

BLASTP search results

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BLASTP 2.0MP-WashU [04-May-2006] [linux26-i686-ILP32F64 2006-05-09T11:47:08]

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Reference: 1. Gish, W. (1996-2006) <http://blast.wustl.edu>

2. Shevchenko A, Sunyaev S, Loboda A, Shevchenko A, Bork P, Ens W, Standing KG. (2001), *Anal Chem* 73(9),1917-26:
Charting the proteomes of organisms with unsequenced genomes by MALDI-quadrupole time-of-flight mass spectrometry and BLAST homology searching

[Abstract](#)

Query= query_sequence
(4552 letters)

Echofilter:

>Unfiltered+0

BNPVDZVZR-BGGPVDZVZR-BNPVDZVGAR-BNPVDZVAGR-BPNVDZVZR-BPGGVDZ
VZR-BACZHNZVZR-BACZHNZVZR-BACZHNZVZR-BPVNDZVZR-BVPNDZVZR-BRGPDZ
VZR-BGRPDZVZR-BGGPVDZVGAR-BGGPVDZVAGR-BNPVDGAVZR-BMGYVSGSVGR
-BMGYVSSGVGR-BMGYVSGWGR-BMGYVSGSRR-BMGYVSGSVGR-BVDHVSGSVGR-BM
ZAYTSVGR-BMZAYTSVGR-BMGYVSGSVGR-BMZASTYVGR-BMZASTYVGR-BMGYVS
SRGR-BMGYADGSVGR-BMGYAATSVGR-BMGYVSSGRR-BVDHAATSVGR-BSTYVSGS
VGR-BTSYVSGSVGR-BMGYVCAVGR-BZVMLGHTDDAK-BNLFLGHTDDAK-BZVYGTH
GRNAK-BZVYGTHGRNAK-BZVYPGHTDDAK-BZVYGTHPDDAK-BZVYGPHTDDAK-BA
GVFLGHTDDAK-BGAVFLGHTDDAK-BGGLFLGHTDDAK-BZVFLGHTDWK-BZVFLGHT
DWK-BZVMLGHTDWK-BZVMLGHTDWK-BNLFLGHTDWK-BNLMLGHTDWK-BAGVYGT
HGRNAK-BGAVYGTGHRNAK-BZVYPGHTDWK-BZVYGTGHPDWK-BZVYGPHTDWK-BZV
YMLPVDZVGR-BZVYGTGHPDWK-BZVYGTGHPDWK-NLYPGHTDWK-BYVMLPVADEGGK-BYV
MLPVDZVGR-BYVMLPVADENK-BYVMLPVDZDK-BYVMLPVADSRK-BYVMLPVADW
GK-BYVMLPVADSGVK-BMMLPVADSVGR-BYVMLPVADEGGK-BFDMLPVADSVGR-B
VYMLPVADSVGR-DFMLPVADSVGR-BYVMLPVADAGDK-BYVMLPVADGADK-BYVMLP
VADGSVK-BYVMLPVADADGK-BYVMLPVADGEGK-YVMLPVADDAGK-BYVMLPVADRS
K-BYVMLPVADDZK-BYVMLPVADGGEK-BYVMLPVADNEK-BYVMLPVADGWK-BMML
PVADZDK-BNSGGFNYSSELLK-BNSGGMNYSSELLK-BASGGFNYSSELLK-BASGGMNYS
