Vaccine induced autoimmunity: The price we pay for a flawed vaccine design and safety process

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Background

In Biotechnology and Safety Assessment (2003)[1], immunotoxicology expert Dr. François Verdier with vaccine maker Aventis Pasteur (now Sanofi Pasteur), writes:
"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."
and
"From these hypothesises (sic), a recommended strategy would be to avoid any vaccine antigen presenting a mimicry with a host antigen involved in an autoimmune disease. Applying this rule, Helicobacter pylori catalase was excluded from the screening of vaccine antigens because first it showed sequence homology with human catalase and second human catalase is reported to be an autoantigen in inflammatory bowel disease".

Method

Human catalase protein sequence was obtained from Uniprot.[2]

BLASTP methodology used for protein sequence alignment was previously described.[3]

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[4,5] and HPV vaccines[6] are produced using this technique. Such vaccines are however, contaminated with all Saccharomyces cerevisiae proteins.

A BLASTP protein sequence alignment check was performed comparing human catalase with vaccine antigens and H. pylori.

Results

BLASTP scores

Autoantigen	Catalase
Vaccine Antigen	
Saccharomyces cerevisiae	464
Streptococcus pneumoniae	569
Corynebacterium diphtheriae	440
Bordetella pertussis	518
Clostridium tetani	26
Neisseria meningitidis	507
Haemophilus influenzae	506
Helicobacter pylori	507

Discussion

The results above show some vaccine antigens have **stronger** alignment to human catalase than H. pylori. Many others have comparable alignment to human catalase as well.
H. pylori catalase was excluded from consideration for a vaccine citing this risk of autoimmunity.

However, we have numerous widely used catalase contaminated vaccines that pose an autoimmunity risk. Using H. pylori catalase in a vaccine risked induction of inflammatory bowel disease (IBD). With S. cerevisiae also showing strong protein sequence alignment to human catalase and with many S. cerevisiae contaminated vaccines, it should come as no surprise that Anti Saccharomyces Cerevisiae Antibodies (ASCA) are observed along with Anti-Neutrophil Cytoplasmic Autoantibodies (ANCA), in IBD patients[7]. ANCA targets include catalase and alpha-enolase.[8] This is evidence that the IBD epidemic and the epidemic of autoimmune diseases in general, are fueled by poorly designed and poorly tested vaccines.

As previously reported[9–12], numerous autoimmune disorders are linked to vaccine antigens or vaccine contaminants due to protein sequence alignment or molecular mimicry.

Action

The vaccine design and test methodology needs a complete overhaul. We need a free market system where vaccine makers have an incentive to improve vaccine safety and effectiveness. We need an independent vaccine safety rating agency like the Insurance Institute for Highway Safety (IIHS) for automobiles. Customers must be able to choose among vaccine brands based on safety rating.

