|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Protein ID | Protein length | Protein mass | Peptides number | Peptides | CV: SA/A |
| TGGT1\_291820 | 1539 | 163316.5514 | 2 | SFLPWLVR; ITLPPLTPFGALTAAGASK | 6.266 |
| TGGT1\_218760 | 329 | 35813.76861 | 2 | GEDTSTQAQMLAEAGNVLKR; SEDTIHDAIQIFEQEGDKATR | 5.7124 |
| TGME49\_207390 | 517 | 56022.65883 | 2 | GIPSAAQGMLAMMNR; SAVYSEAILVDPPPVK | 5.2456 |
| TGME49\_224490 | 646 | 69654.37245 | 2 | AFFGLVLGR; SSPSLSASSLPSSEVLAQK | 4.9196 |
| TGME49\_203400 | 580 | 64578.82991 | 2 | VFLGLLSVQEK; SVTVSDVVQAELEMLDR | 4.6675 |
| TGME49\_304990 | 1281 | 142607.7039 | 2 | MIDAQSLQLLEDLTR; LDLLPVSEMTPVYR | 4.2517 |
| TGME49\_243460 | 2011 | 209738.6885 | 2 | GLAAVAAEIASAQGLGGR; LFEGAAPQEGGQLSDLSR | 3.882 |
| TGGT1\_310300 | 930 | 100718.7247 | 3 | VLAALLSSFLR; KVGDFPLLPLSLLLSR; VGDFPLLPLSLLLSR | 3.7273 |
| TGGT1\_311030 | 3738 | 402558.8031 | 3 | LLLAGEAAHAAAEAVAEADSFAR; LVSSFLLPFLR; LLLQIDAANPLSLPK | 3.6525 |
| TGGT1\_239590 | 684 | 74807.26463 | 3 | AAMLIASGQEPGGRTPEEVEATGVAR; DSASLIPLLQFISK; FSAPFGLPGAR | 3.6208 |
| TGGT1\_267800 | 802 | 87400.25127 | 5 | AALFVPEGAFEILVR; SSVLEALVGR; ALAEFDPLEGLSDHEIR; SLIWSYFQIVR; AFFGGSFAGSALDR | 3.6052 |
| TGGT1\_208540 | 1043 | 114415.562 | 2 | QVVLVSATLPGDLVNFAR; LAFPSAVIYGAMDQTER | 3.486 |
| TGGT1\_254370 | 4367 | 476786.8845 | 2 | AAGQSFASLFR; ATPLDIVNFIQR | 3.3885 |
| TGGT1\_212250 | 767 | 86888.21222 | 2 | HLQTYLSENMLLR; IPTFFVFQGLQPR | 3.3051 |
| TGGT1\_247300 | 903 | 95516.53447 | 2 | TGGWLLGNLLQLPR; LVFEAFEGAQAYR | 3.093 |
| TGGT1\_275490 | 1999 | 216204.3036 | 3 | AFFAGVWQLLR; DAAGLVVFASEVLATTASR; VVSGLGDWIR | 3.0862 |
| TGME49\_243920 | 794 | 88156.71834 | 2 | RGPVQVQINLMDTSATHTPIR; GNDDEEIIPFELLK | 3.0055 |
| TGGT1\_287480 | 4703 | 502361.2972 | 2 | VNAGALLLIGEAK; QLAEIFSPFYSGLSR | 2.9018 |
| TGME49\_243250 | 1513 | 169551.5386 | 3 | LLVAMNPFK; NAFEEIEIPDTK; LLFSPEEEIDYFK | 2.8669 |
| TGGT1\_213300 | 4983 | 538072.8867 | 2 | SLLHNDGLLPPLSESAGDAGGSQSR; FALELLQLTENTR | 2.8094 |
| TGME49\_318410 | 537 | 58628.6328 | 3 | KQMLSIAPTLAQQLLLVDEVLK; RQPVGLNLTTGDALSPSVEGIWDNYR; SIAPTLAQQLLLVDEVLK | 2.7088 |
