Bioinformatics analysis links type 1 diabetes to vaccines contaminated with animal proteins and autoreactive T cells express skin homing receptors consistent with injected vaccines as causal agent

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Vaccines are contaminated with GAD65 (glutamic acid decarboxylase 65 KDa) and AQP4 (aquaporin-4) protein containing chick embryo cell cultures. The role of such contamination in the etiology of type 1 diabetes (T1D) and neuromyelitis optica spectrum disorders (NMOSD), was previously described.[1,2]

Origin of autoreactive T cells

Thymocytes with T cell receptors (TCR) that have high affinity for self peptides are usually negatively selected and destroyed in the thymus.[3] T cells with TCR that recognize peptides that differ by as little as one amino acid from a self peptide, can be positively selected and migrate to the periphery.[4] These low affinity self reactive (LASR) T cells can become autoreactive when they are activated by a peptide that exactly matches a self peptide except for this one amino acid difference (cognate peptide). LASR T cells have the highest possible affinity to self peptides that still qualifies for positive selection in the thymus. This arrangement seems to have worked very well over millions of years of evolution, until human ingenuity intervened …

Vertebrate animal proteins are very similar to human proteins. Animal protein sequences exactly match human proteins except for occasional amino acid differences.[1,2] So animal proteins are an ideal source of peptides to activate such LASR T cells described above. Ingested animal proteins are immunologically processed to produce a tolerogenic response.[5] Injected animal proteins are however another matter. Animal cells and proteins are used as growth media for the culture of viruses and bacteria, and as excipients in the manufacture of vaccines. Such vaccines are contaminated with numerous animal proteins. When animal proteins are injected with vaccines that either contain live viruses or adjuvants that provoke an immune response, LASR T cells can be activated by peptides derived from these animal proteins thus resulting in autoimmunity.

Immunotoxic effects of injected proteins have been known for over a hundred years. But ignorant vaccine regulators have placed no controls on the proteins that contaminate vaccines.[6–8] The outcome was predictable. The Pandemrix vaccine was contaminated with influenza virus nucleoproteins which resulted in narcolepsy.[9] Rabbit and duck embryo neural tissue contaminated rabies vaccines cause "neuroparalytic accidents".[10] Bovine casein and casamino acids used in vaccines are derived from cow's milk.[11] Therefore cow's milk proteins contaminate numerous vaccines, contributing to various disorders.[7,12]

Normally, LASR T cells do not encounter their cognate peptides. Also, due to the lack of innate immune system-derived costimulation, LASR T cells will not be activated if they encounter self peptides complexed with major histocompatibility complex (MHC) molecules on the surface of antigen-presenting cells (APC).[13] Following vaccine administration however, innate immune system costimulation exists. Both live virus vaccines and aluminum adjuvanted subunit vaccines activate the innate immune system.[14] Animal protein derived peptides from the vaccines are complexed with MHC

on the surface of APCs and presented to LASR T cells. This combination of innate immune system costimulation and LASR T cells encountering their cognate peptides on the surface of APCs, can result in LASR T cell activation and abrogation of peripheral tolerance.

During evolution, animal protein injection into humans was a rare event. Therefore our immune systems did not have an opportunity to evolve a defense for this mode of abuse.

Determining animal proteins responsible for activation of autoreactive T cells

Various vaccines are contaminated with cow, pig, African green monkey, guinea pig and chick embryo proteins.[5]
Homology of these animal antigens to epitopes associated with T1D are shown in the table below. $GAD65_{115-127}$[15] is IAFTSEHSHFSLK, $GAD65_{274-286}$[15] is MNILLQYVVKSFD, $GAD65_{555-567}$[16] is NFFRMVISNPAAT, $IA-2_{805-820}$[17] is VIVMLTPLVEDGVKQC and B_{9-23}[18] is SHLVEALYLVCGERG.

Organism	Common name	Contaminated vaccines	$GAD65_{115-127}$	$GAD65_{274-286}$	$IA-2_{805-820}$	B_{9-23}	$GAD65_{555-567}$
Bos taurus	Cow	Tetanus, Diphtheria, Pertussis, Hep A, Polio, Rabies, MMR, Varicella, Zoster etc.	100%	92%	100%	100%	100%
Sus scrofa	Pig	Zoster	100%	92%	100%	100%	100%
Chlorocebus sabaeus	African Green Monkey	Polio, Small pox	100%	100%	100%	100%	100%
Cavia porcellus	Guinea Pig	Varicella	92%	85%	94%	73%	100%
Gallus gallus	Chick	MMR, TBE, Rabies	85%	92%	88%	100%	100%

100% homology is less likely to result in autoimmunity as T cells recognizing those peptides would have been negatively selected in the thymus. Therefore guinea pigs and chick are likely to be the biggest contributor to autoimmunity, followed by cow, pig or monkey proteins.
Since the Varicella vaccine is relatively new compared to the measles, mumps and rubella vaccine, chick proteins are likely the biggest contributor to T1D autoimmunity.

T1D epitope alignment to regions of near identity

Examining the $GAD65_{115-127}$ and $GAD65_{274-286}$ epitopes associated with type 1 diabetes[15], it is clear that the epitopes are from locations where the chick GAD65 residues differ slightly from the human GAD65 protein (highlighted in figure below). This is exactly what we would expect in LASR T cell mediated autoimmunity. Such chick GAD65 epitopes can activate LASR T cells. Such activated LASR T cells can cross react with human GAD65 and destroy beta cells. Such autoreactive T cells are functional even with low affinity or very low affinity binding.[18,19] Peptides from locations where the homology between chick and human proteins is 100% are less likely to activate T cells because such T cells are likely to have been negatively selected in the thymus.

Uniprot[20] and BLASTP[21] are used to perform protein sequence alignment analysis.

