|  |  |  |  |
| --- | --- | --- | --- |
| **Supplementary Table 2: Peptides identificated by LC-MS/MS derived from skim Milk (fraction < 10 kDa)** | | | |
| **Sample** | **Peptide sequence** | **Precursor protein** | |
| **NCBI ID** | **Protein Name** |
| 2,4 | AATPTSCSRNRKKGRITYRKLTLKRCGDRTQGGPISKWKK | gi|119628485 | hCG2045771 |
| 2,7,11 | ADNNAGNMLTFGGGTRLMVKP | gi|631402 | T-cell receptor J-alpha wnV.1 - human (fragment) |
| 5 | AGATVQVTLDGVPAAAPGQPAQLQLNAT | gi|398451 | CDw50, intercellular adhesion molecule-3, ICAM-3=differentiation antigen [human, Peptide Partial, 28 aa, segment 3 of 3] |
| 2 | APQRLSIWGALRQTSSMNAKNTASRRGNWVGLSGSCL | gi|119622684 | hCG1647779 |
| 5,8 | AQYLSLPTVFLHALPCSLE | gi|435833 | Bilirubin UDP-glucuronosyltransferase, bilirubin transferase, HUG-Br1 [human, liver, Peptide PartialMutant, 19 aa] |
| 7 | DSARVPENVGLMQ | gi|635576680 | Chain B, Crystal Structure Of The Synthetic Protein In Complex With Py Peptide |
| 2 | FHRLIILLNLKNQDSGHISLFHFFTPLQKLFLVQCLQGQHGGL | gi|119570367 | hCG2044970 |
| 11 | GAKCGACEKTVYHAEEIQCNGRSFHKTCFHCMACRKALDSTTVAAHESEIYCKVCYGRRA | gi|162329919 | Chain A, Solution Structure Of The N-Terminal Lim Domain Of MlpCRP3 |
| 2,11 | GSHMWDTANNPLYKE | gi|28373682 | Chain A, Crystal Structure Of An Integrin Beta3-Talin Chimera |
| 7 | IVITAEMLMINTSL | gi|247714 | XP group A complementing, partial |
| 4 | KLLNDNIFHMSWRALLRL | gi|1088307 | Retinoblastoma suspectibility protein, partial |
| 4 | KRMLWISLQLTSQVFRFKAGHRKQMAGTIAESCNLVSAKLVSQGHNSLMLTCRC | gi|119600126 | hCG2045376, partial |
| 1 | METDAIDGYITCDNELSPEREHSNMAIDLTSSTPNGQHASPSHMTSMYLPLGHAPVC | gi|46519014 | Helios 1+2b,2c isoform |
| 5 | MKESSIDDLMKSLDKNSDQEIDFKEYSVFLTMLCMAYNDFFLEDNK | gi|396703 | S100D second EF-Hand |
| 12 | MNLLCELCYHKRFMETIVTYSSSINYTSGNNYITGHYPESPISVIDLADTSFSCS | gi|1082714 | Pregnancy-specific beta(1)-glycoprotein-11 - human |
| 11 | MRRAELAGLKTMAWVPAESAVEELMPRLLPDRSSSMSRCCGSSN | gi|9650997 | SMN interacting protein 1-delta |
| 1,11 | NTGTASKLTFGTGTRLQVTL | gi|553742 | Putative, partial |
| 1,4,5,7,8,10,11 | PPPPCPCT | gi|597960322 | Chain C, Crystal Structure Of Gsk-3/axin Complex Bound To Phosphorylated Wnt Receptor Lrp6 E-motif |
| 8 | YLCAWSTRTGXXLHFGNGTRLT | gi|34369259 | T cell receptor beta chain CDR3 region, partial |
| 8 | AAAICLVGINAIFSGGYCSLAVLQNWSMLA | gi|119583859 | hCG2043422, isoform CRA\_a |
| 2,4 | AATPTSCSRNRKKGRITYRKLTLKRCGDRTQGGPISKWKK | gi|119628485 | hCG2045771 |
| 7 | AAVLWEQVRP | gi|249725 | Class IV alcohol dehydrogenase, sigma sigma-ADH |