Detailed Results

Catalase

Vegetative catalase [Streptococcus pneumoniae]
 CON08278.1 483 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
569 bits(1467)	0.0	Compositional matrix adjust.	270/472(57%)	345/472(73%)	3/472(0%)

```
Query   27   LTTGAGNPVGDKLNVITVGPRGPLLVQDVVFTDEMAHFDRERIPERVVHAKGAGAFGYFE   86
             LTT  G PVGD  N +T G RGP L+QDV   +++AHF+RER+PERVVHAKGAGA GYFE
Sbjct   6    LTTSWGAPVGDNQNSMTAGSRGPTLIQDVHLLEKLAHFNRERVPERVVHAKGAGAHGYFE   65

Query   87   VTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDLV   146
             VT+D+TKY+KA     +GK+TP+ +RFSTVAGE GSADTVRDPRGFAVKFYTE+GN+D+V
Sbjct   66   VTNDVTKYTKAAFLSEVGKRTPLFIRFSTVAGELGSADTVRDPRGFAVKFYTEEGNYDIV   125

Query   147  GNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFLFSDRGIP   206
             GNNTP+FFIRD I FP FIH+QKR+P+THLK+P  VWDFWSL PESLHQV+ L SDRGIP
Sbjct   126  GNNTPVFFIRDAIKFPDFIHTQKRDPKTHLKNPTAVWDFWSLSPESLHQVTILMSDRGIP   185

Query   207  DGHRHMNGYGSHTFKLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLF   266
               RHM+G+GSHTFK  NA GE V+ K+H+KT+QG+KNL V  AA+++ E+PDY   DLF
Sbjct   186  ATLRHMHGFGSHTFKWTNAEGEGVWIKYHFKTEQGVKNLDVNTAAKIAGENPDYHTEDLF   245

Query   267  NAIATGKYPSWTFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRNPVNYF   326
             NAI  G YP+W Y+Q+M   A T+ F+PFD+TKVW  KDYPLI VG++VL+RNP NYF
Sbjct   246  NAIENGDYPAWKLYVQIMPLEDANTYRFDPFDVTKVWSQKDYPLIEVGRMVLDRNPENYF   305

Query   327  AEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHRLGPNYLHIPVNCPYRARVANY   386
             AEVEQ  F P  + PGI+ SPDKMLQGRLFAY D HR+R+G N+   +P+N   R +V NY
Sbjct   306  AEVEQATFSPGTLVPGIDVSPDKMLQGRLFAYHDAHRYRVGANHQALPINRA-RNKVNNY   364

Query   387  QRDGPMCMQDNQGGAPNYYPNSFGAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAF   446
             QRDG M   DN GG+ Y PNSFG P++ P  + +    G   + ++D+ TQ
Sbjct   365  QRDGQMRFDDNGGGSVYYEPNSFGGPKESPEDKQAAYPVQGIADSVSYDHNDHYTQAGDL   424

Query   447  YVNVLNEEQRKRLCENIAGHLKDAQI-FIQKKAVKNFTEVHPDYGSHIQALL   497
             Y  +++E++R RL ENI   +K  +    I+ + +++F +  P+YG  +   L
Sbjct   425  Y-RLMSEDERTRLVENIVNAMKPVEKEEIKLRQIEHFYKADPEYGKRVAEGL   475
```

catalase, partial [Bordetella pertussis 2356847]

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
518 bits(1333)	3e-179	Compositional matrix adjust.	252/478(53%)	327/478(68%)	2/478(0%)

```
Query   21   AQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVFTDEMAHFDRERIPERVVHAKGAG    80
             A     LTT AG PV D   N +T GPRGP L+QDV F +++AHFDRERIPERVVHAKG+G
Sbjct   31   AMTNKTLTTAAGAPVADNNNTMTAGPRGPALLQDVWFLEKLAHFDRERIPERVVHAKGSG    90

Query   81   AFGYFEVTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTED   140
             A+G F VTHDI++Y++A++F  +GK+TP+ +RFSTVAGE G+AD  RD RGFA+KFYT++
Sbjct   91   AYGTFTVTHDISRYTRARIFAEVGKQTPLFLRFSTVAGERGAADAERDVRGFAIKFYTDE   150

Query   141  GNWDLVGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFLF   200
             GNWDLVGNNTP+FFIRDP+ FP FIH+QKR+P+T+L++    WDFWSL PESLHQV+ L
Sbjct   151  GNWDLVGNNTPVFFIRDPLKFPDFIHTQKRDPKTNLRNATAAWDFWSLNPESLHQVTILM   210

Query   201  SDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDY   260
             SDRG+P  +R  +G+GSHT+  VN  GE Y KFH+K+ QGI   +  +AA L   D +
Sbjct   211  SDRGLPQNYRQQHGFGSHTYSFVNDAGERFYVKFHFKSQQGIACYTDGEAAELVGRDRES   270

Query   261  GIRDLFNAIATGKYPSWTFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNR   320
                RDLF  I  G++P WT  +QVM   +A T+  NPFDLTKVWPH DYPLI VG L LN+
Sbjct   271  AQRDLFQNIEQGQFPRWTLKVQVMPEAEAATYHINPFDLTKVWPHADYPLIEVGVLELNK   330

Query   321  NPVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHRLGPNYLHIPVNCPYR   380
             NP NYFAEVEQ AF P+N+ PGI  SPDKMLQGRLF+Y DTHR+RLG N+  IPVN P R
Sbjct   331  NPENYFAEVEQAAFTPANVVPGIGFSPDKMLQGRLFSYGDTHRYRLGINHHQIPVNAP-R   389

Query   381  ARVANYQRDGPMCMQDNQGGAPNYYPNSFGAPEQQPSALEHSIQYSGEVR-RFNTANDDN   439
                ++ RDG  +  N G   NY PNSFG  +  A E +   G+   R+N   D++
Sbjct   390  CPFHSFHRDGMGRVDGNGGATLNYEPNSFGEWREAKHAAEPPLALDGQAADRWNHRVDED   449

Query   440  VTQVRAFYVNVLNEEQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL    497
                      ++N++Q+++L  NI  H+        IQ++ +++F    P Y + +   L
Sbjct   450  YYSQPGALFRLMNDDQKQQLFGNIGRHMAGVPEEIQRRQLEHFRRADPAYAAGVAKAL    507
```