ELLK-BNSNFNYSSELLK-BNSGGSGGFNYSSELLK-BGGSGGMNYSSELLK-BNSNFNYSZNL
K-BNSNFNYSZNLK-BMSGGFNYSSELLK-BMSGGMNYSSELLK-BZMMADYSELLK-BZMM
ADYSELLK-BZMMWYSEGGGSK-BZMMWYSEGGGSK-BSSGGFNYSSELLK-BSSGGMNYS
ELLK-BYLWNYSELLK-BZMMWYSELLK-BNSNFNYSSEGLK-BNSNGMYSELLK-BAG
MMADYSELLK-BGAMMADYSELLK-BGGSNGMYSELLK-BNSNFNYSSEGLK-BNSNFN
YSEPEK-BZMMWYSENGSK-BGATAVAEYGVYVK-BGATAVAEYGVYVK-BSCAVAEYGV
YVK-BZTAVAEYGVYVK-BSTAVAEYGVYVK-BDCAVAEYGVYVK-BYAVAEYGVYVK
-BSCAVAEYGVYVK-BSCAVAEYGVYVK-BSCAVAEYGVYVK-BSCAVAEYGVYVK-B
CSAVAEYGVYVK-BMSGAVAEYGVYVK-BSTSVAEYGVYVK-BSGMAVAEYGVYVK-BM
GSVAEYGVYVK-BMSGAVAEYGVYVK-BSCAVAEYGVYVK-BSCAVAEYGVYVK-BSCA
VAEYGVYVK-BSCAVAEYGVYVK-BSCAVAEYGVYVK-BSCAVAEYGVYVK-BSCAVAE
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DYSNVDLGLLK-BPELHPDYSNVDLGLLK-BVVLHPDYSNVDLGLLK-BPTLHPDYSNVD
LGLLK-BDTLHPDYSNVDLGLLK-BESLHPDYSNVDLGLLK-BTDLHPDYSNVDLGLLK-
BTPLHPDYSNVDLGLLK-BZSLHPDYSNVDLGLLK-BAGSLHPDYSNVDLGLLK-BSZLH
PDYSNVDLGLLK-BSGALHPDYSNVDLGLLK-BSAGLHPDYSNVDLGLLK-BNTLHPDYS
NVDLGLLK-BASGLHPDYSNVDLGLLK-BTNLHPDYSNVDLGLLK-BTGGLHPDYSNVDL
GLLK-BEPLHPDYSNVDLGLLK-BTFPLCLPSZDYAEVGR-BTMPLCLPSZDYAEVGR-B
VMPLCLPSZDYAEVGR-BMVPLCLPSZDYAEVGR-BETPLCLPSZDYAEVGR-BTEPLCL
PSZDYAEVGR-BDDPLCLPSZDYAEVGR-BVLPLCLPSZDYAEVGR-BGGSGPLCLPSZD
YAEVGR-BFTPLCLPSZDYAEVGR-BMTPLCLPSZDYAEVGR-BNGLPLCLPSZDYAEV
R-BGGGPLCLPSZDYAEVGR-BGGGSPCLCLPSZDYAEVGR-BGGGPLCLPSZDYAEV
R-BCSPCLCLPSZDYAEVGR-BSCPLCLPSZDYAEVGR-BSGNPLCLPSZDYAEVGR-BVM
PLCLPSZDYAEVGR-BMVPLCLPSZDYAEVGR-BTEPLCLPSZDYAEVGR-BETPLCLPS
ZDYAEVGR-BSPVGVZPLLNEHTFCAGLSK-BLAVGVZPLLNEHTFCAGLSK-BALVGVZ
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SPVGVZPLLNEHTFCAGTVK-BSPVGVZPLLNEHTFCAGLSK-BSPVGVZPLLNEHTFC
LGSK-BSPVGVZPLLNEHTFCAVASK-BSPVGVZPLLNEHTFCAVSK-BSPVGVZPLL
NEHTFCATRK-BSPVGVZPLLNEHTFCAZEK-BSPVGVZPLLNEHTFCAEZK-BSPVGVZP

