

# **Strong protein sequence alignment between autoantigens involved in cardiac arrhythmias and vaccine antigens**

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## **Background**

Autoantibodies against proteins encoded by CACNA1C, CACNA1S, CACNA1D, CACNA1F, SCN5A, TRIM21, K<sub>v</sub>LQT1  $\alpha$ , KCNH2 and KCNA4 have been associated with cardiac arrhythmias<sup>1</sup>. The origin of these autoantibodies is unknown. We know from Pandemrix vaccine induced narcolepsy,<sup>2</sup> that vaccine antigens can induce autoimmunity due to molecular mimicry. Protein sequence alignment between these autoantigens and vaccine antigens or contaminants was examined to check if the autoantibodies could have been induced by vaccines.

## **Method**

Protein sequences for the autoantigens were obtained from Uniprot.<sup>3</sup>

BLASTP methodology was used for protein sequence alignment.

As shown before<sup>4</sup>, 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.<sup>2</sup> 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 the 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<sup>5,6</sup> and HPV vaccines<sup>7</sup> are produced using this technique. Such vaccines are however, contaminated with all *Saccharomyces cerevisiae* proteins.

## Results

The table below shows sequence alignment scores between autoantigens and vaccine antigens. A score equal to or greater than 19.3 indicates high probability of inducing cross-reacting autoantibodies following vaccination.

Autoantigen	CACNA1C	CACNA1S	CACNA1D	CACNA1F	SCN5A	TRIM21	K <sub>v</sub> LQT1 α	KCNH2	KCNA4
Vaccine Antigen									
<i>Saccharomyces cerevisiae</i>	192	172	67.4	146	70.9	39.7		33.5	27.3
<i>Streptococcus pneumoniae</i>	53.1	62.8	71.2	53.1	69.7		62.4	55.1	91.7
<i>Corynebacterium diphtheriae</i>	27.3	32.3	25.8	28.5	26.6	29.6	26.2	37.4	37.4
<i>Bordetella pertussis</i>	28.5		28.9	34.7	31.6	30	38.1	44.7	39.3
<i>Clostridium tetani</i>	29.3	25	25	25	35.8	31.6	23.5	29.6	
<i>Neisseria meningitidis</i>	30.4	27.7	28.5	27.7	28.1	29.6	27.3	26.9	30
<i>Haemophilus influenzae</i>	26.9	27.7	26.9	31.2	32	24.6	27.7	44.3	26.2
Hepatitis B	33.5	32	29.3		27.3		24.3		
Rubella							20.4		
Influenza A									26.6
Hepatitis A			31.2						

## Discussion

The results above show strong sequence alignment between many autoantigens and vaccine antigens. Therefore there is a high probability that these autoantibodies were induced as a result of vaccination.

Most vaccines involve injecting viral or bacterial proteins as an intramuscular injection. The route of exposure during natural infection by these viruses and bacteria is usually through the eyes, nose or mouth and not intramuscular injection. We have evolved immune mechanisms specific to routes of exposure and specific to pathogens. Examples include skin-homing versus gut-homing immune cells produced by different lymph nodes.<sup>8</sup> Pathogen Associated Molecular Patterns (PAMP) or Danger Associated Molecular Patterns (DAMP) recognized by pattern recognition receptors (PRR) expressed on dendritic cells (DC). Aluminum adjuvanted vaccines artificially boost and induce immune responses to viral, bacterial antigens introduced through an artificial route of exposure. This completely disrupts the natural immune response to the vaccine antigens by activating immune pathways quite different from the pathways involved during natural infection. Therefore, protections against autoimmunity during natural infection which have evolved over millions of years, are bypassed in the case of vaccine induced immune responses.

One can therefore logically expect a skewed immune response which could include autoimmunity as was demonstrated in the case of Pandemrix vaccine induced narcolepsy. Pandemrix vaccine contained H1N1 viral proteins along with squalene as an adjuvant.

Similarly, with aluminum adjuvanted vaccines that artificially boost immune response to weakly immunogenic vaccine antigens, the natural protection against autoimmunity can be disrupted.<sup>9</sup>

Dr. François Verdier, an immunotoxicology expert with vaccine maker Aventis Pasteur (now Sanofi Pasteur) wrote in *Biotechnology and Safety Assessment* (2003)<sup>10</sup>:

“Advances in computer software such as LifeSeq from Incyte and the availability of the human genome sequence allow rapid comparison between the protein sequence alignment of a vaccine antigen and a host protein.”

He also explains that this can catch primary structure mimicry but may miss conformational mimicry. He recommends, “From these hypotheses (sic), a recommended strategy would be to avoid any vaccine antigen presenting a mimicry with a host antigen involved in an autoimmune disease.”

A recommendation the vaccine industry has mostly ignored, resulting in devastating consequences.

### **Genetic susceptibility**

The efficiency of producing autoimmunity in the presence of molecular mimicry could of course be influenced by genetic variations. So it may be possible to identify genetic markers for such susceptibility. While such identification would be interesting, the root cause, vaccines, need to be fixed.

### **Action**

All vaccine design aspects including removal of contaminating proteins<sup>11</sup>, handling molecular mimicry and route of administration need to be revisited to avoid such off-target immune responses.

## Detailed Results

### Voltage-dependent L-type calcium channel subunit alpha-1C (CACNA1C)

Cch1p [Saccharomyces cerevisiae YJM270]

[AJR78792.1](#) 2039 2

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

#### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
192 bits(489)	3e-47	Compositional matrix adjust.	239/1063(22%)	434/1063(40%)	167/1063(15%)
Query 625	LRIFKITRYWNSL-----SNLVASLLNSVRSIASLLLLLFLFIIIFSLGMLQFLGGKFN	678	L I F I + R + + + L + L + + I + L F F + + + + F G		
Sbjct 866	LSIFHISRFRYRVIISFKLTKKLWKQILSNGVMIWNLSSFYFFFTFLVAIIMAVYFEGVIP	925			
Query 679	FDEMQTRRSTFDNFPQSLLTVFQILTGEDWNSVMDGIMAYGGPSFPGMLVC-IYFIILF	737	+ E M + + P S L + + F I + E + W + + Y + P + C + + F I I F		
Sbjct 926	PEEMADQPFMYSPLNSFLSLFIIGSTENWTDILY--ALQKHSPNISSTFFCSVFFIIWF	983			
Query 738	ICGN YILLNVFLAI AVDNLADAESL TSAQKEEEEEKERKKLARTASPEKKQELVEKPAV-	796	+ N + + L N + F + A + + + + + E E + + + K + P + K Q E V		
Sbjct 984	LLSNSVILNIFIALISESM-----EVKEEEKRPQKIKHYLKFVYPQKIQEYTHASLVA	1036			
Query 797	-----GESKEEKIELKSITADGESPPATKINMDDLQ-----PNENEDKSP-----	836	G E + + K G + N M + L P + E N K		
Sbjct 1037	RIRKKFFGGHRNEDTRDFKQFLMRGTAIMNIAQNMGELADEFKEPPSENLFKKGLSKLTI	1096			
Query 837	-----YPNPETTGEEDDEEPEMPVGPRPRPLSELHLKE-----KAVP	873	Y N + E + + R L E L + E K P		
Sbjct 1097	GVPSLKRLRMFANNPFYKNSDVVFTETND----INGRTYIL-ELNEYEDEKLDYLKKYP	1150			
Query 874	MPEASAFFIFSSNNRFRQLCHRIVNDTI--FTNLILFFILLSSISLAAEDPVQHTSFRNH	931	+ S + F F S + R F R C R + V + T + F F + D S + + H		
Sbjct 1151	LFNYSYYF-FSPQHRFRFCQRLVPPSTGKRTDGSRFF-----EDSTDLYNKRSYFHH	1202			
Query 932	I--LFYFDIVFTTIFTIEIALKI-----LGN-----ADYVFTSIFTLEIILKMT	973	I + F F T I I + + + G D F F + + E I + K		
Sbjct 1203	IERDVVFVIFALATILLIVCSCYVTPLYRMHHKMGTTWNWSSALDCAFIGAFSIEFIVKTV	1262			
Query 974	AYGAFLHKGSFCRNYFNILD---LLVVSVSLISFGIQSSAINVVKILRVLRVLRPLRAIN	1030	A G + + R N + N + D L + + + + L I + + + N + + I + L L R L R +		
Sbjct 1263	ADGFIYSPNAYLRNPWNFIDFCVLISMWINLIAYLKNNG--NLSRIFKGLTALRALRCLT	1320			
Query 1031	RAKGLKHVVQCV-FVAIRTIGNIVIVTLLQFMFACIGVQLFKGKLYTCSDSSKQTEAEC	1089	+ + V F + I + + + L F F G + + F K G + L T C + D S A + C		
Sbjct 1321	ISNTARQTFNLVDFGLNKIFEAGLISLFLFPFTVWGLSIFKGRGLGTCNDGS-LGRADC	1379			
Query 1090	KGN YITYKDGEVDHPPIQPRSWENSKFDFDNVLAAMMALFTVSTFEGWPELLYRSIDSHT	1149	Y Y + I + P R + + D + + A + L + + + E G W + L L + + S		
Sbjct 1380	---YNEYSNSVFQWDIMSPRVYQQPYLHLD SFASAFNSLYQIISLEGWVDLLENMMNSSG	1436			
Query 1150	EDKGP IYNYRVEISIFFIIIIIIAFFMMNIFVGFVIVTFQEQQEQEYKNCELDKNQRQC	1209	+ + F + + + I + F + + N + F V F + + Y E + K +		
Sbjct 1437	IGTPATVMGSAGNALFLVLFIFLSMVFILNLFVSFIVNNQARTTGSAYFTIE-EKAWLES	1495			