catalase [Helicobacter pylori]

See 1 more title(s)

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
507 bits(1306)	4e-175	Compositional matrix adjust.	258/480(54%)	328/480(68%)	9/480(1%)

```
Query   28   TTGAGNPVGDKLNVITVGPRGPLLVQDVVFTDEMAHFDRERIPERVVHAKGAGAFGYFEV    87
             TT  G PV D  NVIT GPRGP+L+Q    F +++A FDRERIPERVVHAKG+GA+G F V
Sbjct   9    TTAFGAPVWDDNNVITAGPRGPVLLQSTWFLEKLAAFDRERIPERVVHAKGSGAYGTFTV    68

Query   88   THDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDLVG   147
             T DITKY+KAK+F  +GKKT    RFSTVAGE GSAD VRDPRGFA+K+YTE+GNWDLVG
Sbjct   69   TKDITKYTKAKIFSKVGKKTECFFRFSTVAGEKGSADAVRDPRGFAMKYYTEEGNWDLVG   128

Query   148  NNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFLFSDRGIPD   207
             NNTP+FFIRD I FP FIH+QKR+PQT L +PDMVWDFWS  PESL+QV+++ SDRGIP
Sbjct   129  NNTPVFFIRDAIKFPDFIHTQKRDPQTNLPNPDMVWDFWSNVPESLYQVTWVMSDRGIPK   188
```

```
Query  208  GHRHMNGYGSHTFKLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFN  267
                RHM+G+GSHTF L+NA GE  + KFH++T QG+K+L+ E+AA + + DPD   RDLFN
Sbjct  189  SFRHMDGFGSHTFSLINAKGERFWVKFHFETMQGVKHLTNEEAAEIRKHDPDSNQRDLFN  248

Query  268  AIATGKYPSWTFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRNPVNYFA  327
                AIA G +P W   IQVM    A+ + F+PFD+TK+W  KDYPL+ VG + LN+NP NYFA
Sbjct  249  AIARGDFPKWKLSIQVMPEEDAKKYRFHPFDVTKIWYLKDYPLMEVGIVELNKNPENYFA  308

Query  328  EVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHRLGPNYLHIPVNCPYRARVANYQ  387
                EVEQ AF P+N+ PGI  SPD+MLQGRLF+Y DTHR+RLG NY  IPVN P R    +
Sbjct  309  EVEQAAFTPANVVPGIGYSPDRMLQGRLFSYGDTHRYRLGVNYPQIPVNKP-RCPFHSSS  367

Query  388  RDGPMCMQDNQGGAPNYYPNSFGAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFY  447
                RDG M    G  NY P+S   ++ SA +    +  + F  N D   +  +Y
Sbjct  368  RDGYM-QNGYYGSLQNYTPSSLPGYKEDKSARDPKFNLAHIEKEFEVWNWDYRAEDSDYY  426

Query  448  VN------VLNEEQRKRLCENIAGHLKD-AQIFIQKKAVKNFTEVHPDYGSHIQALLDKY  500
                           L  ++++RL + I G L       I K +++F +  P Y   ++  L+K+
Sbjct  427  TQPGDYYRSLPADEKERLYDTIGGSLAHVTHKEIVDKQLEHFKKADPKYAEGVKKALEKH  486
```

catalase [Neisseria meningitidis]