Human GAD65 vs. chick GAD65

PREDICTED: glutamate decarboxylase 2 [Gallus gallus]
<u>XP_015137540.1</u> 588 1

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
1123 bits(2904)	0.0	Compositional matrix adjust.	527/588(90%)	558/588(94%)	3/588(0%)

```
Query 1    MASPGSGFWSFGSEDGSGDSENPGTARAWCQVAQKFTGGIGNKLCALLYGDAEKPAESGG 60
           MASPGSGFW FG+E+GS  +E+PGTARAWCQVAQKFTGGIGNKLCALLYGDAEKPA+ G
Sbjct 1    MASPGSGFWPFGAEEGSAAAESPGTARAWCQVAQKFTGGIGNKLCALLYGDAEKPADPGA 60

Query 61   SQPPRAAARKA---ACACDQKPCSCSKVDVNYAFLHATDLLPACDGERPTLAFLQDVMNI 117
            P A +   AC CD+KPC C + DVNYAFLH+TDLLPACDGE          TL+FLQDV++I
Sbjct 61   RAAPGTAEPRPSCPACTCDKKPCGCRRADVNYAFLHSTDLLPACDGEAATLSFLQDVVDI 120

Query 118  LLQYVVKSFDRSTKVIDFHYPNELLQEYNWELADQPQNLEEILMHCQTTLKYAIKTGHPR 177
           LLQYVVKSFDRSTKVIDFHYPNELLQEYNWELA+QPQ LEEIL++C+TTLKYAIKTGHPR
Sbjct 121  LLQYVVKSFDRSTKVIDFHYPNELLQEYNWELAEQPQTLEEILLNCRTTLKYAIKTGHPR 180

Query 178  YFNQLSTGLDMVGLAADWLTSTANTNMFTYEIAPVFVLLEYVTLKKMREIIGWPGGSGDG 237
           YFNQLSTGLDMVGLAADWLTS ANTNMFTYEIAPVFVLLEYVTL+KMRE++GWPGG GDG
Sbjct 181  YFNQLSTGLDMVGLAADWLTSAANTNMFTYEIAPVFVLLEYVTLRKMREMVGWPGGCGDG 240

Query 238  IFSPGGAISNMYAMMIARFKMFPEVKEKGMAALPRLIAFTSEHSHFSLKKGAAALGIGTD 297
           IFSPGGAISNMYAM+IARFKMFPEVKEKGMAA+PRL+AFTSEHSHFS+KKGAAALGIGTD
Sbjct 241  IFSPGGAISNMYAMLIARFKMFPEVKEKGMAAIPRLVAFTSEHSHFSVKKGAAALGIGTD 300

Query 298  SVILIKCDERGKMIPSDLERRILEAKQKGFVPFLVSATAGTTVYGAFDPLLAVADICKKY 357
           SVILI+CDERGKMIPSDLERRILEAKQKGFVPFLVSATAGTTVYGAFDPL+A+ADICKKY
Sbjct 301  SVILIRCDERGKMIPSDLERRILEAKQKGFVPFLVSATAGTTVYGAFDPLIAIADICKKY 360

Query 358  KIWMHVDAAWGGGLLMSRKHKWKLSGVERANSVTWNPHKMMGVPLQCSALLVREEGLMQN 417
           KIWMHVD AWGGGLLMSRKHKWKL+GVERANSVTWNPHKMMGVPLQCSALLVREEGLMQ+
Sbjct 361  KIWMHVDGAWGGGLLMSRKHKWKLNGVERANSVTWNPHKMMGVPLQCSALLVREEGLMQS 420

Query 418  CNQMHASYLFQQDKHYDLSYDTGDKALQCGRHVDVFKLWLMWRAKGTTGFEAHVDKCLEL 477
           CNQMHASYLFQQDKHYDLSYDTGDKALQCGRHVDVFKLWLMWRAKGTTGFEA +DKCLEL
Sbjct 421  CNQMHASYLFQQDKHYDLSYDTGDKALQCGRHVDVFKLWLMWRAKGTTGFEAQIDKCLEL 480

Query 478  AEYLYNIIKNREGYEMVFDGKPQHTNVCFWYIPPSLRTLEDNEERMSRLSKVAPVIKARM 537
           AEYLYN IKNREGYEMVFDGKPQHTNVCFWYIPPSLR +EDNEERMSRL KVAPVIKARM
Sbjct 481  AEYLYNKIKNREGYEMVFDGKPQHTNVCFWYIPPSLRGMEDNEERMSRLMKVAPVIKARM 540

Query 538  MEYGTTMVSYQPLGDKVNFFRMVISNPAATHQDIDFLIEEIERLGQDL 585
           MEYGTTMVSYQPLGDKVNFFRMVISNPAATHQDIDFLI+EIERLGQDL
Sbjct 541  MEYGTTMVSYQPLGDKVNFFRMVISNPAATHQDIDFLIDEIERLGQDL 588
```

As seen above for the GAD65 protein, the T1D epitope is located at a slightly non-identical region for the tyrosine-protein phosphatase protein as well.

Human vs chick Tyrosine-Protein Phosphatase

PREDICTED: receptor-type tyrosine-protein phosphatase N2 [Gallus gallus]
 <u>XP_015137094.1</u> 1203 2

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
958 bits(2476)	0.0	Compositional matrix adjust.	537/993(54%)	661/993(66%)	90/993(9%)

```
Query 94    FTWQDDYTQYVMDQELADLPKTYLRRP-----EASSPARPSKHSVGSERRYSREGGAALA  148
            FTWQDDYTQ+V+ QEL+++ + + RRP   EAS  R + +ER+  E  LA
Sbjct 230   FTWQDDYTQHVIGQELSNIHRVHNRRPDIFVSEASDTGRILEQNEDNERKSHLENDVNLA  289


Query 149   NALRRHLPFLEALSQAPASDVLARTHTAQDRPPAEGDDRFSESILTYVAH-----TSALT  203
            +L+++L +L LSQ+ A+++ R   D+  +  +++ + Y+      + L
Sbjct 290   ESLQQYLKYLGLLSQSAATNLYPRKRN--DKASVKSY-IYNDPVRYYLMQKPKERATPLA  346


Query 204   YPPGSRTQLREDLLPRTLGQLQPDELSPKVDSGVDRHHLMAALSAYAAQRPPAPPGEGSL  263
            +  S Q E+L  T Q QPD+ S + ++G+D+ LMAAL Y Q  A + S
Sbjct 347    HVSTSHQQYAENLHGMTFKQPQPDKFSAESEAGLDQKALMAALHTYITQNLSAQSNDKSS  406


Query 264   EPQ------YLLRAPSRMPRPLLA------------------PAAPQKWPSP-------  291
            +   Y R S  P            PA+  P+P
Sbjct 407   HSRTKGSHVYADRFYSSQVSPFDGSFSRGKAEDFKMNKLFQPQPASGVLGPAPEMLNHKS  466


Query 292   --LGDSEDPSSTGDG---ARIHTLLKDLQRQPAEVRGLSGLELDGMAELMAGLMQGVD--  344
              D +D   DG   I +LKDL++  V LS ELD +A+ +A  +Q D
Sbjct 467   ASQNDPKDLLRVVDGKVETLIKGILKDLEKHQVNVENLSSTELDEIADTIANAIQAADIQ  526


Query 345   ----HGVARGSPGRAALGESGEQADGPKATLRG-----DSFPDDGVQDDDDRLYQEVHRL  395
                G +  +A    A G   G   + D+GV+  R QE +
Sbjct 527   EKTEDGAVKTQEEKAETKIKKGGAQGRAEIHMGLMENSVNIQDNGVHEASARTDQEEN--  584


Query 396   SATLGGLLQDHGSRLLPGALPFARPLDMERKKSEHPESSLSSEEE------------TA  442
            +A L  L+++    ALP  P D++   PE S  SE +
Sbjct 585   TAKLINYLKNN-------ALPGNTPKDLQ------PEESTKSETKKSEDSDSSSSEEINT  631


Query 443   GVENVKSQTYSKDLLGQQPHSEPGAAAFGELQNQMPGPSKEEQSLPAGAQEALSDGLQLE  502
            GVENVKS+T+S++L  + +E +   E + +   ++ +   Q+  G+QLE
Sbjct 632   GVENVKSETFSRELTAAKS-TESDSKDPSETRYWIKNALMKDGNSSEQPQKNAGQGIQLE  690


Query 503   VQPSEEEARGYIVTDRDPLRPEEGRRLVEDVARLLQVPSSAFADVEVLGPAVTFKVSANV  562
            V+ +EE+ GYIVT +DPL E+G L++DVA LL++ S+F DV +LGPAVTF+V +N+
Sbjct 691   VKSAEEKEYGYIVTVKDPLSVEKGLELIKDVADLLKLQMSSFDDVNMLGPAVTFRVHSNL  750


Query 563   QNVTTEDVEKATVDNKDKLEETSGLKILQTGVGSKSKLKFLPPQAEQEDSTKFIALTLVS  622
            QN++T DV KA   NK+KLE+T+GL+ILQTGVG KS +  LP + E+ +S KF+ LTL+S
Sbjct 751   QNISTADVAKAAAMNKEKLEKTTGLRILQTGVGEKSHVPPLPQRGEEAESAKFLLLTLLS  810


Query 623   LACILGVLLASGLIYCLRHSSQHRLKEKLSGLGGDPGADATAAYQELCRQRMATRPPDRP  682
            LACI GVL ASG++YCLRH + HRLKEKLS LG D G+DATAAYQELCRQRMA + DRP
Sbjct 811   LACIAGVLAASGVVYCLRHRAHHRLKEKLSALGADAGSDATAAYQELCRQRMAVKTSDRP  870


Query 683   EGPHTSRISSVSSQFSDGPIPSPSARSSASSWSEEPVQSNMDISTGHMILSYMEDHLKNK  742
```

```
              E  H SRI+SVSSQFSDGPIPSPSARSS SSW EEPVQSNMDISTGHMILSYMEDHLKNK
Sbjct 871   EPLHASRINSVSSQFSDGPIPSPSARSSTSSWCEEPVQSNMDISTGHMILSYMEDHLKNK  930

Query 743   NRLEKEWEALCAYQAEPNSSFVAQREENVPKNRSLAVLTYDHSRVLLKAENSHSHSDYIN  802
              NRLEKEWEALCAYQAEPN++ VAQ+EEN+ KNRS AV+ YDHSR+ LKAENSH +SDYIN
Sbjct 931   NRLEKEWEALCAYQAEPNATTVAQQEENMQKNRSRAVVPYDHSRICLKAENSHDNSDYIN  990

Query 803   ASPIMDHDPRNPAYIATQGPLPATVADFWQMVWESGCVVIVMLTPLAENGVRQCYHYWPD  862
              ASPIMDHDPRNPA+IATQGPLPATVADFWQMVWE+GCVVIVMLTPL E+GV+QCYHYWPD
Sbjct 991   ASPIMDHDPRNPAFIATQGPLPATVADFWQMVWENGCVVIVMLTPLTESGVKQCYHYWPD  1050

Query 863   EGSNLYHIYEVNLVSEHIWCEDFLVRSFYLKNLQTNETRTVTQFHFLSWYDRGVPSSSRS  922
              EGSNLYHIYEVNLVSEHIWCEDFLVRSFYLKNLQTNETRTVTQFHFLSW D+ VP+S+RS
Sbjct 1051  EGSNLYHIYEVNLVSEHIWCEDFLVRSFYLKNLQTNETRTVTQFHFLSWNDQRVPASTRS  1110

Query 923   LLDFRRKVNKCYRGRSCPIIVHCSDGAGRSGTYVLIDMVLNKMAKGAKEIDIAATLEHLR  982
              LLDFRRKVNKCYRGRSCP++VHCSDGAGRSGTY+LIDMVLNKMAKGAKEIDIAATLEHLR
Sbjct 1111  LLDFRRKVNKCYRGRSCPVVVHCSDGAGRSGTYILIDMVLNKMAKGAKEIDIAATLEHLR  1170

Query 983   DQRPGMVQTKEQFEFALTAVAEEVNAILKALPQ  1015
              DQRPGMVQTKEQFEFALTAVAEEVNAILKALPQ
Sbjct 1171  DQRPGMVQTKEQFEFALTAVAEEVNAILKALPQ  1203
```