| TGGT1\_247330 | 1940 | 209426.2307 | 2 | LALPLVAFFDR; VSSLLDLLFYK | 2.6847 |
| TGME49\_267650 | 3032 | 324068.9064 | 2 | AIAQSAASVFSAPASLR; LFFPAALELLR | 2.679 |
| TGGT1\_222360 | 774 | 83297.21194 | 3 | QFMAVQEAAPTQMLSER; AGADLIDSLQGAAEDSHILLR; SSLALADVQPLWLAVSGGEAGK | 2.5801 |
| TGGT1\_269450 | 350 | 39808.59878 | 2 | TLAALELIEDFIER; HFLDLVEPLEFVSR | 2.5402 |
| TGGT1\_269690 | 865 | 94234.70088 | 4 | KLVTLFLGDEVR; VATLAQALTTGASPSIGMSMASMR; GLQVVVPLPTLEEIQKDGMDR; TQGIETAANKFFESSTQLDR | 2.5258 |
| TGGT1\_308890 | 3132 | 349557.8187 | 2 | RPLTVELEELQLEQQKK; EFGAQLTTEELR | 2.5174 |
| TGGT1\_207720 | 1628 | 176999.7299 | 3 | LSIFHPADVLAAGAVYAEPTSEPLAR; LLFTPASPLFK; FQDAQILNTVLWR | 2.4413 |
| **TGGT1\_225940** | **315** | **33712.9531** | **2** | **YYDGWATFLK; WSNTPLSGPGVLAYIEPK** | **2.4401** |
| TGGT1\_269290 | 4668 | 503002.4193 | 5 | QVSVSSAQLEQFAR; VAVALLSGMAR; AIIASLGDMSLAR; SALDAIAFFADR; LLDLFLSSPLLR | 2.4312 |
| TGGT1\_276210 | 825 | 91792.84964 | 2 | SFVTNVAHAVQSMWR; WLLLPLLR | 2.4219 |
| TGGT1\_216210 | 5565 | 603396.4766 | 2 | GQQLLAALVPGGSLLR; ALPLVLPLIAEELSR | 2.3398 |
| TGGT1\_290160 | 1033 | 113515.5917 | 6 | SWTEITDLLK; SSEAATGTVAVDSIIVSPVDKR; FLLSNGYFFVAK; LAPPRFDEDNVELL; SPKPTEDFELDDSRPLFPSHVSSR; NVDLMYTPDFGATITR | 2.3391 |
| TGGT1\_315670 | 766 | 82656.38129 | 4 | ALGEIAGALEPLAAK; ALGEIAGALEPLAAKEEK; AAGAASAQTVLASLALLLNSREESHVR; LSWISAAMGPVDTR | 2.3266 |
| TGME49\_319658 | 674 | 73848.452 | 2 | DAFWAGVLQR; ENASGDFFLSNVK | 2.2994 |
| TGME49\_294010 | 828 | 86933.66971 | 4 | RGVISAGMIAETLEAVAR; ELSVHPLFEALGAYFR; GVISAGMIAETLEAVAR; GVALAVTAGTR | 2.2726 |
| TGGT1\_283730 | 674 | 76292.24661 | 2 | QLSSPFAPVASDEAEAR; KHFAFLLGYNDGHVVR | 2.2553 |
| TGGT1\_235420 | 4118 | 423266.4744 | 3 | LLSLLAAVEREEVELER; AFLRQEENWLAR; NISSLVDSVLGSR | 2.2339 |
| TGME49\_297880 | 219 | 24137.8013 | 3 | GLLQLFTEK; GVGEHIGGTPVDLVLNDLYPLIVK; SWTDAAHLQIMQLSSSSAR | 2.2338 |
| TGME49\_245710 | 273 | 31239.59138 | 2 | SLIGDTSDEVIFGQDGKR; DGYGVQIWDDGAR | 2.2109 |
