

Strong protein sequence alignment between autoantigens involved in maternal autoantibody related autism and vaccine antigens

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Background

Braunschweig et al.^{1,2} identified seven autoantigens involved in maternal autoantibody related (MAR) autism. The origin of these maternal autoantibodies is unknown. We know from Pandemrix induced narcolepsy³ that vaccine antigens can induce autoimmunity due to molecular mimicry. Protein sequence alignment between these MAR autism 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.⁴

As previously described⁵, a BLASTP sequence alignment score of 19.3 was obtained comparing human hypocretin receptor and H1N1 nucleoprotein. This level of sequence alignment was sufficient to cause autoimmunity that resulted in hypocretin dysregulation and narcolepsy.³ 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^{6,7} and HPV vaccines⁸ 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	LDHA	LDHB	CRMP1	CRMP2	PSD95	STIP1	YBX1
Vaccine Antigen							
Saccharomyces cerevisiae	32.5	29.9	31.6	30.3	85.5	328	35.4
Streptococcus pneumoniae	183	180	79.5	97.3	50.3	37.5	81.7
Corynebacterium diphtheriae	168	152	30.3	32.5	32.5	35.4	59.2
Bordetella pertussis		30.8	30.8	32	29.1	34.6	52.0
Clostridium tetani	258	235	106	184	40.1	36.3	74.4
Neisseria meningitidis	31.2	31.2	29.5	29.9	47.3	32.5	49.6
Haemophilus influenzae	29.9	29.5	32	30.8	34.6	31.2	43.9
Measles					28.2		
Hepatitis B	30.3	29.9					27.8*

*This match is for a Hepatitis B core protein. Therefore this match is relevant for autoimmunity induced by Hepatitis B infection but not immunization with a Hepatitis B recombinant vaccine, which should not contain viral core proteins.

Discussion

The results above show strong sequence alignment between MAR autism 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.⁹ 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 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.¹⁰

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

Vaccine design aspects including removal of contaminating proteins¹¹, molecular mimicry and route of administration need to be revisited to avoid such off-target immune responses.

Detailed Results

LDH A

L-lactate dehydrogenase [Clostridium tetani]

[WP_035109151.1](#) 316 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
258 bits(602)	6e-69	150/337(45%)	177/337(52%)	64/337(18%)	
Query	22	KITVVGVGAVGMACAISILMKDLADELALVDVIEDKLGEMMDLQHGSLFLRTPKIVSGK	81		
		KI ++G G VG A +M LA E VD+ +K KGE MDL HG F I+ G			
Sbjct	7	KISIIIGSGFVGSTTAYALMMEGLASEIIVDINKEKAKGEAMDLSHGVSFVKPVDIAG-	65		
Query	82	DYNVTANSKLVIIITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIVSNPVD	141		
		DY T +S VIITAGA GE RL+L+ N IFK I+P VVKYSP LL+VSNPVD			
Sbjct	66	DYEDTKDSDIIVITAGAGPKPGETRLDLINKNYEIFKGIVPEVVKYSPKSILLVSNPVD	125		

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Query 142 ILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGE-----RLGVHPLSCHGWVLGEHGD 195
          ILTYV K SGFP RVIGSG LD RFRYL+GE R VH +LGEHGD
Sbjct 126 ILTYVTYKLSGFPPQERVIGSGTVLDTSRFRYLLGEHFKIDVR-NVHT-----YILGEHGD 179

Query 196 SSVPVWSGMNVAGVSLKTLHPDLGTD--KD--K-----EQWKEVHKQVVEAYE 240
          S + WS N+AG+S D KD K E EV K AYE
Sbjct 180 SEIAAWSLTNIAGISVE-----DYCKDICKGCEGNFKNRIPE---EV-K---NAAAYE 224

Query 241 VIKLKGYTSSWAIGLSVADLAESIMKN---LRRVHPVSTMIKGLYGIKDDVFLSVPICLG 296
          V KGYTS AI L V E I + L VST+ G YGI +D+++ +P + G
Sbjct 225 VLERKGYTSYAIALAVRRIVEAIRDEDSIL----TVSTLLRGEYGI-NDIYMGIPSVIG 279

Query 297 QNGISDLVK---VTLTSEEEARLKKSADTLWGIQKE 329
          + GI K V L +EE LK SA+ L KE
Sbjct 280 ETGI----KRVLEVKLSKDEEKQLKESAEVL----KE 308

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L-lactate dehydrogenase [Streptococcus pneumoniae]

[CRF99933.1](#) 314 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
183 bits(426)	1e-45	133/333(40%)	153/333(45%)	83/333(24%)	
Query 21		NKITVVGAVGMAC--AISILMKD--LADELALVDVIEDKLGEMMDLQHGSLFLRTPK			76
Sbjct 6		N + VG GAVG C A S M + A+E LVDV E K GE MDL H F P			61
Query 77		IV-SG-----KDYNV TANSKLV IITAGARQQEGESRLNLVQRNVNIFK-----F-			119
Sbjct 62		V SG KD A+ LV+ITAG Q GE RL+LV+ N IFK F			115
Query 120		-IIPNVVKYSPNCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERL			178
Sbjct 116		I LI NPVDILTYV WK SG PK RVIGSG LDSARFRY++G+ L			163
Query 179		GVHPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDK-----DKEQWKEVHK			232
Sbjct 164		V P H + GEHGD PVWS H G K + EQ K			207
Query 233		Q-----VVEAYEVIKLGYSWAIGLS---VADLAESIMKNLRRVHPVSTMIKGL			280
Sbjct 208		Q QEDLDKIFENVRDAAYHIIERKATYYGIGMSLLRV---TKAILNNENSVLTVSAYLEGQ			264
Query 281		YGIKDDVFLSVPICLGQNGISDLVKVTLTSEEE		313	
Sbjct 265		YG K D + VP + G+ + V L EEE		295	

L-lactate dehydrogenase [Corynebacterium diphtheriae]