| 2,8 | ACDTVEKFWGIGASWDTR | gi|950460 | This CDS feature is included to show the translation of the corresponding V\_region. Presently translation qualifiers on V\_region features are illegal, partial |
| 2,7,11 | ADNNAGNMLTFGGGTRLMVKP | gi|631402 | T-cell receptor J-alpha wnV.1 - human (fragment) |
| 3 | ADNNFTQETAMTMITISAQMNPTVFYLCASSRDI | gi|930106 | T-cell receptor beta-chain, partial |
| 7 | ALYFCATSETGLSTDTQ | gi|11323053 | T-cell receptor beta chain, partial |
| 6 | APEAQVSVQPLFHQ | gi|542782 | Cerebrin 30 - human (fragment) |
| 11 | APTQMLEICMATLLCTMPLIMRIYQWQENCLHMVQILKQEARMDIHHFYSL | gi|440575735 | Alternative protein ANKRD62 |
| 5,8 | AQYLSLPTVFLHALPCSLE | gi|435833 | Bilirubin UDP-glucuronosyltransferase, bilirubin transferase, HUG-Br1 [human, liver, Peptide PartialMutant, 19 aa] |
| 7 | ARDSTGGK | gi|672883360 | Chain D, Crystal Structure Of Jmjd2b Complexed With Pyridine-2,4-dicarboxylic Acid And H3k9me3 |
| 7 | ARGSVILFVKP | gi|248842 | Aggrecan core protein [human, synovial fluid, Peptide Partial, 11 aa] |
| 5 | ARTKQTARKSTGGIAPRK | gi|392935539 | Chain Q, Crystal Structure Of Moz |
| 11 | AVLPQEEEGTGGTQLVME | gi|1168118 | Uronic-acid-rich protein, UAP=35 kda uronic-acid-rich inhibitor of calcium oxalate crystallization {N-terminal} [human, urine, Peptide Partial, 18 aa] |
| 7 | AVLSKEYGFVLLTGAASFIMVAHLAINVSKARKKY | gi|86651699 | Microsomal glutathione S-transferase 3, partial |
| 1,7,11 | AWTKQTARKSTGGKA | gi|371927790 | Chain B, Symmetric Dimethylation Of H3 Arginine 2 Is A Novel Histone Mark That Supports Euchromatin Maintenance |
| 8 | CAKSSGWYLGYYYYGMDVWGQGTTVWVSS | gi|29497876 | Immunoglobulin heavy chain complementarity-determining region 3, partial |
| 11 | CQTGANNLFFGTGTRLTVIP | gi|2636656 | Putative, partial |
| 2 | CVVNPNNARLMFGDGTQLVVKPNIQN | gi|245755 | T cell receptor variable alpha chain [human, Peptide Partial, 26 aa] |
| 2 | DGPEAGQTVK | gi|108743992 | FHIT, partial |
| 2,5 | DLYYYGSGGMSAFSIWGQGTMVTVSS | gi|4098684 | Immunoglobulin heavy chain CDR3 region, partial |
| 7 | DSARVRENVGLMQ | gi|635576680 | Chain B, Crystal Structure Of The Synthetic Protein In Complex With Py Peptide |
| 8 | DSRNEVWWTIDGKKPDDITIDVTINESASSKIHSGTGLWFWSHSPASGDS | gi|28629046 | Interleukin-1 receptor accessory protein beta, partial |
| 6 | EGLLQFFRDSLGQFRALQALLNFLDLRIGSSKNW | gi|12804073 | ZNF224 protein, partial |
| 5 | EHLWINTGQEETRRPYRELLSDYQDS | gi|119626204 | hCG1645114, isoform CRA\_a |
| 5 | ENLEINPT | gi|4559413 | Fusion gene, partial |