WP_061727170.1 504 1

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
507 bits(1305)	4e-175	Compositional matrix adjust.	250/473(53%)	326/473(68%)	4/473(0%)

```
Query  27   LTTGAGNPVGDKLNVITVGPRGPLLVQDVVFTDEMAHFDRERIPERVVHAKGAGAFGYFE  86
                LT   G PV D  N +T GPRGPLL QD+    +++A F RE IPER +HAKG+GAFG F
Sbjct  11   LTMNNGAPVADNQNSLTAGPRGPLLAQDLWLNEKLADFVREVIPERRMHAKGSGAFGTFT  70

Query  87   VTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDLV  146
                VTHDITKY++AK+F  +GKKT +  RF+TVAGE G+AD  RD RGFA+KFYTE+GNWD+V
Sbjct  71   VTHDITKYTRAKIFSEVGKKTEMFARFTTVAGERGAADAERDIRGFALKFYTEEGNWDVV  130

Query  147  GNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFLFSDRGIP  206
                GNNTP+FF+RDP  FP + KR+P+T+++     WDFW+L PE+LHQV+ + SDRGIP
Sbjct  131  GNNTPVFFLRDPRKFPDLNKAVKRDPRTNMRSATNNWDFWTLLPEALHQVTIVMSDRGIP  190

Query  207  DGHRHMNGYGSHTFKLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLF  266
                 G+RHM+G+GSHT+  N GE  + KFH++T QGIKNL+ E+AA++  +D +   RDL+
Sbjct  191  AGYRHMHGFGSHTYSFWNEAGERFWVKFHFRTQQGIKNLTNEEAAKIIADDRESHQRDLY  250

Query  267  NAIATGKYPSWTFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRNPVNYF  326
                 AI  G++P WT YIQVM    AE  P++PFDLTKVWP KDYPLI VG+  LNRNP N+F
Sbjct  251  EAIERGEFPKWTMYIQVMPEADAEKVPYHPFDLTKVWPKKDYPLIEVGEFELNRNPENFF  310

Query  327  AEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHRLGPNYLHIPVNCPYRARVANY  386
                A+VEQ AF PSN+ PGI ASPDKMLQ RLF Y D  R+RLG N+  IPVN P R  V +
Sbjct  311  ADVEQSAFAPSNLVPGIGASPDKMLQARLFNYADAQRYRLGVNFRQIPVNRP-RCPVHSN  369

Query  387  QRDGPMCMQDNQGGAPNYYPNSFGAPEQQPSALEHSIQYSGEVRRFNTANDDN--VTQVR  444
                QRDG      N G  P+Y PNSFG +QQP  E  ++ +G+   ++   DD+    +Q R
Sbjct  370  QRDGQGRADGNYGSLPHYEPNSFGQWQQQPDFAEPPLKINGDAAHWDYRQDDDDYFSQPR  429

Query  445  AFYVNVLNEEQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL  497
                A + N++N+ Q++ L  N A  + DA  FI+ + ++N     P YG  +   L
Sbjct  430  ALF-NLMNDAQKQALFGNTAAAMGDAPDFIKYRHIRNCYRCDPAYGESVAKAL  481
```

