

# **Strong protein sequence alignment between autoantigens involved in atherosclerosis-related coronary artery disease, cerebral infarction, diabetes mellitus and vaccine antigens**

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## **Background**

Autoantibodies against RPA2 have been associated with stroke<sup>1</sup>. Autoantibodies against SOSTDC1 and TUBB2C have been associated with cerebral infarction (CI) and diabetes mellitus (DM)<sup>2,3</sup>. Autoantibodies against ATP2B4 and BMP-1 have been associated with atherosclerosis-related diseases, such as CI, DM, coronary artery disease (CAD) and chronic kidney disease<sup>4</sup>. Autoantibodies against adiponectin have been associated with CAD, CI and DM<sup>5</sup>. Decreased serum adiponectin levels and inflammation was reported following typhoid vaccination<sup>6</sup>. Potentially another case of autoantibody induction against adiponectin. The origin of these autoantibodies is unknown. We know from Pandemrix vaccine induced narcolepsy,<sup>7</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>8</sup>

BLASTP methodology used for protein sequence alignment was previously described.<sup>9</sup>

As shown in the article above, 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>7</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>10,11</sup> and HPV vaccines<sup>12</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	RPA2	SOSTDC1	TUBB2C	ATP2B4	BMP1	Adiponectin
Vaccine Antigen						
Saccharomyces cerevisiae	25	28.9	370	556	29.6	25
Streptococcus pneumoniae	26.2		23.9	364	30.4	50.8
Corynebacterium diphtheriae	24.6	23.1		76.6	25.4	28.1
Bordetella pertussis	21.6	24.3		74.3	28.1	30.4
Clostridium tetani			24.3	348	26.2	
Neisseria meningitidis	26.6	27.3	26.2		28.1	55.5
Haemophilus influenzae	23.9	26.6	24.6		25.4	25.4
Hepatitis B					24.6	
Salmonella typhi						23.5
Influenza A						25.8

## 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>13</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>14</sup>

Dr. François Verdier, an immunotoxicology expert with vaccine maker Aventis Pasteur (now Sanofi Pasteur) wrote in *Biotechnology and Safety Assessment* (2003)<sup>15</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>16</sup>, handling molecular mimicry and route of administration need to be revisited to avoid such off-target immune responses.

### **Detailed results**

RPA2

hypothetical protein [Neisseria meningitidis]

[WP\\_079254849.1](#) 81 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)	186	Composition-based stats.	13/36(36%)	19/36(52%)	0/36(0%)
Query	12	SSYGGAGGYTQSPGGFGSPAPSQAEKKSARARAHIV	47		
		+ Y GG TQS F +P PS+ S + ++IV			
Sbjct	2	AKYAERGGLTQSRHDFTPMPSETGFASNFKPENIV	37		

glyoxalase family protein [Streptococcus pneumoniae]

[CIV75181.1](#) 80 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	225	Composition-based stats.	11/29(38%)	17/29(58%)	0/29(0%)
Query	115	SENTVVPPEYVVKVAGHLRSFQNKSLVA	143		
		S+N +VP E + K G LRSF + ++			
Sbjct	48	SQNHLVPLENFXXKTGLLRFSFSQESLFIS	76		

Caf120p [Saccharomyces cerevisiae YJM1355]

[AJT22058.1](#) 1060 1

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

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.0 bits(53)	2141	Compositional matrix adjust.	9/17(53%)	12/17(70%)	0/17(0%)
Query	181	APISNPGMSEAGNFGGN	197		
		+P SNPG+ NFGG+			
Sbjct	13	SPASNPGMLSPSNFGGD	29		

UDP-glucose 6-dehydrogenase [Corynebacterium diphtheriae]

[OLN15394.1](#) 401 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
24.6 bits(52)	2477	Compositional matrix adjust.	9/17(53%)	14/17(82%)	0/17(0%)
Query	174	SQPSAGRAPISNPGMSE	190		
		++ SAGR PIS PG+++			
Sbjct	37	AELSAGRLPISEPLAD	53		

Uncharacterised protein [Bordetella pertussis]

[CFN73851.1](#) 47 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
21.6 bits(44)	6181	Compositional matrix adjust.	8/28(29%)	15/28(53%)	0/28(0%)
Query	99	AAPMDVQRQWVDTDDTSSSENTVVPPEYV	126		
		+APM++R+W		++ PP+ V	
Sbjct	20	SAPMNMRRWPSRSTARPPSSRKPPQNTV	47		

high molecular weight adhesin, partial [Haemophilus influenzae]

[AIY25288.1](#) 932 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
23.9 bits(50)	5818	Compositional matrix adjust.	29/108(27%)	50/108(46%)	12/108(11%)
Query	11	SSSYGGAGGYTQSPGGFGSPAPSQAEEKSRARAQHIVPCTISQLL-SATLVDEVFRIGNV	69		
		SSS+G AG ++ PGG G+ ++ K + + + TIS L S T V + N+			
Sbjct	83	SSSHGNAGIDSEFFGGSGTK---ESPKTNGEQPTVLTNETISNYLKSGTWMNITAKKNL	139		
Query	70	EISQVTIVG----IIRHAEKAPTNIIVYKIDDMTAAAPMDVR----QWVD	109		
		++ +G +I H+E V +D+T+ ++ WVD			
Sbjct	140	TVNSSINIGDSSHLILHSEGKNNGGV KIKEDITSNGGNLTIQSGGWVD	187		

No matches to measles, mumps, rubella, C. tetani, hepatitis B or polio virus in the first 1000 results.

