQGASLHNQDTRT | 93.80% | 52.9 | 39.6 | 1912 | 1928 |
| NOTCH1 Neurogenic locus notch homolog protein 1 | IPI0041298Z | SDFIYQGASLHNQDTR | 90.40% | 46.8 | 39.6 | 1912 | 1927 |
| NPEPPS Puromycin-sensitive aminopeptidase | IPI0002621E | GKLEAAQVRQATNQ | 90.50% | 46.2 | 38.9 | 78 | 92 |
| NUCB1 Nucleobindin-1 | IPI0029554Z | LLIQTATRDLAQYDAAH | 95.00% | 68.3 | 41.1 | 156 | 173 |
| NUCB1 Nucleobindin-1 | IPI0029554Z | LLIQTATRDLAQYDAA | 95.00% | 62.5 | 40.1 | 156 | 171 |
| NUP210 Isoform 1 of Nuclear pore membrane glycoprotein 210 | IPI0029175E | DIGFSVIQAHVQ | 95.00% | 85.2 | 38.6 | 508 | 520 |
| OPTN Isoform 1 of Optineurin | IPI0030418E | EDLETMTILRAQ | 95.00% | 61.5 | 42.1 | 456 | 467 |
| OPTN Isoform 1 of Optineurin | IPI0030418E | EEDLETMTILRAQ | 95.00% | 97.8 | 40.9 | 455 | 467 |
| OPTN Isoform 1 of Optineurin | IPI0030418E | QEEDLETMTILRAQ | 95.00% | 68.5 | 40 | 454 | 467 |
| OPTN Isoform 1 of Optineurin | IPI0030418E | SSEDSFVEIRMAEGEA | 95.00% | 66.3 | 36.2 | 173 | 188 |
| OPTN Isoform 1 of Optineurin | IPI0030418E | ESMLSEIKMEQAKTED | 95.00% | 62.8 | 38.9 | 366 | 381 |
| OPTN Isoform 1 of Optineurin | IPI0030418E | ESMLSEIKMEQAKTEDE | 95.00% | 58.1 | 37.5 | 366 | 382 |
| OPTN Isoform 1 of Optineurin | IPI0030418E | ESMLSEIKMEQAKTEDEK | 90.50% | 47 | 39.6 | 366 | 383 |
| PAFAH1B1 Isoform 1 of Platelet-activating factor acetylhydrolase IB subunit alpha | IPI0021872Z | APESSYSSISEATGSETKKSQKPGP | 95.00% | 76.1 | 40.7 | 284 | 308 |
| PAFAH1B1 Isoform 1 of Platelet-activating factor acetylhydrolase IB subunit alpha | IPI0021872Z | APESYSSISEATGSE | 95.00% | 56.8 | 35.1 | 284 | 299 |
| PAM peptidylglycine alpha-amidating monooxygenase isoform a, preproprotein | IPI0017754Z | VDPNNAAVLQSSGKNL | 95.00% | 81.4 | 39.5 | 454 | 470 |
| PAM peptidylglycine alpha-amidating monooxygenase isoform a, preproprotein | IPI0017754Z | VDPNNAAVLQSSGKN | 95.00% | 77.5 | 40.2 | 454 | 469 |
| PAM peptidylglycine alpha-amidating monooxygenase isoform a, preproprotein | IPI0017754Z | PNNAAVLQSSGKN | 95.00% | 70 | 38 | 457 | 469 |
| PAM peptidylglycine alpha-amidating monooxygenase isoform a, preproprotein | IPI0017754Z | IDPNNAAVLQSSGKN | 95.00% | 107 | 39.5 | 455 | 469 |
| PAM peptidylglycine alpha-amidating monooxygenase isoform a, preproprotein | IPI0017754Z | IDPNNAAVLQSSGKNL | 95.00% | 67.5 | 39.3 | 455 | 470 |
| PAM peptidylglycine alpha-amidating monooxygenase isoform a, preproprotein | IPI0017754Z | WGESSSSPLPGQFT | 95.00% | 69.1 | 37.2 | 562 | 577 |
| PAM peptidylglycine alpha-amidating monooxygenase isoform a, preproprotein | IPI0017754Z | WGESSSSPLPGQ | 95.00% | 84.7 | 35.9 | 562 | 575 |