catalase [Haemophilus influenzae]
 WP_049367712.1 508 1

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
506 bits(1304)	7e-175	Compositional matrix adjust.	251/473(53%)	323/473(68%)	4/473(0%)

```
Query  27   LTTGAGNPVGDKLNVITVGPRGPLLVQDVVFTDEMAHFDRERIPERVVHAKGAGAFGYFE  86
            LT G G PV D  N +T GPRGPLL QD+   +++A F RE IPER +HAKG+GAFG F
Sbjct  15   LTMGNGAPVADNQNSLTAGPRGPLLSQDLWLNEKLADFVREVIPERRMHAKGSGAFGIFT  74

Query  87   VTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDLV  146
            VTHDITKY++AK+F  +GKKT +  RF+TVAGE G+AD  RD RGFA+KFYTE+GNWDLV
Sbjct  75   VTHDITKYTRAKIFSEVGKKTEMFARFTTVAGERGAADAERDIRGFALKFYTEEGNWDLV  134

Query  147  GNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFLFSDRGIP  206
            GNNTP+FF+RDP  FP   + KR+P+T+++    WDFW+L PE+LHQV+ + SDRGIP
Sbjct  135  GNNTPVFFLRDPRKFPDLNKAVKRDPRTNMRSATNNWDFWTLLPEALHQVTIVMSDRGIP  194

Query  207  DGHRHMNGYGSHTFKLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLF  266
             +RHM+G+GSHT+  N GE + KFH++T QGIKNL+ +AA +   D +   RDL+
Sbjct  195  ASYRHMHGFGSHTYSFWNEAGERFWVKFHFRTQQGIKNLTDAEAAAVIANDRESHQRDLY  254

Query  267  NAIATGKYPSWTFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRNPVNYF  326
             AI  G +P WT Y+Q+M    AE  P++PFDLTKVWP KDYPLI VG+  LNRNP N+F
Sbjct  255  EAIERGDFPKWTLYVQIMPETDAEKVPYHPFDLTKVWPKKDYPLIEVGEFELNRNPENFF  314

Query  327  AEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHRLGPNYLHIPVNCPYRARVANY  386
            A+VEQ AF PSN+ PGI ASPDKMLQ RLF Y D  R+RLG NY  IPVN P R  V +
Sbjct  315  ADVEQSAFAPSNLVPGIGASPDKMLQARLFNYADAQRYRLGVNYRQIPVNRP-RCPVHSN  373

Query  387  QRDGPMCMQDNQGGAPNYYPNSFGAPEQQPSALEHSIQYSGEVRRFNTANDDN--VTQVR  444
            QRDG   + N G P+Y PNSF  +QQP  E ++ +G+   ++ NDDN   +Q R
Sbjct  374  QRDGQGRVDGNYGSLPHYEPNSFSQWQQQPDFAEPPLRINGDAAHWDYRNDDNDYFSQPR  433

Query  445  AFYVNVLNEEQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL  497
            A + N++N EQ++ L  N A  + DA FI+ + ++N    P YG  +   L
Sbjct  434  ALF-NLMNPEQKQALFNNTAAAMGDAPEFIKYRHIRNCYWCEPAYGDGVAKAL  485
```


Cta1p [Saccharomyces cerevisiae YJM1342]
 AJU95829.1 515 1

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
464 bits(1194)	5e-158	Compositional matrix adjust.	245/490(50%)	313/490(63%)	13/490(2%)

```
Query  26   VLTTGAGNPVGDKLNVITVGPRGPLLVQDVVFTDEMAHFDRERIPERVVHAKGAGAFGYF  85
            V+T   GNP+ +     +G GPLL+QD   D +AHF+RE IP+R  HA G+GAFGYF
Sbjct  21   VVTNSTGNPINEPFVTQRIGEHGPLLLQDYNLIDSLAHFNRENIPQRNPHAHGSGAFGYF  80

Query  86   EVTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL  145
            EVT DIT   + +F  IGK+T    RFSTV G+ GSADTVRDPRGFA KFYTE+GN D
Sbjct  81   EVTDDITDICGSAMFSKIGKRTKCLTRFSTVGGDKGSADTVRDPRGFATKFYTEEGNLDW  140
```

```
Query  146  VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPE---SLHQVSFLFSD  202
            V NNTP+FFIRDP  FP FIH+QKRNPQT+L+D DM WDF +  PE   ++HQV  LFSD
Sbjct  141  VYNNTPVFFIRDPSKFPHFIHTQKRNPQTNLRDADMFWDFLTT-PENQVAIHQVMILFSD  199

Query  203  RGIPDGHRHMNGYGSHTFKLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGI  262
            RG P  +R M+GY  HT+K  N NG+  Y + H KTDQGIKNL++E+A +++  +PDY
Sbjct  200  RGTPANYRSMHGYSGHTYKWSNKNGDWHYVQVHIKTDQGIKNLTIEEATKIAGSNPDYCQ  259

Query  263  RDLFNAIATGKYPSWTFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRNP  322
            +DLF AI G YPSWT YIQ MT   A+  PF+ FDLTKVWP   +PL VGK+VLN NP
Sbjct  260  QDLFEAIQNGNYPSWTVYIQTMTERDAKKLPFSVFDLTKVWPQGQFPLRRVGKIVLNENP  319

Query  323  VNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHRLGPNYLHIPVNCPYRAR  382
            +N+FA+VEQ AF PS   P  EAS D +LQ RLF+Y D HR+RLGPN+  IPVNCPY ++
Sbjct  320  LNFFAQVEQAAFAPSTTVPYQEASADPVLQARLFSYADAHRYRLGPNFHQIPVNCPYASK  379

Query  383  VAN-YQRDGPMCMQDNQGGAPNYYPN--SFGAPEQQPSALEHSIQYSGEVRRFNTAN---  436
             N   RDGPM +  N G  P Y N  S+   +Q    +H  ++G    ++ A
Sbjct  380  FFNPAIRDGPMNVNGNFGSEPTYLANDKSYTYIQQDRPIQQHQEVWNGPAIPYHWATSPG  439

Query  437  DDNVTQVRAFYVNVLNEE--QRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQ  494
            D +  Q R  Y VL ++  Q+K L  NI H++ A   IQ++A  F V      I+
Sbjct  440  DVDFVQARNLY-RVLGKQPGQQKNLAYNIGIHVEGACPQIQQRAYDMFARVDKGLSEAIK  498

Query  495  ALLDKYNAEK  504
             + +  +A +
Sbjct  499  KVAEAKHASE  508
```