[WP_071575789.1](#) 318 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
168 bits(390)	5e-41	134/351(38%)	161/351(45%)	91/351(25%)	
Query 21	NKITVVGAVGAVGMACAISILMKDLADE-----LALVDVIEDKLGEMMDLQHG-----SL				70
	NK+ +G G VG A A L ++ LA +D+ E KL G MDL HG S				
Sbjct 7	NKVVLIGAGDVGAYAYA-----LVNQGTVDHLAIIIDIDEKKLEGNVMDLNHGCVWASS-				60
Query 71	FLRTPKIVSGKDYNVTANSK-----LVIIITAGARQQEGESRLNLVQRNVNIFKFI				120
	RT K+ SK V+I AGA Q GE RL LV N I K I				
Sbjct 61	--RT-KV-----SKGTYADCEDAAVVVICAGAAQKPGETRLQLVDKNMKIMKSI				106
Query 121	IPNVVKYSPNCKL-----LIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLM				174
	+ NV+ N L+ SNPVDILTY WK SGF RVIGSG LDSARFRY++				
Sbjct 107	VDNVI---AN---NFDGIFLVASNPVDILTYAVWKYSGFDHHRVIGSGTVLDSARFRYML				160
Query 175	GERLGVHPLSCHGWLGEHGDSSVPVWVSGMNVAGVSL-----KTLHPDLGTDKDKEQWKE				229
	GER V P S H + GEHGD PV S VAGVS+ K P L E+ E				
Sbjct 161	GERYDVAPSSIHAYIIEGEGDTELPVLSATVAGVSMRRQLQK--NPGL-----EE--E				210
Query 230	VHK---QVVESAYEVIKLGKGYTSWAIGLSVADLAESIMKNLR--R--VH-----PVSTM				276
	K + + AY +I KG TS IG+ A R R +H PVS				
Sbjct 211	LEKIFEETRDAAYTIIDAKGSTSYGIGMGLA-----RITRAIHNQEVALPVSAY				260
Query 277	IKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEEEARLKKADTLWGIQ 327				
	G YG +D++ P + GI V LT E R SA+TL +Q				
Sbjct 261	LEGQYG-QEDIYIGTPAVINRAGINRVVELELTAHEMERFIHSANTLREVQ 310				

phosphopantothenate synthase [Neisseria meningitidis]

[WP_049331224.1](#) 392 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
31.2 bits(66)	49	21/56(38%)	21/56(37%)	30/56(53%)	
Query 43	DLADELALVDVIEDKLGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKLVIIITAGA				98
	DLAD L ED L TPK SGK K V ITAGA				
Sbjct 168	DLADLL-----ED-----LWTPKLLSGK-----K-VLITAGA				193

polymerase, partial [Hepatitis B virus]

[AIE48321.1](#) 791 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
30.3 bits(64)	91	9/13(69%)	10/13(76%)	0/13(0%)	
Query 64	DLQHGSFLRTPK 76				
	+LQHG LFL T K				
Sbjct 126	ELQHGRFLFKTSK 138				

peptidylprolyl isomerase [Haemophilus influenzae]
[WP_049379987.1](#) 625 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
29.9 bits(63)	121	14/33(42%)	16/33(48%)	15/33(45%)
Query 98	AR-QQEGES	-----RLNLVQRNVN		115
	AR QQEGES		R NL+QR V+	
Sbjct 66	ARAQQEGESFLAKTDSVEFVTALRQNLIQRLVD			98

Mcm10p [Saccharomyces cerevisiae Lalvin QA23]
[EGA82434.1](#) 458 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
32.5 bits(69)	20	15/27(56%)	18/27(66%)	5/27(18%)
Query 296	GQNGISDLVKVT---	LTSEEEARLKKS		319
	G+NG + +K T L	SEEE RLKKS		
Sbjct 260	GENGF-NIIKTRKRL-	SEEEERLKKS		284

STIP1

Sti1p [Saccharomyces cerevisiae YJM1386]
[AJU00305.1](#) 589 3

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
328 bits(766)	5e-89	236/603(39%)	274/603(45%)	155/603(25%)
Query 37	NHVLYSNRSAAYA--KK----	GDYQKAYEDGCKTVDLKPDWKGYSRKA	-----LE	83
	NHVLYSNRSA Y KK D A E C V P W KGY R AA L+			
Sbjct 39	NHVLYSNRSACYTSLKKFSDALND--ANE--C--VKINPSWSKGYNRLGAAHLGLGDLD			91
Query 84	FLNRFEEAKRITYEEGLKHEANNPQLKEGL-----	QNMEARLAERKFMNP-----FNM		130
	EA Y L +A N KEGL Q +AR A+ P F			
Sbjct 92	-----EAESNYKKALELDASNKAAKEGLDQVHRTQ--QARQAQ----	PDLGLTQLFAD		138
Query 131	PNLYQKLESDPRTRTLLSDPTYRELIEQL--RNKPS----	DLGTLQDPRIMTTLVLL		183
	PNL + L +P T ++ DP +L+ L P DL T DPR MT + L+			
Sbjct 139	PNLIENLKKNPKTSEMMKDP---QLVAKLIGYKQNPQAIGQDLFT--DPRLMTIMATLM			192
Query 184	GVDLGSMD-----EEEIATP-----PPP-----	PPP		214
	GVDL MD+ E E P P K E K EPM			
Sbjct 193	GVDL-NMDDINQSNSMPKEPETSKEQKKAEPQSDSTTSKENS	KAPQKEESKESEPM		251

Query 215 E--EDLPENKKQALKEKELGNDAYKKKDFDTALKHYDKAKELDPTNMTYITNQAAVYFEK 272
 E ED + K +A KEK GN YK FD A HY+KA EL + TY N AA +EK
 Sbjct 252 EVDED--DSKIEADKEKAEGNKFYKARQFDEAIEHYNKAWELH-KDITYLNNRAAAEYEK 308

Query 273 GDYNKCRELCEKAI-----EVGRENREDYRQIAKAYARIGNSYFKEEKYKDAIHFYNK 325
 G+Y E AI E GRE R DY I K +ARIGN Y K K I +Y K
 Sbjct 309 GEY-----ETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGLDKKTIEYYQK 361