LLNEHTFCARTK-BSPVGVZPLLNEHTFCAVGTK-BSPVGVZPLLNEHTFCAASVK-BSP
 VGVZPLLNEHTFCAVSAK-BSPVGVZPLLNEHTFCAVTGK-BSPVGVZPLLNEHTFCASV
 AK-BSPVGVZPLLNEHTFCATGVK-BSPVGVZPLLNEHTFCASGLK-BSPVGVZPLLNEH
 TFCASL GK-BSPVGVZPLLNEHTFCATVGK-BSPVGVZPLLNEHTFCAGEAK-BSPVGVZ
 PLLNEHTFCAGAEK-BSPVGVZPLLNEHTFCAWAK-BFNGTHNLTSGATLLNEZWLLTGD
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 NLTSGATLLNEZWLLTTAK-BMNGTHNLTSGATLLNEZWLLTTAK-BTCGTHNLTSGATL
 LNEZWLLTTAK-BFNGTHNLTSGATLLNEZWLLASDK-BFNGTHNLTSGATLLNEZWLLG
 TDK-BMNGTHNLTSGATLLNEZWLLASDK-BTCGTHNLTSGATLLNEZWLLASDK-BMNG
 THNLTSGATLLNEZWLLGTDK-BTCGTHNLTSGATLLNEZWLLGTDK-BFNGTHNLTSGA
 TLLNEZWLLAMAK-BFNGTHNLTSGATLLNEZWLLADSK-BFNGTHNLTSGATLLNEZWL
 LGESK-BMNGTHNLTSGATLLNEZWLLAMAK-BTCGTHNLTSGATLLNEZWLLAMAK-BM
 NGTHNLTSGATLLNEZWLLADSK-BTCGTHNLTSGATLLNEZWLLADSK-BMNGTHNLT
 S
 GATLLNEZWLLGESK-BTCGTHNLTSGATLLNEZWLLGESK-BFNGTHNLTSGATLLNEZ
 WLLTGDK-BCTGTHNLTSGATLLNEZWLLTGDK-BNMGTHNLTSGATLLNEZWLLTGDK-
 BNFGTHNLTSGATLLNEZWLLTTAK-BCTGTHNLTSGATLLNEZWLLTTAK-BNMGTHNL
 TSGATLLNEZWLLTTAK-BNFGTHNLTSGATLLNEZWLLTATK-BCTGTHNLTSGATLLN
 EZWLLTATK-BMNGTHNLTSGATLLNEZWLLTATK-BFNGTHNLTSGATLLNEZWLLSAD
 K-BCPDGGLAEGSTVPEK-BCDPGGLAEGSTVPEK-BCLPHYEGSTVPEK-BCPLEHYGS
 TVPEK-BCPLHYEGSSLP EK-BCLPHYEGSSLP EK-BCLPHYEGSTPEVK-BCPLHYEGS
 TPVEK-BCPLHYEGSTPEVK-BCPLHYEGSTPEK-BCPDGGLAEGSTVEPK-BCDPGGL
 AEGSTVEPK-BCLPHYEGSAEPEK-BCPLHYEGSAEPEK-BCLPHEYGSTVPEK-BCPLH
 EYGSTVPEK-BCLDTFYGSTVPEK-BCPMTFYGSTVPEK-BCEVTFYGSTVPEK-BCVET
 FYGSTVPEK-BCPMTFYGSTVPEK-BCDLTFYGSTVPEK-BCNNTFYGSTVPEK-BSSFP
 LNSAK-BSSFPLNSAK-BSSFPEGZAK-BSFSPPEGZAK-BSCMPEGZAK-BSSFPWZAK-
 BSFSPWZAK-BSCMPWZAK-BSSFPZWAK-BSESDWZAK-BSSMLWZAK-BSSDEWZAK-
 BSFSPWZAK-BSMCPWZAK-BSYAPWZAK-BSSFPEGGA AK-BSSFPEGAGAK-BSSFPL
 NASK-BSSFPLNGTK-BSSFPLNTGK-BSSFPEGZAK-BSSFPCZGPK-BSSFPCZPGK-
 BSEDSWZAK-BSAYPWZAK-BSLMSWZAK-BSSFPWAGAK-BSSFPWGA AK-

Database: swissprot

145,079 sequences; 53,365,827 total letters.