## SOSTDC1

Duo1p [Saccharomyces cerevisiae YJM193]

[AJR76554.1](#) 247 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)	67	Compositional matrix adjust.	24/85(28%)	39/85(45%)	12/85(14%)
Query	109	VLPNWIG----GGYGTKYWSRRSSQEWRCVNDKTRTQRIQLQCQDGGSTRYKITVVTACK	164		
		+L +WI GY K S ++ + +ND+ + + +DGST + V A K			
Sbjct	106	ILDSWINIHSQAGYIHKLMSDQT--YCLKINDRLHNENVTNDEDEGST---LHNVIALK	159		
Query	165	CKRY--TRQHNESSHNFESMSPAKP	187		
		K+ RQ E+ + +PAKP			
Sbjct	160	KKKILDLRQKLENRKGEKDAAPAKP	184		

hypothetical protein AN159\_02290 [Neisseria meningitidis]

[AOT28737.1](#) 92 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.3 bits(59)	75	Compositional matrix adjust.	16/48(33%)	22/48(45%)	4/48(8%)
Query	95	LKELVCAGECLPLPVLPNWIGGGYGTKYWSRRSSQEWRCVNDKTRTQR	142		
		+KE AG VLP W G G GT++ + S +R N + R			
Sbjct	1	MKEARAAGMV----VLPEWQGIGIGTRFLNTPSEMRYRGGNRYNKPMR	44		

alpha-xylosidase [Streptococcus pneumoniae]

[WP\\_050284185.1](#) 737 1

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

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.9 bits(63)	92	Composition-based stats.	13/38(34%)	24/38(63%)	1/38(2%)
Query	108	PVLPNWIGGGYGTKYWSRRSSQEWRCVNDKTRTQRIQL	145		
		P+LP + G + ++YWS +S E+ + D+ T++I L			
Sbjct	177	PLLPRYALGNWWSRYWS-YTSEYLDLIDRFETEKIPL	213		

urease subunit alpha [Haemophilus influenzae]

[WP\\_038439444.1](#) 572 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)	404	Compositional matrix adjust.	11/31(35%)	18/31(58%)	1/31(3%)
Query	83	YISDGQCTSISPLKELVCAGECLPLPVLPNW	113		
		+ G C+S+ PL+E + AG L L + +W			
Sbjct	200	FFGKGNCSLDPLREQIEAG-ALGLKIHW	229		

hypothetical protein BUE64\_10080 [Corynebacterium diphtheriae]

[OLN14942.1](#) 328 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
23.1 bits(48)	4960	Compositional matrix adjust.	9/30(30%)	15/30(50%)	0/30(0%)
Query	110	LPNWIGGGYGTKYWSRRSSQEWRCVNDKTR	139		
		LP WI G+ ++ + WR ++D R			
Sbjct	187	LPVWIHAGHHFSARYQQGADSWRDIDDLAR	216		

Uncharacterised protein [Bordetella pertussis]

[CFN82636.1](#) 90 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
24.3 bits(51)	1129	Compositional matrix adjust.	9/19(47%)	12/19(63%)	0/19(0%)
Query	121	KYWSRRSSQEWRCVNDKTR	139		
		+YW RR S WRC + + R			
Sbjct	18	RYWHRRRSCSWRCASRRPR	36		

No matches to C. tetani, measles, mumps, rubella, polio virus, hepatitis B in the first 1000 results.

## TUBB2C

beta-tubulin [Saccharomyces cerevisiae]

[CAA24603.1](#) 457 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
370 bits(950)	5e-127	Compositional matrix adjust.	167/222(75%)	201/222(90%)	0/222(0%)
Query	2	PTYGDLNHLVSATMSGVTTCLRFPGQLNADLRKLA VNMVFPRLHFFMPGFAPLTSRGSQ	61		
		P+YGD LN+LVS+ MSGVTT LR+PGQLN+DLRKLAVN+VFPRLHFFM G+APLT+ GSQ			
Sbjct	220	PSYGDLN LNVSSVMSGVTTSLRYPGQLNSDLRKLAVNLVFPRLHFFMVG YAPLTAIGSQ	279		
Query	62	QYRALTVPELTQQMFDAKNMMAACDPRHG RYLTVA AVFRGRMSMKEVDEQMLNVQNKNS S	121		
		+R+LTVPELTQQMFDAKNMMAA DPR+GRYLTVA A FRG++S+KEV+++M VQ+KNS			
Sbjct	280	SFRSLTVPELTQQMFDAKNMMAAADPRNG RYLTVA AAFRKGKVSVKEVEDEMHKVQSKNS D	339		
Query	122	YFVEWIPNNVKTAVCDIPPRGLKMSATFI GNSTAIQELFKRISEQFTAMFRRKAFLHWYT	181		
		YFVEWIPNNV+TAVC + P+GL M+ATFI NST+IQELFKR+ +QF+AMF+RKAFLHWYT			
Sbjct	340	YFVEWIPNNVQTAVCSVAPQGLDMAATFI ANSTSIQELFKRVGDQFSAMFKRKAFLHWYT	399		
Query	182	GEGMDEMEFTEAESNMNDLVSEYQQYQD ATEEEGEFEEEEAE	223		
		EGMDE+EF+EAESNMNDLVSEYQQYQ+AT E++ E +E +			
Sbjct	400	SEGMDLEFSEAESNMNDLVSEYQQYQEAT VEDDEEVDENG D	441		

DNA mismatch repair protein MutL [Neisseria meningitidis]

[WP\\_061731970.1](#) 658 1

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

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
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26.2 bits(56) 689 Compositional matrix adjust. 19/66(29%) 33/66(50%) 7/66(10%)  
 Query 52 FAPLTSRGS-QQYRALTVPELTQQMFDAKNMMAACDPRHGRYLTVAAVFRGRMSMKEVDE 110  
 A ++ GS + R LT+PE+ + D +N + +HGR V +++++KE+D  
 Sbjct 599 LATMSCHGSIRAGRRLTLPENALLRDMENPTPRSNQCKHGRPTWV-----KLTLKELDA 652