SUPPLEMENTARY DATA

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|---|-------------|----------------------|--------|------|------|------|------|
| PAM peptidylglycine alpha-amidating monooxygenase isoform a, preproprotein | IPI0017754C | GEESGSSPLPGQFT | 95.00% | 64.4 | 37.5 | 563 | 577 |
| PCBP1 Poly(rC)-binding protein 1 | IPI0001661C | EIRESTGAQVQVAGDM | 95.00% | 95.3 | 39.9 | 122 | 137 |
| PCBP1 Poly(rC)-binding protein 1 | IPI0001661C | IRESTGAQVQVAGDM | 95.00% | 91.3 | 40.6 | 123 | 137 |
| PCBP1 Poly(rC)-binding protein 1 | IPI0001661C | EIRESTGAQVQV | 94.80% | 49.2 | 40.4 | 122 | 132 |
| PCBP1 Poly(rC)-binding protein 1 | IPI0001661C | EESGARINISEGN | 95.00% | 61.8 | 38.7 | 41 | 53 |
| PCBP1 Poly(rC)-binding protein 1 | IPI0001661C | RQQSHFAMMHGGTG | 94.70% | 51.7 | 36.2 | 243 | 256 |
| PCBP1 Poly(rC)-binding protein 1 | IPI0001661C | ARQQSHFAMMHGGTG | 93.90% | 48.7 | 35.3 | 242 | 256 |
| PDCD6 Programmed cell death protein 6 | IPI00025277 | SGVISDTELQQLSN | 95.00% | 104 | 40.8 | 49 | 63 |
| PDCD6 Programmed cell death protein 6 | IPI00025277 | SGVISDTELQQLS | 95.00% | 57.7 | 41 | 49 | 62 |
| PDI A6 Isoform 2 of Protein disulfide-isomerase A6 | IPI00299571 | EPEWAAAASEVKEQTKG | 95.00% | 84.5 | 40.2 | 197 | 213 |
| PDLIM1 PDZ and LIM domain protein 1 | IPI00010414 | TNQYNNPAGLYSSENI | 95.00% | 92.5 | 37.3 | 141 | 157 |
| PDXDC1 Isoform 1 of Pyridoxal-dependent decarboxylase domain-containing prc | IPI0038468E | GIQEAQVELQKASEER | 93.10% | 51.8 | 40.1 | 616 | 631 |
| PGK1 Phosphoglycerate kinase 1 | IPI0016938E | DEEGAKIVKDLMS | 95.00% | 58.6 | 40.5 | 259 | 271 |
| PGK1 Phosphoglycerate kinase 1 | IPI0016938E | KELNYFAKALESPERP | 95.00% | 69.3 | 40.4 | 192 | 207 |
| PGK1 Phosphoglycerate kinase 1 | IPI0016938E | ELNYFAKALESPERP | 92.60% | 51.5 | 40.8 | 193 | 207 |
| PGK1 Phosphoglycerate kinase 1 | IPI0016938E | KELNYFAKALESPERPF | 92.30% | 50.7 | 40.5 | 192 | 208 |
| PIK3IP1 Isoform 1 of Phosphoinositide-3-kinase-interacting protein 1 | IPI0029838E | LPARSEAAAVQPVIGIS | 95.00% | 46.6 | 36.7 | 137 | 153 |
| PKM2 Isoform M1 of Pyruvate kinase isozymes M1/M2 | IPI00220644 | DLRVNFAMNVGKARG | 94.10% | 53.7 | 39.9 | 299 | 313 |
| PLA1A Isoform 1 of Phospholipase A1 member A | IPI0064279C | TDTNLRGIRIPVGHVDY | 95.00% | 63.4 | 41.1 | 218 | 234 |
| PLA1A Isoform 1 of Phospholipase A1 member A | IPI0064279C | TDTNLRGIRIPVGHVD | 93.50% | 53.4 | 41 | 218 | 233 |
| PLD1 Isoform PLD1A of Phospholipase D1 | IPI0001286E | NEPVGNLPIQKSIDDVD | 95.00% | 70.5 | 40.4 | 529 | 545 |
| PLEKHB2 Isoform 1 of Pleckstrin homology domain-containing family B member | IPI00335457 | LGMLAGAATGMALGSL | 95.00% | 127 | 39.4 | 202 | 217 |
| PLEKHB2 Isoform 1 of Pleckstrin homology domain-containing family B member | IPI00335457 | LGMLAGAATGMALGS | 95.00% | 88.9 | 39.4 | 202 | 216 |
| PLOD1 Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 | IPI0002719E | IYLKGSALRGELQ | 95.00% | 67.3 | 36.1 | 454 | 467 |
| PLOD1 Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 | IPI0002719E | SDQLFYTKIFLDPEKRE | 95.00% | 64.7 | 41.5 | 178 | 194 |
| PLOD1 Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 | IPI0002719E | DSDQLFYTKIFLDPEKRE | 95.00% | 57.7 | 41.4 | 177 | 194 |
| PLSCR1 Phospholipid scramblase 1 | IPI00005181 | LSQIDQLIHQQIE | 95.00% | 77 | 39.1 | 85 | 98 |
| PLSCR1 Phospholipid scramblase 1 | IPI00005181 | SQIDQLIHQQIE | 95.00% | 69.7 | 40.2 | 86 | 98 |
| PLSCR1 Phospholipid scramblase 1 | IPI00005181 | QIDQLIHQQIE | 95.00% | 64.1 | 39.7 | 87 | 98 |
| PLSCR1 Phospholipid scramblase 1 | IPI00005181 | FFESTGSQEQKSG | 95.00% | 64.4 | 36.6 | 287 | 299 |
| PLTP 45 kDa protein | IPI0002273E | NSLLDTPVPRSSVDE | 95.00% | 68.8 | 40.8 | 197 | 211 |
| PLXNB2 Plexin B2 | IPI0085262E | TNLNKAMTLQEAEAFVG | 95.00% | 96.4 | 40.9 | 1117 | 1133 |
| PLXNB2 Plexin B2 | IPI0085262E | TNLNKAMTLQEAEA | 95.00% | 72.1 | 40.2 | 1117 | 1130 |
| PLXNB2 Plexin B2 | IPI0085262E | TNLNKAMTLQEAEAFV | 95.00% | 59.3 | 41.2 | 1117 | 1132 |
| PLXNB2 Plexin B2 | IPI0085262E | TNLNKAMTLQEAEAF | 95.00% | 54.2 | 40.6 | 1117 | 1131 |
| PLXNB2 Plexin B2 | IPI0085262E | LDTVKGSSLVHVGSDLL | 95.00% | 75.7 | 40.3 | 692 | 706 |
| PLXNB2 Plexin B2 | IPI0085262E | NLDTVKGSSLVHVGSDLL | 95.00% | 71 | 39 | 691 | 707 |
| PLXNB2 Plexin B2 | IPI0085262E | NLDTVKGSSLVHVGSDLL | 95.00% | 66.9 | 40.2 | 691 | 706 |
| PLXNB2 Plexin B2 | IPI0085262E | NLDTVKGSSLVHVGSDLLK | 95.00% | 56.5 | 39.5 | 691 | 708 |
| PLXNB2 Plexin B2 | IPI0085262E | LKFMEPVMTQESGTF | 95.00% | 56.4 | 38.9 | 707 | 721 |
| PLXNB2 Plexin B2 | IPI0085262E | VVYLGAVNALYQLDAK | 95.00% | 63.3 | 39.1 | 45 | 60 |
| PLXNB2 Plexin B2 | IPI0085262E | GPSPLVIPMNHETDVNFQGN | 89.30% | 47.3 | 41.5 | 671 | 691 |
| POU2AF1 POU domain class 2-associating factor 1 | IPI00293727 | SPPLITNVITRRSATPA | 95.00% | 89.2 | 39.7 | 143 | 159 |
| PPP2R1A cDNA FLJ34068 fis, clone FCBBF3001918, highly similar to SERINE/1 | IPI00168184 | GPEITKTDLVPAFQ | 93.70% | 47.4 | 39.4 | 96 | 109 |
| PPT1 Palmitoyl-protein thioesterase 1 | IPI0000241E | EMDNAGQLVFLATEGDH | 95.00% | 108 | 37.5 | 72 | 88 |
| PSEN1 Isoform 1 of Presenilin-1 | IPI00028077 | RNETLFPALIYSST | 95.00% | 59.2 | 40.1 | 186 | 199 |
| PSEN1 Isoform 1 of Presenilin-1 | IPI00028077 | NSKYNAESTERESQDTV | 95.00% | 57.6 | 37.2 | 220 | 236 |
| PSEN1 Isoform 1 of Presenilin-1 | IPI00028077 | NSKYNAESTERESQDT | 95.00% | 53.5 | 35.5 | 220 | 235 |
| PSMA5 Proteasome subunit alpha type-5 | IPI00291922 | ATNIELATVQPGQNFH | 95.00% | 68.7 | 40.6 | 212 | 227 |
| PSMA5 Proteasome subunit alpha type-5 | IPI00291922 | NIELATVQPGQNFH | 95.00% | 66.4 | 40.5 | 214 | 227 |
| PSMB10 Proteasome subunit beta type-10 | IPI0002793E | DGVLGDATRATNDS | 95.00% | 74.1 | 39.9 | 49 | 63 |
| RAB11A Ras-related protein Rab-11A | IPI0042919C | FAEKNGLSFIETSALD | 95.00% | 64.1 | 40.7 | 142 | 157 |
| RAB11A Ras-related protein Rab-11A | IPI0042919C | TSALDSTNVEAAFQ | 95.00% | 53.4 | 39.2 | 153 | 166 |
| RAB11FIP1 Isoform 1 of Rab11 family-interacting protein 1 | IPI0041943E | GPGGTSDAYAVIQVGEKEY | 95.00% | 62.2 | 41 | 34 | 52 |
| RAB11FIP1 Isoform 1 of Rab11 family-interacting protein 1 | IPI0041943E | GPGGTSDAYAVIQVGEKEYA | 95.00% | 57.9 | 41.2 | 34 | 53 |
| RAB21 Ras-related protein Rab-21 | IPI0000775E | YRDSNGAILVYDITDE | 95.00% | 87.4 | 39.4 | 89 | 104 |
| RAB21 Ras-related protein Rab-21 | IPI0000775E | RDSNGAILVYDITDE | 95.00% | 79.8 | 40 | 90 | 104 |
| RAB21 Ras-related protein Rab-21 | IPI0000775E | RDSNGAILVYDITDED | 95.00% | 71.8 | 39 | 90 | 105 |
| RAB21 Ras-related protein Rab-21 | IPI0000775E | YRDSNGAILVYDITD | 95.00% | 57.3 | 39.3 | 89 | 103 |
| RAB4A RAB4A, member RAS oncogene family variant | IPI0048005E | KDDSNHTIGVEFGSKIIN | 95.00% | 87.8 | 41.2 | 39 | 56 |
| RAB4A RAB4A, member RAS oncogene family variant | IPI0048005E | TNWLTDARMLASQN | 95.00% | 73 | 39.4 | 105 | 118 |
| RAB4B Isoform 2 of Ras-related protein Rab-4B | IPI0018714C | AAWLTARTLASPNI | 95.00% | 59.4 | 40.1 | 100 | 115 |
| RAB5C Ras-related protein Rab-5C | IPI0001633E | ADDNSLLFMETSAK | 95.00% | 117 | 38.4 | 153 | 166 |
| RAB5C Ras-related protein Rab-5C | IPI0001633E | ADDNSLLFMETSAKT | 95.00% | 93.8 | 39.1 | 153 | 167 |
| RAB5C Ras-related protein Rab-5C | IPI0001633E | ADDNSLLFMETSAKTA | 95.00% | 89.4 | 39.4 | 153 | 168 |
| RAB5C Ras-related protein Rab-5C | IPI0001633E | DDNSLLFMETSAK | 95.00% | 87.1 | 38.8 | 154 | 166 |
| RAB5C Ras-related protein Rab-5C | IPI0001633E | DDNSLLFMETSAKT | 95.00% | 79.3 | 38.4 | 154 | 167 |
| RAB5C Ras-related protein Rab-5C | IPI0001633E | DDNSLLFMETSAKTA | 95.00% | 70.7 | 38.9 | 154 | 168 |
| RAB8B Ras-related protein Rab-8B | IPI0002428E | IKNWIRNIEEHSSDVER | 95.00% | 57.2 | 41.1 | 99 | 116 |
| RALB Ras-related protein Rab-B | IPI00004397 | AGQEDYAAIRDNYFR | 90.00% | 45.6 | 39 | 70 | 84 |