Homing marker provides evidence of T cell activation site

Hedman et al.[22] write:
"No significant differences were seen in any of the Th1-associated receptors, and only the percentages of CD8+ cells expressing the Th2-associated receptor CCR4 was higher in the diabetic group in comparison with healthy individuals (Fig. 2a,b), but not observed on CD4+ cells."

As Berin et al.[23] describe, the CCR4 receptor indicates skin homing and the site of initial priming. Skin homing would be expected since the animal antigen containing vaccines were administered via the subcutaneous or intramuscular route. Such CD8 T cells expressing CCR4 are involved in the destruction of beta cells.[24]

Vaccines disable at least one layer of natural protection against autoimmunity

T cells with high affinity to self peptides being negatively selected in the thymus is one major layer of natural defense against autoimmunity.
T cells in the periphery need to be activated with a self peptide. This is another major layer of natural defense against autoimmunity.
Vaccines are contaminated with numerous animal proteins. Animal proteins contain numerous peptides identical to self peptides. Upon administration of such vaccines, with innate immune system-derived costimulation active, these animal protein derived peptides activate T cells that have escaped thymic negative selection. So this layer of defense is disabled.

Protein sequence alignment

Here we analyze protein sequence alignment between T1D autoantigens and various viral, bacterial, fungal proteins that contaminate vaccines along with animal proteins. Chick and Coxsackievirus

protein sequence alignment scores are also included for comparison. Natural infection with Coxsackievirus has been linked to T1D.[25]

Method

BLASTP methodology was used for protein sequence alignment. As shown before[26], a BLASTP sequence alignment score of 19.3 was obtained comparing human hypocretin receptor and H1N1 nucleoprotein contained in the Pandemrix vaccine. This level of sequence alignment was sufficient to cause autoimmunity that resulted in hypocretin dysregulation and narcolepsy.[9] Therefore any score equal to or higher than 19.3 suggests high probability of autoimmunity.

While vaccines target one or a few particular viral, bacterial proteins, most vaccines are contaminated with all proteins from that virus or bacteria. Example: the Pandemrix vaccine contained both H1N1 hemagglutinin (target) and H1N1 nucleoproteins (contaminant). The exceptions are recombinant vaccines. In recombinant vaccines, the vaccine contains only the target protein from the target organism. The target protein is produced usually by genetically modifying yeast (*Saccharomyces cerevisiae*). Hepatitis B[27,28] and HPV vaccines[29] are produced using this technique. Such vaccines are however, contaminated with all *Saccharomyces cerevisiae* proteins.

Autoantigen	Insulin B 10-18	PPI 15–24 ALWGPDPAAA	IGRP 265–273 VLFGLGFAI	IA-2 797–805 WQMVWESGCTV	GAD65 115–127 IAFTSEHSHFSLK	GAD65 274–286 MNILLQYVVKSFD
Organism						
Gallus Gallus	32	21.8	22.7	38.8	38	39.7
Haemophilus Influenzae	25.2	21	21	20.2	20.6	23.5
Streptococcus pneumoniae	23.1	23.5	24.4	23.1	23.1	26.1
Corynebacterium diphtheriae	21.8	21	22.7	21	20.2	20.6
Bordetella Pertussis	20.2	24.8	24.4	21	19.3	20.6
Clostridium tetani	21.8	18.5	20.6	19.7	19.3	22.7
Neisseria meningitidis	21.4	21	18.9	21.8	21	24
Hepatitis B virus	18.9	21*	21.4	16.8	19.7	21*
Coxsackievirus	20.6	16.3	18.9			
Influenza A virus	18.5	17.6		19.7	19.7	18.9
Saccharomyces cerevisiae	21.8	26.5	21.4	21.8	23.5	24
Rubella virus		18.5				
Mumps virus			18.5			

* Hepatitis core protein match. Applicable to Hepatitis B infection, but not recombinant vaccines, as they do not contain core proteins.

As we can see above, there are numerous scores above the 19.3 baseline that corresponds to the level of sequence alignment in Pandemrix vaccine induced narcolepsy. So these contaminants can contribute to autoimmune diseases.