Query 111 QMLNVQ 116  
 L Q  
 Sbjct 653 LFLRGQ 658

hypothetical protein [Streptococcus pneumoniae]

[WP\\_081509436.1](#) 60 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
23.9 bits(50)	1073	Compositional matrix adjust.	7/15(47%)	12/15(80%)	0/15(0%)
Query 167	FTAMFRRKAFLEHWYT 181				
	++ MF+RK F H+Y+				
Sbjct 40	YSHMFKRKLFTHYYS 54				

tRNA(Met) cytidine acetyltransferase [Haemophilus influenzae]

[WP\\_050948471.1](#) 656 1

[See 6 more title\(s\)](#)

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
24.6 bits(52)	2186	Compositional matrix adjust.	18/60(30%)	31/60(51%)	9/60(15%)
Query 4	YGDLNHLVSATMSGVT-TCLRFPGQLNADLRKLA VNMVFPRLHFFMPGFAPLTSRGSQQ 62				
	Y D+ + + ++ CLR G++ RK +++ P+ P APLTS+GSQ+				
Sbjct 319	YSDITYNIEKNAKNSLFPCLR--GKVPVG-RKGDLDIASSPQ-----PSVAPLTSKGSQE 370				

spore germination protein [Clostridium tetani]

[WP\\_035141345.1](#) 470 1

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

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
24.3 bits(51)	3200	Compositional matrix adjust.	10/20(50%)	14/20(70%)	0/20(0%)
Query 115	VQKNSSYFVEWIPNNVKTA 134				
	++NKNS VE+I NN+ A				
Sbjct 53	IKNKNSILSVEYIKNNIEA 72				



No matches to measles, mumps, rubella, Hepatitis B, polio virus, C. diphtheriae or B. pertussis in the first 1000 results.

ATP2B4

Pmc1p [Saccharomyces cerevisiae YJM1342]

[AJS23320.1](#) 1173 1

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

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
556 bits(1434)	2e-176	Compositional matrix adjust.	399/1120(36%)	573/1120(51%)	230/1120(20%)
Query 76		RRQVFGHNVIPPKPKTFLELVWEALQDVTLIILEIAAIISLVLSFYRPAGEENELCGQV			135
		R + +G N +P + PK+FL+LVW A D T+ +L +AA++S VL Y EL Q			
Sbjct 87		RYKNYGDNSLPERIPKSFLQLVWAAFNDKTMQLLTVAAVVSFVLGLY-----ELWMQP			139
Query 136		AT-TPEDENEAQAGWIEGAAILFSVIVVLTAFNDWSKEKQFRGLQCRIEQEQKFSIIR			194
		PE Q WIEG AI+ +V +VVLV+A ND+ KE QF L + ++ +K +IR			
Sbjct 140		PQYDPEGNKIKQVDWIEGVAIMIAVFWVVLVSAANDYQKELQFAKLNKK-KENRKIIVIR			198
Query 195		NGQLIQLPVAEIVVGDIAQVKYGDLLPADGILIQGNDLKIDESSLTGESDHVKK-----			248
		N Q I + + ++VGD+ ++ GD++PAD ++I G + DESS+TGES+ ++K			
Sbjct 199		NDQEILISIHVHLVGDVLSLQTDGDDVADCVMSISGK-CEADESSITGESNTIQKFPVDNS			257
Query 249		-----SLDK-----DPMLLSGTHVMEGSGRMVTVAVGVNSQT			280
		S+D D ML+SG+ ++ G GR V+T+VG+NS			
Sbjct 258		LRDFKKFNSIDSHNHSKPLDIGDVNEDGNKIADCMLISGSRIISGLGRGVITSVGINSVY			317
Query 281		GIIITLLGVNEDDEGEKKKKGKQGVPENRNKAKTQDGALEIQPLNSQEGIDNEEKDKK			340
		G +T +L +P			
Sbjct 318		GQTMT-----SLNAEP-----			328
Query 341		AVKVPKKEKSVLQGKLRVAVQIGKAGLLMSALTVFILILYFVIDNFVNRRLPWLPECTP			400
		E + LQ L++LA I G + SA+ +F L+L+ ++I + P			
Sbjct 329		-----ESTPLQLHLSQLADNISVYGCV-SAILLF-LVLFTRYLFYIIPEDGRFHDLDP			379
Query 401		IYI-QYFVKFFIIGITVLVAVPEGLPLAVTISLAYSVKMMKDNLVRHLDACETMGNA			459
		F+ FI ITV+VVAVPEGLPLAVT++LA++ +M KD NLVR L +CETMG+A			
Sbjct 380		AQKGSKFMNIFITSITVIVVAVPEGLPLAVTLALAFATTRMTKDGNLVRLRSCETMGSA			439
Query 460		TAICSDKTGTLTMRMTVVQAYIGGIHY-----RQIPSPDVFVLPKVL-----DL			503
		TA+CSDKTGTLT N MTVV+ ++G + R++ S VF DL			
Sbjct 440		TAVCSDKTGTLTENVMTVVRGFLGNSKFDNKSPLVSEQRKLNKSKVFEENCSSSLRNDL			499
Query 504		IVNGISINSAY-----TSKILP-----PEKEGGLPR			529
		+ N + ++A+ SK L + E L +			
Sbjct 500		LNIIVLNSTAFENRDYKKNKNTNGSKNMSKNLSFLDKCKSRLSFFKKNREDDEDQLFK			559

Query 530 QV-----GNKTECALLG---FVTDLKQ-DYQAVRNEVPE----EKLYKVYTFNSVR 572  
 V G+KTE ALL F L+ + Q +R++ E EK+ + F S R  
 Sbjct 560 NVNKGQRQEPFIGSKTETALLSLARFSLGLQPGELQYLRDQPMKFNIEKVVQTIPFESSR 619