Query 1210 VEYALKARPLRRYIPK-----NQHQYKVVWYVNSTYFEYLMFVLILLNTICLAMQHYG 1262  
 + +A+P +IP Q Y++ +Y+ +V++L+IL +Y  
 Sbjct 1496 QKLLSQAKP--KAIPNLIELSRVRQFFYQLAVEKKNFYASFLQVVLYLHIIMLLSRSYN 1553

Query 1263 QSCLFKIAMNILNMLFTGLFTVEMILKLI AFKPKGYFSDPWNVDFLIVIGSIIDVILSE 1322  
 L + M T+F++ L+ P+YF WN  
 Sbjct 1554 PGNLIG-YQGVYFMFSTSVFLIQEALHMCGEPRLYFRQKWNSIRL----- 1598

Query 1323 TNHYFCDAWNTFDALIVVGSIVDIAITEVNPAEHTQCSPSMNAEENSRSITFFRLFRVM 1382  
 ++I++ I++ VPAH +I FL +  
 Sbjct 1599 -----SIIIIAFIMNAFAHV-PASHYWFFH-----NIKGFLLVIF 1633

Query 1383 RLVKLLSRGEGIRTLLWTFIKSFQALPYVALLIVMLFFIYAVIGMQVFGKIALNDTTEIN 1442  
 + +++++ LL T+S + + +LF+YA+ Q+FG L T  
 Sbjct 1634 LFI-IPQNDLTELLETAMASLPPILSLTYTWGVLFLVYAIALNQIFGLTRLGSNT--T 1689

Query 1443 RNNNFQTFPQAVLLLFRFCATGEAWQDIMLACMPGKKCAPESEPSNSTEGETPCGS-SFAV 1501  
 NNF+T +++++LFRC+ GE W IM + S NST T CGS ++A  
 Sbjct 1690 DNINFRTVIKSMIVLFRCSFGEGWNYIMADLTVSEPYC--SSDDNST--YTDCGSETYAY 1745

Query 1502 FYFISFYMLCAFLIINLFVAVIMDNFDYLTRDW---SILGPHHLDEFKRIWAEYDPEAKG 1558  
 +S+ ++ ++ +N+V++I+ NF Y+ R S+ + ++ W+++D+ G  
 Sbjct 1746 LLLMSWNIISMYIFVNMVSLIIGNFSYVYRSGGSRSGINRSEIKKYIEAWSKFDTDGTG 1805

Query 1559 RIKHLDVVTLLRRIQPPLGFGKLCPHRVACKRLVSMNMPLNSD 1601  
 ++ + ++ PL F K+ R+ KLV M+N D  
 Sbjct 1806 ELELSYLPRIMHSFDGPLSF-KIWEGRLTIKSLVENYMEVNPD 1847

Ion transport protein [Streptococcus pneumoniae]

[CJK91097.1](#) 279 2

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
53.1 bits(126)	3e-05	Compositional matrix adjust.	57/267(21%)	113/267(42%)	63/267(23%)
Query 957	DYVFTSIFTLEILKMTAYGAFLHKGSFCRNYFNILDLLVVSLSIFGIQSSAINVVKI	1016			
	D + ++F EI ++ ++H+ +F R+ +++ D VV+++L+ S + +++				
Sbjct 57	DSLILAVFVAEIAARI-----YVHRAAFFRDPWSLFDVSVVAIALVPASGPFSILRALRV	111			
Query 1017	LRVLRVLRPLRAINRAKGLKHVVQCVFAIRTIGNIVIVTLLQFMFACIGVQLFKGKLY	1076			
	LRV+R+ + ++VV + AI +G+I +V L+ ++ A I LF				
Sbjct 112	LRVMRM-----VTMVPSMRRVVGALLSAIPGLGSIAMVLALVFYSAVIATGLFAA---	162			
Query 1077	TCSDSSKQTEAECKGNYITYKDGEVDHPHIIQPRSWENSKFDFDNVLAAMMALFTVSTFEG	1136			
	D P W F++ ++ LF V T E				
Sbjct 163	-----DFP-----EW-----FGSLGRSVYTLFQVMTLES	186			
Query 1137	WPELLYRSIDSHTEDKGPIYNRVEISIFFIIYIIIIAFFMMNIFVGFVIVTFQEQQEQE	1196			
	W + R + I+Y +FFI+I+I F M+N+F+ ++ Q ++				
Sbjct 187	WSMGIVRPVME-----IFPYA---WVFFIPFILIATFTMLNLFIAIIVNAMQTVTDAD	236			
Query 1197	YKNCELD-KNQRQCVEYAL--KARPLR	1220			
	+ + + R+ +E L + R LR				
Sbjct 237	REATQASIEAAREHIETDLHDEVRLR	263			

S protein, partial [Hepatitis B virus]

[AOF42255.1](#) 134 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
33.5 bits(75)	22	Composition-based stats.	19/41(46%)	22/41(53%)	2/41(4%)
Query	2012	ALAVAGLSP--LLQRSHSPASFPRPFATPPATPGSRGWPPQ	2050		
		+L V G SP L Q S SP S P + PP PG RG P+			
Sbjct	9	SLNVLGGSPVCLGQNSQSPTSNSHPTSCPPICPGYRGM CPR	49		

Uncharacterised protein [Bordetella pertussis]

[CFN80739.1](#) 30 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.5 bits(62)	135	Composition-based stats.	14/28(50%)	17/28(60%)	0/28(0%)
Query	1826	LPRPAGYPSTVSTVEGHGPPLSPAIRVQ	1853		
		+P P G S VS G GP LSPA+ V+			
Sbjct	1	MPLPLGPSSAVSVPCGKGPRLSPAMTVR	28		

DNA repair protein RecO [Neisseria meningitidis]

[WP\\_025455575.1](#) 247 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
30.4 bits(67)	431	Compositional matrix adjust.	21/67(31%)	33/67(49%)	13/67(19%)
Query	1277	LFTGLFTVEMILKLI AFKPKGYFSDPW-NVFDLIVIGSIIDVILSETNH YF---CDAWN	1332		
		LF+GL+ E++LKL A + DP ++D L +++ + E NH C W			
Sbjct	90	LFSGLYVNELVLKLTARE-----DMPPELYDAL---AKVMEAVCREANHIADLRCFEWK	140		
Query	1333	TFDALIV	1339		
		+AL V			
Sbjct	141	LLNALGV	147		

hypothetical protein W5M\_06852 [Corynebacterium diphtheriae bv. intermedius str. NCTC 5011]

[EIK56196.1](#) 91 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.3 bits(59)	1424	Composition-based stats.	10/23(43%)	13/23(56%)	0/23(0%)
Query	2022	LQRSHSPASFPRPFATPPATPGS	2044		
		+ SH+P PRP A P PG+			
Sbjct	1	MSTSHTPKPGPRPGAVPGRPGA	23		

serine/threonine protein kinase [Clostridium tetani]

[WP\\_052219511.1](#) 619 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.3 bits(64)	1432	Composition-based stats.	14/32(44%)	19/32(59%)	2/32(6%)
Query	1939	TEMLSYQDDENRQLTLPEED--KRDIRQSPKR	1968		
		TE + Q+DEN +T PEED K D +Q +			
Sbjct	585	TEEPTDQEEDENNNITTPPEEDGKKEDTKQDKNK	616		

hypothetical protein [Haemophilus influenzae]

[WP\\_041174642.1](#) 112 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.9 bits(58)	2520	Composition-based stats.	15/55(27%)	31/55(56%)	7/55(12%)
Query	654	LLLLLFLFIIIFSLGMLQFLGGKFNFDQMTRRSTFDNFPQSLLTVFQILTGEDW	708		
		+ L+LFLFI + SL+G++ +++++ ++ F+ TVF+ GE++			
Sbjct	3	ICLVLFLFISLSSMLGLK-----YNKLSQLFIFNIIYFFTVFRYDVGEY	50		

No matches to measles, mumps, rubella, polio or human influenza A viruses, in the first 10000 results.

### E3 ubiquitin-protein ligase TRIM21 (Ro/SSA)

Slx8p [Saccharomyces cerevisiae YJM1248]

[AJU44904.1](#) 274 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
39.7 bits(91)	0.097	Compositional matrix adjust.	18/54(33%)	27/54(50%)	5/54(9%)
Query	16	CPICLDPFVEPVSIIECGHSFCQECISQVGGGGSV-----CPVCRQRFLKLNLR	64		
		CPIC +P + CGH FC C+ Q+ + C +CR + LK++R			
Sbjct	206	CPICFEPETALMTLCGHVFCPCPLFQMVNSSRTRCRQFGHCALCRSKVYLKDVR	259		

flagellar export protein FliJ [Clostridium tetani]

[WP\\_035109535.1](#) 145 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
31.6 bits(70)	21	Composition-based stats.	14/54(26%)	36/54(66%)	1/54(1%)
Query	139	LQVALGELRRKQELAEKLEVEIAIKRADWKKTVETQKSRIHAEFVQQKNFLVEE	192		
		+++ EL++++E EK+ + + K+ + +KTVET + + + F++++N L ++			
Sbjct	76	IELTTEELKKREEEVEKVRISLKKQKQIE-RKTVETLREKDKSAFIKEQNLLEQK	128		

PqiA, partial [Neisseria meningitidis]

[AAK08046.1](#) 103 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.6 bits(65)	57	Composition-based stats.	10/36(28%)	19/36(52%)	0/36(0%)
Query	19	CLDPFVEPVSIIECGHSFCQECISQVGKGGGVCPC	54		
		C D + P +++C C+ + Q+ +G + CP C			
Sbjct	16	CRDEALPPHTVDCPECGCRADVPQLDRGEAAFCPRC	51		

hypothetical protein BXA20\_11850 [Corynebacterium diphtheriae]