SUPPLEMENTARY DATA

| | | | | | | | |
|--|-------------|------------------------|--------|------|------|-----|-----|
| RELT Tumor necrosis factor receptor superfamily member 19L | IPI00064377 | DANEDTIGVLVR | 95.00% | 69.1 | 41 | 218 | 229 |
| RHBD2 Isoform 1 of Rhomboid family member 2 | IPI0043349E | EPASSGAHIWPPD | 95.00% | 64.1 | 35.2 | 529 | 541 |
| RHBD2 Isoform 1 of Rhomboid family member 2 | IPI0043349E | EEPASSGAHIWPPD | 95.00% | 58.6 | 35 | 528 | 541 |
| RHBD2 Isoform 1 of Rhomboid family member 2 | IPI0043349E | EEPASSGAHIWPPDIT | 95.00% | 56.8 | 38.1 | 528 | 543 |
| RHBD2 Isoform 1 of Rhomboid family member 2 | IPI0043349E | EPASSGAHIWPPDIT | 95.00% | 56.8 | 38.9 | 529 | 543 |
| RNF19A Isoform 1 of E3 ubiquitin-protein ligase RNF19A | IPI0001905E | DNASTKAMAGSIL | 95.00% | 92.7 | 40.2 | 558 | 570 |
| RNF19A Isoform 1 of E3 ubiquitin-protein ligase RNF19A | IPI0001905E | VSDNASTKAMAGSILN | 95.00% | 77.3 | 41.1 | 556 | 571 |
| RNF19A Isoform 1 of E3 ubiquitin-protein ligase RNF19A | IPI0001905E | SDNASTKAMAGSIL | 95.00% | 70 | 39.7 | 557 | 570 |
| RNF19A Isoform 1 of E3 ubiquitin-protein ligase RNF19A | IPI0001905E | VSDNASTKAMAGSIL | 95.00% | 63.3 | 39.4 | 556 | 570 |
| RNF19B Isoform 1 of E3 ubiquitin-protein ligase RNF19B | IPI0047747E | EAEAAAAAEPGFDEE | 95.00% | 82.1 | 31.8 | 89 | 105 |
| RNF19B Isoform 1 of E3 ubiquitin-protein ligase RNF19B | IPI0047747E | AEAEAAAAAEPGFDEE | 95.00% | 73.3 | 31.9 | 88 | 105 |
| RNF19B Isoform 1 of E3 ubiquitin-protein ligase RNF19B | IPI0047747E | ISDNASTRAMAGSIS | 95.00% | 56.5 | 40.8 | 559 | 574 |
| RPL9 60S ribosomal protein L9 | IPI0003169I | LVSNSAALIQQATTVK | 95.00% | 119 | 37.4 | 26 | 41 |
| RPL9 60S ribosomal protein L9 | IPI0003169I | LVSNSAALIQQATTVKN | 95.00% | 96.1 | 38.2 | 26 | 42 |
| RPL9 60S ribosomal protein L9 | IPI0003169I | LVSNSAALIQQATT | 95.00% | 94.8 | 40.5 | 26 | 39 |
| RPL9 60S ribosomal protein L9 | IPI0003169I | LVSNSAALIQQAT | 95.00% | 85.3 | 40.9 | 26 | 38 |
| RPL9 60S ribosomal protein L9 | IPI0003169I | LVSNSAALIQQATTV | 95.00% | 83.6 | 39.7 | 26 | 40 |
| RPL9 60S ribosomal protein L9 | IPI0003169I | ELVNSAALIQQATTVK | 95.00% | 79.5 | 38.8 | 25 | 41 |
| RPS20 40S ribosomal protein S20 | IPI0001249E | IVKQITSISIEPGVE | 95.00% | 79.6 | 38.4 | 16 | 30 |
| RPS20 40S ribosomal protein S20 | IPI0001249E | IVKQITSISIEPGVEE | 95.00% | 67.7 | 37.2 | 16 | 32 |
| S100A8 Protein S100-A8 | IPI00007047 | DINTDGVNFE | 95.00% | 83.6 | 38.3 | 59 | 70 |
| S100A8 Protein S100-A8 | IPI00007047 | FKELDINTDGVN | 95.00% | 81.5 | 40.6 | 55 | 67 |
| S100A8 Protein S100-A8 | IPI00007047 | DINTDGVN | 95.00% | 52.4 | 40.2 | 59 | 67 |
| S100A8 Protein S100-A8 | IPI00007047 | DINTDGVNFE | 95.00% | 46.7 | 39.5 | 59 | 69 |
| S100A8 Protein S100-A8 | IPI00007047 | MLTELEKALNS | 95.00% | 80.1 | 40.3 | 1 | 11 |
| S100A8 Protein S100-A8 | IPI00007047 | MLTELEKAL | 95.00% | 58.6 | 37.1 | 1 | 9 |
| S100A8 Protein S100-A8 | IPI00007047 | TELEKALNSIID | 95.00% | 51.8 | 39.4 | 3 | 14 |
| S100A8 Protein S100-A8 | IPI00007047 | MLTELEKALN | 95.00% | 52.1 | 38.4 | 1 | 10 |
| S100A8 Protein S100-A8 | IPI00007047 | NSIIDVYHKYS | 95.00% | 53.5 | 37.4 | 10 | 20 |
| S100A9 Protein S100-A9 | IPI0002746E | DTNADKQLSFE | 95.00% | 72.5 | 37.2 | 67 | 78 |
| S100A9 Protein S100-A9 | IPI0002746E | LDTNADKQLS | 95.00% | 70.7 | 40.5 | 66 | 75 |
| S100A9 Protein S100-A9 | IPI0002746E | DTNADKQLSF | 95.00% | 65.4 | 38.8 | 67 | 76 |
| S100A9 Protein S100-A9 | IPI0002746E | DTNADKQLSFE | 95.00% | 61 | 37.6 | 67 | 77 |
| S100A9 Protein S100-A9 | IPI0002746E | DLDTNADKQ | 95.00% | 60 | 39.3 | 65 | 73 |
| S100A9 Protein S100-A9 | IPI0002746E | LDTNADKQL | 95.00% | 59 | 41.9 | 66 | 74 |
| S100A9 Protein S100-A9 | IPI0002746E | LDTNADKQ | 95.00% | 53 | 41.6 | 66 | 73 |
| S100A9 Protein S100-A9 | IPI0002746E | DTNADKQLS | 95.00% | 48.1 | 39.7 | 67 | 75 |
| S100A9 Protein S100-A9 | IPI0002746E | DTNADKQL | 95.00% | 48 | 41.6 | 67 | 74 |
| S100A9 Protein S100-A9 | IPI0002746E | LGHPTLNQGEFK | 95.00% | 58.8 | 38.9 | 26 | 38 |
| S100A9 Protein S100-A9 | IPI0002746E | SVKLGHPDTL | 95.00% | 53.6 | 39.6 | 23 | 32 |
| S100A9 Protein S100-A9 | IPI0002746E | IINTFHQY | 95.00% | 67 | 38.8 | 15 | 22 |
| S100A9 Protein S100-A9 | IPI0002746E | TIINTFHQY | 95.00% | 53.5 | 38.1 | 14 | 22 |
| SCAMP2 Secretory carrier-associated membrane protein 2 | IPI0021885C | LPGSSQPAVLQPSVEPTQ | 95.00% | 91 | 40.7 | 54 | 71 |
| SCAMP2 Secretory carrier-associated membrane protein 2 | IPI0021885C | LPGSSQPAVLQPSVEPTQPT | 95.00% | 79.7 | 40.9 | 54 | 73 |
| SCAMP2 Secretory carrier-associated membrane protein 2 | IPI0021885C | LPGSSQPAVLQPSVEPT | 95.00% | 77 | 40.6 | 54 | 70 |
| SCAMP2 Secretory carrier-associated membrane protein 2 | IPI0021885C | LPGSSQPAVLQPSVEPTQP | 95.00% | 66.9 | 40.9 | 54 | 72 |
| SCAMP2 Secretory carrier-associated membrane protein 2 | IPI0021885C | LPGSSQPAVLQPSVE | 95.00% | 65 | 40.3 | 54 | 68 |
| SCAMP2 Secretory carrier-associated membrane protein 2 | IPI0021885C | LPGSSQPAVLQPSVEPTQPTP | 95.00% | 60.8 | 40.8 | 54 | 74 |
| SCAMP2 Secretory carrier-associated membrane protein 2 | IPI0021885C | LPGSSQPAVLQPSVEP | 95.00% | 59.1 | 40.8 | 54 | 69 |
| SCARB1 Isoform 1 of Scavenger receptor class B member 1 | IPI0017796E | SAPKGSVLQAEKL | 95.00% | 58.7 | 39.4 | 462 | 474 |
| SCPEP1 Isoform 1 of Retinoid-inducible serine carboxypeptidase | IPI0001242E | IFGSEYGGKMAAGIGLE | 95.00% | 77.2 | 40.6 | 163 | 179 |
| SCPEP1 Isoform 1 of Retinoid-inducible serine carboxypeptidase | IPI0001242E | TDGVNFFYNIKTSTPT | 95.00% | 62.1 | 40.8 | 264 | 279 |
| SDCBP Syntenin-1 | IPI0029908E | VIQAQTAFSANPANPAIL | 95.00% | 89.7 | 39.9 | 15 | 32 |
| SDCBP Syntenin-1 | IPI0029908E | IQAQTAFSANPANPAIL | 95.00% | 68.6 | 38.8 | 16 | 32 |
| SDF4 45 kDa calcium-binding protein | IPI0010664E | YNALNEAKQMIADEN | 95.00% | 81.1 | 39.8 | 313 | 329 |
| SDF4 45 kDa calcium-binding protein | IPI0010664E | DPMNEYNALNEAKQ | 95.00% | 97.7 | 37 | 308 | 321 |
| SDF4 45 kDa calcium-binding protein | IPI0010664E | MDPMNEYNALNEAKQM | 95.00% | 89.3 | 34.5 | 307 | 322 |
| SDF4 45 kDa calcium-binding protein | IPI0010664E | DPMNEYNALNEAKQM | 95.00% | 84.5 | 36.1 | 308 | 322 |
| SDF4 45 kDa calcium-binding protein | IPI0010664E | MDPMNEYNALNEAKQ | 95.00% | 82.3 | 35.5 | 307 | 321 |
| SDF4 45 kDa calcium-binding protein | IPI0010664E | YNALNEAKQMIADENQNH | 95.00% | 58.3 | 39.7 | 313 | 333 |
| SDF4 45 kDa calcium-binding protein | IPI0010664E | NALNEAKQMIADENQNH | 89.30% | 45.5 | 39.7 | 314 | 333 |
| SEMA4A Semaphorin-4A | IPI00149097 | LPFNVRHVAVLLPADSPTAPH | 93.60% | 51.4 | 38.7 | 167 | 187 |
| SEMA4A Semaphorin-4A | IPI00149097 | LPFNVRHVAVLLPADSPT | 92.30% | 47.9 | 37.7 | 167 | 184 |
| SEMA4D Semaphorin-4D | IPI00023807 | EPSFVFADVIRKSPDSDGEDDR | 95.00% | 65.1 | 39.8 | 208 | 230 |
| SEMA4D Semaphorin-4D | IPI00023807 | EPSFVFADVIRKSPDSDG | 95.00% | 64.3 | 40.4 | 208 | 226 |
| SEMA4D Semaphorin-4D | IPI00023807 | EPSFVFADVIRKSPDSD | 95.00% | 60 | 41 | 208 | 225 |
| SEMA4D Semaphorin-4D | IPI00023807 | EPSFVFADVIRKSPDSDP | 95.00% | 50.5 | 40.9 | 208 | 224 |
| SEMA7A Semaphorin-7A | IPI00025257 | NPQFIKATIVHQDQAYD | 95.00% | 70.2 | 40.5 | 221 | 237 |
| SEMA7A Semaphorin-7A | IPI00025257 | NPQFIKATIVHQDQAYDD | 95.00% | 67.2 | 40.4 | 221 | 238 |
| SEMA7A Semaphorin-7A | IPI00025257 | NPQFIKATIVHQDQAYDDK | 92.00% | 51 | 41.3 | 221 | 239 |