Searching....10....20....30....40....50....60....70....80....90....100% done

Color Key: red = positive hit; green = borderline hit; black = negative result

Summary:	Get the selected sequences		Zurücksetze	
Sequences producing High-scoring Segment Pairs:	High Score	Total Score		
sp P19006 HPT_CANFA Haptoglobin alpha and beta chains	137	4.3e-40	5	-40 5
sp P19007 HPT_RABIT Haptoglobin precursor	131	3.8e-33	5	-33 5
sp P00738 HPT_HUMAN Haptoglobin precursor	137	3.5e-31	5	-31 5
sp Q8SPS7 HPT_PIG Haptoglobin precursor	142	3.7e-28	5	-28 5
sp Q61646 HPT_MOUSE Haptoglobin precursor	133	1.2e-24	5	-24 5
sp O35086 HPT_MESAU Haptoglobin precursor	127	6.7e-24	5	-24 5
sp P50417 HPT_ATEGE Haptoglobin precursor	128	1.1e-27	5	-27 5
sp Q60574 HPT_MUSCR Haptoglobin precursor	133	2.4e-24	5	-24 5
sp P06866 HPT_RAT Haptoglobin precursor	115	1.1e-21	5	-21 5
sp P00739 HPTR_HUMAN Haptoglobin-related protein precursor	129	1.1e-27	5	-27 5
sp Q62558 HPT_MUSSA Haptoglobin precursor	122	5.6e-21	6	-21 6
sp Q91507 VSP1_TRIMU Mucrofibrase 1 precursor	66	1.00000	2	0000 2
sp Q91508 VSP2_TRIMU Mucrofibrase 2 precursor (Trimubin)	66	1.00000	2	0000 2
sp Q9DG84 VSP7_TRIMU Serpentokallikrein-2 precursor	66	1.00000	2	0000 2
sp Q91511 VSP5_TRIMU Mucrofibrase 5 precursor	66	1.00000	2	0000 2
sp Q91509 VSP3_TRIMU Mucrofibrase 3 precursor	66	1.00000	2	0000 2
sp Q9I8X0 VSP3_AGKAC Venom serine proteinase Dav-KN precu...	66	1.00000	2	0000 2
sp O13062 VSPC_TRIGA Venom serine proteinase 2C precursor	66	1.00000	2	0000 2
sp Q91510 VSP4_TRIMU Mucrofibrase 4 precursor	66	1.00000	2	0000 2

sp P16295 FA9_CAVPO	Coagulation factor IX (Christmas factor)	60	1.00000	2	00000	2
sp Q9UKQ9 KLK9_HUMAN	Kallikrein 9 precursor (Kallikrein-1...	66	0.997	1	997	1
sp P03953 CFAD_MOUSE	Complement factor D precursor (C3 co...	65	0.9999	1	9999	1
sp Q26422 LFC_CARRO	Limulus clotting factor C precursor (FC)	65	1.00000	1	00000	1
sp P28175 LFC_TACTR	Limulus clotting factor C precursor (FC)	65	1.00000	1	00000	1
sp P16296 FA9_RAT	Coagulation factor IX (Christmas factor)	64	1.00000	1	00000	1
sp P16294 FA9_MOUSE	Coagulation factor IX precursor (Chri...	64	1.00000	1	00000	1
sp P44507 GRK_HAEIN	Glycerate kinase	61	1.00000	1	00000	1
sp P23524 GRK2_ECOLI	Glycerate kinase 2	61	1.00000	1	00000	1
sp Q9UL52 DES1_HUMAN	Serine protease DESC1 precursor	61	1.00000	1	00000	1
sp P39808 YVYG_BACSU	Hypothetical protein yvyG	60	1.00000	1	00000	1
sp P32038 CFAD_RAT	Complement factor D precursor (C3 conv...	60	1.00000	1	00000	1
sp P16293 FA9_PIG	Coagulation factor IX (Christmas factor)	60	1.00000	1	00000	1
sp P16292 FA9_RABIT	Coagulation factor IX (Christmas factor)	60	1.00000	1	00000	1
sp P19540 FA9_CANFA	Coagulation factor IX precursor (Chri...	60	1.00000	1	00000	1
sp Q95ND7 FA9_PANTR	Coagulation factor IX precursor (Chri...	60	1.00000	1	00000	1
sp P00740 FA9_HUMAN	Coagulation factor IX precursor (Chri...	60	1.00000	1	00000	1
sp P07477 TRY1_HUMAN	Trypsin I precursor (Cationic trypsi...	59	1.00000	1	00000	1
sp O13058 VSP3_TRIFL	Venom serine proteinase 3 precursor	59	1.00000	1	00000	1
sp P09092 HXA6_MOUSE	Homeobox protein Hox-A6 (Hox-1.2) (M...	58	1.00000	1	00000	1
sp P31267 HXA6_HUMAN	Homeobox protein Hox-A6 (Hox-1B)	58	1.00000	1	00000	1
sp P48336 YCXF_CYAPA	Hypothetical 11.2 kDa protein in YCF...	57	1.00000	1	00000	1
sp Q8KC50 RL31_CHLTE	50S ribosomal protein L31	55	1.00000	1	00000	1
sp Q9KTM4 R31B_VIBCH	50S ribosomal protein L31 type B	55	1.00000	1	00000	1