catalase [Corynebacterium diphtheriae]

WP_014311206.1 512 1

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
440 bits(1131)	1e-148	Compositional matrix adjust.	216/486(44%)	302/486(62%)	21/486(4%)

```
Query  28   TTGAGNPVGDKLNVITVGPRGPLLVQDVVFTDEMAHFDRERIPERVVHAKGAGAFGYFEV  87
            T   G PV +  IT GP+G ++ D+  +++AHF+RER+PER  HAKG GAFG   +
Sbjct  22   TRAGGQPVASENISITAGPQGANVLNDLYLIEKLAHFNRERVPERNPHAKGHGAFGELHI  81

Query  88   THDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDLVG  147
            T D+++Y KAK+F+  G  TP+AVRFSTVAGE GS DT RD  GFA++FYT+DGN+D+VG
Sbjct  82   TEDVSQYTKAKLFQK-GTVTPMAVRFSTVAGEKGSPDTWRDVHGFALRFYTQDGNYDIVG  140

Query  148  NNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFLFSDRGIPD  207
            NNTP FF+RD + FP FIHSQKR   + L+D DM WDFW+  PES HQV++L  DRG P
Sbjct  141  NNTPTFFLRDAMKFPDFIHSQKRLGSSGLRDADMQWDFWTRTPESAHQVTYLMGDRGTPK  200

Query  208  GHRHMNGYGSHTFKLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFN  267
             RH +G+GSHT++ +N +G+ V+ K+H+KT QG +  +  +A ++ ++ ++ DY   DL+N
Sbjct  201  TSRHQDGFGSHTYQWINEDGQPVWVKYHFKTRQGWETFTDAEAQEMAGKNADYQREDLYN  260

Query  268  AIATGKYPSWTFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRNPVNYFA  327
```

```
         AI  G +P W   +Q+MTF++AET+ +NPFDLTK W  KDYPLI VG  VLNRNP N+FA
Sbjct  261  AIERGDFPIWDVKVQIMTFDEAETYRWNPFDLTKTWSQKDYPLINVGYFVLNRNPQNFFA  320

Query  328  EVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHRLGPNYLHIPVNCPYRARVANYQ  387
         ++EQ+A DP+N+ PG+  SPD+ML  R FAY D  R+R+GPNY  +P+N P    V  YQ
Sbjct  321  QIEQLALDPANLVPGVGLSPDRMLMARAFAYADAQRYRIGPNYQQLPINQPV-VPVNTYQ  379

Query  388  RDGPMCMQDNQGGAPNYYPNSF--GAPEQQPSALEHSIQYSGEVRRFNT-----------  434
          +GPM   N  AP Y PN F  GA        S    G+ +
Sbjct  380  HEGPMAYHFNPADAPVYTPNRFGKGAGYLDDGQTSSSGATYGQAQDLYVNPDPHGTDLTR  439

Query  435  ------ANDDNVTQVRAFYVNVLNEEQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPD  488
               A DD+  Q    Y V ++ ++R +N+  +       +++    +T+V  +
Sbjct  440  AAYVKHAEDDDFMQAGILYREVYDDAAKERFVDNVTNAMAGVSPETEERVYWYWTQVDEN  499

Query  489  YGSHIQ  494
          G+ I+
Sbjct  500  LGAKIR  505
```