Most epidemiological studies are invalid

Most epidemiological studies investigating the role of vaccines in autoimmune diseases, ignore the mechanism of causation. Hypothesizing a mechanism allows for a study design that accounts for appropriate controls. By ignoring the mechanism, these studies have the wrong controls and the results are invalidated due to confounding factors. Relying on such invalid epidemiological studies have lead researchers down blind alleys for decades. Researchers must determine root cause by focusing on mechanisms of causation.

Conclusion

The above findings add to the growing evidence of vaccines inducing autoimmune diseases. While the analysis above focused on T1D, the mechanisms described are obviously likely to be active in any number of autoimmune diseases.[2]

It is quite obvious that there are fundamental problems with vaccine design and safety. Vaccine designers need to go back to the drawing board. We need vaccines that are safe by design. [8,30]

Detailed BLASTP Results

Sequence alignment between human GAD65 epitopes and various animal species GAD65 proteins that contaminate vaccines

glutamate decarboxylase 2 [Bos taurus]
 NP_001192652.1 585 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	8e-07	13/13(100%)	13/13(100%)	0/13(0%)

Query 1   IAFTSEHSHFSLK 13
           IAFTSEHSHFSLK
Sbjct 274 IAFTSEHSHFSLK 286

glutamate decarboxylase 2 [Sus scrofa]
 NP_999060.2 585 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	8e-07	13/13(100%)	13/13(100%)	0/13(0%)

Query 1   IAFTSEHSHFSLK 13
           IAFTSEHSHFSLK
Sbjct 274 IAFTSEHSHFSLK 286

PREDICTED: glutamate decarboxylase 2 [Chlorocebus sabaeus]

Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	8e-07	13/13(100%)	13/13(100%)	0/13(0%)

```
Query 1    IAFTSEHSHFSLK  13
           IAFTSEHSHFSLK
Sbjct 274  IAFTSEHSHFSLK  286
```

PREDICTED: glutamate decarboxylase 2 [Cavia porcellus]

Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	7e-06	12/13(92%)	13/13(100%)	0/13(0%)

```
Query 1    IAFTSEHSHFSLK  13
           +AFTSEHSHFSLK
Sbjct 274  VAFTSEHSHFSLK  286
```

PREDICTED: glutamate decarboxylase 2 [Gallus gallus]

Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
38.0 bits(82)	2e-04	11/13(85%)	12/13(92%)	0/13(0%)

```
Query 1    IAFTSEHSHFSLK  13
           +AFTSEHSHFS K
Sbjct 277  VAFTSEHSHFSVK  289
```

PREDICTED: glutamate decarboxylase 2 [Chlorocebus sabaeus]

Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	1e-07	13/13(100%)	13/13(100%)	0/13(0%)

```
Query 1    MNILLQYVVKSFD  13
           MNILLQYVVKSFD
Sbjct 115  MNILLQYVVKSFD  127
```

glutamate decarboxylase 2 [Bos taurus]

NP_001192652.1 585 2

See 1 more title(s)

GenPeptGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	8e-07	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1    MNILLQYVVKSFD  13
            M+ILLQYVVKSFD
Sbjct  115  MDILLQYVVKSFD  127
```

glutamate decarboxylase 2 [Sus scrofa]

NP_999060.2 585 2

See 1 more title(s)

GenPeptGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	8e-07	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1    MNILLQYVVKSFD  13
            M+ILLQYVVKSFD
Sbjct  115  MDILLQYVVKSFD  127
```

PREDICTED: glutamate decarboxylase 2 [Cavia porcellus]

XP_003463212.1 585 2

GenPeptGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	7e-06	11/13(85%)	12/13(92%)	0/13(0%)

```
Query  1    MNILLQYVVKSFD  13
            M+ILLQYVVK FD
Sbjct  115  MDILLQYVVKTFD  127
```

PREDICTED: glutamate decarboxylase 2 [Gallus gallus]

XP_015137540.1 588 2

GenPeptGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
39.7 bits(86)	4e-05	11/12(92%)	12/12(100%)	0/12(0%)

```
Query  2    NILLQYVVKSFD  13
            +ILLQYVVKSFD
Sbjct  119  DILLQYVVKSFD  130
```

PREDICTED: glutamate decarboxylase 2 [Gallus gallus]

XP_015137540.1 588 2

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
39.7 bits(86)	1e-04	11/12(92%)	12/12(100%)	0/12(0%)

```
Query 2    NILLQYVVKSFD  13
           +ILLQYVVKSFD
Sbjct 119  DILLQYVVKSFD  130
```

Alignment statistics for match #2

Score	Expect	Identities	Positives	Gaps
17.6 bits(34)	10826	4/6(67%)	6/6(100%)	0/6(0%)

```
Query 3    ILLQYV  8
           +LL+YV
Sbjct 217  VLLEYV  222
```

Sequence alignment between human insulin and various animal species insulin that contaminate vaccines

PREDICTED: insulin isoform X2 [Chlorocebus sabaeus]

XP_008002825.1 144 1

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
218 bits(556)	4e-74	Compositional matrix adjust.	107/110(97%)	107/110(97%)	0/110(0%)

```
Query 1   MALWMRLLPLLALLALWGPDPAAAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAED  60
          MALWMRLLPLLALLALWGPDP AFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAED
Sbjct 35  MALWMRLLPLLALLALWGPDPVPAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAED  94

Query 61  LQVGQVELGGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQLENYCN  110
           QVGQVELGGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQLENYCN
Sbjct 95  PQVGQVELGGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQLENYCN  144
```

preproinsulin, partial [Sus scrofa]

AAC77920.1 127 1

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
132 bits(333)	2e-40	Compositional matrix adjust.	94/110(85%)	95/110(86%)	2/110(1%)

```
Query 1   MALWMRLLPLLALLALWGPDPAAAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAED  60
          MALW RLLPLLALLALW P PA AFVNQHLCGSHLVEALYLVCGERGFFYTPK RREAE+
Sbjct 20  MALWTRLLPLLALLALWAPAPAQAFVNQHLCGSHLVEALYLVCGERGFFYTPKARREAEN  79
```

```
Query  61  LQVGQVELGGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQLENYCN  110
               Q G VELGG  G G LQ LALEG  QKRGIVEQCCTSICSLYQLENYCN
Sbjct  80  PQAGAVELGG--GLGGLQALALEGPPQKRGIVEQCCTSICSLYQLENYCN  127
```

insulin preproinsulin precursor [Gallus gallus]

NP_990553.1 107 1

See 3 more title(s)

GenPeptGraphics Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
129 bits(325)	2e-39	Compositional matrix adjust.	70/110(64%)	75/110(68%)	3/110(2%)

```
Query  1  MALWMRLLPLLALLALWGPDPAAAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAED  60
             MALW+R LPLLALL  GP + A NQHLCGSHLVEALYLVCGERGFFY+PK RR+ E
Sbjct  1  MALWIRSLPLLALLVFSGPGTSYAAANQHLCGSHLVEALYLVCGERGFFYSPKARRDVEQ  60

Query  61  LQVGQVELGGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQLENYCN  110
                V  L G G  Q  E   KRGIVEQCC + CSLYQLENYCN
Sbjct  61  PLVSS-PLRGEAGVLPFQQEEYEKV--KRGIVEQCCHNTCSLYQLENYCN  107
```

insulin [Cavia porcellus]