SUPPLEMENTARY DATA

| | | | | | | | |
|---|-------------|-----------------------|--------|------|------|------|------|
| SGCE sarcoglycan, epsilon isoform 1 | IPI00414984 | GDFLGAVKNVWQPER | 95.00% | 65.7 | 39.4 | 181 | 195 |
| SGMS2 Phosphatidylcholine:ceramide cholinephosphotransferase 2 | IPI00169331 | QPSDPTNTYARPAEPVE | 95.00% | 67.2 | 39.6 | 16 | 32 |
| SGTA Small glutamine-rich tetratricopeptide repeat-containing protein alpha | IPI0001394E | SPSQNDLASLIQAGQQ | 95.00% | 98.9 | 39.6 | 264 | 279 |
| SILV Melanocyte protein Pmel 17 | IPI0003163C | DFGDSSGTLISRAL | 95.00% | 84.5 | 40.5 | 84 | 97 |
| SILV Melanocyte protein Pmel 17 | IPI0003163C | DFGDSSGTLISRALVVT | 95.00% | 57.8 | 40.4 | 84 | 100 |
| SLAMF6 SLAM family member 6 | IPI00513714 | SPTNNTVYASVTHSNRET | 95.00% | 66.2 | 39.3 | 277 | 294 |
| SLC12A7 Isoform 1 of Solute carrier family 12 member 7 | IPI0000861E | LNGVVLNKSQDAQ | 95.00% | 73.1 | 40.1 | 1023 | 1035 |
| SLC19A1 Folate transporter 1 | IPI0037545Z | VDPTNSARVYNGAAD | 95.00% | 81.9 | 38.7 | 295 | 310 |
| SLC19A1 Folate transporter 1 | IPI0037545Z | VDPTNSARVYNGAADA | 95.00% | 79.9 | 39.2 | 295 | 311 |
| SLC19A1 Folate transporter 1 | IPI0037545Z | PTTNSARVYNGAADA | 95.00% | 58 | 39.9 | 297 | 311 |
| SLC19A1 Folate transporter 1 | IPI0037545Z | ASTLLGAITSFAAG | 95.00% | 52.9 | 40.3 | 312 | 325 |
| SLC20A1 Sodium-dependent phosphate transporter 1 | IPI0002303E | DSTVNGAVQLPNGNL | 95.00% | 60.1 | 39.6 | 345 | 359 |
| SLC2A6 Putative uncharacterized protein | IPI0017996E | VPSAAGYALMAGAAGH | 95.00% | 110 | 39.1 | 117 | 131 |
| SLC35F2 Isoform 1 of Solute carrier family 35 member F2 | IPI0029336Z | EDNSGSDVLIGDIL | 95.00% | 99.2 | 40.3 | 188 | 201 |
| SLC35F2 Isoform 1 of Solute carrier family 35 member F2 | IPI0029336Z | REDNSGSDVLIGDIL | 95.00% | 93.7 | 40.8 | 187 | 201 |
| SLC35F2 Isoform 1 of Solute carrier family 35 member F2 | IPI0029336Z | GREDNSGSDVLIGDIL | 95.00% | 90.1 | 40.2 | 186 | 201 |
| SLC35F2 Isoform 1 of Solute carrier family 35 member F2 | IPI0029336Z | GVGTMVSGADILAGREDN | 95.00% | 93.4 | 40.2 | 174 | 190 |
| SLC35F2 Isoform 1 of Solute carrier family 35 member F2 | IPI0029336Z | VGTMVSGADILAGRED | 95.00% | 115 | 41.2 | 175 | 189 |
| SLC35F2 Isoform 1 of Solute carrier family 35 member F2 | IPI0029336Z | VGTMVSGADILAGREDN | 95.00% | 114 | 40.6 | 175 | 190 |
| SLC35F2 Isoform 1 of Solute carrier family 35 member F2 | IPI0029336Z | TMVGDILAGREDN | 95.00% | 77.1 | 38.4 | 177 | 190 |
| SLC38A2 Isoform 1 of Sodium-coupled neutral amino acid transporter 2 | IPI00410034 | TANEGGSLLYEQLGYK | 95.00% | 83.6 | 40.7 | 34 | 49 |
| SLC38A2 Isoform 1 of Sodium-coupled neutral amino acid transporter 2 | IPI00410034 | TANEGGSLLYEQLG | 95.00% | 49.8 | 39.9 | 34 | 47 |
| SLC38A5 Isoform 1 of Sodium-coupled neutral amino acid transporter 5 | IPI0010250E | DPKMNGALPSDAVGY | 95.00% | 83.3 | 38.5 | 5 | 19 |
| SLC38A5 Isoform 1 of Sodium-coupled neutral amino acid transporter 5 | IPI0010250E | DPKMNGALPSDAVG | 95.00% | 63.1 | 38.1 | 5 | 18 |
| SLC38A5 Isoform 1 of Sodium-coupled neutral amino acid transporter 5 | IPI0010250E | LQDPKMNGALPSDAVG | 95.00% | 62.8 | 40.3 | 3 | 18 |
| SLC38A5 Isoform 1 of Sodium-coupled neutral amino acid transporter 5 | IPI0010250E | PKMNGALPSDAVG | 95.00% | 58.6 | 38.8 | 6 | 18 |
| SLC38A5 Isoform 1 of Sodium-coupled neutral amino acid transporter 5 | IPI0010250E | QDPKMNGALPSDAVG | 91.30% | 46.5 | 39.9 | 4 | 18 |
| SLC38A5 Isoform 1 of Sodium-coupled neutral amino acid transporter 5 | IPI0010250E | QDPKMNGALPSDAVGY | 90.60% | 45.7 | 39.4 | 4 | 19 |
| SLC39A3 Isoform 1 of Zinc transporter ZIP3 | IPI00029337 | VPGSVASVLLQLLGG | 95.00% | 65.2 | 37.7 | 353 | 368 |
| SLC4A2 Isoform A of Anion exchange protein 2 | IPI00383597 | KGAQAGTQVEEAEAEA | 95.00% | 83.9 | 39.4 | 174 | 189 |
| SLC4A2 Isoform A of Anion exchange protein 2 | IPI00383597 | TPRASKGAQAGTQVEEAEAEA | 95.00% | 59.6 | 41.1 | 169 | 189 |
| SLC7A1 High affinity cationic amino acid transporter 1 | IPI0002772E | IIGTSSVARAWSAT | 95.00% | 56 | 39.8 | 122 | 135 |
| SLC7A5 Large neutral amino acids transporter small subunit 1 | IPI0000898E | VTLQRNITLLNGVA | 95.00% | 47.8 | 35.8 | 44 | 57 |
| SNX17 Sorting nexin-17 | IPI0001421E | SASDVHGNFAFEGIGDED | 95.00% | 66.3 | 33.1 | 452 | 469 |
| SNX17 Sorting nexin-17 | IPI0001421E | SASDVHGNFAFEGIGDE | 95.00% | 57.8 | 35.3 | 452 | 468 |
| SNX17 Sorting nexin-17 | IPI0001421E | ASDVHGNFAFEGIGDED | 95.00% | 55.7 | 33.5 | 453 | 469 |
| SORL1 Sortilin-related receptor | IPI0002260E | ENQEVIILEVRDFQ | 95.00% | 93.5 | 40.1 | 288 | 301 |
| SORL1 Sortilin-related receptor | IPI0002260E | SRENQEVIILEVRDFQ | 95.00% | 74.2 | 40.4 | 286 | 301 |
| SORL1 Sortilin-related receptor | IPI0002260E | GADASATQAARSTDVA | 95.00% | 80.6 | 38.7 | 2122 | 2137 |
| SORL1 Sortilin-related receptor | IPI0002260E | GADASATQAARSTDVAA | 95.00% | 53.6 | 38.6 | 2122 | 2138 |
| SORL1 Sortilin-related receptor | IPI0002260E | GADASATQAARSTD | 95.00% | 65.6 | 35.5 | 2122 | 2135 |
| SORL1 Sortilin-related receptor | IPI0002260E | DASATQAARSTDVA | 95.00% | 55.7 | 36.7 | 2124 | 2137 |
| SORL1 Sortilin-related receptor | IPI0002260E | GADASATQAARSTDVAVVVP | 91.50% | 47.9 | 41.1 | 2122 | 2142 |
| SORL1 Sortilin-related receptor | IPI0002260E | NLQGFISIPFRAADL | 95.00% | 70.2 | 40.3 | 195 | 209 |
| SORL1 Sortilin-related receptor | IPI0002260E | NLQGFISIPFRAAD | 95.00% | 69.6 | 39 | 195 | 208 |
| SORL1 Sortilin-related receptor | IPI0002260E | NLQGFISIPFRAADLL | 95.00% | 60.4 | 40 | 195 | 210 |
| SORL1 Sortilin-related receptor | IPI0002260E | VINSGLTVEALA | 95.00% | 77.3 | 38.4 | 825 | 838 |
| SORL1 Sortilin-related receptor | IPI0002260E | QSRENQEVIILEVRDFQ | 92.60% | 51.3 | 40.5 | 285 | 301 |
| SORL1 Sortilin-related receptor | IPI0002260E | VVHLLGSEQSSVF | 95.00% | 81.2 | 39.5 | 312 | 325 |
| SORL1 Sortilin-related receptor | IPI0002260E | SEQQSSVQLWVSFGRKP | 87.80% | 46 | 41.8 | 318 | 334 |
| SQSTM1 Isoform 1 of Sequestosome-1 | IPI0017947Z | DPSKPGGNVEGATQSLAEQM | 95.00% | 83.7 | 38.7 | 208 | 227 |
| SQSTM1 Isoform 1 of Sequestosome-1 | IPI0017947Z | DPSKPGGNVEGATQSLAEQ | 95.00% | 82.9 | 39.7 | 208 | 226 |
| STAM2 Isoform 1 of Signal transducing adapter molecule 2 | IPI0029054Z | NPTYMNQNSNLQSATGT | 95.00% | 111 | 36.8 | 458 | 474 |
| STAM2 Isoform 1 of Signal transducing adapter molecule 2 | IPI0029054Z | NPTYMNQNSNLQSATGTT | 95.00% | 88.2 | 37 | 458 | 475 |
| STAM2 Isoform 1 of Signal transducing adapter molecule 2 | IPI0029054Z | LQSATGTTAYTQQMG | 95.00% | 66.8 | 39.3 | 468 | 482 |
| STX12 Syntaxin-12 | IPI0032933Z | ANVESSEVHVERATEQLQ | 95.00% | 81.7 | 40.3 | 244 | 261 |
| STX12 Syntaxin-12 | IPI0032933Z | ANVESSEVHVERATEQ | 95.00% | 87.6 | 39.5 | 244 | 259 |
| STX12 Syntaxin-12 | IPI0032933Z | LQLQHQSTNQLAKETN | 95.00% | 69.3 | 41 | 63 | 78 |
| STX12 Syntaxin-12 | IPI0032933Z | LQLQHQSTNQLAKETNEL | 95.00% | 83.1 | 40.7 | 63 | 80 |
| STX12 Syntaxin-12 | IPI0032933Z | LQLQHQSTNQLAKETNE | 94.30% | 55 | 40.6 | 63 | 79 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | IEANVENAEVHVQQAN | 95.00% | 109 | 40 | 206 | 221 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | ANVENAEVHVQQAN | 95.00% | 104 | 38.8 | 208 | 221 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | NVENAEVHVQQANQQ | 95.00% | 99.4 | 39.7 | 209 | 223 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | ANVENAEVHVQQANQQ | 95.00% | 88.8 | 40.2 | 208 | 223 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | IEANVENAEVHVQQ | 95.00% | 86.5 | 40.7 | 206 | 219 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | ANVENAEVHVQQANQQL | 95.00% | 79.8 | 40.8 | 208 | 224 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | ANVENAEVHVQQANQ | 95.00% | 76.9 | 39.2 | 208 | 222 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | ANVENAEVHVQQANQQLS | 95.00% | 74.4 | 40.8 | 208 | 225 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | VENAEVHVQQANQQ | 95.00% | 71.9 | 40.4 | 210 | 223 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | NVENAEVHVQQAN | 95.00% | 70.7 | 38.8 | 209 | 221 |