ABC transporter ATP-binding protein [Clostridium tetani]
[WP_011099592.1](#) 397 1

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

[GenPeptGraphics](#)Next MatchPrevious Match

<div align="center">Alignment statistics for match #1</div>

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	3292	Compositional matrix adjust.	21/73(29%)	34/73(46%)	6/73(8%)

```
Query  213  NGYGSHTF-----KLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFN  267
         NG G  T    KL++   VY +   D  K LS + + L+ + + G+ +FN
Sbjct  38   NGAGKTTILRTVSKLLDPIKGTVYIEGENIQDVANKELSKKMSVVLTNK-FNGGLMTVFN  96

Query  268  AIATGKYPSWTFY  280
          +A G+YP  F+
Sbjct  97   VVAMGRYPYTGFF  109
```

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

References

1. Verdier F. Chapter 14 - Preclinical Safety Evaluation of Vaccines A2 - Thomas, John A. In: Fuchs RLBT-B and SA (Third E, editor. San Diego: Academic Press; 2003. p. 397–412.

2. UniProt: the universal protein knowledgebase. Nucleic Acids Res. 2017 Jan 4;45(D1):D158–69.

3. Arumugham V. Significant protein sequence alignment between peanut allergen epitopes and vaccine antigens [Internet]. 2016. Available from: https://www.zenodo.org/record/1034555

4.   Engerix B Package Insert [Internet]. [cited 2016 May 8]. Available from: http://www.fda.gov/downloads/BiologicsBloodVaccines/Vaccines/ApprovedProducts/UCM224503.pdf

5.   Recombivax HB Package Insert [Internet]. [cited 2016 May 8]. Available from: http://www.fda.gov/downloads/BiologicsBloodVaccines/Vaccines/ApprovedProducts/UCM110114.pdf

6.   Gardasil Package Insert [Internet]. Available from: http://www.fda.gov/downloads/BiologicsBloodVaccines/Vaccines/ApprovedProducts/UCM111263.pdf

7.   Mokrowiecka A, Gasiorowska A, Malecka-Panas E. pANCA and ASCA in the diagnosis of different subtypes of inflammatory bowel disease. Hepatogastroenterology. Greece; 2007;54(77):1443–8.

8.   Roozendaal C, Zhao MH, Horst G, Lockwood CM, Kleibeuker JH, Limburg PC, et al. Catalase and alpha-enolase: two novel granulocyte autoantigens in inflammatory bowel disease (IBD). Clin Exp Immunol. England; 1998 Apr;112(1):10–6.

9.   Arumugham V. Strong protein sequence alignment between autoantigens involved in atherosclerosis-related coronary artery disease, cerebral infarction, diabetes mellitus and vaccine antigens [Internet]. 2017. Available from: https://www.zenodo.org/record/1034569

10.   Arumugham V. Strong protein sequence alignment between autoantigens involved in maternal autoantibody related autism and vaccine antigens [Internet]. 2017. Available from: https://www.zenodo.org/record/1034571

11.   Arumugham V. Significant protein sequence alignment between Saccharomyces cerevisiae proteins (a vaccine contaminant) and Systemic Lupus Erythematosus associated autoepitopes [Internet]. 2017. Available from: https://www.zenodo.org/record/1034585

12.   Arumugham V. Significant protein sequence alignment between vaccine antigens and Alopecia Areata associated autoantigen [Internet]. 2017. Available from: https://www.zenodo.org/record/1034591