Query 326 SLAEHRTPDVLKCCQQAELK--EQRERLAYINPDLA---LEEKNKGNECFQKGDYPQA 379
 SL EHRT D+L K AEK LK E E AY+NP+ A LE G E F K D P A
 Sbjct 362 SLTEHRTADILTKLRNAEKELKAEAE--AYVNPEKAEERLE----GKEYFTKSDWPNA 415

Query 380 MKHYTEAIKRNPDKAKLYSNRAACYTKLLEFQLALKDCEECIQLEPTFIKGYTRKAAALE 439
 K YTE IKR P DA YSNRAA KL+ F A DC I+ +P F+ Y RKA A
 Sbjct 416 VKAYTEMIKRAPEDARGYSNRAAALAKLMSFPEAIADCNKAIEKDPNFVFRAYIRKATAQI 475

Query 440 AMKDYTKAMDVYQKALDLD-----SSCKE-----AADGYQRCMMAQY---N 477
 A K+Y A++ LD SS E A QR +
 Sbjct 476 AVKEYASALET-----LDAARTKDTEVNGSSAREIDQLYYKASQ--QR-----FQPGT 522

Query 478 RHDSPEDVKKRRAMADPEVQQIMSDPAMRLILEQMOKDPQALSEHLKNPVIAQKIQLMDV 537
 + PE+ RAM DPEV IM DP M IL+Q Q +P AL EH+KNP + KI Q L
 Sbjct 523 SNETPEETYQRAMKDPEVAAIMQDPVMQSLQQAQNPAAALQEHEMKNPEVFKKIQTILIAA 582

Query 538 GLI 540
 G I
 Sbjct 583 GII 585

SPOR domain-containing protein, partial [Bordetella pertussis]

[WP_055311347.1](#) 154 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
34.6 bits(74)	6.7	13/22(59%)	13/22(59%)	5/22(22%)
Query 197	ATPP-----PPPPPKKETKPEP	213		
	ATPP PP PK E KPEP			
Sbjct 20	ATPPQAATPPAAPKPEAKPEP	41		

DNA polymerase III subunits gamma and tau [Corynebacterium diphtheriae bv. intermedius str. NCTC 5011]

[EIK57148.1](#) 670 3

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
35.4 bits(76)	4.4	15/28(54%)	16/28(57%)	4/28(14%)
Query 195	EIATPPPPPPPKKETKPEPMEEDLPENK	222		
	E+A P P P PK E KPEP PE K			
Sbjct 386	EVAAPAPAPEPKPEPKPEPK----PEPK	409		

hypothetical protein [Clostridium tetani]
[WP_023437697.1](#) 393 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
36.3 bits(78)	2.3	20/46(43%)	21/46(45%)	16/46(34%)	
Query 224	QALKEK	---ELGNDAY	-----KKKDFDTALK	-----HYDKAKE	253
	QAL EK	E N AY	K K FD ALK	+YDK E	
Sbjct 217	QALLEKIKGEISNIA	YTNADNYLKRKH	FDEALKEIDKALQYDKDNE		262

immunoglobulin A1 protease autotransporter [Haemophilus influenzae]
[WP_005693332.1](#) 1694 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
31.2 bits(66)	86	21/43(49%)	21/43(48%)	12/43(27%)	
Query 194	EEIA	---TPPPPPPKK	KETKPEPME	--EDLPENKKQALK	--EK 229
	EEIA	TP PPP P	T P E E	EN KQ K EK	
Sbjct 1021	EEIARVETP	PPPAP	--AT	---PSETTETVAENSKQESKTVEK	1058

putative PKS biosynthesis protein [Streptococcus pneumoniae]
[COC41047.1](#) 1152 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
37.5 bits(81)	1.0	20/49(41%)	21/49(42%)	23/49(46%)	
Query 212	EPMEE	-----DLPENKKQALKEK	-----E	--LGNDAYK	---KKDFD 242
	EPME+	DLPE	LKEK	E G YK	KDFD
Sbjct 704	EPMEDRLAVVASD	DLPE	-----LKEKLRIFCTEGTIGEGVYKGNVT	KDFD	747

excinuclease ABC subunit A [Neisseria meningitidis]
[CKJ75081.1](#) 755 2

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

Alignment statistics for match #1

Score Expect Identities Positives Gaps
32.5 bits(69) 35 15/22(68%) 16/22(72%) 3/22(13%)
Query 337 KKCQQA EKILKE-QERLAY-IN 356
KK Q AEKILKE ERL + IN
Sbjct 461 KK-QIAEKILKEITERLGFLIN 481

No matches to measles, mumps, rubella, Hepatitis B, or polio.

CRMP1

dihydropyrimidinase [*Clostridium tetani*]

[WP_039261451.1](#) 461 2

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

Alignment statistics for match #1

Score Expect Identities Positives Gaps
106 bits(243) 2e-21 50/102(49%) 55/102(53%) 22/102(21%)
Query 326 LQVTGSGHCPYSTAQKAVGKDNFTLIPEGVNGIEERMT-----VWWDKAVATGKMDEN- 378
LQV HCP+ QK G D F IP G G+E RM V E+
Sbjct 310 LQVVATDHCPFFMEQKRMGIDSFNKIPNGAPGVELRMSLMYTYGVL-----EDR 358

Query 379 ---Q-FVAVTSTNAAKIFNLYPRKGRIAVGSDADVVIWDPDK 416
Q FV VTSTNAAKIF +YP KG IAVGSDAD VI DP+K
Sbjct 359 ISLQRFVEVTSTNAAKIFGMYPQKGTIAVGSDADLVIFDPNK 400

dihydroorotase [*Streptococcus pneumoniae*]