| 8 | EPERGSLTRQGWNAMVRSQLNATSASLVQAILLPQPPE | gi|119598842 | hCG2045390 |
| 2 | EQWLVLSNFDYWGQGTLVTVSS | gi|299347 | Immunoglobulin H chain VDJ segment, partial |
| 7 | ETTSFHLEKGSVQVSDSAVYFCALSLNNNDMRFGAGTRLTVKP | gi|1041561356 | T-cell receptor alpha chain variable region, partial |
| 1 | EVHLKNASRGSAGNKNYRM | gi|1335141 | IGF-I precursor C-terminus |
| 1 | FSGTQISTIAESEDSQSVDSV | gi|1042011 | Cyclic AMP response element-binding protein-1 alpha isoform, partial |
| 4 | GCWRTSGGHKCSFSWRRNSSSHGVFIVSCNAIDLEFQHRTHMKCHC | gi|119595003 | hCG1815675 |
| 1,2 | GEGRTVSILSWWGIPHSSWDTRQMF | gi|802069 | T cell receptor delta chain variable region, partial |
| 11 | GERGLWAGGYKNK | gi|245018 | Gamma delta T cell antigen receptor delta-chain=CDR3 region [human, skin lesion, Peptide Partial, 13 aa] |
| 8 | GFFKRQYKCILQEENRRDSWSYINSKSNDD | gi|514829847 | Chain B, 14-3-3-zeta In Complex With S1011 Phosphorylated Integrin Alpha-4 Peptide |
| 4 | GGIRAMALSYDQRCIISGMASGSIVLFYNDFNRWHHEYQTRY | gi|211825989 | LRBA protein, partial |
| 1 | GGTMENLSRRLKVTGDLFDIMSG | gi|159164772 | Chain A, Solution Structure Of The Bcl-XlBECLIN-1 Complex |
| 11 | GIHKQKEKSRLQGGVLVNEILNHMKRATQIPSYKKLIMF | gi|308198396 | Chain A, Nmr Structure In A Membrane Environment Reveals Putative Amyloidogenic Regions Of The Sevi Precursor Peptide Pap248-286 |
| 3 | GKSNSSAPWRGPGSVLQRGTVTRASTLTV | gi|119599074 | hCG1786995 |
| 4 | GLHPCPAPSSMGSDAKTEAQGSEVTHPRSHSLSVAELGFNPREKPMQCCTSNHY | gi|119605725 | hCG1816600 |
| 1,3,7,8,11 | GNTQHSKIDSGILSQHIRRMVQKN | gi|119587667 | hCG2045237 |
| 2,11 | GSHMWDTANNPLYKE | gi|28373682 | Chain A, Crystal Structure Of An Integrin Beta3-Talin Chimera |
| 3 | GSNCEPKVAPTTAWNAATMPPQMGSVPVMTQPTLIYSQPVMRPPNPFGPVSGAQIQFM | gi|3139031 | Type II CALM protein, partial |
| 2 | GWEPSQGSGPSQVLQPSQDMETGWEQRPSQWPEPSQVLPLKMALDQALEGVENPR | gi|119605844 | hCG1644958, isoform CRA\_b, partial |
| 2 | GWGIWKIMKLPAGWGEIGSSPLAMSCRSASAPAPAGLWQP | gi|119628290 | hCG2044003 |
| 8 | HCGRGRSSWQAFHLWPQ | gi|1063659 | YRRM, partial |
| 7 | HGKIMEAMEKLKSGMRFNEVAAQYS | gi|157886800 | Parvulin, partial |
| 7 | IDEAGSQLSGGQRQAVALARALIRKPCVLILDDATSALDANSQL | gi|1200314 | Similar to human TAP1 gene exon 10, Genbank Accession Number X66401, partial |
| 11 | IDECSENMCAQLCVNYPGGYTCYCDGKKGFKLAQDQKSWE | gi|27597166 | PROS1, partial |
| 11 | ILLNACCPGWVRTDMAGPWATK | gi|298222 | NADP(+)-dependent prostaglandin dehydrogenase unmodified isoform, carbonyl reductase {EC 1.1.1.141, 1.1.1.184, 1.1.1.189} [human, placenta, Peptide Partial, 22 aa] |