[ONF63907.1](#) 115 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.6 bits(65)	59	Compositional matrix adjust.	14/34(41%)	19/34(55%)	4/34(11%)
Query	94	VHGERLHLFCEKDGKALCWV----CAQSRKHRDH	123		
		+HG+RLH FC+ LC+ QS+ H DH			
Sbjct	24	LHGDRLHSFCDYRHILLCYSRSLPTPQSQPHTDH	57		

IclR family transcriptional regulator [Bordetella pertussis]

[WP\\_023852623.1](#) 256 1

[See 554 more title\(s\)](#)

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
30.0 bits(66)	106	Compositional matrix adjust.	23/76(30%)	36/76(47%)	8/76(10%)
Query	96	GERLHLFCEKDGKALCWCAQSRKHRDHAMVPLEEAAQEYQEKLVQALGELRRKQELAEK	155		
		G R + GKAL + Q+ + DH A + + E V+L L KQELA+			
Sbjct	128	GGRAPAYAVATGKAL--LACQTADYLDH----YGAAIKRHTEDTHVSL--LALKQELADV	179		
Query	156	LEVEIAIKRADWKKTV	171		
		+ AI R +W++ +			
Sbjct	180	NRIGYAINRGEWRQGI	195		



diphosphonucleoside choline transferase [Haemophilus influenzae]

[ADQ55242.1](#) 265 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
24.6 bits(52)	6481	Compositional matrix adjust.	12/52(23%)	23/52(44%)	9/52(17%)
Query	6	RLTMMWEEVTCPICLDPFVEPVSIIECGHSFCQECISQVGKGGGSVCPVCRQR	57		
		+LT+ +++ C LD F H+ C++ GGG++ R +			
Sbjct	3	KLTLREQQLVCLDILDYF-----HALCEKYQIHYSLGGGTIGAIRHK	45		

No matches to measles, mumps, rubella, polio, hepatitis A/B or human influenza A viruses, in the first 10000 results.

### Potassium voltage-gated channel subfamily KQT member 1 (K<sub>v</sub>LQT1 α)

ion transport protein [Streptococcus pneumoniae]

[CJL53225.1](#) 283 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
62.4 bits(150)	8e-11	Compositional matrix adjust.	64/256(25%)	111/256(43%)	46/256(17%)
Query	129	VFLIVLVCLIFSVLSTIEQYAALATGTLFWMEIVLVVFFGTEYVRLWSAGCRSKYV-GL	187		
		+F ++V ++ S+ S E++ L T +E F EYV+R+++ KY+			
Sbjct	38	IFASLVVVMLDSIASFNERHGQLLTN----LEWGFTAIFAVEYVLRITYTHPEPRKYILSF	93		
Query	188	WGRLRFARKPISIIDLIVVASMVVLCVSGKQVFATSAIRGIRFLQILRM-----	238		
		+G ++DL V+ + + L + IR +R ++L++			
Sbjct	94	YG-----MVDLFSVLPAFIALFPDAQYLLVVRVIRMLRIFRVLKLAPYLSQANF	143		
Query	239	LHVDRQGGTWRLGSSVFIHRQELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGS	298		
		L V QG ++ +VF+ +TTL I + L++ V E F S			
Sbjct	144	LLVALQGSRQKI---IVFLLS---VTTLIIIVYGTLMY-----VIEGPSNGFTS	185		
Query	299	YADALWGWVVTVTITIGYDVKVPQTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQK	358		
		+++W VVT+TT+G+GD VP T +GK +A+ + S A+P GI F ++			
Sbjct	186	IPISIIYWAVTLTTVFGFDIVPLTPLGKALATVVMITGYSIIAVPTGI---FTAELANA	241		
Query	359	QRQKHFNRQIPAAASL	374		
		RQ P L			
Sbjct	242	MRQDSL RHNCPTCDKL	257		

potassium channel protein [Bordetella pertussis]

[CFW09189.1](#) 319 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
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38.1 bits(87) 0.006 Compositional matrix adjust. 25/87(29%) 41/87(47%) 7/87(8%)

Query 300 ADALWGVVTVTTIGYGDKVPQTWGKTIASCFVFAISFFALPAGILGS---GFALKVQ 356  
 A A ++ +V+++T+GYGD PQT + A+ + I+ FA + G LK

Sbjct 96 ATAFYFSIVSMSTVGYGDITPQTTAARLFAASIIILGITVFATSISAIAGPVIGGNLKR 155

Query 357 QKQRQKHFNRQ---IPAAASLIQTAW 379  
 + R H R+ I A L Q+ +

Sbjct 156 VRGRISHAMRKHIIIAGATPLAQSIV 182

hypothetical protein [Corynebacterium diphtheriae]

[WP\\_072588026.1](#) 162 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	20	Compositional matrix adjust.	25/84(30%)	35/84(41%)	12/84(14%)
Query 249	RLGGSVFIHRQELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEF--GSYADALWWG				306
	R+LG HR EL+T G VY A + R+ F S A +WW				
Sbjct 32	RILG-----HRVELVDASRGPEQDRHHREVVY-----AWLQGLRIPFLIASMATYMWWH				81
Query 307	VTVTTIGYGDKVPQTWGKTIAS				330
	V V+ I + +P W+ IA+				
Sbjct 82	NVVSVILFVICIPLPWIAVVIAN				105

30S ribosomal protein S11 [Clostridium tetani]

[WP\\_011100698.1](#) 132 1

[See 9 more title\(s\)](#)

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
23.5 bits(49)	151	Compositional matrix adjust.	7/14(50%)	10/14(71%)	0/14(0%)
Query 440	VPHITCDPPEERRL				453
	+PH C PP+ RR+				
Sbjct 119	IPHNGCRPPKRRRV				132

helix-hairpin-helix motif family protein [Neisseria meningitidis NM045]

[EQD03286.1](#) 69 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.3 bits(59)	3.0	Composition-based stats.	11/16(69%)	11/16(68%)	0/16(0%)
Query 57	GAPGPAPPASPAAPAA				72
	GAP P PA PA PAA				
Sbjct 52	GAPAPKPAKPAIPAA				67

DNA internalization-related competence protein ComEC/Rec2 [Haemophilus influenzae]

[WP\\_042603513.1](#) 788 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.7 bits(60)	12	Compositional matrix adjust.	17/45(38%)	18/45(40%)	3/45(6%)
Query	370	AAASLIQTAWRCYAAENPDSSTWKIYIRKAPRSHTLLSPSPKPKK		414	
		A + WR Y SSTWKI K PR TL P K			
Sbjct	464	CAGIFMLIIWRIYREPEASSSTWKI---KRPRFFTLNLSKPLLKN		505	

non-structural polyprotein p200 [Rubella virus]

[AEN94545.1](#) 2116 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
20.4 bits(41)	2684	Compositional matrix adjust.	19/61(31%)	24/61(39%)	3/61(4%)
Query	65	ASPAAPAAPPVASD-LGPRPPVSLDPRVSIYSTRRPVLARTHVQGRVYNFLERPTGWKCF		123	
		A A A VA D GP P DP I + H+ RV + ++ P G K			
Sbjct	779	ADRARDAEQEVACDPSPGAAPTRADPNSDIVESYARAAGPVHL--RVRDIMDPPPGCKVV		836	

  

Query	124	V	124
		V	
Sbjct	837	V	837

surface antigen, partial [Hepatitis B virus]

[AAR87403.1](#) 101 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
24.3 bits(51)	58	Compositional matrix adjust.	13/22(59%)	16/22(72%)	2/22(9%)
Query	119	GWKCFVYHFAVFL-IVLVCLIF	139		
		GW C + F +FL I+LVCLIF			
Sbjct	14	GWMC-LRRFIIFLIFILLVCLIF	34		

No matches to measles, mumps, polio, hepatitis A or human influenza A viruses, in the first 10000 results.

## Sodium channel protein type 5 subunit alpha (SCN5A)

Ion transport protein [Streptococcus pneumoniae]

[CJK91097.1](#) 279 2

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
69.7 bits(169)	1e-10	Compositional matrix adjust.	67/279(24%)	115/279(41%)	63/279(22%)
Query 1195	RKTCYHIVEHSWFETFIIFMILLSSGALAFE-DIYLEERKTIKVLLEYADKMFTYVFLVLE	1253			
	R +E F+ I+ +I++++ L + L R ++L D+ VFV E				
Sbjct 10	RSRLGQFIERPAFQRGILLIVINAAILGMQTSALVARWGEALVL--LDLILAVFVAE	67			
Query 1254	MLLKWVAYGFKKYFTNAWCWLDLFLIVDVSLSLVANTLGAEMGPIKSLRTRLRALRPLRA	1313			
	+ + + +F+ W DF +V ++LV GP LR LR LR +R				
Sbjct 68	IAARIYVHR-AAFFRDPWSLFDVSVVAIALVP-----ASGPFSILRALRVLRVMMR	117			
Query 1314	LSRFEGMRVVNALVGAIPSIMNVLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPL	1373			
	++ MR VV AL+ AIP +++ +V +++++ LFA F				
Sbjct 118	VTMVPSMRRVVGALLSAIPGLGSIAMVLALVFYVSAVIATGLFAADFPE-----	166			
Query 1374	NYTIVNNKSQCESLNTGELYWTKVKVNFNDVNGAGYLALLQVATFKGW-MDIMYAAVDSR	1432			
	W F ++G L QV T + W M I+				
Sbjct 167	-----W-----FGSLGRSVYTLFQVMTLESWSMGIV-----	192			
Query 1433	GYEEQPQWEYNLYMYIYFVIFIFGSFFTLNLFIVIID	1471			
	+P E Y +++F+ FI+ +F LNLFI +I++				
Sbjct 193	---RPVMEIFPYAWVFFIPFILIATFTMLNLFIAIIVN	227			

Cch1p [Saccharomyces cerevisiae YJM270]