[CWH90672.1](#) 457 2

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

Alignment statistics for match #1

Score Expect Identities Positives Gaps
79.5 bits(180) 2e-13 73/209(35%) 89/209(42%) 60/209(28%)
Query 65 VIPGGIDVNTYLQ---KPSQGMTAADDFFQGTRAALVGGTTMIIDHVVPPEGSSL---L 117
V PG ID TL+ KS + AD+F G AA GTT +ID P G SL L
Sbjct 50 VLPGFIDAHTHLELNNKGKS--LSTADNFTTGSQAAVAKGTTTVIDMATPNKGGSLKDCL 107

Query 118 TSFEKWHEAADTKSCCDYSLHVDITSWYDGVV-----EELEVLVQDK---GVNSFQVYMA 169
W + A+ KS CDY H W E +Q+ G+ SF YMA
Sbjct 108 AT---WNQLAEGKSSCDYTYHMSMIEW---KPTIAAE-----IQEMIAAGITSFKMYMA 155

Query 170 YKD VYQMSDSQLYEAFTFLK-----G-LGAVILVHAENGDLIAQEQRILEMGITG--P 220
Y + D + +EA +K G LG VH ENGD L+ E + I
Sbjct 156 YDNL-RTTDAEIFEA---MKEIKVNGMLG---VHCENGD LVD-----EL-IQSYVS 199

Query 221 EG-----HALSRPEELEAEAVFRAITIA 243
+G H LSRP EAEAV R IA
Sbjct 200 QGKLTPHYHPLSRPAAVEAEAVARYLMIA 228

Probable type I restriction-modification system specificity determinant [Haemophilus influenzae]
[CWX46791.1](#) 426 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
32.0 bits(68)	48	24/64(38%)	26/64(40%)	30/64(46%)	
Query	9	IPHITS-DRLLIKGGRI-----INDDQSLYADVYLE-----DGLIKQ---IGE	47		
		IP ITS + IKGG I IN+ VYLE D LI IGE			
Sbjct	45	IPYITSKN---IKGGKIDFQNTKYINE-----HVYLELSRTRCIIENDILISMIGTIGE	95		
Query	48	NLIV 51			
		IV			
Sbjct	96	AVIV 99			

Ptk1p [Saccharomyces cerevisiae YJM1400]
[AJS49424.1](#) 660 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
31.6 bits(67)	66	12/15(80%)	12/15(80%)	2/15(13%)	
Query	505	EVPATPKYATPAPSA 519			
		E PATP ATPAPSA			
Sbjct	612	EPPATP--ATPAPSA 624			

enoyl-CoA hydratase/isomerase family protein [Bordetella pertussis]
[CFN74911.1](#) 148 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
30.8 bits(65)	103	14/27(52%)	17/27(62%)	4/27(14%)	
Query	233	AEAVFRAITIAGRIN-CPVYITKVMMSK 258			
		AEA RAI +AGR+ CP + MSK			
Sbjct	82	AEA--RAIEVAGRVSQCPAHVVR-MSK 105			

fructose-bisphosphatase class II [Corynebacterium diphtheriae]

[WP_014308186.1](#) 338 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
30.3 bits(64)	155	18/39(46%)	19/39(48%)	14/39(35%)
Query	395	YPRKGRIAVGSDADVVIWDPDKLKTITAKSHKSAVEYNI	433	
		Y RK IAVGS+A I D I A VEYNI		
Sbjct	128	YMRK--IAVGSEAAGTI-D-----INA-----PVEYNI	152	

ATP-binding protein [Neisseria meningitidis]

[WP_014581964.1](#) 630 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
29.5 bits(62)	290	8/8(100%)	8/8(100%)	0/8(0%)
Query	207	QEQKRILE	214	
		QEQKRILE		
Sbjct	366	QEQKRILE	373	

No matches to measles, mumps, rubella or Hepatitis B viral proteins.

PSD95

Guk1p [Saccharomyces cerevisiae YJM1250]

[AJU88218.1](#) 187 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
85.5 bits(194)	3e-15	63/172(37%)	73/172(42%)	57/172(33%)
Query	535	RPIIILGPT-----KDRANDLLSEFPDKFGSCVPHTTRPKREYEIDGRDYHFVS-	584	
		RPI+I GP K L E+PD FG V TTR R E++G DY FVS		
Sbjct	3	RPIVISGPGSGTGKSTLLKK-----LFAEYPDSFGFSVSSTTRTPRAGEVNGKDYNFVSV	56	

Query 585 ----SREKMEKDIQAHKFIE----AGQYNHLYGTSVQSVREVAEQGKHCILDV----- 630
 S M K+ + FIE G Y YG V SV +V GK CILD+
 Sbjct 57 DEFKS---MIKNNE---FIEWAQFSGNY----YGSTVASVKQVSKSGKTCILDIDMQGVK 106

Query 631 SANAVRRLQAAHLHPIAIFIRPRSLLENV---LE-----INKRITEEQ 670
 S A+ L A L F I P S E+ LE INKR QA
 Sbjct 107 SVKAIPELNARFL-----FIAPPSVEDLKKRLEGRGTETEESINKRLSAAQA 153

guanylate kinase [Neisseria meningitidis]

[WP_055390214.1](#) 205 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
47.3 bits(104) 0.001 48/110(44%) 53/110(48%) 28/110(25%)					
Query 563	VPHTTRPKREYEIDGRDYHFVSSREKMEKDI--QAHKFIE-A---GQYNHLYGTSVQSV	616			
	V H T T R P R E E + G Y H F V S E E I + A F E A G Y Y G T S + V				
Sbjct 38	VSHTTRPPREGEANGVHYHFV-SKEEFESLIAQEA--FLEYADVFVGNV----YGTSAEGV	90			
Query 617	REVAEQGKHCIL--DV---SA---NAVRRLQAAHLHPIAIFIRPRSLLENV	659			
	A E G I L D V A N A L A + I F I P S + V L				
Sbjct 91	NALAEAGYDVILEIDVQGAQVRNA---LPEA---VGIFILPPSF-DVL	132			

guanylate kinase [Clostridium tetani]