AAA37041.1 110 1

GenPeptGraphics Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
127 bits(319)	2e-38	Compositional matrix adjust.	76/110(69%)	88/110(80%)	0/110(0%)

```
Query  1  MALWMRLLPLLALLALWGPDPAAAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAED  60
             MALWM LL +LALLALWGP+  AFV++HLCGS+LVE LY VC + GFFY PK RRE ED
Sbjct  1  MALWMHLLTVLALLALWGPNTNQAFVSRHLCGSNLVETLYSVCQDDGFFYIPKDRRELED  60

Query  61  LQVGQVELGGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQLENYCN  110
              QV Q ELG G GAG LQPLALE +LQKRGIV+QCCT  C+ +QL++YCN
Sbjct  61  PQVEQTELGMGLGAGGLQPLALEMALQKRGIVDQCCTGTCTRHQLQSYCN  110
```

PREDICTED: insulin isoform X1 [Bos taurus]

XP_015316816.1 221 1

GenPeptGraphics Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
123 bits(308)	2e-35	Compositional matrix adjust.	84/110(76%)	86/110(78%)	5/110(4%)

```
Query  1  MALWMRLLPLLALLALWGPDPAAAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAED  60
             MALW RL PLLALLALW P PA AFVNQHLCGSHLVEALYLVCGERGFFYTPK RRE E
Sbjct  117  MALWTRLAPLLALLALWAPAPARAFVNQHLCGSHLVEALYLVCGERGFFYTPKARREVEG  176

Query  61  LQVGQVELGGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQLENYCN  110
              QVG +EL  AG   LEG  QKRGIVEQCC S+CSLYQLENYCN
Sbjct  177  PQVGALEL-----AGGPGAGGLEGPPQKRGIVEQCCASVCSLYQLENYCN  221
```

Sequence alignment between human preproinsulin epitopes and various animal species preproinsulin that contaminate vaccines

SHLVEALYLVCGERG

preproinsulin, partial [Gallus gallus]
AAP45961.1 55 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
50.7 bits(112)	6e-09	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1   SHLVEALYLVCGERG  15
           SHLVEALYLVCGERG
Sbjct  26  SHLVEALYLVCGERG  40
```

Chain B, Porcine Desb1-2 Despentapeptide(B26-B30) Insulin
1SDB_B 23 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
50.7 bits(112)	9e-10	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1  SHLVEALYLVCGERG  15
          SHLVEALYLVCGERG
Sbjct  7  SHLVEALYLVCGERG  21
```

Chain B, Bovine Despentapeptide Insulin
1PID_B 25 1

See 1 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
50.7 bits(112)	1e-09	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1  SHLVEALYLVCGERG  15
          SHLVEALYLVCGERG
Sbjct  9  SHLVEALYLVCGERG  23
```

PREDICTED: insulin isoform X1 [Chlorocebus sabaeus]
XP_008002752.1 209 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
50.7 bits(112)	7e-09	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    SHLVEALYLVCGERG  15
            SHLVEALYLVCGERG
Sbjct  132  SHLVEALYLVCGERG  146
```

insulin isoform X1 [Sus scrofa]
XP_020936937.1 175 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
50.7 bits(112)	7e-09	15/15(100%)	15/15(100%)	0/15(0%)

```
Query 1    SHLVEALYLVCGERG 15
           SHLVEALYLVCGERG
Sbjct 100  SHLVEALYLVCGERG 114
```

insulin, partial [Cavia porcellus]
AAX33329.1 51 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
25.7 bits(53)	5.1	8/11(73%)	8/11(72%)	0/11(0%)

```
Query 1   SHLVEALYLVC 11
          S LVE LY VC
Sbjct 9   SNLVETLYSVC 19
```

PPI 15–24
ALWGPDPAAA

PREDICTED: insulin isoform X1 [Chlorocebus sabaeus]
XP_008002752.1 209 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
27.8 bits(58)	0.36	8/10(80%)	8/10(80%)	0/10(0%)

```
Query 1    ALWGPDPAAA 10
           ALWGPDP A
Sbjct 114  ALWGPDPVPA 123
```

class E basic helix-loop-helix protein 41 isoform X1 [Sus scrofa]
XP_003355589.2 482 4

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
26.5 bits(55)	1.0	9/10(90%)	9/10(90%)	0/10(0%)

```
Query 1    ALWGPDPAAA 10
           AL GPDPAAA
Sbjct 303  ALLGPDPAAA 312
```

lon protease homolog, mitochondrial precursor [Bos taurus]

NP_001015569.2 961 2

See 2 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score   Expect   Identities   Positives   Gaps

24.8 bits(51)   4.1   8/10(80%)   8/10(80%)   0/10(0%)

Query 1 ALWGPDPAAA 10

       ALWG PAAA

Sbjct 53 ALWGQSPAAA 62

PREDICTED: mucin-6, partial [Cavia porcellus]

XP_003460756.2 1096 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score   Expect   Identities   Positives   Gaps

24.4 bits(50)   5.8   6/6(100%)   6/6(100%)   0/6(0%)

Query 2 LWGPDP 7

       LWGPDP

Sbjct 139 LWGPDP 144

PREDICTED: rab11 family-interacting protein 3 isoform X1 [Gallus gallus]

XP_004945476.1 681 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score   Expect   Identities   Positives   Gaps

21.8 bits(44)   48   6/9(67%)   7/9(77%)   0/9(0%)

Query 1 ALWGPDPAA 9

       ALW +PAA

Sbjct 45 ALWAAEPAA 53

Sequence alignment between human PTPRS epitope and various animal species PTPRS proteins that contaminate vaccines

PREDICTED: receptor-type tyrosine-protein phosphatase N2 [Gallus gallus]

XP_015137094.1 1203 2

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score   Expect   Identities   Positives   Gaps

46.0 bits(101)   7e-08   14/16(88%)   14/16(87%)   0/16(0%)

Query 1 VIVMLTPLVEDGVKQC 16

       VIVMLTPL E GVKQC

Sbjct 1029 VIVMLTPLTESGVKQC 1044

Alignment statistics for match #2

Score	Expect	Identities	Positives	Gaps
15.9 bits(30)	3611	4/4(100%)	4/4(100%)	0/4(0%)

Query 8 LVED 11
          LVED
Sbjct 43 LVED 46

LOW QUALITY PROTEIN: receptor-type tyrosine-protein phosphatase-like N [Sus scrofa]
XP_003133717.2 979 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	1e-10	16/16(100%)	16/16(100%)	0/16(0%)

Query 1   VIVMLTPLVEDGVKQC 16
           VIVMLTPLVEDGVKQC
Sbjct 805 VIVMLTPLVEDGVKQC 820

receptor-type tyrosine-protein phosphatase-like N precursor [Bos taurus]
NP_001068599.1 979 1

See 4 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	1e-10	16/16(100%)	16/16(100%)	0/16(0%)

Query 1   VIVMLTPLVEDGVKQC 16
           VIVMLTPLVEDGVKQC
Sbjct 805 VIVMLTPLVEDGVKQC 820

PREDICTED: receptor-type tyrosine-protein phosphatase-like N isoform X3 [Cavia porcellus]
XP_005001098.1 980 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	8e-10	15/16(94%)	16/16(100%)	0/16(0%)

Query 1   VIVMLTPLVEDGVKQC 16
           VIVMLTPLVEDG+KQC
Sbjct 806 VIVMLTPLVEDGIKQC 821

PREDICTED: receptor-type tyrosine-protein phosphatase N2 [Gallus gallus]

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	3e-07	14/16(88%)	14/16(87%)	0/16(0%)

```
Query  1     VIVMLTPLVEDGVKQC  16
             VIVMLTPL E GVKQC
Sbjct  1029  VIVMLTPLTESGVKQC  1044
```