[AJR78792.1](#) 2039 2

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
70.9 bits(172)	3e-10	Compositional matrix adjust.	75/349(21%)	140/349(40%)	65/349(18%)
Query 115	SPFHPIRRAAVKILVHSLFNMLIMCTILTNCVMAQHDPPPW--TKYVEYFTTAIYTFES	172			
	S F H I R + +LI+C+ ++ H W + ++ F ++ E				
Sbjct 1198	SYFHHERDVFVFIFALATILLIVCSCYVTPLYRMHMKMGTTWNWSSALDCAFIFAFSIEF	1257			
Query 173	LVKILARGFCLHAFTFLRDPWNWLDVSVIIMAYTTEFVDLGNVSAL-RTFRVLRALKTIS	231			
	+VK +A GF +LR+PWN++DF V+I + L N L R F+ L AL+ +				
Sbjct 1258	IVKTVADGFIYSPNAYLRNPWNFIDFCVLISMWINLIAYLKNNGNLSRIFKGLTALRALR	1317			
Query 232	VI---SGLKTIVGALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTAL	287			
	+ + +T + +K+ + +++ L F + GL +F G L T				
Sbjct 1318	CLTISNTARQTFNLVMDGLNKFIEAGLISLLEFPFTVWGLSIFKGRGLG-----TCN	1370			
Query 288	NGTNGSVEADGLVWESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGEN	347			
	+G+ G + C N + +				
Sbjct 1371	DGSLGRAD-----CYNEYSNSVFQWDIMSPRVYQQ	1400			
Query 348	PDHGYTSFDSFAWAFALFRLMTQDCWERLYQQTLRSAG-----KIYMIFFMLVI	397			
	P Y DSFA AF +L++++ + W L + +S+G +F +L I				
Sbjct 1401	P---YLHLSDFASAFNSLYQIISLEGWVDLLENMMNSSGIGTPATVMGSAGNALFLVFI	1457			

Query 398 FLGSFYLVNLLAVVAMAYEEQNQATIAETEE---KEKRFQEAMEMLKK 443  
 FL +++NL +++ NQA + +EK +E+ ++L +  
 Sbjct 1458 FLSMVFILNLFVSFIV----NNQARTTGSAYFTIEEKAWLESQKLLSQ 1501

dihydroorotase, partial [Bordetella pertussis]

[WP\\_019249695.1](#) 337 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
31.6 bits(70)	193	Composition-based stats.	28/92(30%)	36/92(39%)	23/92(25%)
Query 569	RTSAQGQPSPGTSAPGHALHGKKNSTVDCNGVVSLLGAGDPEATSPGSHLLRPVMLEH--				626
	R +A GQ G A H +D G+ L G D A G+ L P+ E				
Sbjct 32	RIAAIGQAPAGFQAQQH-----IDARGLAVLPGLVDLSARVHGAGL-APLACEMQA				81
Query 627	-----PPDTTTPSEEPGGPQMLTSQA		647		
	PPDT P +EPG +ML +A				
Sbjct 82	ALAGGVTRLVPPDTPPLDEPGRVEMLRHRA		113		

hypothetical protein KY52\_09675 [Clostridium tetani]

[KGI37804.1](#) 553 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
35.8 bits(81)	12	Composition-based stats.	48/193(25%)	87/193(45%)	33/193(17%)
Query 1432	RGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIVGVIIDNFNQKKKLGQDIFMTEEQ				1491
	R Y+ + +++ Y+Y +I + LF +I N+ D+ +T				
Sbjct 282	RSYKIKKNIVRDIFFVYNIISFNIIILVFVILFFASVIKNWPY-----DLSIT---				330
Query 1492	KKYYNAMKGLGSKKPQKPIRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDD				1551
	KYYN +K +G+ LN Y+ IF AF ++ I + + +VE				
Sbjct 331	LKYYN-VKSVGTSL-----LNVYKNTIF-----VAFTTALIGTIVVFITAYIVERYK				376
Query 1552	QSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDI				1611
	+ + NIL I L ++I ++ L+ + +F SWN+F+F+ I+ +L++I				
Sbjct 377	EFSKIRNIIYIIASLPLSI--SGMVIGLSYI--LFFNKSWNVFNFLYGTFFIL--ILANI				430
Query 1612	IQKYFFSPTLFRV		1624		
	I +FFS F +				
Sbjct 431	I--HFFSVPFFTI		441		

hypothetical protein, partial [Corynebacterium diphtheriae]

[WP\\_071575429.1](#) 144 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.6 bits(57)	4634	Composition-based stats.	9/17(53%)	13/17(76%)	0/17(0%)
Query	1493	KYYNAMKKLGSKKPQKP	1509		
		KYYN+ + G KKP++P			
Sbjct	123	KYYNSDQSSGPKKPERP	139		

hypothetical protein, partial [Haemophilus influenzae]

[WP\\_005655715.1](#) 133 1

[See 7 more title\(s\)](#)

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
32.0 bits(71)	54	Composition-based stats.	20/70(29%)	34/70(48%)	5/70(7%)
Query	1212	IFMILLSSGALAFEDIYLEERKTIKVLLEYADKM-----FTYVFEVLEMLLKWVAYGFKKY	1266		
		+++ +S +L F IYLE R + +LL+YAD + +Y+ + + L W+ K			
Sbjct	18	LYLTFVSVTSLFFISIYLENRPLLSLLLDYADNIDRLSSLSYITSVLLSLFWIYKAHKNI	77		
Query	1267	FTNAWCWLDF	1276		
		LDF			
Sbjct	78	EQKGIKNLDF	87		

Uncharacterised protein [Neisseria meningitidis]

[CWS47831.1](#) 109 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.1 bits(61)	980	Compositional matrix adjust.	13/33(39%)	17/33(51%)	0/33(0%)
Query	978	WDFCCGLLRQPQKPAALAAQGQLPSCIATPYS	1010		
		W LL Q+ +PA LAA +LP C+ S			
Sbjct	45	WSAASFLLWQKQPAYLAAAARLPDCLLVAVS	77		

surface antigen, partial [Hepatitis B virus]

[AGZ62121.1](#) 148 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.3 bits(59)	2332	Composition-based stats.	25/97(26%)	32/97(32%)	5/97(5%)
Query	564	PWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGVVSLLGAGDPEATSPGSHLLRPVM	623		
		PWP G PG + P L G + G++ L A P A++ +P			
Sbjct	50	PWPDANKVAGAFGPGVTPPHGGLLG--WSPQAQGILQLPANPPPASTNRQSGRQPTP	106		
Query	624	LEHPPDTTTPSEEPGGPQML--TSQAPCVDGFEEPGA	658		
		L P T P T Q P V G P			
Sbjct	107	LSPPLRDTHPQAMQWNSTTFQQTLQDPXVRGLYFPAG	143		

No matches to measles, mumps, rubella, hepatitis A, human influenza A, human papilloma or polio viruses, in the first 10000 results.

### Potassium voltage-gated channel subfamily H member 2 (KCNH2)

Phototropin homolog [Streptococcus pneumoniae]

[CON50322.1](#) 261 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

#### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
55.1 bits(131)	2e-06	Composition-based stats.	30/105(29%)	52/105(49%)	2/105(1%)
Query 15	LDTIIRKFEGQSRKFI	ANARVENCAVIYCNDGFC	ELCGYSRAEVMQRPCTC	DFLHGPR	74
	L+ I + +	+I + +E+ ++Y N GF ++	GY E++ + C FL G T		
Sbjct 13	LEVIKKALDHVRVGV	ITDPALEDNPIVYVYV	NQGFVQMTGYETEEILGK	--NCRFLQGKHT	70
Query 75	QRRAAAQIAQALLGAEERK	VEIAFYRKDGSCFLCLVDV	VPVKNE	119	
	I AL E V+I Y+KDG+ F	+++ P++ ED			
Sbjct 71	DPAEVYNIRTALQNK	EPVTVQIQNYKKDGMTF	WNELNIDPMEIED	115	

transcriptional regulator Crp [Haemophilus influenzae]

[WP\\_050846696.1](#) 224 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

#### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
44.3 bits(103)	0.006	Compositional matrix adjust.	25/90(28%)	44/90(48%)	6/90(6%)
Query 764	PPGDTLVHAGDLLTALYFIS	RGSIEILRGD-----VV	VAILGKNDFGEPLNLYAR	PGKS	818
	P TL+HAG+ T LY++ +GS+ +	D +++ LG FGE L+ K			
Sbjct 39	PAKSTLIHAGEDATTLYYVI	KGSVMVSSKDDDEGKEMIL	TYLGAGQFFGEA-GLFDE	GSKR	97
Query 819	NGDVRALTYCDLHKIHRD	DLLEVLDMYPEF	848		
	+ V+ T C++ +I +++ PE				
Sbjct 98	SAWVKTKTTCEIAEISYK	KYRQLIQANPEI	127		

potassium channel protein [Bordetella pertussis]

[CFU09599.1](#) 364 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

#### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
44.7 bits(104)	0.009	Compositional matrix adjust.	24/89(27%)	51/89(57%)	8/89(8%)
Query 613	TALYFTFSSLTSVGF	GNVSPNTNSEKIFSICV	MLIGSLMYASIFGNVSA	IIQRLYSGTAR	672
	TA YF+ S+++VG+G+++P	T + ++F+ ++++G ++A+	++SAI + G +		
Sbjct 142	TAFYFSIVSMSTVGYG	DITPQTAAARLFAASII	ILGITVFAT---SISAI	AGPVIGNLK	198

Query 673 YHTQMLRVREFIRFHQI- - - -PNPLRQRL 697  
 + R+ +R H I PL Q +  
 Sbjct 199 RLVRG-RISHAMRKHIIIAGATPLAQS 226

hypothetical protein [Clostridium tetani]