SUPPLEMENTARY DATA

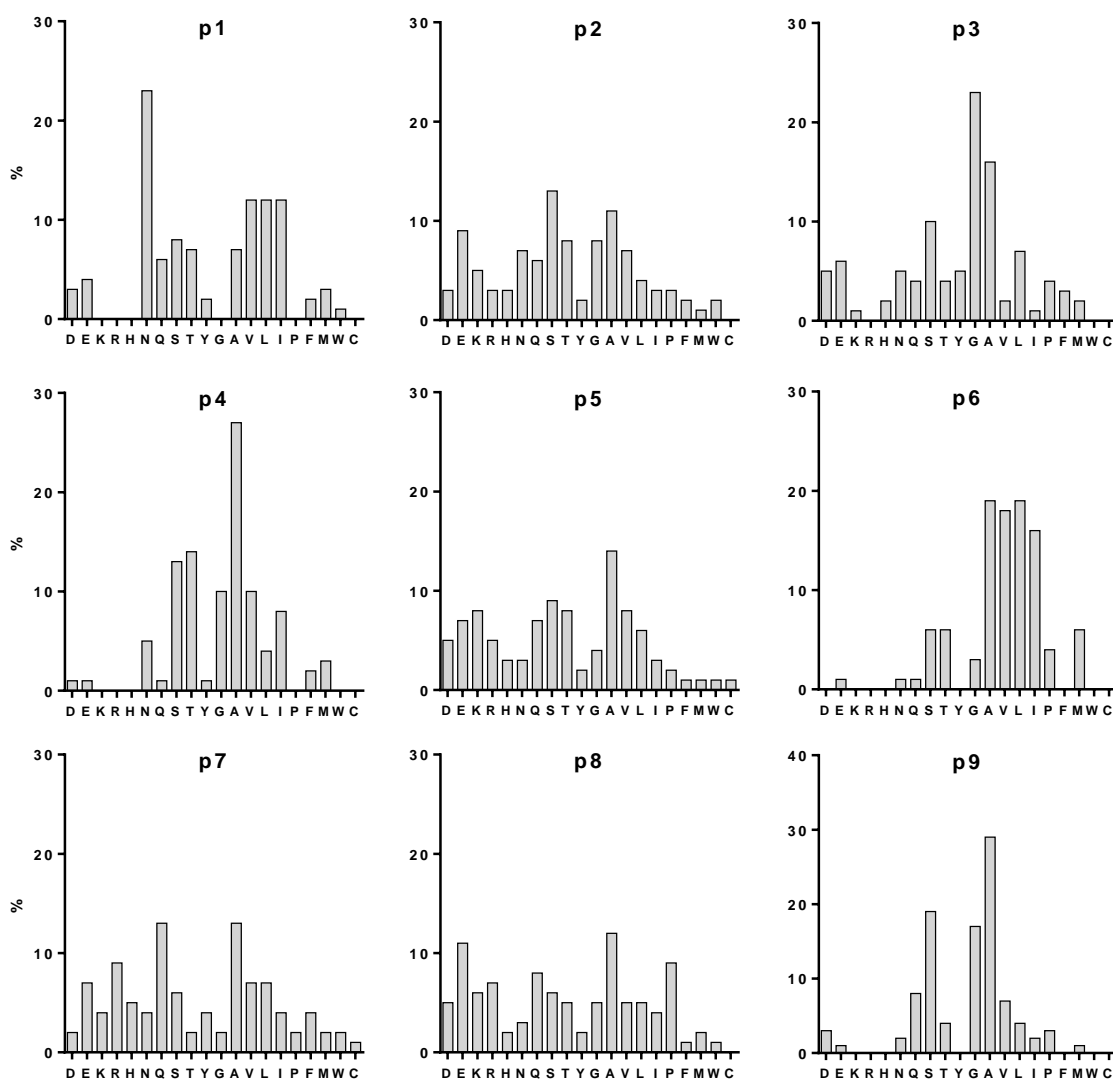
| | | | | | | | |
|---|-------------|------------------------|--------|------|------|------|------|
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | NVENAEVHVQQANQQL | 95.00% | 66.6 | 40.7 | 209 | 224 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | IEANVNAEVHVQ | 95.00% | 61.4 | 39.9 | 206 | 218 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | NVENAEVHVQQANQ | 95.00% | 57.9 | 40.1 | 209 | 222 |
| STX7 Isoform 1 of Syntaxin-7 | IPI0028987E | IFKDLGMMIHEQGDV | 95.00% | 53.9 | 40.3 | 188 | 202 |
| SYNGR2 Synaptogyrin-2 | IPI0001394E | NPKDVLVGADSVRAAIT | 95.00% | 67.7 | 39.5 | 134 | 150 |
| SYNGR2 Synaptogyrin-2 | IPI0001394E | NPKDVLVGADSVRAA | 95.00% | 58.8 | 38.7 | 134 | 148 |
| TCEB1P3 similar to elongation factor SIII p15 subunit | IPI0001310E | VNETNEVNF | 95.00% | 50.4 | 38.3 | 54 | 62 |
| TFG Protein TFG | IPI0029461E | GPPSAPAEDRSGTPD | 95.00% | 75.8 | 37.7 | 194 | 208 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | NPGGYVAYSKAATVTGKL | 95.00% | 106 | 40 | 215 | 232 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | NPGGYVAYSKAATVTGK | 95.00% | 105 | 40.2 | 215 | 231 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | NPGGYVAYSKAATVTG | 95.00% | 97.5 | 40 | 215 | 230 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | NPGGYVAYSKAATVTGKLV | 95.00% | 95.8 | 39.6 | 215 | 233 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | PGGYVAYSKAATVTG | 95.00% | 93.2 | 39.7 | 216 | 230 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | GGYVAYSKAATVTG | 95.00% | 79.9 | 39.2 | 217 | 230 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | ENPGGYVAYSKAATVTG | 95.00% | 62.8 | 40.5 | 214 | 230 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | NPGGYVAYSKAATVTGKLVH | 93.50% | 52.8 | 40.2 | 215 | 234 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | VDGDNSHVEMKLAVDDEENADN | 95.00% | 76.3 | 33.5 | 29 | 50 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | VDGDNSHVEMKLAVDDEEN | 95.00% | 74.7 | 35.9 | 29 | 47 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | VDGDNSHVEMKLAVDDEE | 95.00% | 72.6 | 36.8 | 29 | 45 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | VDGDNSHVEMKLAVDDEE | 94.80% | 51.9 | 36.1 | 29 | 46 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | QDSNWASKVEKLT | 94.00% | 48.3 | 40.1 | 524 | 536 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | LPALLENLKRKQNN | 94.20% | 46 | 32 | 709 | 723 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | DQARSASFNLFGGEP | 95.00% | 92.8 | 39.3 | 3 | 17 |
| TFRC Transferrin receptor protein 1 | IPI0002246Z | TWTIQGAANALSGDV | 91.30% | 45.6 | 39 | 739 | 753 |
| TGFB1 Transforming growth factor beta-1 | IPI0000007E | MNRPFLMLMATP | 95.00% | 53.6 | 40.6 | 253 | 264 |
| TLN1 Talin-1 | IPI0029899A | QGLISAARMVAAATN | 95.00% | 90 | 38.2 | 2391 | 2405 |
| TLN1 Talin-1 | IPI0029899A | GDLISATKAAAGKVG | 95.00% | 88.5 | 40.4 | 2092 | 2107 |
| TLN1 Talin-1 | IPI0029899A | GDLISATKAAAGKVG | 95.00% | 62.4 | 39.1 | 2092 | 2106 |
| TLN1 Talin-1 | IPI0029899A | LGDLISATKAAAGKVG | 95.00% | 62.3 | 37.6 | 2091 | 2106 |
| TLN1 Talin-1 | IPI0029899A | DLISATKAAAGKVG | 95.00% | 54.2 | 39 | 2093 | 2106 |
| TLN1 Talin-1 | IPI0029899A | GDLISATKAAAGKVGDDPA | 93.00% | 52 | 40.5 | 2092 | 2110 |
| TMED2 Transmembrane emp24 domain-containing protein 2 | IPI0001660E | EMINELAVAMTAVK | 95.00% | 127 | 40.8 | 47 | 60 |
| TMED2 Transmembrane emp24 domain-containing protein 2 | IPI0001660E | EEMINELAVAMTAVK | 95.00% | 125 | 41.2 | 46 | 60 |
| TMEM123 Isoform 1 of Porimin | IPI0021736E | HESAAAMAASANIEN | 95.00% | 74.6 | 34.7 | 27 | 40 |
| TMEM161A Transmembrane protein 161A | IPI0030184I | DEVQQTAAARIAGALGG | 95.00% | 67.2 | 39.5 | 322 | 337 |
| TMEM161A Transmembrane protein 161A | IPI0030184I | EVQQTAAARIAGALG | 95.00% | 50.3 | 38.9 | 323 | 336 |