Query 573 KSMSTVIRNPNNG-----FRMYSKGASEIILRKC--RILDRKGEAVPFKNKDRDDMVRT 625  
 K V++ G +R + KGA+EI+ + C+ R D E + NK + D  
 Sbjct 620 KWAGLVVYKKEGKKNKPFYRFFIKGAAEIVSKNCSYKRNSDDTLEEINEDNKKKTD---D 676

Query 626 VIEPMACDGLRTICIAIYRDFDDTEPSW-----DNENEILTELTCI-----AVVG 669  
 I+ +A D LR I +A++DF + + SW D ++ + L + ++G  
 Sbjct 677 EIKNLASDALRAISVAHKDFCECD-SWPPEQLRDKDSPNIAALDLLFNSQKGLILDGLLG 735

Query 670 IEDPVRPEVPDAIAKCKQAGITVRMVTGDNINTARAIATKCGILT---PGDDFLCLEGKE 726  
 I+DP+R V +++ +C++AG+TVRMTGDNIT A+AIA C IL+ + + +EG E  
 Sbjct 736 IQDPLRAGVRESVQQCQRAGVTVRMTGDNILTAKAIARNCAILSTDISSEAYSAMEGTE 795

Query 727 FNRLIRNEKGEVEQEKLDKIWPKLRLVARSSPTDKHTLVKGIIDSTVGEHRQVAVTGDG 786  
 F +L +NE+ +I P LRLVARSSP DK LV+ T+ VVAVTGDG  
 Sbjct 796 FRKLTKNER-----IRILPNLRLVARSSPEDKRLLE-----TLKMGDVVAVTGDG 842

Query 787 TNDGPALKKADVGFAMGIAGTDVAKEASDIILTDDNFTSIVKAVMWGRNVYDSISKFLQF 846  
 TND PALK ADVGF+MGI+GT+VA+EASDIIL D+F++IV A+ WGR V SI KF+QF  
 Sbjct 843 TNDAPALKLADVGFSMGISGTEVAREASDIILMTDDFSAIVNAIKWGRCVSVSIKKFIQF 902

Query 847 QLTVNVAIVAVTFTGACITQD--SPLKAVQMLWNLIMDTFASLALATEPPTESLLKRRP 904  
 QL VN+ AVI+ F + + D S L AVQ+LW+NLIMDT A+LALAT+ P +++ R+P  
 Sbjct 903 QLIVNITAVILTFVSSVASSDETSVLTAQQLLWINLIMDTLAALALATDKPDPNIMDRKP 962

Query 905 YGRNKPLISRTMMKILGHAFYQLIVIFILVFAGEKFFDIDSGRKAPLHSPPSQHYTIVF 964  
 GR+ LIS + K IL A QLIV FIL F G + F + H Q + F  
 Sbjct 963 RGRSTSLISVSTWKMILSQATLQLIVTFILHFYGPPELFFKKHEDEITSHQ-QQQLNAMTF 1021

Query 965 NTFVLMQLFNEINSRKIH-----GEKNVFSGIYRNIIFCSVVLGTFICQIF 1010  
 NTFV +Q F + SRK+ N F + RN F +++ CQ+  
 Sbjct 1022 NTFVWLQFFTMLVSRKLEDEGDGISNWRGRISAANLNFFQDLGRNYYFLTIMAIIGSCQVL 1081

Query 1011 IVEFGGKPFSCSLSLSQWLWCLFIGIGELLWGQFISAIP 1050  
 I+ FGG PFS + S W+ + G+ L+ G + P  
 Sbjct 1082 IMFFGGAPFSIARQTKSMWITAVLCGMLSLIMGVLRICP 1121

putative potassium/sodium efflux P-type ATPase%2C fungal-type [Streptococcus pneumoniae]  
[CW164661.1](#) 901 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
364 bits(934)	2e-107	Compositional matrix adjust.	296/988(30%)	463/988(46%)	160/988(16%)
Query 61	SPVEGLSGNPADLEKRRQVFGHNVIPPKKPKTFLELVWEALQDVTLIILEIAAIIISLVLS				120
	+ +GLS A +KR + +G NV+ K K+ +E +D +I+L AA+IS V S				
Sbjct 27	TTTDGLSAQEA--QKRLETYGENVLDEGKKKSLAVKFFEQFKDFMIIIVLLAAAVISAVFS				84
Query 121	FYRPAGEENELCGQVATTPEDENEAQAGWIEGAAILFSVIVVLVTAFNDSKEKQFRGL				180
	++ IL VI+ + + E+ L				
Sbjct 85	H-----DVVDSIIILVVVILNAIFGVIQEAQAEQAEAL				118
Query 181	QCRIEQEQKFSIIRNGQLIQLPVAEIVVGDIAQVKYGDLLPADGILIQGNDLKIDESSLT				240
	+ ++ R+G +I + E+V GDI ++ GD++PAD L++ N LKI+E++LT				
Sbjct 119	KEM--SSPNANVRRDGHVITVKSDELVPGDIVLLEAGDVVPADLRLLEANSLKIEEAALT				176