[WP_011099447.1](#) 208 2

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
40.1 bits(87) 0.20 46/122(38%) 51/122(41%) 36/122(29%)					
Query 566	TTR-PKREYEIDGRDYHFVSSREKMEKDIQAHKFIE-A---GQYNHLYGTSVQS-VREV	619			
	T T R P R E E I G Y F S E E I F E A G Y Y G T S V E				
Sbjct 37	TTRDP-REGEIQGKSYFM-SKEEFEDKIKENDFLEYAKVYGNV----YGTP-KSKVIEM	89			
Query 620	AEQGKHCILDVSNANAVRRLQAAHLH-----PIAIFIRPRSLLENVLEINKRI-----T	666			
	+ G K I L + + Q A L + I I F I P S + E E R I T				
Sbjct 90	LDKGGKDVILEID-----IQGA-LQVKENYKEGIFIFILPPSME---ELKNRIIKRGTT	139			
Query 667	EE	668			
	EE				
Sbjct 140	EE	141			

zinc metalloprotease [Haemophilus influenzae]

[WP_049379821.1](#) 443 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
36.3 bits(78)	3.2	16/29(55%)	19/29(65%)	1/29(3%)
Query	193	KIIEGGAHKDGRLLQIGDKILAVNSVGL	E	221
		K++E A K G L IGDKILA NS L+		
Sbjct	227	KVVESSPAEKAG-LLIGDKILAENSTALD		254

guanylate kinase [Streptococcus pneumoniae]

[CVX81048.1](#) 207 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
50.3 bits(111)	2e-04	50/133(38%)	55/133(41%)	43/133(32%)
Query	566	TTRPKREYEIDGRDYHFVSSREKME---KDIQAHKFIEAGQYNSHLYGTSVQSVREVAEQ		622
		TTR RE EIDG DY F E E KD Q FIE QY YGT VQ V + E+		
Sbjct	41	TTRHMRERGEIDGVDFYFF-KTKEEFEALIKDDQ---FIEYAQYVGNYYGTPVQYVKDTMEE		96
Query	623	GKHCILDV-----SANAVRR--LQAAHLHPA--IFIRPRSLENVLE-----		660
		G H DV A VR P A IF P SL++ E		
Sbjct	97	G-H---DVFLEIEVEGAKQVRKKF-----PDALFIFLAPPSLDDLKERLVGRGTSDE		145
Query	661	-INKRITEEQARK	672	
		I R+ E ARK		
Sbjct	146	KIQSRVNE--ARK	156	

transcriptional regulator, PadR domain protein [Bordetella pertussis STO1-CHOC-0017]

[ETH82602.1](#) 84 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
29.1 bits(61)	373	12/25(48%)	14/25(56%)	9/25(36%)
Query	619	VAEQGKHCILDVSANAVR----RLQ		639
		+AE +LDV A AVR RLQ		
Sbjct	14	IAE-----VLDVTAEAVRQQMARLQ		33

trigger factor, partial [Corynebacterium diphtheriae]

[WP_021335150.1](#) 305 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
32.5 bits(69)	45	27/65(42%)	31/65(47%)	28/65(43%)	
Query 86	PHIGDDPSIFITKIIPGGAAAQDGRRLRVNDSILFVNEVDVR-EVT---HSA-AVE--ALK				138
	PHI D ITK +D N+ + F EVDVR E+T SA AVE ALK				
Sbjct 91	PHI--D----ITKL-----ED-----NEVVEFTAEDVRPEITVPDFSAFAVEVPALK				132
Query 139	---EA 140				
	EA				
Sbjct 133	SNDEA 137				

nucleoprotein, partial [Measles virus genotype H1]

[AID53682.1](#) 151 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
28.2 bits(59)	794	13/20(65%)	13/20(65%)	3/20(15%)	
Query 249	AYLSDSYAPPDI-TTS-YSQ		266		
	AYL S PPDI T S YSQ				
Sbjct 91	AYLPPTS-TPPIDTASEYSQ		109		

No matches to mumps, polio, rubella or hepatitis B viral proteins.

YBX1

cold shock protein [Streptococcus pneumoniae]

[CVY15617.1](#) 66 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
81.7 bits(185)	1e-15	36/73(49%)	41/73(56%)	21/73(28%)	
Query 61	GTVKWFNVRNGYGFINRNDTKE---DVFVHQTAI-----KKNNPRKYLRVSGDGETVEFD				112
	GTVKWFN G+GFI R E DVFVH AI K S +G+ VEFD				
Sbjct 4	GTVKWFNAEKGFGERIER---ENGGDVFVHFS AIVEDGYK-----SLEEGQSV EFD				50
Query 113	VVEGEKGAEAA NV 125				
	+VEGE G +AANV				
Sbjct 51	IVEGERGEQAANV 63				

cold-shock protein [Clostridium tetani]

[WP_023437243.1](#) 67 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
74.4 bits(168)	3e-13	35/70(50%)	42/70(60%)	14/70(20%)	
Query 61	GTVKWFNVRNGYGF	INRNDTKE	-----DVFVHQ	TAIKKNNPRKYL	RSVGDGETVEFDVVE 115
	GTVKWFN	G+GFI	E	DVFVH TAI	+ PRK L +GE V+F+V +
Sbjct 4	GTVKWFNSEKGF	GFI	-----EVEGED	DVVFHFTAI	QSDSPRKNL---EEGEKVQFEVEQ 54
Query 116	GEKGAEAA	NV 125			
	G KG	+A NV			
Sbjct 55	GPKGLQAS	NV 64			

cold-shock protein [Corynebacterium diphtheriae]

[WP_003850453.1](#) 67 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
59.2 bits(132)	3e-08	29/62(47%)	34/62(54%)	4/62(6%)	
Query 61	GTVKWFNVRNGYGF	INRNDTKED	VFVHQ	TAIKKNNPRKYL	RSVGDGETVEFDVVEGEKGA 120
	GTVKWFN	G+GFI	D	DVFVH I N	R + + VEF+V EG KG
Sbjct 4	GTVKWFNAEKGF	GFI	APEDG	SADVFVHYSEI	QNGG---FRTLEENQKVEFEVGEKAKGP 59
Query 121	EA	122			
	+A				
Sbjct 60	QA	61			

cold-shock protein [Bordetella pertussis]