| 11 | ILLSKCGCYEMQAQIYRTETSSTVHNTHPRNGHCSSAPRVTSGSTYILVPLSHLAQN | gi|209978904 | FSHR, partial |
| 7 | IPETPPPG | gi|339717345 | Chain B, Structure Of The Ww Domain Of Pin1 In Complex With A Human Phosphorylated Smad3 Derived Peptide |
| 8 | IQRTQQEDSAVYLCASNPAGQLETQYF | gi|311902980 | T-cell receptor beta VJ region, partial |
| 11 | IQRTQQEDSAVYLCASSLVGQLETQYF | gi|311902990 | T-cell receptor beta VJ region, partial |
| 2 | ITNNTCSWIHIPGICSQMRNWTERSCVALKSPVCCISKF | gi|444739109 | Alternative protein PCDHB9 |
| 4 | IVSISALSTTEVAMHTSTSSSVTKSYISSQTNGEMGQLVHRFTVP | gi|347961913 | Glycophorin B, partial |
| 6 | KFFVFALILALMLSMTGADSHAKRHHGYKRKFHEKHHSHRGYRSNYLYDN | gi|4557653 | Histatin-3 precursor |
| 2 | KKATQAIQEY | gi|88192187 | Chain C, Crystal Structure Of The Mdc1 Brct Repeat In Complex With The Histone Tail Of Gamma-H2ax |
| 2,3,4,5,6,8,11 | KTSAAAQLDELMAHLTEMQ | gi|970841982 | Chain C, Pyk2-fat Domain In Complex With Leupaxin Ld4 Motif |
| 3 | LCHVAQTYGSEVILSESR | gi|182627807 | Mediator complex subunit MED24 variant MED24\_i10, partial |
| 11 | LEDSAKYFCALGCPWGTFVTWDTRQMF | gi|12698584 | T-cell receptor delta chain, partial |
| 11 | LHNVYKTPCVHSMEIIINERSNIILISCTVKQKKKKKKKTTSLKSRSTK | gi|119587287 | hCG2036995 |
| 7 | LINGATQSGPGTGLRRLTTAPCCHVDWC | gi|219526 | Cell adhesion regulator, partial |
| 4 | LLSDSGFYLCAWSVGDRGNQPQHF | gi|6841662 | T-cell receptor beta chain, partial |
| 5 | LPKPPKPVSKMRMATPLLMQ | gi|545489 | HLA-DR1-associated li peptide [human, Epstein-Barr virus-transformed homozygous B-cell line WT-100, Peptide, 20 aa] |
| 1 | LWNTDSRSKVADCRGHLS | gi|6687822 | APAF1 protein, partial |
| 1 | MAAVPMVLSAMGFTAAG | gi|32394714 | Interferon-induced ISG12-S short isoform, partial |
| 2 | MAGSRLTATSTSWVQAILLPQPPE | gi|119600294 | hCG2045403 |
| 5 | MAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP | gi|253722711 | Chain B, Cleaved Substrate Variant Of Plasminogen Activator Inhibitor-1 |
| 1,7,11 | MAPTKQTARKSTGGKA | gi|371927790 | Chain B, Symmetric Dimethylation Of H3 Arginine 2 Is A Novel Histone Mark That Supports Euchromatin Maintenance |
| 11 | MDLLLLMEMRLSHISLAPLWNLRQPPPQTLTRL | gi|119598463 | hCG2039151 |
| 8 | MDNTLLSFSDHHPCTMLVACCNRDSTSGCQLLCNKPPQHSVA | gi|444733537 | Alternative protein LOC100129033 |
| 11 | MDQSSEGCMKKISSVNLDKLINDFSQIEKKMVETNGKNNILDIQLEKSNCLLKVMQAKEVS | gi|60499120 | CH5400, partial |
| 11 | MESIFHEKQPSGNMDDSGFFSIQTAAKAATAAAAAAAGGPIRTEFTSM | gi|258614027 | Ataxin-3 isoform j |
| 8 | MHEFPPQKLTSTPILSGLQLPSPYITPTPIEPPSESSRNTSMQIN | gi|242381092 | Hypothetical protein |