Query	241	GESDHVKKSL-----DKDPMLLSGTHVMEGSGRMVVTAVGVNSQTGIILTLLGV	289
		GES V+K + D+ M S ++V G G VV VG T +	
Sbjct	177	GESVPVEKEVTILEGTDIGDRINMAYSNSNVTYGRGLGVV--VGTGMNTEV-----	227
Query	290	NEDDEGEKKKKGKKQGVPENRNKAKTQDQVALEIQPLNSQEGIDNEEKDKKAVKVPKKEK	349
		GK G+ + + +T P K+	
Sbjct	228	-----GKIAGMLASEQETET-----PLKQN	247
Query	350	SVLQGKLTRLAVQIGKAGLLMSALTVFILILYFVIDNFVINRRPWLPPECTPIYIQYFVKF	409
		GK+ +A+ + I + FV+ ++N R W +	
Sbjct	248	LNQLGKMLTIAILV-----IAAVMFVVG--MMNGRSW-----IDM	280
Query	410	FIIGITVLVVAVPEGLPLAVTISLAYSVKMMKDNLLVRHLDACETMGNATAICSDKTGT	469
		+ I++ V A+PEGLP VTI LA +KM K N +VR L A ET+G+ ICSDKTGT	
Sbjct	281	LLTSISLAVAAIPEGLPAIVTIIALGTQKMAKKNAIVRKLPVAVETLGGSTDIICSDKTGT	340
Query	470	LTMNRMTVVQAYIGGIHYRQIPSPDVFLPKVLDLIVNGISINSAYTSKILPPEKEGGLPR	529
		LT+N+MTV Y G Q+ S +P D + I +N +KI ++G L	
Sbjct	341	LTLNQMTVEALYTDG----QVLSASTEIPA--DNMALKI-MNFTNDTKI---AQDGS---	388
Query	530	QVGNKTECALLGFVTDLKQDYQAVRNEVPEEKLYKVYTFNSVRKSMSTVIRNPNNGFRMY	589
		+G+ TE AL+ F L + E ++ ++ F+S RK M+TV GGF +	
Sbjct	389	-IGDPTETALVQF--GLDHAFNVTEKVAEPRVAEI-PFSDRKLMTTVHELKTGGFLVS	444
Query	590	SKGASEIILRKCNRILDRKGEAVPFKNKDRDDMVRTVIEPMACDGLRTICIAYRDFDDE	649
		KGA + +L++C IL GE P R ++++T +A LR + +AY+ + +T	
Sbjct	445	VKGAPDELLKRCTEILSN-GETSPLDETRQEILKTNTS-LAKQALRVLGMAYK-YVETI	501
Query	650	PSWDNENEILTELTCIAVVGIEDPVRPEVPDAIAKCKQAGITVRMVTGDNINTARAIATK	709
		P+ + + +LT +VG+ DP R E DA+ K+AGI M+TGD+ +TA AIA +	
Sbjct	502	PAEMSELVEKDLTFAGLVGMIDPERKEAADAVKVAKEAGIRPIMITGDHRDTAEAIAAR	561
Query	710	CGILTPGDDFLCLEGKEFNRLIRNEKEVEQEKLDKIWPKLRVLARSSPTDKHTLVKGII	769
		GI+ GDD + G E N E+ EK ++ V AR SP K +VK	
Sbjct	562	LGIIEGDDDAVITGAELN-----ELSDEKFAQVVGHYSVYARVSPHEKVRIVKAW-	612
Query	770	DSTVGEHRQVVAVTGDGTNDGPALKKADVGFAMGIAGTDVAKEASDIILTDDNFTSIVKA	829
		+ +VVA+TGDG ND PALK AD+G MGI GT+V+K ASD++L DDNF++I+ A	
Sbjct	613	----QQEGKVVAMTGDGVNDAPALKAADIGIGMGITGTEVSKGASDMVLADDNFSTIIVA	668
Query	830	VMWGRNVYDSISKFLQFQLTVNVVAVIVAFTGACITQDSPLKAVQMLWVNLIMDTFASLA	889
		V GR V+ +I K +Q+ L+ N+ V+ F + D+ L V +LW+NL+ DTF ++A	
Sbjct	669	VEEGRKVFNSIQKTIQYLLSANLGEVLTFLFIATMLNWDTLV-VHLLWINLVTDTFPAIA	727
Query	890	LATEPPTESLLKRRPYGRNKPLISRTMMKNILGHAFYQLIVIFI-----LVFAGEKFFDI	944
		L EP ++ P G+ S ++ +++ Q + I ++F +	
Sbjct	728	LGVEPAERDVMSHEPRGKSNFFSGGVLSVVYQGITQGALTLIVYKMSIMFPAHTAANT	787
Query	945	DSGRKAPLHSPPSQHYTIVFNTFVLMQLFNEINSRKHGKKNVFS-GIYRNIIFCSVVLG	1003
		+ +A T+ F T L+QLF+ N + I+ +++F G++RN F +L	
Sbjct	788	NLSAQALYDLQHGDALTMAFATLGLIQLFHAFNVKSIY--QSIFKVLFRNKSFNYGILV	845
Query	1004	TFICQIFIVEFGG--KPFCTSLSLSQW	1029
		+F+ + G FS T L QW	
Sbjct	846	SFLLLAATIVIPGFNDLFSVTHLDAYQW	873

ATPase [Clostridium tetani]