[WP\\_035125131.1](#) 88 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.6 bits(65)	95	Composition-based stats.	9/19(47%)	14/19(73%)	0/19(0%)
Query 695	QRLEEFQHAW	SYTNGIDM	713		
	+++ EY	HAW Y NG	+++M		
Sbjct 70	KQINEYVDHAWI	YENGVEM	88		

NAD-binding protein of Kef-type K<sup>+</sup> transporter [Corynebacterium diphtheriae]

[WP\\_004567149.1](#) 362 1

[See 90 more title\(s\)](#)

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
37.4 bits(85)	1.9	Compositional matrix adjust.	14/43(33%)	29/43(67%)	0/43(0%)
Query 603	GGPSIKDKYVT	ALYFTFSSLTSVGF	GNVSPNTNSEKIFSICVM	645	
	GG S	++ ALY++	SL++ G+G+++P T S ++ +I ++		
Sbjct 69	GGYSEHLTFIDAL	YSAVSLSTTGYGDITPITQSARLLNIIII	111		

Sod1p [Saccharomyces cerevisiae YJM1304]

[AJV39167.1](#) 154 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
33.5 bits(75)	13	Composition-based stats.	23/80(29%)	38/80(47%)	9/80(11%)
Query 739	HCKPFRGATKG	CLRALAM- -KFKTTHAPPGDTLVHAGDL- - -LTALYFISIRGSIEILRGD	793		
	H F AT GC+ A	FK TH P D + H GD+ T	+++GS + D		
Sbjct 47	HIHEFGDATNGCVS	SAGPHFNPFKKTHTGAPTDEVRHVGDMGNVKTDENGVAKGSFK- - - -D	102		
Query 794	VVAILGKNDIF	GEPLNLYA	813		
	++ ++G + G + ++A				
Sbjct 103	SLIKLIGPTS	VVGRSVVIHA	122		



glycosyltransferase 25 family protein, partial [Neisseria meningitidis 69096]

[ELL13802.1](#) 44 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.9 bits(58)	302	Compositional matrix adjust.	16/40(40%)	18/40(45%)	5/40(12%)
Query	218	MDNHVAGLGPAAEERRALVGPSPPRSAPGQ-----LPSPR	252		
		M NHV L A ERRA + R P Q +PS R			
Sbjct	1	MQNHVISLASAAERRAHIAATFGARGIPFQFFDALMPSER	40		

No matches to measles, mumps, rubella, polio, hepatitis A/B, human influenza A or human papilloma viruses, in the first 10000 results.

### Potassium voltage-gated channel subfamily A member 4 (KCNA4)

ion transport protein [Streptococcus pneumoniae]

[CJL53225.1](#) 283 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
91.7 bits(226)	9e-19	Compositional matrix adjust.	53/174(30%)	95/174(54%)	15/174(8%)
Query	382	FSFEFVRCFACPSQALFFKNIMNIIDIVSILPYFITLGTDLAQGGGNGQQQAMSFA	441		
		F+ E+V+R + P + + ++D+ S+LP FI L AQ			
Sbjct	72	FAVEYVLRITYHPEPRKYILSFYGMVDLFSVLPAFIALLLFPDAQY-----LL	118		
Query	442	ILRIIRLVRFRIKLSRHSKGLQILGHTLRASMRELGLLIFFLFIGVILFSSAVYFAEA	501		
		++R+IR++R+FR+ KL+ + L L+ S +++ + + + +I++ + +Y E			
Sbjct	119	VVRVIRMLRIFRVLKLPAPYLSQANFLLVALQGSRQKIIIVFLLSVTTLIIIVYGTLMYVIEG	178		
Query	502	DEPTTHFQSIPDAFWAVVTMTTVGYGDMKPITVGGKIVGSLCAIAGVLTIALP	555		
		P+ F SIP + +WAVVT+TTVG+GD+ P+T GK + ++ I G IA+P			
Sbjct	179	--PSNGFTSIPISIIYWAVVTLTTVGFQDIVPLPLGKALATVVMITGYSIIAVP	230		

potassium channel protein [Bordetella pertussis]

[CFW09189.1](#) 319 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
39.3 bits(90)	0.21	Compositional matrix adjust.	37/141(26%)	65/141(46%)	20/141(14%)
Query	429	GGNGQQQAMSFAILRIIRLVRFRIKLSRHSKGLQILGHTLRASMRELGLLIFFLFIG	488		
		G +G +++ + I LV +R F + + G +L A + LLI+ +F			
Sbjct	28	GWDGGHLLLAYTGVLIAALVCFWRRFDRASLAAG-----SLFAVISITSLLIYAVF--	79		
Query	489	VILFSSAVYFAEADEPTTHFQSIPDAFWAVVTMTTVGYGDMKPITVGGKIVGSLCAIAG	548		
		L+ A + + + P T AF++++V+M+TVGYGD+ P T ++ + I G			
Sbjct	80	GTLYLGAEFSPKVESPAT-----AFYFSIVSMSTVGYGDITPQTAAARLFAASIIILG	132		

Query 549 VLTIALPV-----PVI VSNFN 564  
 + A + PVI N  
 Sbjct 133 ITVFATSISAIAGPVI GGNLK 153

NAD-binding protein of Kef-type K<sup>+</sup> transporter [Corynebacterium diphtheriae]

[WP\\_004567149.1](#) 362 1

[See 90 more title\(s\)](#)

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
37.4 bits(85)	1.00	Compositional matrix adjust.	21/81(26%)	43/81(53%)	2/81(2%)
Query 464	LQILGHTLRASMR	ELGLLIFFLFIGVILFSSAVYFAE	ADEPTTHFQSIPDAFWWAVVTMT		523
	++I G+ L + +R +	+ + +I+ + VY E + H	I DA +++ V+++		
Sbjct 32	IRIPGNPLVSP	IRLIARRFGYALALIIIVALVVYLDEGGY	-SEHLTFI-DALYYS	AVSLS	89
Query 524	TVGYGDMKPITVGGKIVGSLC				544
	T GYGD+ PIT +++ +				
Sbjct 90	TTGYGDITPITQSARLLNIII				110

hypothetical protein H760\_YJM456O00189 [Saccharomyces cerevisiae YJM456]

[AJT77342.1](#) 715 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.3 bits(59)	1490	Compositional matrix adjust.	15/53(28%)	27/53(50%)	5/53(9%)
Query 92	KKKAHYRQSSFPHCS	DLMPSGSE-----EKILRELS	EEEEEEEEEEEEEEEE	EGR	139
	K+ AHY Q+ PHCS+	S+ E I ++L +E+ + ++	E +		
Sbjct 588	KEMAHYEQTYLPHCSEAYGLTSKVL	EFGENIWKDLPGTDENNLQSKKNSPEKK			640

neuraminidase [Influenza A virus (A/swine/Iowa/A01203491/2012(H1N1))]

[AFN66863.1](#) 469 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.6 bits(57)	2736	Compositional matrix adjust.	13/45(29%)	27/45(60%)	1/45(2%)
Query 540	VGSLCAIAGVLTIALPVPVIVSNFN	FYFHRETENEEQTQLTQNAV			584
	+G++C IAG++++ L + IVS + + +T E T++ +V				
Sbjct 10	IGTVMIAIGIISLLLQIGNIVSLW-	ISHSIQTGWENHTEMCNQSV			53

hypothetical protein [Haemophilus influenzae]

[WP\\_050845276.1](#) 458 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	3554	Compositional matrix adjust.	12/33(36%)	18/33(54%)	1/33(3%)
Query 511	IPDAFWAVVTMTTVGYGDMKPITVGGKIVGSL		543		
	I D WWA T+ +G +KP T+ G I ++				
Sbjct 7	IYDNTWAKAHQFTITHGGLKP-TLRGTIKNTM		38		

DNA damage-inducible protein DnaD [Neisseria meningitidis]

[WP\\_049344716.1](#) 283 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
30.0 bits(66)	158	Compositional matrix adjust.	21/66(32%)	27/66(40%)	17/66(25%)
Query 498	FAEADEPTTHFQSIIPDAFWAVVTMTTVGYGDMKPITVGGKIVGSLCAIAGVLTIALPVP		557		
	FA+ADE T FW+A +GY DM+ I S+C L +P				
Sbjct 26	FAQADENT-----FWYASDLAMMLGYNDMQAILKAINRAHSVC-----FQLDIP		69		
Query 558	VIVSNF 563				
	I NF				
Sbjct 70	-ITENF 74				

No matches to C. tetani, measles, mumps, rubella, polio, hepatitis A/B or human papilloma viruses, in the first 10000 results.