| TMEM50A Transmembrane protein 50A | IPI0000061Z | GCLGQGTGARIW | 95.00% | 60.2 | 39.4 | 86 | 96 |
| TMEM87A cDNA FLJ76697 | IPI0017142Z | QEPNGNSKVNKAQEDD | 93.00% | 49.7 | 38.2 | 441 | 456 |
| TMEM87B Isoform 1 of Transmembrane protein 87B | IPI0078338C | SVSNGTAKPATSENF | 95.00% | 59.3 | 38.3 | 494 | 509 |
| TNFAIP3 Tumor necrosis factor, alpha-induced protein 3 | IPI0000944E | THLINAAKLDEANLPK | 93.80% | 51.5 | 38.3 | 322 | 337 |
| TNFAIP3 Tumor necrosis factor, alpha-induced protein 3 | IPI0000944E | THLINAAKLDEANLPKE | 92.20% | 50.4 | 40.4 | 322 | 338 |
| TNFRSF21 Tumor necrosis factor receptor superfamily member 21 | IPI0000441Z | LFEIIGVKSQEASQTL | 95.00% | 106 | 39.6 | 628 | 643 |
| TNFRSF21 Tumor necrosis factor receptor superfamily member 21 | IPI0000441Z | LFEIIGVKSQEASQT | 95.00% | 94.9 | 40.5 | 628 | 642 |
| TNFRSF21 Tumor necrosis factor receptor superfamily member 21 | IPI0000441Z | LFEIIGVKSQEASQ | 95.00% | 69.5 | 40.9 | 628 | 641 |
| TNFSF9 Tumor necrosis factor ligand superfamily member 9 | IPI0001330I | SDPGLAGVSLTGGLS | 95.00% | 82.2 | 41.7 | 111 | 125 |
| TNFSF9 Tumor necrosis factor ligand superfamily member 9 | IPI0001330I | AVSGARSPSGAASPR | 94.10% | 54.5 | 40.6 | 54 | 69 |
| TNIP1 Isoform 2 of TNFAIP3-interacting protein 1 | IPI0021661E | SPEGAGALLRKQE | 95.00% | 80.4 | 39.3 | 442 | 454 |
| TNIP1 Isoform 2 of TNFAIP3-interacting protein 1 | IPI0021661E | SPEGAGALLRKQ | 95.00% | 79.5 | 38 | 442 | 453 |
| TNIP1 Isoform 2 of TNFAIP3-interacting protein 1 | IPI0021661E | SPEGAGALLRKQEL | 95.00% | 66.8 | 38.3 | 442 | 455 |
| TNIP1 Isoform 2 of TNFAIP3-interacting protein 1 | IPI0021661E | SPEGAGALLRKQELVT | 95.00% | 66.6 | 37.3 | 442 | 457 |
| TNIP1 Isoform 2 of TNFAIP3-interacting protein 1 | IPI0021661E | SPEGAGALLRKQELV | 95.00% | 60.4 | 37.1 | 442 | 456 |
| TNIP1 Isoform 2 of TNFAIP3-interacting protein 1 | IPI0021661E | TELRQKLADLQKQVTDLE | 93.10% | 51.8 | 40.2 | 336 | 353 |
| TPP1 Isoform 1 of Tripeptidyl-peptidase 1 | IPI00298237 | GDEEDLSAYIQRVNTE | 95.00% | 117 | 36.8 | 326 | 343 |
| TPP1 Isoform 1 of Tripeptidyl-peptidase 1 | IPI00298237 | DEDSLSAYIQRVNTE | 95.00% | 93.3 | 38.5 | 328 | 343 |
| TPP1 Isoform 1 of Tripeptidyl-peptidase 1 | IPI00298237 | LENVADLVRPSP | 95.00% | 108 | 39.3 | 82 | 93 |
| TPP1 Isoform 1 of Tripeptidyl-peptidase 1 | IPI00298237 | LTVENVADLVRPSP | 95.00% | 80.7 | 38.8 | 80 | 93 |
| TPP1 Isoform 1 of Tripeptidyl-peptidase 1 | IPI00298237 | TLENVADLVRPSP | 95.00% | 75.1 | 38.8 | 81 | 95 |
| TPP1 Isoform 1 of Tripeptidyl-peptidase 1 | IPI00298237 | ENVADLVRPSP | 95.00% | 73.8 | 39.8 | 83 | 93 |
| TPP1 Isoform 1 of Tripeptidyl-peptidase 1 | IPI00298237 | TLENVADLVRPSP | 95.00% | 70.5 | 39.7 | 81 | 93 |
| TPP1 Isoform 1 of Tripeptidyl-peptidase 1 | IPI00298237 | TLENVADLVRPSP | 95.00% | 62.6 | 38.9 | 81 | 94 |
| TPP1 Isoform 1 of Tripeptidyl-peptidase 1 | IPI00298237 | LENVADLVRPSP | 95.00% | 58.4 | 38.5 | 82 | 94 |
| TPP1 Isoform 1 of Tripeptidyl-peptidase 1 | IPI00298237 | LENVADLVRPSP | 95.00% | 57.5 | 38.8 | 82 | 95 |
| TPT1 Tumor protein, translationally-controlled 1 | IPI0000994Z | GPEGETESTVITGVDIVMHH | 95.00% | 61.6 | 39.7 | 22 | 43 |
| Tyrosine-protein kinase receptor | IPI00884937 | ATPLLMQALPMGALPQGP | 95.00% | 126 | 40.2 | 110 | 127 |
| Tyrosine-protein kinase receptor | IPI00884937 | TPLLMQALPMGALPQGPMC | 95.00% | 107 | 40.8 | 111 | 129 |
| Tyrosine-protein kinase receptor | IPI00884937 | ATPLLMQALPMGALPQGPMC | 95.00% | 104 | 41.2 | 110 | 129 |
| Tyrosine-protein kinase receptor | IPI00884937 | TPLLMQALPMGALPQGPM | 95.00% | 103 | 40.6 | 111 | 128 |
| Tyrosine-protein kinase receptor | IPI00884937 | ATPLLMQALPMGALPQGPM | 95.00% | 100 | 40.6 | 110 | 128 |
| Tyrosine-protein kinase receptor | IPI00884937 | TPLLMQALPMGALPQGP | 95.00% | 91.6 | 40.1 | 111 | 127 |
| Tyrosine-protein kinase receptor | IPI00884937 | TPLLMQALPMGALPQGP | 95.00% | 87.9 | 40 | 111 | 126 |