[WP\\_035110785.1](#) 887 1

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

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
348 bits(894)	6e-102	Compositional matrix adjust.	316/988(32%)	471/988(47%)	168/988(17%)
Query 73	LEKRRQVFGHNVI	PKPKPTFLELW	EALQDVTLIILEIA	AAISLVLSFYRPA	GEENELC 132
Sbjct 27	+++ R+ +G N +	K K+ +++E L D+ +	IL AA+IS L	GE ++	
Query 133	GQVATTPEDENEA	QAGWIEGAAILF	SVIIIVLVTA	FNDWSK-EKQFRGL	QCRIEQEQKFS 191
Sbjct 79	-----AIIIFL	VIIILNSVIGVV	QESKAEKALEA	LKKM--STPKAM	116
Query 192	IIRNGQLIQLPVA	EIVVGDIAQVKY	GDLLPADGILIQ	GNDLKIDESSLT	GESDHVKKSLD 251
Sbjct 117	VRREGELREIPSE	EVVPGDIIILDAG	RYVPCDLRLIET	ASLKVEESALT	GESVPV---D 172
Query 252	KDP-MLLSGTHVME	GSGRMVVAVGVNS	QTGIILTLLGVNE	DEGEKKKKGGKQ	GVPENR 310
Sbjct 173	KD ++LSG	TA+G	+ TL		
Query 311	NKAKTQDGVALEI	QPLNSQEGIDNE	-EKDKKAVKVPK	KEKSVLQGKLTR	LAVQIGKAGLL 369
Sbjct 199	--ATYGRGVAIA	VAT----GMDTEI	GKIAKMLDTEEK	NLTPLQKLEELG	KTLGLGALA 251
Query 370	MSALTVFILILYF	IDNFVINRRPWL	PECTPIYIQYFVK	FFIIGITVLVVA	VEGLPLAV 429
Sbjct 252	VCALMFGVGLL-	-----QKRDMF-	-----EMFLIAIS	LAVAAIPEGLPA	IV 290
Query 430	TISLAYSVKMMKDN	NLVRHLDACETMG	NATAICSDKTGTL	TMRMTVVQAYIG	GIHYRQ 489
Sbjct 291	TIVLAMGVQMKIK	NAIVRKLPAVETL	GAVNVICSDKTG	TLTQNKMTVTKFY	-ADTYYG 349
Query 490	IPSPDVFLPKVLD	LIVNGISINSAYT	SKILPPEKEGGL	PRQVGNKTECALL	--GFVTDLK 547
Sbjct 350	ISTLDIEKSGHKLL	LENLILCNDATYSE	-----DKQTDG	PTEIALLEAGYK	YGIK 399
Query 548	QD-----YQAVRNE	VPEEKLYKYVTF	NSVRKSMSTVIR	NPNGGFRMYSKG	ASEIILRKN 602
Sbjct 400	KEELEEVHQRV-N	ELP-----FSD	RKMLTTVNKYD	NEIYVM-TKGAID	NLFNICT 448
Query 603	RILDRKGEAVPFK	NDRDDMVRTVIEP	MACDGLRTICIA	YRDFDDTEPSWD	NENEILTEL 662
Sbjct 449	HVY-RNGEIVELT	EIKNEFMEGA-N	NMSDALRVLGG	AYKKSQDEINSD	---LEG 503
Query 663	TCIAVVGIEDPVR	PEVPDAIAKCKQ	AGITVRMVTGDN	INTARAIATKCG	ILTPGDDFLCL 722
Sbjct 504	TLIGLVGMIDPP	REEVKDSIMECK	SGIKTVMITGDH	KDTALAIKELAI	--AEDKSQAV 561
Query 723	EGKEFNRLIRNEK	GEVEQEKLDKI	WPKLRVLARSS	PTDKHTLVKGI	IDSTVGEHRQVVAV 782
Sbjct 562	FGKELDKM-----	SDEELSQRIDN	LRVRFARVSPEH	KVRIVKAF-----	KEKGNIVSM 608
Query 783	TGDGTNDGPALK	KADVGFAMGIAG	TDVAKASDIIL	TDDNFTSIVKAV	MWGRNVYDSISK 842
Sbjct 609	TGDGVNDAPSLK	IAADVGVAMGIT	GTVDVAKGASD	VILTDDNFSTIV	SAVKEGRNIFNIIK 668
Query 843	FLQFQLTVNVVAV	IVAFGTGACITQ	DSPLKAVQMLW	NLIMDTFASLAL	APEPTESLLKR 902

Sbjct 669 + F L+ N+ +I F + +PL+ + +LWVNI DT +L+L +P ++  
 SIIIFLLSCNIGEIIISLFFAILLGGWPAPLRPIHLLWVNLITDTLPALSLGIDPGDPDMDE 728

Query 903 RPYGRNKPLIS----RTMMKNILGHAFYQL--IVIFILVFAGE-KFFDI---DSGRKAPL 952  
 +P L + ++ N L F L ++ + V+ F + D ++A

Sbjct 729 KPRDPKASLFAGGTGTFILINGLLIGFLTAAAFIVGVKYVTNSTTLFPLIPEDVSKEALT 788

Query 953 HSPPSQHYTIVFNTFVLMQLFNEINSRKIHGEKNVFS-GIYRN-IIFCSVVLGTFICQIF 1010  
 H+ T+ F + QLF+ +N R H +K++F GI+ N + +++LG + I

Sbjct 789 HAQ-----TMAFVLSVSQLFHSLNLR--HPKKSIFQLGIFTNKYLIGAILGIVLQDIV 841

Query 1011 I-VEFGGKPFCTSLSLSQLWLWCLFIGI 1037  
 I + F F L L WL + I

Sbjct 842 ITIPFLANIFKVYDLLLKDWLLVGLSI 869

copper-translocating P-type ATPase [Corynebacterium diphtheriae]

[WP\\_070795185.1](#) 740 1

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

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
76.6 bits(187)	2e-12	Compositional matrix adjust.	63/219(29%)	96/219(43%)	47/219(21%)
Query 644	DFDDTEPSWDNEN----	EILTELTCIAVVGIEDPVRPEVPDAIAKCKQAGITVRMVTGDN	699		
	+ DT +W	I+ + I V +ED +RPE A+ + G+ V M+TGD			
Sbjct 501	ELTDTTSAWTGRGAGVLHIVRDGQIIGAVAVEDKIRPESRAAVKALQDRGVKAMITGDA		560		
Query 700	INTARAIATKCGIILTPGDDFLCLEGKEFNRLIRNEKGEVEQEKLDKIWPKLRVLARSSPT		759		
	A+A+ GI	EV E L P			
Sbjct 561	QQVAQAVGQDLGI-----	DEVFAEVL-----PQ	583		
Query 760	DKHTLVKGIIDSTVGEHRQVAVTGDGTNDGPALKKADVGFAMGIAGTDVAKEASDIILT		819		
	DK T V + D +	VA+ GDG ND PAL +ADVG A+G AGTDVA E++ ++L			
Sbjct 584	DKDTKVTQLQDRGLS-----	VAMVGDGVNDAPALTRADVIGIAIG-AGTDVAMESAGVVLA	637		
Query 820	DDNFTSIVKAVMWGRNVYDSISKFLQFLTVNVVAVIVA		858		
	D+ +++ + + Y + + L +	N++AV +A			
Sbjct 638	SDDPRAVLSMIELSQASYRKMIQNLIWASGYNILAVPLA		676		

membrane transport ATPase [Bordetella pertussis]

