|  |
| --- |
| **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] |