Voltage-dependent L-type calcium channel subunit alpha-1S (CACNA1S)

Cch1p [Saccharomyces cerevisiae YJM1385]

[AJS26017.1](#) 2039 2

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
172 bits(437)	3e-41	Compositional matrix adjust.	228/1043(22%)	427/1043(40%)	152/1043(14%)
Query 526	VLRCIRLLRIFKITYWTSLNSLNASLLNSIRSIALLLLLLFLFVIFALLGMQLFGGRY		585		
	+R R++ FK+TK L +L++ I+L FF +A++ FG				
Sbjct 871	ISRFYRVIISFKLTK-----KLWKQILSNGVMIWNLSSFYFFFTFLVAIIMAVYFEGVI		924		
Query 586	DFEDETVRRSNFDNFPQALISVFQVLTGEDWTSMMYNGIMAYGGPSYPGMLVC-IYFIIL		644		
	E+ + +P++S+F++E+WT++Y + P+ C++FII				
Sbjct 925	PPEEMADQPFGMYSLNSLFLSFIIGSTENWTDILY--ALQKHSPNISSAFFCSVFFIIW		982		
Query 645	FVCGNYILLNVFLAIVDNLAEAESLTSQAQKAKAEKRRKMSKGL---PDKSEE--EK		698		
	F+ N++LN+F+A+ ++ ++KEEK+ +++ L PK+E				
Sbjct 983	FLLSNSVILNIFIAL-----ISESMEVKEEEKRPQQIKHYLKFVYPQKIQEYTHA		1032		

Query 699 STMAKKLEQKPKGEGIPTTAKLK-----IDEFESNVNEVKDPY---PSAD-FPGDDE 746  
S+A+ ++ G T K I N+E+D+ PS+F D  
Sbjct 1033 SLVARIRKKFFGGHRNEDTRDFKQFLMRGTAIMNIAQNMGELADEFEKPPSENLFKKDLS 1092

Query 747 EDEPEIPLSPRRPLAE-----LQLKE-----KAVPIP 774  
+ +P R R A L+L E K P+  
Sbjct 1093 KLTIGVPSLKRLRMFANNPFYKNSDVVFTETNDINGRTYILELNEYEDEKLDYLKKYPLF 1152

Query 775 EASSFFIFSPTNKIRVLCHRIV-----NATWFTN-----FILL 807  
S +F FSP ++R C R+V ++T N F++  
Sbjct 1153 NYSYF-FSPQHRFRFCQRLVPPSTGKRTDGSRFFEDSTDLYNKRSYFHIERDVFVFI 1211

Query 808 FILLSSAALAAEDPIRADSMRNQIL-----KHFDIGFTSVFTVEIVLKMTTYGAFLHKG 861  
F L + + + + D F F++E++K G  
Sbjct 1212 FALATILLIVCSCYVTPLYRMHMKMGTTWNWSSALDCAFIFAGSIEFIVKTVADGFIYSPN 1271

Query 862 SFCRNYFNMLDLLVVA---VSLISMGLESSAIS-VVKILRVLRLRPLRAINRAKGLKHV 917  
++ RN +N +D V+ ++L+ + +S +K L R L R L N A+ ++  
Sbjct 1272 AYLRNPWNFIDFCVLISMWINLIAYLKNNGNLSRIFKGLTALRALRCLTISNTARQTFNL 1331

Query 918 VQCMFVAISTIGNIVLVTLLQFMFACIGVQLFKGKFFRCTDLSKMTEEECRGYVVYKD 977  
V M F ++I L++ L F F G+ +F K G+ C D S+ +C Y Y +  
Sbjct 1332 V--MFDGLNKIFEAGLISLSLLFPFTVWGLSIFKGRGTGNDGS-LGRADC---YNEYSN 1385

Query 978 GDPMQIELRHREWHSDFFHDNVLSAMMSLFTVSTFEGWPQLLYKAIDSNAEDVGPIYNN 1037  
+ R+ H D+ SA SL+++EGW LL ++S+  
Sbjct 1386 SVFQWDIMSPRVYQPYLHLD SFASAFNSLYQIISLEGWVDLLENMMNSSGIGTPATVMG 1445

Query 1038 RVEMAIFIIYIILIAFFMMNIFVGFVIVTFQEGETEYKNCELD---KNQRQCVQYALK 1094  
A+F +++ L F++N+V F++ +Y E ++Q+ Q K  
Sbjct 1446 SAGNALFLVLFNLSMVFILNLFVSVFVNQARTTGSAYFTIEEKAWLESQKLLSQAKPK 1505

Query 1095 ARPLRCYIPK-NPYQYQVWYIVTSSYFEYLMFALIMLNTICLGMQHYNQSEQMNHISDIL 1153  
A P ++ +YQ+ +Y+ + ++L+I L +Y N ++ +  
Sbjct 1506 AIPNLIELSRVRQFFYQLAVEKKNFYASFLQVVLYLHIIMLLSRYPGNLIGY-QGVY 1564

Query 1154 NVAFTIIFTLEMILKLMFAFKARGYFGDPWNVDFD-LIVIGSIIDVILSEIDTFLASSGGL 1212  
+ T +F ++ L+ R Y F W N +I+I I+++ + AS  
Sbjct 1565 FMFSTSVFLIQEALHMCGEPRLYFRQKWN SIRLSIIIIAFIMNAFAFHVP---ASHYWF 1621

Query 1213 YCLGGGCGNVPDESARISSAFFRLFRVMRLIKLLSRAEGVRTLLWTFIKSFQALPYVAL 1272  
+ +G F++ ++++++ LL T+S + +  
Sbjct 1622 HNIKG-----FLLVIFLFIIPQNDTLTELLETAMASLPPILSLTY 1662

Query 1273 LIVMLFFIYAVIGMQMFGKIALVDGTQINRNNNFQTFPQAVLLLFRCATGEAWQEILLAC 1332  
+LF +YA+ Q+FG L G+ N NF+T +++++LFRC+ GE W I+  
Sbjct 1663 TWGVFLVYAIALNQIFGLTRL--GSNTDNINFRTVIKSMIVLFRCSFGEGWNYIMADL 1720

Query 1333 SYGKLCDPESDYAPGEEYT-CGT-NFAYYYFISFYMLCAFLVINLFVAVIMDNFDYLTRD 1390  
+ + +P Y T C G+ +A Y +S+ ++ ++ +N+V++I+ N F Y+ R  
Sbjct 1721 T---VSEPYCSDDNSTYTDCGSETYAYLLLMSWNIISMYIFVNMVSLIIGNFSYVYRS 1777

Query 1391 W---SILGPHHLDEFKAIWAEYDPEAKGRIKHLDDVVTLLRRIQPPLGFGKFCPHRVACKR 1447  
S + +++ W+++D+ G ++ + ++ P L F K R+ K  
Sbjct 1778 GGSRSGINRSEIKKYIEAWSKFDTDGTELELSYLPRIMHSFDGPLSF-KIWEGRLTIKS 1836

Query 1448 LVGMNMPNLSGDGTVTFNATLFAL 1470  
L V M +N D L L  
Sbjct 1837 LVENYMEVNPDDPYDVKIDLIGL 1859

Ion transport protein [Streptococcus pneumoniae]

[CJK91097.1](#) 279 2

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
62.8 bits(151)	1e-08	Compositional matrix adjust.	57/270(21%)	118/270(43%)	59/270(21%)
Query 1120	FEYLMFALIMLNTICLGMQHYNQ-SEQMNHISDILNVAFTIIFTLEMILKLMFAFKARGYF		1178		
	F+ + LI++N LGMQ + +L+ +F E+ ++ +A +F				
Sbjct 22	FQRGILLIVINAAILGMQTSAAALVARWGEALVLLDSLILAVFVAEIAARIYVHRA-AFF		80		
Query 1179	GDPWNVDFDLIVIGSIIDVILSEIDTFLASSGGLYCLGGGCGNVDPEDESARISSAFFRLF		1238		
	DPW++FDF +V +++ +SG L R				
Sbjct 81	RDPWSLFDVSVVAIALVP-----ASGPFSIL-----RAL		109		
Query 1239	RVMRLIKLLSRAEGVRTLLWTFIKSFQALPYVALLIVMLFFIYAVIGMQMFGKIALVDGT		1298		
	RV+R+++++ +R ++ ++ L +A+++ ++F++ AVI +F				
Sbjct 110	RVLRVMRMVTMVPSMRRVGALLSAIPGLGSIAMVLALVFYVSAVIATGLFAA-----		162		
Query 1299	QINRNNNFQTFPQAVLLLFRCATGEAWQEILLACSYGKLCDPESDYAPGEEYTCGTNFAY		1358		
	+ F+ ++V LF+ TE+W SG + P + P +A+				
Sbjct 163	--DFPEWFGSLGRSVYTLFQVMTLESW-----SMG-IVRPVMEIFP-----YAW		203		
Query 1359	YFISFYMLCAFLVINLFVAVIMDNFDYLT		1388		
	+FI F ++ F ++NLF+A+I++ +T				
Sbjct 204	VFFIPFILIATFTMLNLFIAIIVNAMQTVT		233		

X protein [Hepatitis B virus]

[ACM40559.1](#) 154 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
32.0 bits(71)	63	Composition-based stats.	25/75(33%)	35/75(46%)	9/75(12%)
Query 1699	TRGRALGQPCRVLGPHSKPCVEMLKGL-LTQRAMPARGQAPPA-PC-----QCPRVSSMP		1751		
	+RGR L P L P S PCV G L+ R +P A PC R+E+++				
Sbjct 25	SRGRPLPGPLGTLSPASPPCVPTDHGAHLSLRGLPVCAFSSAGPCALRFTSARRMETTVN		84		
Query 1752	EDRSSTPGSLHEET		1766		
	+ R + P LH+ T				
Sbjct 85	DHR--NLPKVLHKRT		97		

multicopper oxidase [Corynebacterium diphtheriae PW8]

[AEX68733.1](#) 397 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
32.3 bits(72)	137	Composition-based stats.	15/35(43%)	18/35(51%)	5/35(14%)
Query 1734	GQAPPAPCQCPRV-----ESSMPEDRKSSTPGSLH		1763		
	GQAPP C+ PRV S +PE + TP H				
Sbjct 347	GQAPPRCRLPRVVHRTASVLPESARPCTPARGH		381		

ABC transporter permease, partial [Clostridium tetani]

[KHO33579.1](#) 71 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.0 bits(53)	5621	Composition-based stats.	7/22(32%)	16/22(72%)	0/22(0%)
Query	1366	MLCAFLVINLFFVAVIMDNFDYL	1387		
		++CA +V++L + + DNF ++			
Sbjct	37	IICALIVHLLIPFVKDNFTHI	58		

hypothetical protein, partial [Bordetella pertussis]

[WP\\_023997416.1](#) 94 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.0 bits(53)	7523	Composition-based stats.	8/18(44%)	13/18(72%)	0/18(0%)
Query	977	DGDPMQIELRHREWVHSD	994		
		DGD +++ ++ R WVH D			
Sbjct	54	DGDALRLAVKLRRLWVHVD	71		

hypothetical protein [Haemophilus influenzae]

[WP\\_085024506.1](#) 495 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.7 bits(60)	2998	Composition-based stats.	13/53(25%)	33/53(62%)	5/53(9%)
Query	664	LAEAESLTSQAKAKAEKRR-----KMSKGLPDKSEEEKSTMAKKLEQKPKG	711		
		+A+A++ Q+AKAE+ KR+ K+++ +++++ ++ +A++ E+ K			
Sbjct	1	MAQAQAEARRQAKAEQVKRQAEAEKVARQKAEAKRQEALARQQEARKA	53		

peptidase [Neisseria meningitidis]

[WP\\_049328404.1](#) 286 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.7 bits(60)	3308	Compositional matrix adjust.	11/20(55%)	14/20(70%)	0/20(0%)
Query	566	LFLFIVIFALLGMQLFGGRY	585		
		L+LF+ +F LL LFGG Y			
Sbjct	89	LYLFLAVFPLLAALLFGGNY	108		

No matches to hepatitis A, polio, measles, mumps, rubella, human influenza A or human papilloma viruses, in the first 10000 results.