SUPPLEMENTARY DATA

| | | | | | | | |
|---|-------------|---------------------------|--------|------|------|-----|-----|
| Tyrosine-protein kinase receptor | IPI00884937 | TPLLMLQALPMGALPQ | 95.00% | 81.5 | 39 | 111 | 125 |
| Tyrosine-protein kinase receptor | IPI00884937 | MRMATPLLMLQALPM | 95.00% | 62.4 | 40 | 107 | 120 |
| Tyrosine-protein kinase receptor | IPI00884937 | MRMATPLLMLQALP | 95.00% | 59.5 | 38.7 | 107 | 119 |
| Tyrosine-protein kinase receptor | IPI00884937 | LMQALPMGALPQGP | 95.00% | 49 | 39.1 | 114 | 127 |
| Tyrosine-protein kinase receptor | IPI00884937 | SKMRMATPLLMLQA | 90.10% | 46.4 | 40.3 | 105 | 117 |
| UBC;UBB;RPS27A ubiquitin and ribosomal protein S27a precursor | IPI0017933C | IPDQQRLLIFAGKQLED | 92.50% | 50.7 | 40.2 | 52 | 68 |
| UBC;UBB;RPS27A ubiquitin and ribosomal protein S27a precursor | IPI0017933C | IPDQQRLLIFAGKQLEDG | 94.00% | 48.9 | 40.7 | 52 | 69 |
| UBC;UBB;RPS27A ubiquitin and ribosomal protein S27a precursor | IPI0017933C | DYNIQKESTLHLVLR | 95.00% | 85.3 | 39.8 | 74 | 88 |
| UBC;UBB;RPS27A ubiquitin and ribosomal protein S27a precursor | IPI0017933C | YNIQKESTLHLVLR | 95.00% | 79.6 | 38 | 75 | 88 |
| UBC;UBB;RPS27A ubiquitin and ribosomal protein S27a precursor | IPI0017933C | EPSDTIENVKAKIQDKEGIPDDQ | 92.90% | 53 | 41.7 | 34 | 56 |
| UBC;UBB;RPS27A ubiquitin and ribosomal protein S27a precursor | IPI0017933C | EPSDTIENVKAKIQDKEGIPPD | 92.30% | 51.7 | 41.5 | 34 | 55 |
| UBC;UBB;RPS27A ubiquitin and ribosomal protein S27a precursor | IPI0017933C | EPSDTIENVKAKIQDKEGIPP | 89.80% | 47.3 | 40.9 | 34 | 54 |
| UBC;UBB;RPS27A ubiquitin and ribosomal protein S27a precursor | IPI0017933C | EPSDTIENVKAKIQDK | 89.00% | 46.4 | 40.9 | 34 | 49 |
| UBE2V2 Ubiquitin-conjugating enzyme E2 variant 2 | IPI0001960C | NGINSSGMVDARS | 95.00% | 89 | 35.9 | 89 | 102 |
| UBE2V2 Ubiquitin-conjugating enzyme E2 variant 2 | IPI0001960C | GINSSGMVDARS | 95.00% | 85.3 | 36.6 | 90 | 102 |
| UBQLN4 Ubiquilin-4 | IPI0002450C | NREANLQALITGGDIN | 95.00% | 101 | 39.6 | 561 | 577 |
| UBQLN4 Ubiquilin-4 | IPI0002450C | REANLQALITGGDIN | 95.00% | 96.6 | 40.2 | 562 | 577 |
| UFM1 Ubiquitin-fold modifier 1 | IPI0001020T | AITNDGGINPAQTAG | 95.00% | 56.9 | 40.1 | 49 | 65 |
| UFM1 Ubiquitin-fold modifier 1 | IPI0001020T | IITNDGGINPAQTA | 93.80% | 48.1 | 40.1 | 50 | 64 |
| VASP Vasodilator-stimulated phosphoprotein | IPI0030105E | DAAQFAAGMASALE | 95.00% | 76.2 | 37.1 | 98 | 111 |
| VCP Transitional endoplasmic reticulum ATPase | IPI00022774 | EAEKNAPAIIFIDEL | 95.00% | 68.6 | 40.9 | 292 | 306 |
| VCP Transitional endoplasmic reticulum ATPase | IPI00022774 | EAEKNAPAIIFIDE | 95.00% | 65.9 | 40.9 | 292 | 305 |
| VDAC1 Voltage-dependent anion-selective channel protein 1 | IPI0021630E | SAKVNNSLIGLYTQT | 95.00% | 76.2 | 40.1 | 202 | 218 |
| VPS35 Vacuolar protein sorting-associated protein 35 | IPI00018931 | EDEISDSKAQLAAIT | 95.00% | 56.8 | 40.8 | 615 | 629 |
| WBP2 WW domain-binding protein 2 | IPI0003205C | TPAAEAKAAEAAASAYYN | 95.00% | 106 | 38.6 | 171 | 188 |
| WBP2 WW domain-binding protein 2 | IPI0003205C | TPAAEAKAAEAAASAYY | 95.00% | 84.2 | 39.8 | 171 | 187 |
| WBP2 WW domain-binding protein 2 | IPI0003205C | TPAAEAKAAEAAASA | 95.00% | 82.1 | 40.8 | 171 | 185 |
| WBP2 WW domain-binding protein 2 | IPI0003205C | TPAAEAKAAEAAASAY | 95.00% | 79.8 | 40.2 | 171 | 186 |
| WBP2 WW domain-binding protein 2 | IPI0003205C | TPAAEAKAAEAAASAYNPGN | 95.00% | 69.5 | 39.1 | 171 | 194 |
| WBP2 WW domain-binding protein 2 | IPI0003205C | TPAAEAKAAEAAASAYNPGN | 95.00% | 68.7 | 39.8 | 171 | 193 |
| WBP2 WW domain-binding protein 2 | IPI0003205C | GPDVPSTPAEAKAAEAAASA | 95.00% | 55.4 | 40.3 | 165 | 185 |
| WBP2 WW domain-binding protein 2 | IPI0003205C | GPDVPSTPAEAKAAEAAASAYNPGN | 94.30% | 53.8 | 39.4 | 165 | 194 |
| WBP2 WW domain-binding protein 2 | IPI0003205C | GPDVPSTPAEAKAAEAAA | 95.00% | 52.4 | 40.2 | 165 | 183 |
| WBP2 WW domain-binding protein 2 | IPI0003205C | GPDVPSTPAEAKAAEAAA | 95.00% | 50.5 | 40.4 | 165 | 182 |
| WWP2 NEDD4-like E3 ubiquitin-protein ligase WWP2 | IPI0001301C | LPSRDSSTAVAPEN | 95.00% | 78.5 | 39.5 | 163 | 177 |
| WWP2 NEDD4-like E3 ubiquitin-protein ligase WWP2 | IPI0001301C | ENKGSVSGGELT | 95.00% | 71.4 | 41.1 | 126 | 138 |
| YWHAE 14-3-3 protein epsilon | IPI0000081E | EDLVYQAKLAEQAE | 95.00% | 74.2 | 40.8 | 5 | 18 |
| YWHAE 14-3-3 protein epsilon | IPI0000081E | EDLVYQAKLAEQAERYD | 95.00% | 62.4 | 40 | 5 | 21 |
| YWHAE 14-3-3 protein epsilon | IPI0000081E | EDLVYQAKLAEQAER | 91.20% | 48.9 | 40.5 | 5 | 19 |
| YWHAE 14-3-3 protein epsilon | IPI0000081E | DREDLVYQAKLAEQAERYD | 90.50% | 47.8 | 40.5 | 3 | 21 |
| ZDHHC18 Palmitoyltransferase ZDHHC18 | IPI0018397E | IDNTGSSTYRPPP | 95.00% | 52 | 39.8 | 165 | 177 |
| ZSWIM6 zinc finger, SWIM domain containing 6 | IPI00015424 | AAAAAAAAAAAAA | 95.00% | 90.2 | 39.2 | 241 | 254 |
| ZSWIM6 zinc finger, SWIM domain containing 6 | IPI00015424 | AAAAAAAAAAAAA | 95.00% | 74.5 | 38.6 | 241 | 255 |
| ZSWIM6 zinc finger, SWIM domain containing 6 | IPI00015424 | AAAAAAAAAAAAAAG | 95.00% | 54.7 | 38.8 | 248 | 261 |

SUPPLEMENTARY DATA
SUPPLEMENTAL FIGURE 1

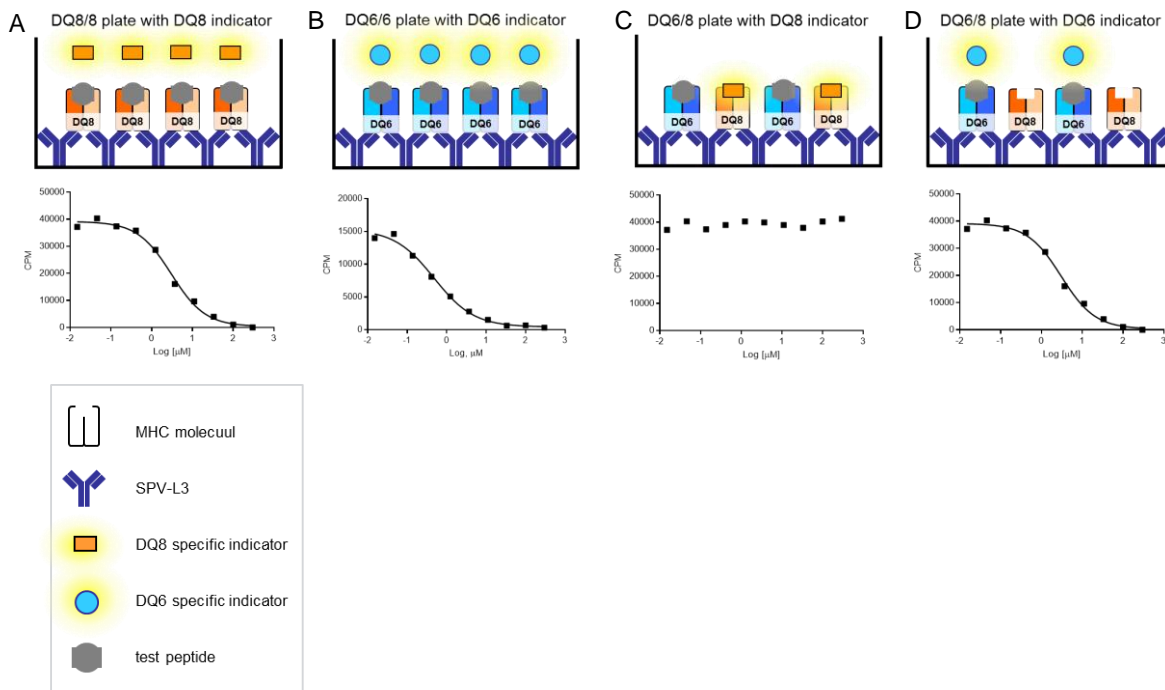
Amino acid distributions at the anchor and non-anchor positions within the peptide-binding groove of T1D protective DQ6. Amino acids with a frequency of 1.5 times higher compared to the same amino acids in the human proteome were considered as preferred residues. The frequencies of amino acids in the human proteome were adapted from the human assembly database Expert Protein Analysis System (ExPASy).