| 4,7 | MLLITSMLVLWMQLS | gi|70913339 | T cell receptor alpha variable 25, partial |
| 8 | MLMESVTVSSLKEKSLYITNSLLLSLQRTLKQKGSTM | gi|119616908 | hCG1773884 |
| 7 | MMAVEQMPKKDWYSILGADPSANISDLKQKYQKLILMVH | gi|119588647 | Zinc finger, CSL-type containing 3, isoform CRA\_a |
| 7 | MMCGVSCGKRLRQARGLPVTCSHVQTRSPHPPSLRPRQTWASW | gi|440575937 | Alternative protein NDST1 |
| 4 | MMREWVLFMS | gi|90110532 | Interstitial retinol binding protein 3, partial |
| 6 | MMRVCWLVRQDSRHQRIRLPHLEAVVIGRGPETKITDKKCSRQQVESRV | gi|34538285 | Aprataxin variant LP2 |
| 1 | MMTMVCLLGIGAALTPVAGTQGAGTAAWRSSKIGKNLASAQSDMASAGSLLGPSTQRCGLWGFLPG | gi|444738287 | Alternative protein TGM3 |
| 5 | MMVLQVSAAPRTVALTALLTVLLTSVVQGRATP | gi|37719423 | MHC class II antigen, partial |
| 7 | MNQTASVSHHIKCQPSKTIK | gi|62822381 | Unknown, partial |
| 4 | MPAPNFWMELASMQGSAAGLRGPAAEALRPGVTRPGFQAVWPQTSTSASVDLVAPFVKWKKTT | gi|119572075 | hCG2041075 |
| 11 | MPMILISLCHQGWSAAAEFQLTATSTCWVQGISQVAGTTGAHHHAWLIFCRDGVLPCCPGWS | gi|119597721 | Chromosome 15 open reading frame 21 |
| 11 | MPTPPNNNNNTSRGKMSYFLDLPQCTENNRQCYQIPLYVF | gi|55139850 | DIPLA1-antisense expressed |
| 2 | MRAHSFLPSHSLGP | [gi|478715](http://www.matrixscience.com/cgi/master_results.pl?file=..%2Fdata%2F20160913%2FFTiArbsnh.dat;sessionID=guest_guestsession#Hit1) | Hypothetical protein 1 estrogen receptor 5'-region - human |
| 8 | MSFIDPYQHIIVEHQYSHKFTVVVLRATKVTKGAFGDMPKVTKGAFGDM | gi|1401032 | Cytosolic phospholipase A2, partial |
| 4 | MSKRFRQSSHLTTHKIIHTGEKPYKCEECWKLSTDSFTLLHIREFTLERN | gi|3021386 | Zinc finger protein, partial |
| 6 | MSPFSWTHTPTTRWCGSLAPGSTSMPMPSSSWRGFLMCSFHITAPVMKRPG | gi|444737871 | Alternative protein PTGIS |
| 2 | MSSQIRHNYSTDVEAAVNSLVNLYL | gi|449331665 | L-ferritin, partial |
| 2 | MTPMRKTNPLMKLIN | gi|587654138 | Cytochrome b, partial (mitochondrion) |
| 8 | MVALQGTKPLEGRMKKWFNVSLMDGLLNQPVGKNMKHVWLLNYIMEIIPQHRKHSK | gi|444738185 | Alternative protein F13B |
| 7 | MVCLKLPGGSCMAALTVTLTVLSSPLALA | gi|296275 | HLA-DRB4$0101, partial |
| 2 | MVCLRLPGGSCMAALTVTLMVLSSPLALA | gi|296267 | HLA-DRB2, partial |
| 8 | MVHLTPEEKSAVTAL | gi|193244943 | truncated beta globin |
| 3 | MVQAFSAQSGMKLEWSQKCLQDNKWNYIRAGQVFTMLQTEGKIPVEAFKQIP | gi|444737765 | Alternative protein NXF5 |
| 8 | NINQFFKYLLIFLITMLILVTANNLFQLFIGWEGVGIMSFLLI | gi|283838238 | NADH dehydrogenase subunit 5, partial (mitochondrion) |
| 1,6 | NMTPQDHEKAALIMQVLQLTADQIAMLPPEQRQSILILKEQIQKSTGAP | gi|119390445 | Chain A, Nmr Structure Of C-Terminal Domain Of Human Cstf-64 |