### Voltage-dependent L-type calcium channel subunit alpha-1D (CACNA1D)

Ion transport protein [Streptococcus pneumoniae]

[CJK91097.1](#) 279 2

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

#### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
71.2 bits(173)	3e-11	Composition-based stats.	57/266(21%)	119/266(44%)	55/266(20%)
Query 1207	FEYMMFVLIIMLNTLCLAMQHYEQ-SKMFNDAMDILNMVFTGVFTVEMVLKVIKPKGYF	1265			
	F+ ++LI++N L MQ ++A++L+++ VF E+ ++ + +F				
Sbjct 22	FQRGILLIVINAAILGMQTSAAALVARWGEALVLLDSLILAVFVAEIAARIYVHR-AAFF	80			
Query 1266	SDAWNTFDLSLIVIGSIIDVALSEADPTSESENPVPTATPGNSEESNRISITFFRLFRVMR	1325			
	D W+ FD S++ +AL VP +P + R RV+R				
Sbjct 81	RDPWSLFDLFD-----SVVAIAL-----VPASGP-----FSILRALRVLR	113			
Query 1326	LVKLLSRGEGIRTLWTFIKSFQALPYVALLIAMLFFIYAVIGMQMFGKVAMRDNNQINR	1385			
	+++++ +R ++ ++ L +A+++A++F++ AVI +F +				
Sbjct 114	VMRMVTMVPSMRRVVGALLSAIPGLGSIAMVLALVFYVSAVIATGLFAA-----DF	164			
Query 1386	NNNFQTFPQAVLLFRFCATGEAWQEIMLACLPGKLCDPESDYNPGEETYCGSNFAIVYFI	1445			
	F + ++V LF+ T E+W + P + P +A V+FI				
Sbjct 165	PEWFGSLGRSVYTLFQVMTLESWSM-----GIVRPVMEIFP-----YAWVFFI	207			
Query 1446	SFYMLCAFLIINLFVAVIMDNFDYLT	1471			
	F ++ F ++NLF+A+I++ +T				
Sbjct 208	PFILIATFTMLNLFIAIIVNAMQTVT	233			

Cch1p [Saccharomyces cerevisiae YJM993]

[AHY79558.1](#) 2039 4

[See 4 more title\(s\)](#)

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

#### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
67.4 bits(163)	4e-09	Compositional matrix adjust.	74/287(26%)	120/287(41%)	48/287(16%)
Query 167	AFLIIFTVETFLKIIAYGLLLHPNAYVRNGWNLLDFVIVIVGLFSVILEQLTKETEGGNH	226			
	AF+ F++E +K +A G + PNAY+RN WN +DF ++I S+ + + GN				
Sbjct 1248	AFIGAFSIEFIVKTVADGFIYSPNAYLRNPWNFIDFCVLI----SMWINLIAYLKNNGNL	1303			
Query 227	SSGKSGGFDVKALRAFVRVLRPLRLVSGVPSLQVV--LNSIIKAMVPLLHIALLVLFVIII	284			
	S G + ALR A R L +L + LN I +A L + L ++				
Sbjct 1304	SRIFKG---LTALRALRCLTISNTARQTFNLVFMFDGLNKIFEA-----GLISLSLLFP	1353			
Query 285	YAIIGLELFIGMKHKTCCFFADSDIVAEEDPAPCAFSGNGR-QCTANGTECRSGW--VGP-	340			
	++ GL +F G++ C GR C + W + P				
Sbjct 1354	FTVWGLSIFKGRL-----GTCNDGSLGRADCYNEYSNSVQWDIMSPR	1396			

Query 341 --NGGITNFDNFAMFLTQFQITMEGWTDVLYWMNDAMGFELPWV-----YFVSLV 390  
 + D+FA A +++Q I++EGW D+L M++ G P F+L  
 Sbjct 1397 VYQQPYLHLD SFASAFNSLYQIISLEGWVDLLENMMNSSGIGTPATVMGSAGNALFLVLF 1456

Query 391 IFGSF-FVLNLVLGVLSGEFSKEREKAKARGDFQKLREKQLEEDLK 436  
 IF S F+LNL + + ++ A + + E Q+L K  
 Sbjct 1457 IFLSMVFILNLFVSFIVNNQARTTGSAYFTIEEKAWLESQKLLSQAK 1503

polyprotein [Human hepatitis A virus]

[APD15889.1](#) 2227 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
31.2 bits(69)	457	Compositional matrix adjust.	20/74(27%)	38/74(51%)	8/74(10%)
Query 793	VNQIANS DNKVTIDDYREED-----	EDKDPYPPCDVPVGE EEEEEEEDEPEVPAGPR	844		
	+++IA D + ++DD R E+	E ++PY + VG++ + ++E P			
Sbjct 767	MSRIAAGDLESSVDDPRSEEDKRFESHIECRNPYKELRLEVQKRLKYAQEELSNEVLPP		826		
Query 845	PRRISELNMKEKIA	858			
	PR+I L + KI+				
Sbjct 827	PRKIKGLFSQAKIS	840			

large S protein, partial [Hepatitis B virus]

[AGP15125.1](#) 162 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.3 bits(64)	679	Composition-based stats.	17/55(31%)	25/55(45%)	1/55(1%)
Query 1716	PSIPPASDTEKPLFPAGNSVCHNHHNHSIGKQVPTSTNANLNNA-NMSKAAHG	1769			
	P+ PP + T +PL+ PAG S	+ + + N N A NM A G			
Sbjct 89	PAAPPPASTNRPLYFPAGGSSSGTASPAQNTVSAISSILSKNGNPAPNMENIASG	143			

DNA polymerase III subunits gamma and tau [Haemophilus influenzae 22.4-21]

[EDK14149.1](#) 688 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.9 bits(58)	7024	Compositional matrix adjust.	21/74(28%)	33/74(44%)	11/74(14%)
Query 1706	TTHRPLHVQRPSIPPASDTEKPLFPAGNSVCHNHHNHN-SIGKQVPTSTNANL-----N	1759			
	T +P H+++P+ PP + P NS N + N I + +A+ N				
Sbjct 472	TEPKPKHIEKPTSPNAAQ-----APQKNSTEENSSDDNVEIAQDEQEILSADTYRWEWN	526			
Query 1760	NANMSKAAHGKRPS	1773			
	N ++KA G RPS				
Sbjct 527	NPELAKADTGVRPS	540			



bacterioferritin [Neisseria meningitidis]

[WP\\_061725459.1](#) 157 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.5 bits(62)	1133	Composition-based stats.	16/50(32%)	25/50(50%)	0/50(0%)
Query	2054	KQRSADSLVEAVLISEGLGRYARDPKFVSATKHEIADACDLTIDEMESAA	2103		
		+ ++AD L+E +L EGL K + E ACDLT ++ + A			
Sbjct	51	EMKAADDLIERILFLEGLPNLQELGKLLIGESTEEIIACDLTKEQEKEHA	100		

ABC transporter permease, partial [Clostridium tetani]

[KHO33579.1](#) 71 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.0 bits(53)	5827	Composition-based stats.	6/22(27%)	16/22(72%)	0/22(0%)
Query	1449	MLCAFLIINLFAVAVIMDNFDYL	1470		
		++CA ++++L + + DNF ++			
Sbjct	37	IICALIVHLLIPFVKDNFTHI	58		

hypothetical protein [Bordetella pertussis]

[WP\\_050849081.1](#) 160 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.9 bits(63)	804	Composition-based stats.	8/16(50%)	9/16(56%)	0/16(0%)
Query	1981	WATPPATPPYRDWTPC	1996		
		W PPA+ P W PC			
Sbjct	133	WVLPPASSPTTSWIPC	148		

hypothetical protein [Corynebacterium diphtheriae]

[WP\\_010934020.1](#) 86 1

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

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.8 bits(55)	4962	Composition-based stats.	14/43(33%)	24/43(55%)	3/43(6%)
Query	24	ANYARGTRLP---LSGEGPQSQPNSKQTVLSWQAAIDAARQA	63		
		A +A+ T L L+GE P QPN+ ++ V + A+ + +A			
Sbjct	2	ATHAQSTELLEALLAGEAPRFQPN TGQELVDDIEIALSPSARA	44		

No matches to measles, mumps, rubella, polio, human papilloma or human influenza viruses, in the first 10000 results.