PREDICTED: receptor-type tyrosine-protein phosphatase-like N isoform X1 [Chlorocebus sabaeus]

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-10	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    VIVMLTPLVEDGVKQC  16
            VIVMLTPLVEDGVKQC
Sbjct  806  VIVMLTPLVEDGVKQC  821
```

Sequence alignment between various T1D associated human epitopes and proteins of various organisms that contaminate vaccines

insulin B10–18
HLVEALYLV

PREDICTED: insulin isoform X1 [Gallus gallus]

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
32.0 bits(68)	0.033	9/9(100%)	9/9(100%)	0/9(0%)

```
Query  1   HLVEALYLV  9
           HLVEALYLV
Sbjct  59  HLVEALYLV  67
```

dTDP-glucose 4,6-dehydratase [Haemophilus influenzae]
 WP_015701908.1 334 1

See 14 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
25.2 bits(52)	8.5	7/7(100%)	7/7(100%)	0/7(0%)

```
Query 3   VEALYLV  9
          VEALYLV
Sbjct 232 VEALYLV  238
```

sensor histidine kinase [Streptococcus pneumoniae]
 COD91922.1 452 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
23.1 bits(47)	49	6/9(67%)	7/9(77%)	0/9(0%)

```
Query 1   HLVEALYLV  9
          HLV+ LY V
Sbjct 150 HLVQSLYIV  158
```

ATP-dependent dethiobiotin synthetase BioD [Corynebacterium diphtheriae]
 WP_071579533.1 222 1

See 1 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.8 bits(44)	142	6/8(75%)	7/8(87%)	0/8(0%)

```
Query 1   HLVEALYL  8
           +LVE LYL
Sbjct 210 QLVEDLYL  217
```

ABC transporter permease [Bordetella pertussis]
 WP_080379438.1 378 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
20.2 bits(40)	584	6/8(75%)	7/8(87%)	0/8(0%)

```
Query 2   LVEALYLV  9
          LV+ALY V
Sbjct 364 LVDALYAV  371
```

2-hydroxyglutaryl-CoA dehydratase [Clostridium tetani]
WP_011098753.1 321 1

See 8 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.8 bits(44)	142	6/7(86%)	6/7(85%)	0/7(0%)

```
Query  2  LVEALYL  8
          LVE LYL
Sbjct 24  LVEGLYL  30
```

conserved hypothetical inner membrane protein [Neisseria meningitidis]
AHW76735.1 145 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.4 bits(43)	204	6/8(75%)	7/8(87%)	0/8(0%)

```
Query   2  LVEALYLV  9
            +V ALYLV
Sbjct 133  MVAALYLV  140
```

polymerase [Hepatitis B virus]
APC26029.1 845 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
18.9 bits(37)	1694	6/7(86%)	6/7(85%)	1/7(14%)

```
Query   1  HLVEALY  7
           HL EALY
Sbjct 564  HL-EALY  569
```

polyprotein [Coxsackievirus A6]*
AFN53722.1 2201 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	408	7/9(78%)	7/9(77%)	2/9(22%)

```
Query    3  VEAL--YLV  9
            VEAL  YLV
Sbjct 1045  VEALKNYLV  1053
```

* Live virus, not vaccine

polymerase basic subunit 1, partial [Influenza A virus (A/guinea fowl/Shantou/7211/2004(H6N1))]
ABS53766.1 487 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
18.5 bits(36)	2423	5/6(83%)	5/6(83%)	0/6(0%)

```
Query 1   HLVEAL  6
          H VEAL
Sbjct 253 HIVEAL  258
```

NDI1 [Saccharomyces cerevisiae]
KZV08718.1 513 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.8 bits(44)	142	6/6(100%)	6/6(100%)	0/6(0%)

```
Query 1   HLVEAL  6
          HLVEAL
Sbjct 269 HLVEAL  274
```

No matches were found to measles, mumps, rubella, polio, HPV or Hep A viruses in the first 10000 results.

PPI15–24
ALWGPDPAAA

hypothetical protein BON23_3140, partial [Saccharomyces cerevisiae]
ONH77559.1 513 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
26.5 bits(55)	0.20	7/7(100%)	7/7(100%)	0/7(0%)

```
Query 3   WGPDPAA  9
          WGPDPAA
Sbjct 360 WGPDPAA  366
```

RNA 2',3'-cyclic phosphodiesterase [Bordetella pertussis]
WP_049805779.1 188 1

See 1 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
24.8 bits(51)	0.82	8/10(80%)	8/10(80%)	1/10(10%)

Query 1 ALWGPDPAAA 10
          ALW PDPA A
Sbjct 31 ALW-PDPATA 39

hypothetical protein [Corynebacterium diphtheriae]
  WP_088774760.1 638 1

See 1 more title(s)

  GenPeptGraphics Next Match Previous Match
                              Alignment statistics for match #1
Score   Expect Identities Positives Gaps
21.0 bits(42) 19   5/6(83%) 6/6(100%) 0/6(0%)
Query 1 ALWGPD 6
          A+WGPD
Sbjct 258 AMWGPD 263

PREDICTED: rab11 family-interacting protein 3 isoform X1 [Gallus gallus]
  XP_004945476.1 681 1

  GenPeptGraphics Next Match Previous Match
                              Alignment statistics for match #1
Score   Expect Identities Positives Gaps
21.8 bits(44) 9.6   6/9(67%) 7/9(77%) 0/9(0%)
Query 1 ALWGPDPAA 9
          ALW +PAA
Sbjct 45 ALWAAEPAA 53

flagellar hook-associated protein FlgK [Clostridium tetani]
  WP_035109447.1 579 1

See 1 more title(s)

  GenPeptGraphics Next Match Previous Match
                              Alignment statistics for match #1
Score   Expect Identities Positives Gaps
18.5 bits(36) 165   5/6(83%) 5/6(83%) 0/6(0%)
Query 3 WGPDPA 8
          WGPD A
Sbjct 479 WGPDEA 484

non-structural polyprotein p200 [Rubella virus]
  APC23134.1 2116 1

  GenPeptGraphics Next Match Previous Match
                              Alignment statistics for match #1
Score   Expect Identities Positives Gaps
18.5 bits(36) 165   5/5(100%) 5/5(100%) 0/5(0%)

Query 5   PDPAA 9
           PDPAA
Sbjct 900 PDPAA 904

precore/core protein, partial [Hepatitis B virus]*
  AGP07765.1 78 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.0 bits(42)	20	5/5(100%)	5/5(100%)	0/5(0%)

Query 2   LWGPD 6
           LWGPD
Sbjct 27 LWGPD 31

*Core protein match, only applies to natural infection, not vaccines

serine/threonine protein phosphatase [Streptococcus pneumoniae]
  CVM85803.1 571 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
23.5 bits(48)	2.3	7/7(100%)	7/7(100%)	0/7(0%)

Query 4   GPDPAAA 10
           GPDPAAA
Sbjct 334 GPDPAAA 340

class I SAM-dependent methyltransferase [Haemophilus influenzae]
  WP_005661787.1 211 1

See 11 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.0 bits(42)	20	5/6(83%)	5/6(83%)	0/6(0%)

Query 2   LWGPDP 7
           LW PDP
Sbjct 163 LWSPDP 168

neuraminidase, partial [Influenza A virus (A/India/D058688/2005(H3N2))]
  AGR55093.1 375 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
17.6 bits(34)	337	4/4(100%)	4/4(100%)	0/4(0%)

Query 2 LWGP 5
          LWGP
Sbjct 43 LWGP 46

N utilisation substance protein A [Neisseria meningitidis Z2491]
CAM09013.1 505 1

GenPeptGraphics

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.0 bits(42)	19	5/7(71%)	6/7(85%)	0/7(0%)

Query 2   LWGPDPA 8
           LW P+PA
Sbjct 288 LWSPEPA 294

capsid protein VP1, partial [Coxsackievirus A4]
AHJ38809.1 296 1

GenPeptGraphics

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
16.3 bits(31)	993	5/7(71%)	5/7(71%)	0/7(0%)

Query 4 GPDPAAA 10
          GPD AA
Sbjct 25 GPDATAA 31

No matches to measles, mumps, polio, HPV, or Hep A viruses in the first 10000 results.

IGRP265–273

VLFGLGFAI

MULTISPECIES: membrane protein [Bordetella]
WP_003818983.1 188 1

See 583 more title(s)

GenPeptGraphics

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
24.4 bits(50)	17	7/8(88%)	7/8(87%)	0/8(0%)

Query 2 LFGLGFAI 9
          LFGL FAI
Sbjct 71 LFGLAFAI 78

DUF4887 domain-containing protein, partial [Streptococcus pneumoniae]

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
24.4 bits(50)	17	7/8(88%)	7/8(87%)	0/8(0%)