| 1 | NQMEQSECDMLHDAVCFGSKKKKLGGFSKVALLGSKTAGFFFLKYLGLTLHRGSQSMI | gi|444738851 | Alternative protein COBL [Homo sapiens] |
| 1,11 | NTGTASKLTFGTGTRLQVTL | gi|553742 | Putative, partial |
| 2 | NVQTTHRPMLVSTTAMRKNIQINHPAAGCQLPSGSGSPSQWILQCSLHQ | gi|119609319 | hCG1814338 |
| 5 | PGVPAIHPVLSGLSEQPD | gi|386121 | Chymotrypsinogen homolog {N-terminal} [human, Peptide Partial, 18 aa] |
| 8 | PQPEGVNQPD | gi|34809626 | Chain B, Solution Structure Of The Human Grb7-Sh2 Domain In Complex With A 10 Amino Acid Peptide Py1139 |
| 2 | QMSPALTC | gi|189580 | Plasminogen activator inhibitor type 1, partial |
| 2 | QNTQNSHHTIEGQSLRTDTT | gi|20809563 | Unknown (protein for IMAGE:4734918), partial |
| 11 | RASQSISSYLNAASSLQSQQSYSTPPYT | gi|189231272 | Anti-fluorescein immunoglobulin light chain variable region, partial |
| 8 | RASQSVSSNYVAGASSRATQQYAYSPYT | gi|189231260 | Anti-fluorescein immunoglobulin light chain variable region, partial |
| 7 | REWLSIRNMRIKCEIFSCSVKPMSANCISCRMKNATCWLSMRLRN | gi|444738783 | Alternative protein SLK |
| 4 | RQAHIELPSMAV | gi|723586803 | Chain C, Crystal Structure Of Rqa\_v Phosphopeptide Bound To Hla-a2 |
| 4 | RSEMNVSTLELGDSALYLCASSLETSGMVNTYEQYFGPGTRLTVTEDLKN | gi|312273763 | TCR, partial |
| 6 | RTIMRKTIFCMWPTVMRVSMGNEWLEAQQMGAPGLGGRGGVCVRDMGKEGGSHRKETEGEDI | gi|119616576 | GABA(A) receptor-associated protein like 1, isoform CRA\_f |
| 2 | SCPQNRETRHCISRQQSIYRWGSSYNMQFFGPGTRLTVLEDLKNVFP | gi|4028224 | T-cell receptor beta chain, partial |
| 7 | SDNMNMTP | gi|588292799 | Chain B, Grb2 Sh2 Domain/cd28-derived Peptide Complex |
| 7 | SIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK | gi|231241 | Chain B, The S Variant Of Human Alpha1-Antitrypsin, Structure And Implications For Function And Metabolism |
| 2 | SLNESLNALFI | gi|249889 | cGMP-inhibited low K(m) cAMP phosphodiesterase Peak 43, cGI-PDE [human, placenta, Peptide Partial, 11 aa] |
| 2 | SLVAEAFVSQIA | gi|62822246 | Unknown, partial |
| 2,8 | SMALNLMPTTPLMWKPKMECQGWAALAMPAPQSASAWGMQSHCQACL | gi|444738485 | Alternative protein EPHA1 |
| 11 | SMGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIVQPMIDQS | gi|946926289 | Chain A, Homodimer Of Tale Type Homeobox Transcription Factor Meis1 Complexes With Specific Dna |
| 5 | SPPDYSAAPRGRFGIPFFPVHLKRLLILLLLS | gi|253723240 | Chain A, Structure And Influence On Stability And Activity Of The N- Terminal Propetide Part Of Lung Surfactant Protein C |