[WP_010931694.1](#) 68 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps		
52.0 bits(115)	8e-06	31/65(48%)	37/65(56%)	8/65(12%)		
Query 61	GTVKWFNVRNGYGF	I	NRNDTKED	VFVHQ	TAIKKNNPRKYL	RSVGDGETVEFDVVEGEK 118
	G VKWFN	GYGFI	+ T	DVF H AI	R Y RS +G+ VEF+V + K	
Sbjct 5	GKVKWFNADKGY	GFI	FITPDSGGT	---DVF	AHFSAI---QGRGY-RSLNEGQVEFEVKDVPK 58	
Query 119	GAEAA	123				
	G +AA					
Sbjct 59	GPQAA	63				

cold shock domain protein CspD [Haemophilus influenzae]

[WP_050847617.1](#) 72 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
43.9 bits(96)	0.003	26/64(41%)	34/64(53%)	8/64(12%)
Query 61	GTVKWFNVRN	--GYGFINRNDTKEDV	FVHQTAIKKNNPRKYLRSV	GDGETVEFDVVEGEK 118
	G VKWFN N	G+GFI	D+F H I +	Y RS G+ V+F+V+ G+K
Sbjct 4	GIVKWFN	--NAKGFGEISAEGVDADIF	AHYSVIEMDG	---Y-RSLKAGQKVQFEVIHGDK 57
Query 119	GAEA	122		
	G A			
Sbjct 58	GSHA	61		

Ume6p [*Saccharomyces cerevisiae* Vin13]

[EGA79399.1](#) 615 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
35.4 bits(76)	2.5	16/26(62%)	16/26(61%)	6/26(23%)
Query 14	PPAAPALSAADTKPGTT	--GSGAGSG	37	
	PP APA S	PGTT GSGAG G		
Sbjct 210	PPQAPAVSS	---PGTTAAGSGAGTG	231	

truncated core protein [*Hepatitis B virus*]

[ABY65690.1](#) 181 3

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
27.8 bits(58)	474	9/11(82%)	9/11(81%)	1/11(9%)
Query 147	RYPRRRG	P-R 156		
	RYPRRR	P PR		
Sbjct 154	RYPRRRT	PSPR 164		

Chain A, Crystal Structure Of The Cold Shock Domain Protein From *Neisseria Meningitidis*

[3CAM_A](#) 67 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
46.9 bits(103) 3e-04 31/74(42%) 38/74(51%) 15/74(20%)				
Query	56	ATKVLGTVKWFNVRNGYGFINRNDTKEDVFVHQTAIK-----KNNPRKYLRVSGDGETVEF	111	
		AT G VKWFN G+GFI ++ ED F H AI K L +G+ V F		
Sbjct	2	AT---GIVKWFNDAKGFGFITPDEGGEDLFAHFSAINXEGFKT-----LK---EGQRVSF	50	
Query	112	DVVEGEKGAEAA NV 125		
		DV G KG +AAN+		
Sbjct	51	DVTTGPKGKQAANI 64		

No matches to measles, mumps, rubella or polio viral proteins.

LDH B

L-lactate dehydrogenase [Clostridium tetani]

[WP_035109151.1](#) 316 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
235 bits(547) 1e-61 134/298(45%) 162/298(54%) 38/298(12%)				
Query	45	LADELALVDVLEDKLGEMMDLQHGSLFLQTPKIVADKDYSVTANSKIVVVTAGVRQQEG	104	
		LA E VD+ +K KGE MDL HG F I+A DY T +S IV++TAG G		
Sbjct	29	LASEIVIVDINKEKAKGEAMDLSHGVSFVKPVDIAG-DYEDTKDSDIVIITAGAGPKPG	87	
Query	105	ESRLNLVQRNVVFKFIIPQIVKYSPODCIIIVVSNPVDILTYVTWKL SGLPKHRVIGSGC	164	
		E RL+L+ N +FK I+P++VKYSP I VVSNPVDILTYVT KLSG P RVIGSG		
Sbjct	88	ETRLDLINKNYEIFKGIVPEVVKYSPKISILLVSNPVDILTYVTYKLSGFPQERVIGSGT	147	
Query	165	NLDSARFRYLMAE--KLG IHPSSCHGWILGEHGDS SVAWVSGVNVAGVSLQ-----	213	
		LD RFRYL+ E K + H ILGEHGDS +A WS N+AG+S +		
Sbjct	148	VLDTSRFRYLLGEHFKIDVR--NVHTYILGEHGDS EIAAWSLTNIAGISVEDYCKDICKG	205	
Query	214	-ELN-----PEMGTDNDS ENWKEVHKM VVESAYEVIKLG YTNWAI GLSVADLIESMLKN	267	
		E N PE EV K AYE V KGYT AI L V +E +		
Sbjct	206	CEGNFKNRIPE-----EV-K---NAAYEVLERKGYTSYAIALAVRRIVEAIRD	250	
Query	268	LSRIHPVSTMVKGMYGIENEVFLSLPCILNARGLT SVINQKL-KDDEVAQLKKSADTL	324	
		I VST+ G YGI N++++ P + G V KL KD+E QLK SA+ L		
Sbjct	251	EDSILTVSTLLRGEYGI-NDIYMGIPSVIGETGIKRVLEVKLSKDEE-KQLKESAEVL	306	

L-lactate dehydrogenase [Streptococcus pneumoniae]