### Voltage-dependent L-type calcium channel subunit alpha-1F (CACNA1F)

Cch1p [Saccharomyces cerevisiae YJM1399]

[AJS28472.1](#) 2039 5

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

#### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
146 bits(369)	3e-33	Compositional matrix adjust.	168/732(23%)	314/732(42%)	56/732(7%)
Query 847	EGSAFFCLSQTNPLRKGCHTLIIHHVFTNLILVFIILSSVSLAAEDPI-RAHSFRNHILG	905	+GS FF S ++ I VF ++ IL V P+ R H H+G		
Sbjct 1182	DGSRFFEDSTDLYNKRSYFHIERDVFVIFALATILLIVCSCYVTPLYRMH----	HKMG 1237			
Query 906	YFDY-----AFTSIFTVEILLKMTVFGAFLHRGSFCRSWFNMLD---LLVSVSLISFG	956	+++ AF F++E ++K G ++ R+ +N +D L+ + ++LI++		
Sbjct 1238	TWNWSSALDCAFIGAFSIEFIVKTVDAGFIYSPNAYLRNPWNFIDFCVLISMWINLIAYL	1297			
Query 957	IHSSAIS-VVKILRVLRVLRPLRAINRAKGLKHVVQCVFVAIRTIGNIMIVTLLQFMFA	1015	++ +S+K L LR LR L NA+ ++V +F + I +++ L F F		
Sbjct 1298	KNNGNLSRIFKGLTALRALRCLTISNTARQTFNLV--MFDGLNKIFEAGLISLSLLFPFT	1355			
Query 1016	CIGVQLFKGKFYCTDEAKHTPQECKGSFLVYPDGDVSRPLVRERLWVNSDFNFDNLSA	1075	G+ +FKG+ TC DE+ +C Y+ ++ R++ +D+ SA		
Sbjct 1356	VWGLSIFKGRGLGTCNDESLGR-ADCYNE---YSNSVFQWDIMSPRVYQQPYLHLSDFASA	1411			
Query 1076	MMALFTVSTFEGWPALLYKAIDAYAEDHGPIYNYRVEISVFFIVYIIIIAFFMMNIFVGF	1135	+L+ ++ EGW LL +++ ++F +++ + F++N+FV F		
Sbjct 1412	FNSLYQIISLEGWVDLLENMMNSSGIGTPATVMGSAGNALFLVLFNFLSMVFILNLFVSF	1471			
Query 1136	VIITFRAQGEQEYQNCELDKNQRQCVEYALKAQPLRRYIPK-----NPHQYRVWATVNSA	1190	++ Y E +K ++ +A+P +IP Q+ V		
Sbjct 1472	IVNNQARTTGSAYFTIE-EKAWLESQKLLSQAKP--KAIPNLIELSRVRQFFYQLAVEKK	1528			
Query 1191	AFEYLMFL--LILLNTVALAMQHYEQTAPFNAMDILNMVFTGLFTIEMVLKIIAFKPKH	1248	F Y FL ++ L+ +L +Y Y + M T +F I+ L+ P+		
Sbjct 1529	NFYASFLQVVLYLHIIMLLSRYPGNLIGY-QGVYFMFSTSVFLIQEALHMCGEPRRL	1587			
Query 1249	YFTDAWNTFDALIVVGSIVDIAVTEVNNGGHLGESSSEDSSRISITFFRLFRVMRLVKLLS	1308	YF WN+ I++++ AV H+ S I F++ +++		
Sbjct 1588	YFRQKWNISIRLSIIIIAFIMNAV-----AFHVPASHYWFHNIK----GFFLLVIFLFIIP	1638			
Query 1309	KGEGIRTLWTFIKSFQALPYVALLIAMIFFIYAVIGMQMFGKVALQDGTQINRNNNFQT	1368	+++ LL T+S + + ++F +YA+ Q+FG L G+ N NF+T		
Sbjct 1639	QNDLTLETLETAMASLPILSLTYTWGVFLVYAIALNQIFGLTRL--GSNTTDNINFRT	1696			
Query 1369	FPQAVLLLFRCATGEAWQEIM---LASLPGNRCDPESDFGPGEEFTCGS-NFAIAYFISF	1424	+++++LFRC+ GE W IM SP D S+ CGS +A +S+		
Sbjct 1697	VIKSMIVLFRCSFGEGWNYIMADLTVSEPYCSSDDNSTYT-----DCGSETYAYLLMSW	1751			
Query 1425	FMLCAFLIINLFVAVIMDNFDYLTR---DWSILGPHHLDEFKRIWSEYDPGAKGRIKHLD	1481	++ ++ +N+FV++I+ NF Y+ R S+ +++ WS++D G ++		
Sbjct 1752	NIISMYIFVNMVSLIIGNFSYVYRSGGSRGINRSEIKKYIEAWSKFDTDGTGELELSY	1811			

Query 1482 VVALLRRIQPPLGFGKLCPHRVACKRLVAMNMLNSDGTVTFNATLFALVRTSLKIKTEG 1541  
 + ++ PL F K+ R+ K L V M + N D L L + I  
 Sbjct 1812 LPRIMHSFDGPLSF-KIWEGRLTIKSLVENYMEVNPDDPYDVKIDLIGLNKELNTIDKAK 1870

Query 1542 NLEQANQELRIV 1553  
 +++ Q R V  
 Sbjct 1871 IQRKLYRRFV 1882

Ion transport protein [Streptococcus pneumoniae]  
[CJK91097.1](#) 279 1

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### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
53.1 bits(126)	2e-05	Compositional matrix adjust.	58/277(21%)	110/277(39%)	60/277(21%)
Query 861		RKGCHTLIHHHVFTNLILVFIILSSVSLAAEDPIRAHSFRNHILGYFDYAFTSIFTVEIL			920
		R I F IL+ I++++ L + + L D ++F EI			
Sbjct 10		RSRLGQFIERPAFQRGILLLLIVINAAILGMQTSAAALVARWGEALVLLDSLILAVFVAEIA			69
Query 921		LKMTVFGAFLHRGSFCRSWFNMLDLLVSVSLISFGIHSSAISVVKILRVLRLRPLRAI			980
		++ ++HR +F R +++ D VV+++L+ S + +++LRV+R+ +			
Sbjct 70		ARI-----YVHRAAFFRDPWLSLFDVSVVAIALVPASGPFILRALRVLVRMRM-----V			118
Query 981		NRAKGLKHVVQCVFVAIRTIGNIMIVTLLQFMFACIGVQLFKGKFTCTDEAKHTPQEC			1040
		++ VV + AI +G+I +V L+ ++ A I LF F			
Sbjct 119		TMVPSMRRVVGALLSAIPGLGSIAMVLALVFYVSAVIATGLFAADF-----			164
Query 1041		KGSFLVYPDGDVSRPLVRERLWNDSFNFDNVLSAMMALFTVSTFEGWPALLYKAIDAYA			1100
		P+ W F ++ ++ LF V T E W + +			
Sbjct 165		-----PE-----W-----FGSLGRSVYTLFQVMTLESWSMGIVR-----			193
Query 1101		EDHGPIYNYRVEISVFFIVYIIIIAFFMMNIFVGFVI			1137
		P+ VFFI +I+I F M+N+F+ ++			
Sbjct 194		----PVMEIFPYAWVFFIPFILIATFTMLNLFIAIIV			226

polyketide synthase [Corynebacterium diphtheriae]  
[WP\\_014308834.1](#) 2639 1

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

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### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.5 bits(62)	2308	Compositional matrix adjust.	18/48(38%)	28/48(58%)	3/48(6%)
Query 1898		LVEAVLISEG--LGLFARDPRFVALAKQEIADACRLTLDDEMNAASDL			1943
		++ A++ EG L L A DP+ VA E+ D C T DE+D A +++			
Sbjct 1867		MLRAIVTDEGHQLILDADDPQ-VATPPVEVDLDCATADEVDQAITEV			1913

aminopeptidase, partial [Bordetella pertussis]  
[WP\\_055345188.1](#) 253 1

[GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
34.7 bits(78)	20	Compositional matrix adjust.	18/46(39%)	22/46(47%)	0/46(0%)
Query	1170	LRRYIPKNPHQYRVWATVNSAAFEYLMFLLILLNTVALAMQHYEQT	1215		
		+R+ I NP R W TVN FE L + A+A HYEQ			
Sbjct	128	IRQAIAANPEIGRAWPTVNPLVFECNDGYLNDIQAQVAEAEHYEQA	173		

ABC transporter permease, partial [Clostridium tetani]

[KHO33579.1](#) 71 1

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### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.0 bits(53)	5220	Composition-based stats.	6/22(27%)	16/22(72%)	0/22(0%)
Query	1426	MLCAFLIINLFVAVIMDNFDYL	1447		
		++CA ++++L + + DNF ++			
Sbjct	37	IICALIVHLLIPFVKDNFTHI	58		

conserved hypothetical metabolite transport protein [Haemophilus influenzae PittHH]

[EDK10412.1](#) 344 1

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### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
31.2 bits(69)	298	Composition-based stats.	19/57(33%)	26/57(45%)	10/57(17%)
Query	717	MYDGIMAYGGPFPPGMLVCIYFIILFCIGNYILLNVFLAIAVDNLASGDAGTAKDKG	773		
		M + I Y PFF GMLVCI +LF ++ IA + + A T + G			
Sbjct	136	MLEVITTYFKPFFLGLVCIAGYVLF-----YIMIAFSQIYAKSAPTVEAG	182		

hypothetical protein, partial [Neisseria meningitidis]

[AEQ62062.1](#) 327 1

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### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.7 bits(60)	3354	Composition-based stats.	17/44(39%)	23/44(52%)	2/44(4%)
Query	34	AVEGESSGASGLGTPKRRNQHSKHKT--VAVASQRSRALFCL	75		
		A +G + A LG +N H + + ASAQR P+ALF L			
Sbjct	32	AEQGYTEAAFVLGNHLLQNGHPEQAFPWLETASAQRHPKALFTL	75		

No matches to measles, mumps, rubella, polio, hepatitis A/B, human papilloma or human influenza A viruses, in the first 10000 results.

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