| 2 | SQRERAEQNRIIFDSVA | gi|309319989 | Chain E, Crystal Structure Of Human Crfr2 Alpha Extracellular Domain In Complex With Urocortin 1 |
| 5 | SRKAGVGQSWKENSPLNVS | gi|428698310 | Chain A, Phosphorylation Of The Cytoplasmic Tail Of Tissue Factor And Its Role In Modulating Structure And Binding Affinity |
| 8 | SSASQSNHSCTSMPSSPATPASGTK | gi|17426162 | Macrophin 1 isoform, partial |
| 6 | SVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDPD | gi|1402823 | Immunoglobulin heavy chain, partial |
| 2,11 | SVVAKDNATC | gi|4261525 | Proacrosin, partial |
| 7,8 | TARPSTG | gi|971826030 | Chain C, Human Sirt2 In Complex With Myristoylated Peptide (h3k9myr) |
| 4 | TAVYYCTTHRSTGDKIRFDPWGQGTLVTVSSG | gi|4096460 | Ig heavy chain, partial |
| 4 | TETCWLVLLNTGSVGRIITSSMTLSYPSWMHIKTLLKTEGQVIHLP | gi|444739009 | Alternative protein CHD7 |
| 4 | TLQMKNPSMQYKIGQLKSKHTLGTMPKLFWLGTSVTWKTSGSSQLSEVNI | gi|444733267 | Alternative protein RAB3C |
| 4 | TLTVTSAHPEDSSFYICSALRQGGNNSPLHFGNGTRLTVT | gi|1041562730 | T-cell receptor beta chain variable region, partial |
| 8 | TMTLHTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRG | gi|197311346 | Estrogen receptor alpha delta 1\*,2,3\*/663 choroid plexus isoform, partial |
| 1,6 | TMTPQDHEKAALIMQVLQLTADQIAMLPPEQRQSILILKEQIQKSTGAP | gi|119390445 | Chain A, Nmr Structure Of C-Terminal Domain Of Human Cstf-64 |
| 11 | TNPTPGSLGPWK | gi|828178119 | Crystallin beta A3/A1, partial |
| 5,8,11 | TRKAGVGQSWKENSPLNVS | gi|428698310 | Chain A, Phosphorylation Of The Cytoplasmic Tail Of Tissue Factor And Its Role In Modulating Structure And Binding Affinity |
| 4 | TTSHQPQDRYKAVWLIFFMLGLGTLLPWNFFMTATQYFTNRLDMSQNVSLV | gi|257900389 | Equilibrative nucleoside transporter 1, partial |
| 3 | VCSQPHLWCTQLQGPAGQ | gi|87074 | Choline O-acetyltransferase (EC 2.3.1.6) - human (fragment) |
| 4 | VDLERTFTFRNSKQTYSGIPIIVANMDTVGTFEMAAVMSQ | gi|529233 | glucose-6-phosphate dehydrogenase, partial |
| 7 | VDTAVYYCTTDSSSSFDYWGQGTLVTVSS | gi|4103709 | Immunoglobulin heavy chain, partial |
| 4 | VFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTFRMELMGCDLN | gi|116008323 | Coagulation factor VIII, partial |
| 7 | VLLGDQIPKSGSAADTQAVADAVTYQL | gi|1082611 | Proteasome endopeptidase complex (EC 3.4.25.1), delta chain - human (fragments) |
| 7 | VTMPALTMVLTVRSLPILLPVGGLSTASKLCCAPVERTW | gi|444738773 | Alternative protein KDM4A |
| 2 | YICAVLFGNQFYFGTGTSLTVIPNIQN | gi|1245945 | TCR V alpha {V-J junction, clone MS8-4} [human, multiple sclerosis patient, myelin basic protein-reactive T cells before vaccination, Peptide Partial, 27 aa] |