| TGME49\_291140 | 2562 | 265701.8437 | 3 | LTTMTELMESYYSVNPVR; NLIGPSNASSFLGR; LMEAAAAVASAAAGMGR | 2.2105 |
| TGGT1\_274060 | 323 | 35049.20561 | 2 | KAVAGLAAGGLGSFFGNPADLALIR; AVAGLAAGGLGSFFGNPADLALIR | 2.2065 |
| TGGT1\_306060 | 2980 | 328828.9664 | 4 | LLSSVPIDDLNAPGVDIGTLK; SIIDLVGASDGTQPLVLK; LLDLASPVTIVGDLTR; IVPMFSTPNVTVK | 2.1814 |
| TGGT1\_314970 | 893 | 98038.0167 | 5 | NFFSELLDDLHTQAIHQK; GAASSPASSSVFFATSPLSEAEKEELSVLPR; YATSIWEVIK; DWAEVMTPLEIVR; ASVLSSLGAAVAATNAMVQR | 2.1724 |
| TGGT1\_202550 | 2212 | 232808.7943 | 3 | FVQPVLFVGNK; TNSVAFGSLVSVPGAR; LVDALSGFPLLSK | 2.1597 |
| TGME49\_259200 | 2288 | 248035.6279 | 4 | GVAEGLPNTFLGSR; LLSPASSGLGLPR; AAFSMALDQVR; FAGATALPSLWEGR | 2.1287 |
| TGME49\_273580 | 1423 | 155099.7887 | 2 | VLQPLLLFR; SALLFLLEQK | 2.1123 |
| TGGT1\_239400 | 1265 | 133853.6323 | 4 | GMLPHIVEYFFLDAR; TAGSVGGQPSPPSSFSASLPQTR; SPQVPVSGLGSAAGLVFYQPEK; TLPSAPAVVQVLPTPQTQR | 2.1086 |
| TGME49\_239820 | 604 | 65152.95785 | 2 | AVAEALMANELAGAALDVFEEEKEFSKDNPLIQAK; SQQLVSLVHLAEILGR | 2.0903 |
| TGGT1\_318260 | 1094 | 117948.5345 | 3 | AAPSAEEAAVVALGTLGGR; MLDSLQEAISSFK; AWAPLLLPVVDGEAR | 2.0861 |
| TGGT1\_206470 | 519 | 55072.72447 | 5 | VVSTLTQGIEHLFR; VIISSTGALALDKVPKR; IDGLSIDIDK; ASAGGKYDVVVVGGGPGGYVAAIK; NLGLEELGIETDR | 2.0778 |
| TGGT1\_236930 | 5651 | 609557.949 | 2 | ILTTSLFLR; SSLLPASSLLPLVDR | 2.0525 |
| TGME49\_233220 | 1476 | 159606.1291 | 2 | ANLGWDPSLVGVGMAR; TVNSMEEFASLVR | 2.0478 |
| TGME49\_228190 | 346 | 38045.31725 | 3 | HFDILPYPPLKVR; VHPVVVLTILDAYLR; HSLTDEGLLQIIKDHHETMYELK | 2.0476 |
| TGME49\_230960 | 1233 | 135657.7719 | 3 | ASFLAVGGLDNMVR; NLALVDELQSLSPITDLK; SVVDPVLGTLLDQR | 2.0364 |
| TGME49\_233080 | 1415 | 156336.0192 | 2 | ALTALDILLGK; FLIEDVVLQK | 2.0208 |
| TGGT1\_300290 | 226 | 25247.02763 | 2 | LLDDLDVDVVR; VEALKDEIFSLLQQR | 2.0172 |
| TGGT1\_222900 | 1766 | 191336.5396 | 2 | LGAEAALHAVSLTR; VSFAVQAAAEAK | 2.012 |
| TGGT1\_299130 | 3218 | 346910.0262 | 2 | GAFPSLELLLLR; SGDTEGDSLLLSHLPLLLR | 2.005 |

SA: eluted proteins identified from sialic acid-agarose beads

A: eluted proteins identified from agarose beads