[CFN98132.1](#) 184 1

[See 6 more title\(s\)](#)

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
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74.3 bits(181) 2e-13 Composition-based stats. 61/219(28%) 90/219(41%) 53/219(24%)

Query 670 IEDPVRPEVPDAIAKCKQAGITVRMVTGDNINTARAIATKCGILTPGDDFLCLEGKEFNR 729  
 + D ++ A+A + G+ M+TGDN A+A+A + GI D L

Sbjct 1 MADTLKASSAAVADLHRLGVRTLMLTGDNTRAAQAVAAQAGIDEARGDLL----- 51

Query 730 LIRNEKGEVEQEKLDKIWPKLRVLRSSPTDKHTLVKGIIDSTVGEHRQVVAVTGDGTND 789  
 Q+KLD + KL R V + GDG ND

Sbjct 52 -----PQDKLDAVEAKLDPALR-----VGMVGDGIND 78

Query 790 GPALKKADVGFAMGIAGTDVAKEASDIILTDDNFTSIVKAVMWGRNVYDSISKFLQFQLT 849  
 PAL +AD+GFAMG AGT A E +D+ L DD+ I V R + +++ + L

Sbjct 79 APALARADIGFAMGAAGTGTAIETADVALMDDDLRKIGTFVRLSRATHRILTQNIVLALG 138

Query 850 VNVVAVIVAFTGACITQDSPLKAVQMLWVNLIMDTFASL 888  
 + V +++A G LW+ + D ASL

Sbjct 139 IKAVFLVLAMAGQA-----TLWMAVFADVGASL 166

No matches to Hepatitis B, measles, mumps, rubella, polio virus, N. meningitidis or H. influenzae in the first 1000 results.

BMP-1

hypothetical protein [Streptococcus pneumoniae]

[WP\\_055310881.1](#) 127 1

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

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

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
30.4 bits(67)	70	Composition-based stats.	25/67(37%)	32/67(47%)	11/67(16%)
Query 910	EVEEETDCGYDYMELFDGYDSTAPRLGRYCGSGPPEEVYSAGDSVLVKFHSDDTITKKG				969
	+ EE DY ELF+GYD R RY P + GD LV+ + +T GF				
Sbjct 15	KAEEMRRQAIDYQELFEGYD-----RSRRY----PVRLLRHEGD--LVELEATNTGVS				64
Query 970	HLRYTST 976				
	H R+T T				
Sbjct 65	H-RFTDT 70				

hypothetical protein, partial [Neisseria meningitidis]

[WP\\_080179636.1](#) 85 1

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

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.1 bits(61)	221	Composition-based stats.	8/24(33%)	16/24(66%)	0/24(0%)
Query 404	PIVSTDSRLWVEFRSSSNWVGKGF 427				
	P++S D +L+ ++S NW +G+				
Sbjct 19	PVISPDKLYAPYKSGGNWYFEGY 42				

DTW domain protein [Bordetella pertussis STO1-CHOC-0017]

[ETH81502.1](#) 163 1

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

### Alignment statistics for match #1

Score	Expect	Method		Identities	Positives	Gaps
28.1 bits(61)	521	Composition-based stats.		10/23(43%)	13/23(56%)	0/23(0%)
Query	759	TSPNWPDKYPSKKECTWAISSTP	781			
		T P WP ++ CTWA +S P				
Sbjct	4	TPPAWPRSGCARPSCTWASASIP	26			

3-isopropylmalate dehydratase large subunit [Corynebacterium diphtheriae]

[WP\\_082258445.1](#) 480 1

[See 8 more title\(s\)](#)

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

### Alignment statistics for match #1

Score	Expect	Method		Identities	Positives	Gaps
25.4 bits(54)	6756	Compositional matrix adjust.		13/39(33%)	21/39(53%)	7/39(17%)
Query	197	QAISIGKNCDFGIVVHELG-----HVVGFWHEHTRP	228			
		Q ++ KNC++FG+ +H +G H VG T+P				
Sbjct	96	QVETLRKNCEEFVRLHAMGDKKQIVHVGSQLGATQP	134			

surface antigen, partial [Hepatitis B virus]

[AKR80495.1](#) 76 1

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

### Alignment statistics for match #1

Score	Expect	Method		Identities	Positives	Gaps
24.6 bits(52)	2961	Composition-based stats.		11/23(48%)	14/23(60%)	2/23(8%)
Query	87	AVPGNTSTPSCQSTNGQPQRGAC	109			
		+ PGN+S PSC T +P G C				
Sbjct	4	SAPGNSSFPSCCCT--KPTAGNC	24			

myo-inositol 2-dehydrogenase [Clostridium tetani E88]

[AAO35136.1](#) 345 1

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

### Alignment statistics for match #1

Score	Expect	Method		Identities	Positives	Gaps
26.2 bits(56)	4179	Compositional matrix adjust.		8/22(36%)	16/22(72%)	0/22(0%)
Query	266	FDSIMHYARNTF\$RGIFLDTIV	287			
		+S +++A+N +S G+FLD +				
Sbjct	167	IESFLNFAKNNYSGLFLDMAI	188			

hypothetical protein CGSHiR3021\_00447 [Haemophilus influenzae 22.4-21]