```
Query  2  LFGLGFAI  9
          LFGL FAI
Sbjct  29 LFGLAFAI  36
```

ER membrane protein complex subunit 1 precursor [Gallus gallus]

See 2 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
22.7 bits(46)	70	7/8(88%)	7/8(87%)	0/8(0%)

```
Query  1   VLFGLGFA  8
           VLFGL FA
Sbjct  958 VLFGLVFA  965
```

fusion protein [Mumps virus genotype A]

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
18.5 bits(36)	2422	5/5(100%)	5/5(100%)	0/5(0%)

```
Query  5  LGFAI  9
          LGFAI
Sbjct  9  LGFAI  13
```

EamA/RhaT family transporter [Haemophilus influenzae]

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.0 bits(42)	286	6/6(100%)	6/6(100%)	0/6(0%)

```
Query  1  VLFGLG  6
          VLFGLG
Sbjct  17 VLFGLG  22
```

bifunctional acetaldehyde-CoA/alcohol dehydrogenase [Clostridium tetani]

 WP_035142045.1 876 1

See 1 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	405	6/8(75%)	7/8(87%)	0/8(0%)

```
Query 1   VLFGLGFA  8
             VL+ LGFA
Sbjct 487  VLYNLGFA  494
```

iron ABC transporter permease [Corynebacterium diphtheriae]

 WP_094078792.1 343 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
22.7 bits(46)	70	7/8(88%)	7/8(87%)	0/8(0%)

```
Query 2   LFGLGFAI  9
            L GLGFAI
Sbjct 210  LLGLGFAI  217
```

mitochondrial genome required [Saccharomyces cerevisiae YJM789]

 EDN61044.1 113 1

See 97 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.4 bits(43)	203	7/9(78%)	8/9(88%)	1/9(11%)

```
Query 1   VLFGLGFAI  9
            +LFG GFAI
Sbjct 35  ILFG-GFAI  42
```

large surface protein [Hepatitis B virus]

 AGT40581.1 389 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.4 bits(43)	200	6/6(100%)	6/6(100%)	0/6(0%)

```
Query 3  FGLGFA  8
           FGLGFA
Sbjct 52  FGLGFA  57
```

polyprotein [Coxsackievirus B1]
 AKF40402.1 2182 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
18.9 bits(37)	1680	5/5(100%)	5/5(100%)	0/5(0%)

```
Query  3    FGLGF  7
            FGLGF
Sbjct  1011 FGLGF  1015
```

hypothetical protein NMA510612_1536 [Neisseria meningitidis]
 AHW75823.1 359 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
18.9 bits(37)	1684	8/11(73%)	8/11(72%)	2/11(18%)

```
Query  1    VLFGL--GFAI  9
            VL GL GFAI
Sbjct  233  VLVGLDSGFAI  243
```

No matches to measles, rubella, polio, HPV, influenza A, Hep A or Varicella viruses in the first 10000 results.

IA-2 797–805

WQMVWESGCTV

PREDICTED: receptor-type tyrosine-protein phosphatase-like N [Gallus gallus]
 XP_015145574.1 946 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
38.8 bits(84)	2e-04	10/11(91%)	10/11(90%)	0/11(0%)

```
Query  1    WQMVWESGCTV  11
            WQMVWE GCTV
Sbjct  762  WQMVWEHGCTV  772
```

surface antigen, partial [Hepatitis B virus]
 AAG44620.1 185 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
16.8 bits(32)	15344	4/8(50%)	6/8(75%)	1/8(12%)

```
Query  1  WQMVWESG  8
          W M+W+ G
Sbjct 179  W-MIWDWG  185
```

Histone demethylase JHD2 [Saccharomyces cerevisiae]
ONH78554.1 728 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.8 bits(44)	214	7/11(64%)	7/11(63%)	4/11(36%)

```
Query  4  VW----ESGCT  10
          VW   ESGCT
Sbjct 446  VWYSIPESGCT  456
```

ABC transporter ATP-binding protein (plasmid) [Clostridium tetani E88]
AAO37426.1 168 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
19.7 bits(39)	1260	4/4(100%)	4/4(100%)	0/4(0%)

```
Query  3  MVWE  6
          MVWE
Sbjct 100  MVWE  103
```

ABC transporter permease [Corynebacterium diphtheriae]
WP_088246176.1 854 1

See 4 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.0 bits(42)	435	5/6(83%)	5/6(83%)	1/6(16%)

```
Query  1  W-QMVW  5
          W QMVW
Sbjct 818  WSQMVW  823
```

ABC transporter ATP-binding protein [Bordetella pertussis]
WP_077069045.1 307 1

See 1 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.0 bits(42)	435	7/14(50%)	8/14(57%)	3/14(21%)

```
Query  1  WQMV---WESGCTV  11
          WQMV   E G T+
Sbjct 174  WQMVRRLRENGVTI  187
```

N-substituted formamide deformylase precursor [Streptococcus pneumoniae]
COE25659.1 580 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
23.1 bits(47)	74	6/8(75%)	6/8(75%)	0/8(0%)

```
Query  3  MVWESGCT  10
          MVW S CT
Sbjct 14  MVWISACT  21
```

antirestriction protein, partial [Haemophilus influenzae]
OKQ01777.1 291 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
20.2 bits(40)	884	5/8(63%)	6/8(75%)	0/8(0%)

```
Query  1  WQMVWESG  8
          WQ  W+SG
Sbjct 30  WQKPWDSG  37
```

nucleocapsid protein [Influenza A virus (A/Malaysia/33464/2006(H3N2))]
AFJ78038.1 498 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
19.7 bits(39)	1261	4/4(100%)	4/4(100%)	0/4(0%)

```
Query   2  QMVW  5
           QMVW
Sbjct 327  QMVW  330
```

hypothetical protein NMB0306 [Neisseria meningitidis MC58]
AAF40752.1 64 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.8 bits(44)	216	5/7(71%)	5/7(71%)	0/7(0%)

```
Query  5  WESGCTV  11
          WE GC V
Sbjct 33  WENGCSV  39
```

No matches to measles, mumps, rubella, polio, HPV, Hep A, Varicella or Coxsackievirus in the first 10000 results.

GAD65 115–127
IAFTSEHSHFSLK

PREDICTED: glutamate decarboxylase 2 [Gallus gallus]
588 1

Next MatchPrevious Match
Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
38.0 bits(82)	5e-04	11/13(85%)	12/13(92%)	0/13(0%)