[CKE55230.1](#) 314 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
180 bits(417)	1e-44	94/196(48%)	107/196(54%)	28/196(14%)	
Query 22		NKITVVGVGQVGMAC--AISILGKSLADELALVDVLEDKLGEMMDLQHGSFLQTPKIV			79
Sbjct 6		N + VG G VG C A S A+E LVDV E K GE MDL H F P V			63
Query 80	-----AD-KDYSVTANSKIVVVTAGVRQEGESRLNLVQRNVNVFKFIIPQIVK-----				127
Sbjct 64	WSGSYADCKD----AD--LVVITAGLPQKPGETRLDLVEKNTKIFK----QIVRGIMDSG				113
Query 128	YSPDCIIIVSNPVDILTIVTWKLSGLPKHRVIGSGCNLDSARFRYLMAEKLGIHPSSCH				187
Sbjct 114	F--DGIFLIATNPVDILTIVTWKESGLPKERVIGSGTTLDSARFRYMLGDYLDVDPNRVH				171
Query 188	GWILGEHGDSVAVWS	203			
Sbjct 172	AYIVGEHGDTLPVWS	187			

L-lactate dehydrogenase [Corynebacterium diphtheriae]

[WP_004567410.1](#) 318 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps	
152 bits(353)	3e-36	130/340(38%)	154/340(45%)	69/340(20%)	
Query 22		NKITVVGVGQVGMAC AISILGKSLADELALVDVLEDKLGEMMDLQHGSFLQTPKIV--			79
Sbjct 7		NK+ +G G VG A A D LA +D+ E KL G MDL HG +V			58
Query 80	-----AD-KDYSVTANSKIVVVTAGVRQEGESRLNLVQRNVNVFKFIIPQIVK				127
Sbjct 59	SSRTKVSFGTYADCEAAV-----VVICAGAAQKPGETRLQLVDKNMKIMKSIVDNVMA				112
Query 128	YSPDCIIIVSNPVDILTIVTWKLSGLPKHRVIGSGCNLDSARFRYLMAEKLGIHPSSCH				187
Sbjct 113	NNFDGIFLVASNPVDILTIVTWKSGFHHRVIGSGTVLDSARFRYMLGERYDVAPSSIH				172
Query 188	GWILGEHGDSVAVWVSGVNVAGVS----LQELNPEMGTDNDSENWK---EVHKMVVESAY				240
Sbjct 173	AYIIEHGDTLPVLSATVAGVSMRRQLQK-NP--GLEEELE--KIFEETR----DAAY				223
Query 241	EVIKLKGTYNWAIGLSVADLIESMLKNLSR-----IH-----PVSTMVKGMYGIENEVF				289
Sbjct 224	TIIDAKGSTSYGIG-----M--GLARITRAIHNQEVALPVSAYLEGQYGQE-DIY				271

Query 290 LSLPCILNAR-GLTSVINQKLKDEVAQLKKSADTLWDIQ 328
P + N R GL V+ L E SA+TL ++Q
Sbjct 272 IGTPAVIN-RGGLNRVVELELTAHEMERFIHSANTLREVQ 310

zinc protease [Bordetella pertussis]

[CRE05023.1](#) 338 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
30.8 bits(65)	65	12/18(67%)	13/18(72%)	1/18(5%)
Query 38	ISILGKSLADELALV-DV	54		
	IS LGK L D +ALV DV			
Sbjct 4	ISTLGKNLPDVMALVLDV	21		

DDE superendonuclease family protein [Neisseria meningitidis 97027]

[EOB72617.1](#) 93 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	38	13/21(62%)	13/21(61%)	7/21(33%)
Query 166	LDSARFRY----L--MAEKLG	180		
	LD ARF Y L MAEKLG			
Sbjct 26	LDNARF-YRMGVLREMAEKLG	45		

hemoglobin and hemoglobin-haptoglobin binding protein A [Haemophilus influenzae HK1212]

[EFA29506.1](#) 150 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
29.5 bits(62)	144	10/14(71%)	10/14(71%)	2/14(14%)
Query 114	NVNVFKFIIPQIVK	127		
	NVNVF F IP VK			
Sbjct 128	NVNVFSFLIP--VK	139		

polymerase, partial [Hepatitis B virus]

[ALK24765.1](#) 327 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
29.9 bits(63)	117	12/18(67%)	12/18(66%)	0/18(0%)
Query 65	DLQHGSFLQTPKIVADK		82	
	DLQHG L LQT K DK			
Sbjct 8	DLQHGRLLVLTQSKRHGDK		25	

Bfr1p [Saccharomyces cerevisiae FostersO]

[EGA60504.1](#) 428 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
29.9 bits(63)	120	15/28(54%)	16/28(57%)	4/28(14%)
Query 3	TLKEKLIAPVAEEEEATVPNN---KITV		26	
	TL LIA AE + TVP N KITV			
Sbjct 379	TLEPTLIATLAELDVTVPINSDDVKITV		406	

No matches to measles, mumps, rubella, Hep A, HPV or polio viral proteins.

CRMP2

dihydropyrimidinase [Clostridium tetani]

[WP_039261451.1](#) 461 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
184 bits(427)	3e-45	178/488(36%)	197/488(40%)	187/488(38%)
Query 19	IKGGKIVNDDQSFYADIYMED-GLIK-----QIGENLIVPGGVKTIEAHSRMVI-----P		67	
	IK G IV D Y D G IK QIG +L G K I+A I P			
Sbjct 8	IKNGTIVTA-----SDTYKGDIG- IKDGKIVQIGLDLE-SSGKKIIDA-----IGKYIFP		55	
Query 68	GGIDVHTRFQMPDQ-GMT-SADDFQGTKAALAGGTTMIDHVVPEP-GTSLLAAFDQ--		122	
	GGID HT MP G T S DDF GTKAA GGTT I+D V +P G L +			
Sbjct 56	GGIDPHTHMDMP--FGGTFSSDDFLTGTCAAACGGTTTIVDFAV-QPKGKTL----KETT		108	
Query 123	--WREWADSKCCDYSLHVDIS---EWHKGIQEEMEALVKDHGVNSFLVYMAFKDRFQL		176	
	WRE AD K C DY H+ I E I EEM +K+ G SF +M			
Sbjct 109	KIWREKADNKACIDYGIHIAITDMNDE----ILEEMGEIIE-KYSSFKLFMT-----		156	