SUPPLEMENTARY DATA

SUPPLEMENTAL FIGURE 2

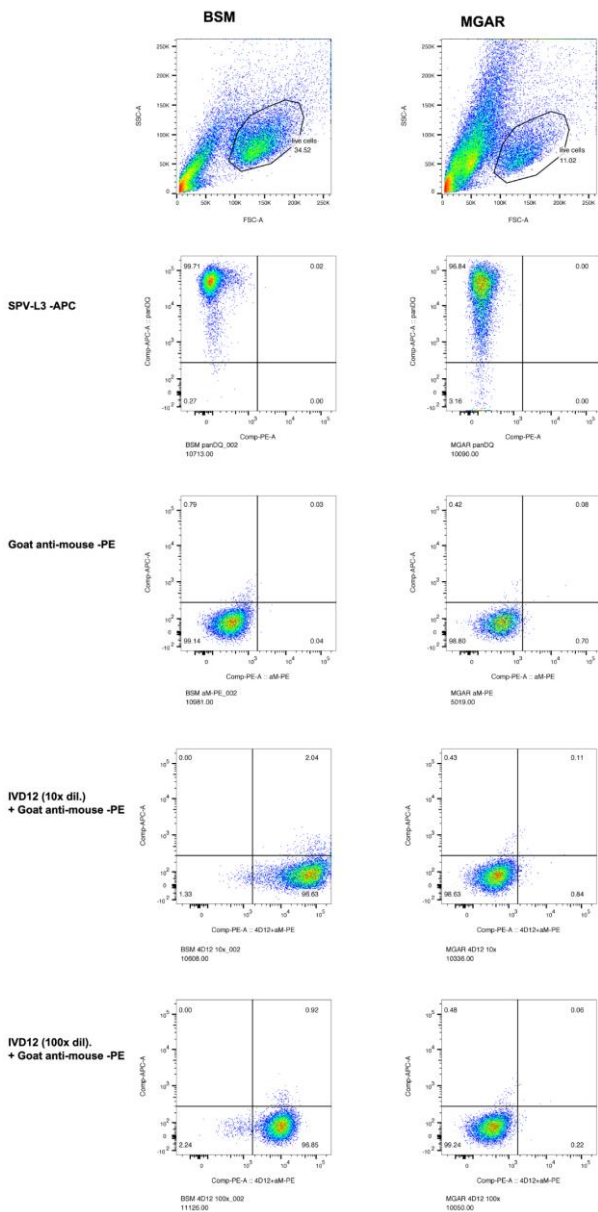
Competitive HLA-DQ peptide binding assays. To demonstrate peptide stealing from DQ8 by DQ6, binding of a test peptide is tested in 96-well plates coated with to DQ8 (A), DQ6 (B) or DQ6+DQ8 (C and D). Here, it is assumed that the test peptide can bind both DQ6 and DQ8 but with a preferential binding to DQ6 in the presence of DQ8. Below each representation of a DQ coated experimental well the expected outcome is shown by binding curves, with increasing concentrations of test peptide on the x-axis (log μM) and signal (count per minute; CPM) on the y-axis. Once a peptide binds to DQ, the indicator peptide is outcompeted resulting in a decreasing signal with increasing concentrations of test peptide. Subsequently, a typical S-shaped binding curve originates. Once a test peptide does not bind, the indicator peptide is not outcompeted, stays bound to the DQ molecule resulting in a stable signal giving rise to a horizontal binding curve. **A** and **B**. Binding of a test peptide to DQ8 and DQ6, respectively, resulting in the S-shaped curves. **C**. Binding of the test peptide to DQ6 in the presence of DQ8 using the DQ8 indicator. As the test peptide preferentially binds DQ6, the DQ8 indicator is not outcompeted resulting in the horizontal binding curve. **D**. As **C**, but using the DQ6 indicator. Here, the indicator peptide is outcompeted since the test peptide binds preferentially to DQ6. Once a test peptide preferentially binds DQ8, the expected binding curves in C and D will be the opposite.



SUPPLEMENTARY DATA

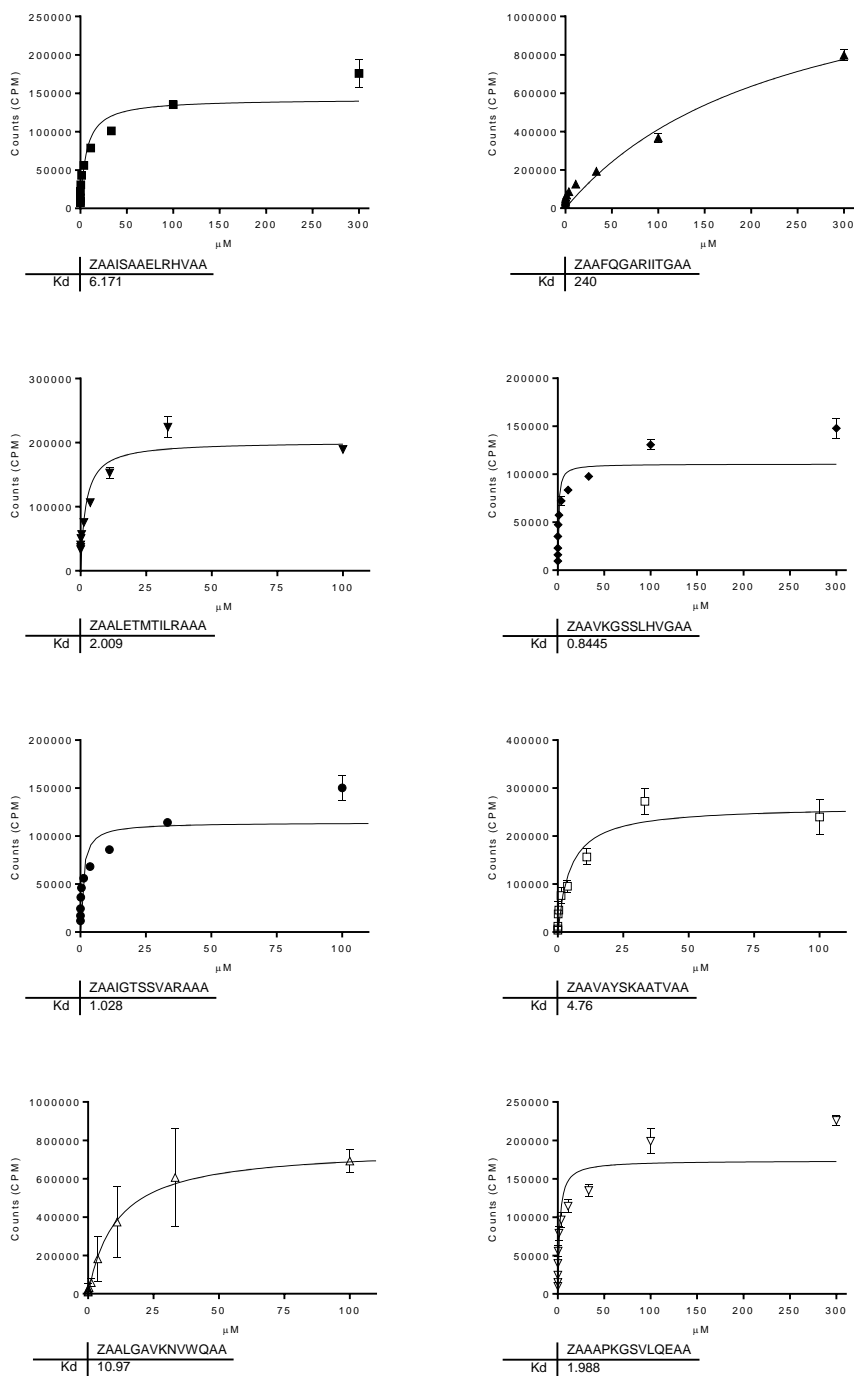
SUPPLEMENTAL FIGURE 3

Staining of EBV-BLCL with IVD12 and SPV-L3. Homozygous HLA-DQ6 (MGAR) and HLA-DQ8 (BSM) EBV-BLCL were stained with APC-conjugated SPV-L3 or with unconjugated IVD12 followed by staining with the secondary antibody GAM-PE. As control, MGAR and BSM were also stained with GAM-PE. IVD12 was used as ascites and two dilutions were used, namely 10x and 100x diluted. SPV-L3 recognizes both HLA-DQ6 and HLA-DQ8 expressed on MGAR and BSM, respectively. IVD12 only recognizes HLA-DQ8 on BSM, irrespective of the used IVD12 ascites dilution.



SUPPLEMENTARY DATA
SUPPLEMENTAL FIGURE 4

To obtain an indicator peptide for the peptide-binding studies with HLA-DQ6, eluted peptides from HLA-DQ6/6 homozygous EBV-BLCL were tested in direct peptide-binding assays. For this, predicted core-nonamers of DQ6-eluted peptides were extended with two alanine residues both at the N- and C-terminus and a biotin label was added at the N-terminus. Peptide sequences of the tested biotinylated peptides are shown. Data are obtained from two independent experiments each in duplicate. Curves are fitted according to a one-site binding hyperbola using GraphPad Prism. Data represent \pm SEM.



SUPPLEMENTARY DATA

SUPPLEMENTAL FIGURE 5

Natural processed and DQ6-presented peptides eluted from DQ6/8 expressing DC were tested for binding DQ6.2 and DQ8. The following peptides were confirmed: in the upper panel PPI 14-22 and in the lower panel IA-2₃₇₄₋₃₈₆, IA-2₄₉₈₋₅₁₁, IA-2₅₄₃₋₅₆₆ and IA-2₅₈₂₋₅₉ (from left to right) eluted from the four distinct core regions of IA-2. EC₅₀ values were calculated on the basis of competition between the biotinylated indicator peptide and the test peptides. Data represent mean ± SEM (n=3). Shown on the x-axes is 1/EC₅₀, illustrating that larger bars represent better binding.