```
Query  1    IAFTSEHSHFSLK  13
            +AFTSEHSHFS K
Sbjct  277  VAFTSEHSHFSVK  289
```
Bst1p [Saccharomyces cerevisiae YJM1478]
1029 1

Next MatchPrevious Match
Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
23.5 bits(48)	77	8/12(67%)	8/12(66%)	1/12(8%)

```
Query  1    IAFTSEHSHFSL  12
            I FT EH HF L
Sbjct  457  ISFT-EHLHFTL  467
```

ferrochelatase [Streptococcus pneumoniae]
364 1

See 1 more title(s)

Next MatchPrevious Match
Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
23.1 bits(47)	109	6/7(86%)	6/7(85%)	0/7(0%)

```
Query  1    IAFTSEH  7
            I FTSEH
Sbjct  242  ISFTSEH  248
```

hypothetical protein [Neisseria meningitidis]
78 1

Next MatchPrevious Match
Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.0 bits(42)	627	7/11(64%)	7/11(63%)	3/11(27%)

```
Query  5    SEHS---HFSL  12
            SEHS  HF L
Sbjct  3    SEHSFRRHFAL  13
```

polymerase [Hepatitis B virus]

[ACP20559.1](#) 834 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
19.7 bits(39)	1837	5/5(100%)	5/5(100%)	0/5(0%)

```
Query  7   HSHFS  11
           HSHFS
Sbjct  288 HSHFS  292
```

sulfatase [Haemophilus influenzae]

[CWX23282.1](#) 421 2

[See 5 more title(s)](#)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	904	5/10(50%)	9/10(90%)	0/10(0%)

```
Query  1   IAFTSEHSHF  10
           IA+TS+H ++
Sbjct  318 IAYTSDHGQY  327
```

Alignment statistics for match #2

Score	Expect	Identities	Positives	Gaps
16.8 bits(32)	22054	6/8(75%)	6/8(75%)	2/8(25%)

```
Query  4   TSEHSHFS  11
           TS SHFS
Sbjct  123 TS--SHFS  128
```

chromosomal replication initiator protein DnaA [Corynebacterium diphtheriae]

[WP_072590166.1](#) 558 1

[See 2 more title(s)](#)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
20.2 bits(40)	1288	5/6(83%)	6/6(100%)	0/6(0%)

```
Query  6   EHSHFS  11
           EHSH+S
Sbjct  119 EHSHYS  124
```

ImmA/IrrE family metallo-endopeptidase [Clostridium tetani]
 WP_035109316.1 137 1

See 7 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
19.3 bits(38)	2589	5/6(83%)	5/6(83%)	0/6(0%)

```
Query  8  SHFSLK  13
          SHF LK
Sbjct  59  SHFTLK  64
```

NADH pyrophosphatase [Bordetella pertussis]
 CFN66976.1 166 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
19.3 bits(38)	2595	5/6(83%)	5/6(83%)	0/6(0%)

```
Query  1  IAFTSE  6
          IAFT E
Sbjct  111  IAFTAE  116
```

polymerase PA, partial [Influenza A virus (A/Sendai/TU13/2008(H1N1))]
 BAI59538.1 161 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
19.7 bits(39)	1821	6/7(86%)	6/7(85%)	0/7(0%)

```
Query  3  FTSEHSH  9
          FTSE SH
Sbjct  139  FTSEVSH  145
```

No matches to measles, mumps, rubella, Hep A, polio, HPV, Coxsackievirus or Varicella viruses in the first 10000 results.

GAD65 274–286
MNILLQYVVKSFD

PREDICTED: glutamate decarboxylase 2 [Gallus gallus]
 XP_015137540.1 588 2

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
39.7 bits(86)	1e-04	11/12(92%)	12/12(100%)	0/12(0%)

```
Query  2   NILLQYVVKSFD  13
           +ILLQYVVKSFD
Sbjct  119 DILLQYVVKSFD  130
```

Alignment statistics for match #2

Score	Expect	Identities	Positives	Gaps
17.6 bits(34)	10833	4/6(67%)	6/6(100%)	0/6(0%)

```
Query  3   ILLQYV  8
           +LL+YV
Sbjct  217 VLLEYV  222
```

acyltransferase [Streptococcus pneumoniae]
  WP_061750393.1 332 1

See 2 more title(s)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
26.1 bits(54)	9.4	9/16(56%)	9/16(56%)	5/16(31%)

```
Query  2   NILLQ-----YVVKSF  12
           NILLQ    YVV  F
Sbjct  162 NILLQMPIQTYVVQTF  177
```

K7_Ylr446wbp [Saccharomyces cerevisiae Kyokai no. 7]
  GAA25300.1 177 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
24.0 bits(49)	54	8/13(62%)	9/13(69%)	2/13(15%)

```
Query  2   NILLQY--VVKSF  12
           NILLQY + K F
Sbjct  48  NILLQYNIIPKNF  60
```

hypothetical protein [Neisseria meningitidis]
  WP_049331678.1 360 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
24.0 bits(49)	54	7/9(78%)	8/9(88%)	1/9(11%)

```
Query  1   MNILLQYVV  9
           MN+LL YVV
Sbjct  1   MNVLL-YVV  8
```

core protein [Hepatitis B virus]*
  AMQ48152.1 183 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
21.0 bits(42)	632	7/11(64%)	8/11(72%)	1/11(9%)

```
Query 2   NILLQYVVKSF  12
          NI L+Y V SF
Sbjct 113 NIVLEYLV-SF  122
```

* Core protein match. Only applies to natural infection, not vaccines.

sporulation transcription factor Spo0A, partial [Clostridium tetani]
  WP_040053750.1 243 1

[See 1 more title(s)](#)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
22.7 bits(46)	155	6/7(86%)	6/7(85%)	0/7(0%)

```
Query 7   YVVKSFD  13
          YVVK FD
Sbjct 107 YVVKPFD  113
```

phage tail protein [Corynebacterium diphtheriae]
  WP_071574087.1 658 1

[See 3 more title(s)](#)

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	905	5/5(100%)	5/5(100%)	0/5(0%)

```
Query 1   MNILL  5
          MNILL
Sbjct 533 MNILL  537
```

dTDP-4-dehydrorhamnose reductase [Bordetella pertussis]
  CFO36417.1 44 1

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	878	5/5(100%)	5/5(100%)	0/5(0%)

```
Query 1 MNILL  5
        MNILL
Sbjct 1 MNILL  5
```

polymerase PA [Influenza A virus (A/Netherlands/001R1/1953(H1N1))]
 ADT78907.1 716 1

See 1 more title(s)

Next MatchPrevious Match
Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
18.9 bits(37)	3732	5/5(100%)	5/5(100%)	0/5(0%)

```
Query  7   YVVKS  11
           YVVKS
Sbjct  321 YVVKS  325
```

hypothetical protein NTHI1209_01601 [Haemophilus influenzae]
 KIS35978.1 50 1

Next MatchPrevious Match
Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
23.5 bits(48)	76	7/8(88%)	7/8(87%)	0/8(0%)

```
Query  3   ILLQYVVK  10
           ILL YVVK
Sbjct  8   ILLLYVVK  15
```

No matches to Hep A, measles, mumps, rubella, polio, HPV, Varicella or Coxsackievirus in the first 10000 results.

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