Query 177 TDCQIYEVLSVI-----RDIGAIQVHAENGDIIEEQQRILD-----LGITG 219
 YE + V RD G I VHAEN + + D L
 Sbjct 157 -----YEGMRVEDDTLMRALMKARDKGGIICVHAEN-----HYVIDYFIKKLLS--- 200

Query 220 PEG-----HVLSRPEEVEAEAVNRAITIANQTNC--PLYITKVMKSSAEV--IAQARK 269
 EG H SRPE E EA RAI A C PLYI V A V I ARK
 Sbjct 201 -EGKTEPKYHAISRPELCEGEAAGRAIKLAE--ICGAPLYI--VHNSCEASVSEIERARK 255

Query 270 KGTVVYGEPIASLG-T-----DGSHYWSKNWAKAAAFVTSPPL----- 307
 G Y PI +G T +G AK +V SPPL
 Sbjct 256 LG---Y--PI---MGETCPQYLLLSYENYEEEGFNG-----AK---YVMSPLRDKK 296

Query 308 -----SPDPTTPDFLNSLLSCGDLQVTGSAHCTFNQAQKAVGKDNFTLIPEGTNGT 358
 S D T LQV HC F QK G D F IP G G
 Sbjct 297 NWEHIWKALSKD--T-----LQVVATDHCPFFMEQKRMGIDSFNKIPNGAPGV 342

Query 359 EERMS-----VIWDKAVVTGKMDEN----Q-FVAVTSTNAAKFVNLPRKGRIAVGSDA 407
 E RMS V E+ Q FV VTSTNAAK+F +YP KG IAVGSDA
 Sbjct 343 ELRMSLMYTYGVL-----EDRISLQRFVEVTSTNAAKIFGMPYQKGTIAVGSDA 391

Query 408 DLVIWDPD 415
 DLVI DP+
 Sbjct 392 DLVIFDPN 399

dihydroorotase [Streptococcus pneumoniae]

[CWH90672.1](#) 457 2

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
97.3 bits(222)	8e-19	90/236(38%)	111/236(47%)	46/236(19%)
Query 65	VIPGGIDVHTRFQMPDQG--MTSADDFQGTKAALAGGTTMIIDHVPEPGTSL--LA 118			
	V PG ID HT ++ + G + AD+F G AA A GTT +ID P G SL LA			
Sbjct 50	VLPGFIDAHTHLEL-NNGKGSLSSTADNFTTGSQAAVAKGTTTVIDMATPNKGGSLKDCLA 108			
Query 119	AFDQWREWADSKSCCDYSLHVDISEWHK-----GIQEEMEALVKDHGVNSFLVYMAFKDR 173			
	W + A+ KS CDY H EW K IQ EM A G+ SF YMA+ +			
Sbjct 109	T--WNQLAEGKSSCDYTYHMSMIEW-KPTIAAEIQ-EMIAA----GITSFKMYMAYDN- 158			
Query 174	FQL--TDCQIYEVLSVIRDIGAIQVHAENGDIIEEQQRILDLGITG--PEG-----H 223			
	L TD +I+E + I + VH ENGD +E L I +G H			
Sbjct 159	--LRTTDAEIFEAMKEIKKVNGLGVHCENGLVDE----L---IQSYVSQGKLTPHYH 208			
Query 224	VLSRPEEVEAEAVNRAITIANQTNCPLYITKV-MS-KSSAEVIAQARKKGTVVYGE 277			
	LSRP VEA EAV R IA + L + V +S K S E + AR G V Y E			
Sbjct 209	PLSRPAAVEAEAVARYLMAEMAD--LSVNIVHLSTKRSLEAVERARQRGQSVYVE 262			

Allantoinase [Saccharomyces cerevisiae]

[ONH77022.1](#) 207 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
30.3 bits(64)	147	21/47(45%)	22/47(46%)	14/47(29%)
Query 398	KGRIAVGSDADLVIWDPDSVKTISAKTHNSL-----EYNIFE			GM 437
	KG IA G DADLV+ D S IS NSS YN GM			
Sbjct 131	KGTIAPGYDADLVVFDTASEHKIS----NSSVYFKNKLTAYN---GM			170

nuclease [Corynebacterium diphtheriae]

[WP_072564720.1](#) 382 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
32.5 bits(69)	36	13/30(43%)	14/30(46%)	11/30(36%)
Query 141	ISEWHKGIQEEMEALVKDHGVNSFLVYMAF			170
	+SEW I EMEAL D Y AF			
Sbjct 64	VSEW---IDAEMEALTDD-----YVAF			82

N-acyl-D-amino-acid deacylase domain protein [Bordetella pertussis I002]

[ETH55497.1](#) 379 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
32.0 bits(68)	48	19/46(41%)	24/46(52%)	10/46(21%)
Query 33	ADIYMEDG----LIKQIGENLIVPGGVKTIEAHSRMVIPGGIDVHT			74
	ADI G LI +IG+ I PG I+A V PG +D+HT			
Sbjct 27	ADI----GVRGALIAEIGD--IAPGAAAEIDARGKIVTPGFVDIHT			66

GntR family transcriptional regulator [Neisseria meningitidis]

[WP_061702841.1](#) 238 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
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29.9 bits(63) 202 18/44(41%) 19/44(43%) 22/44(50%)
 Query 200 ENGDII-A-----EEQQ-----RILDLGITGPEGHVL 225
 EN DII A EE + RILD GIT HVL
 Sbjct 4 ENDDIIHAPTTSSLILEERHSELFRVYARILD-GIT---DHVL 43

cytidine deaminase [Haemophilus influenzae]

[WP_061720754.1](#) 292 1

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

Alignment statistics for match #1

Score	Expect	Identities	Positives	Gaps
30.8 bits(65)	114	10/14(71%)	10/14(71%)	0/14(0%)
Query 236	VNRAITIANQTNCP	249		
	VNRAI ANQ CP			
Sbjct 192	VNRAILAAQSHCP	205		

No matches to Hep A, B, human papillomavirus, measles, mumps, rubella or polio viral proteins.

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