[EDK12737.1](#) 78 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.4 bits(54)	1721	Compositional matrix adjust.	12/26(46%)	15/26(57%)	4/26(15%)
Query 313	ARKLYKCPACGETLQDSTGNFSSPEY	338			
	A YKCP CG L+D F +P+Y				
Sbjct 4	AMTSYKCPKCGAELED----	FYTPDY	25		

Ski7p [Saccharomyces cerevisiae YJM1381]

[AJT98873.1](#) 747 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.6 bits(65)	350	Compositional matrix adjust.	16/33(48%)	20/33(60%)	4/33(12%)
Query 954	VLVKFHSDDTITKKGFHLRYTSTKFQDTLHSRK	986			
	VLVK H+ + TTK FH+R K +HSRK				
Sbjct 607	VLVKIHNTEDFTKKQFHIR----	KGDIIHSRK	635		

No matches to measles, mumps, rubella or polio virus in the first 1000 results.

## Adiponectin

hypothetical protein [Neisseria meningitidis]

[WP\\_079453994.1](#) 421 6

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
55.5 bits(132)	3e-07	Compositional matrix adjust.	33/65(51%)	41/65(63%)	0/65(0%)
Query 42	GIPGHPGHNGAPGRDGRDGTPEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQGRK	101			
	G+ G PG G G G DG PGE+GE+G G G KGD GE G G +GP+G G QG++				
Sbjct 64	GLDGLPGA KGDAGPKGADGLPGERGERGADGAKGDKGDTGERGPIGPQGPQGLTGPQQQR	123			
Query 102	GEPGE	106			
	GE G+				
Sbjct 124	GETGQ	128			



collagen triple helix repeat family protein [Streptococcus pneumoniae GA17971]

[EHE09278.1](#) 953 13

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
50.8 bits(120)	2e-05	Compositional matrix adjust.	32/67(48%)	35/67(52%)	0/67(0%)
Query 40	MAGIPGHPGHNGAPGRDGRDGTPEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQG	99			
	+ G G G GA G G G G KGEKGD G G G G GA+G RG G QG				
Sbjct 521	LTGAQGAKEKGAQGERGLTGAQGAKEKGDGRGERGLTGAQGAKEKGAQGERGLTGAQG	580			
Query 100	RKGEPEGE	106			
	KGE G+				
Sbjct 581	AKGEKGD	587			

translation initiation factor IF-2 [Bordetella pertussis]

[WP\\_010930271.1](#) 997 1

[See 349 more title\(s\)](#)

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
30.4 bits(67)	67	Composition-based stats.	14/37(38%)	19/37(51%)	1/37(2%)
Query 30	PLPK-GACTGWMAGIPGHPGHNGAPGRDGRDGTPEK	65			
	P P+ GA +G + G P AP +D + G PG K				
Sbjct 314	PEPQAGALSGTLHKPAGKPATTAAPKKDAKPGAPGAK	350			

transpeptidase [Corynebacterium diphtheriae]

[WP\\_041631009.1](#) 417 1

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

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.1 bits(61)	364	Compositional matrix adjust.	15/31(48%)	21/31(67%)	2/31(6%)
Query 206	EVGDQVWLQ--VYGERNGLYADNDNDSTF	234			
	E G QV ++ +YG+ NG+Y DNDN +TF				
Sbjct 227	EPGTQVTVKADLYGKDLGNGIYGDNDNSATF	257			

type I restriction-modification protein subunit M [Haemophilus influenzae]

[WP\\_048954411.1](#) 673 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.4 bits(54)	2651	Compositional matrix adjust.	15/42(36%)	22/42(52%)	3/42(7%)
Query	195	DQASGSVLLHLEVGDVWLQVYGEGER--NGLYADNDNDSTF	234		
		D+ +G+ + VGD WL YGEG + L A D++ F			
Sbjct	438	DEKTGNTKKEI-VGDTEWLDTYGEGWKKIRKLRASKDSNRDF	478		

neuraminidase, partial [Influenza A virus (A/Ceara/119142/2012(H1N1))]

[AGO02431.1](#) 357 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.8 bits(55)	1816	Compositional matrix adjust.	15/34(44%)	19/34(55%)	3/34(8%)
Query	36	CTGWMAGIPGHPGHNGAPGRDGRDGTPEKGEKG	69		
		C+G++ G HP N PG G + G KGEKG			
Sbjct	214	CSGFLGG---HPPLNDRPGSCGPGSSNGAKGEKG	244		

hypothetical protein H758\_YJM451D00125 [Saccharomyces cerevisiae YJM451]

[AJU65427.1](#) 126 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.0 bits(53)	1955	Compositional matrix adjust.	13/32(41%)	20/32(62%)	2/32(6%)
Query	175	LFKKDKAMLFTYDQYQENNVD--QASGSVLLH	204		
		LF KD+ + F +D+Y+ +D A G+V LH			
Sbjct	14	LFAKDERIRFKHKYKALPIDVRNAEGNVPLH	45		

Uncharacterised protein [Salmonella enterica subsp. enterica serovar Typhi]

[CHZ58626.1](#) 49 1

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

### Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
23.5 bits(49)	2319	Composition-based stats.	7/14(50%)	10/14(71%)	0/14(0%)
Query	149	KFHCNIPGLYFAY	162		
		+ +CN P L+YF Y			
Sbjct	12	RINC NAPQLFYFWY	25		

No matches to measles, mumps, rubella, polio virus, Hepatitis B, C, tetani, influenza B or C in the first 10000 results.

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