Query sequence and locally-aligned HSPs from database sequences

	0	910	1820	2730	3640	4550	4552
query_sequence							
^ v sp P19006 HPT_CANF							
^ v sp P19007 HPT_RABI							
^ v sp P00738 HPT_HUMA							
^ v sp Q8SPS7 HPT_PIG							
^ v sp Q61646 HPT_MOUS							
^ v sp Q35086 HPT_MESA							
^ v sp P50417 HPT_ATEG							
^ v sp Q60574 HPT_MUSC							
^ v sp P06866 HPT_RAT							
^ v sp P00739 HPTR_HUM							
^ v sp Q62558 HPT_MUSS							
^ v sp Q91507 VSP1_TRI							
^ v sp Q91508 VSP2_TRI							
^ v sp Q9DG84 VSP7_TRI							
^ v sp Q91511 VSP5_TRI							
^ v sp Q91509 VSP3_TRI							
^ v sp Q9I8X0 VSP3_AGK							
^ v sp O13062 VSPC_TRI							
^ v sp Q91510 VSP4_TRI							
^ v sp P16295 FA9_CAVP							
^ v sp Q9UKQ9 KLK9_HUM							
^ v sp P03953 CFAD_MOU							
^ v sp Q26422 LFC_CARR							
^ v sp P28175 LFC_TACT							
^ v sp P16296 FA9_RAT							
^ v sp P16294 FA9_MOUS							
^ v sp P44507 GRK_HAEI							

```

^ v sp|P23524|GRK2\_ECO |           -
^ v sp|Q9UL52|DES1\_HUM |           -
^ v sp|P39808|YVYG\_BAC |           -
^ v sp|P32038|CFAD\_RAT |           -
^ v sp|P16293|FA9\_PIG  |           -
^ v sp|P16292|FA9\_RABI |           -
^ v sp|P19540|FA9\_CANF |           -
^ v sp|Q95ND7|FA9\_PANT |           -
^ v sp|P00740|FA9\_HUMA |           -
^ v sp|P07477|TRY1\_HUM |           -
^ v sp|O13058|VSP3\_TRI |           -
^ v sp|P09092|HXA6\_MOU |           -
^ v sp|P31267|HXA6\_HUM |           -
^ v sp|P48336|YCXF\_CYA |           -
^ v sp|Q8KC50|RL31\_CHL |           -
^ v sp|Q9KTM4|R31B\_VIB |           -

```

Alignments:

^ = [sp|P19006|HPT_CANFA](#) Haptoglobin alpha and beta chains
Length = 329

```

          0          70          140          210          280          |329
sp|P19006|HPT_CANFA |-----|
Local hits (HSPs)  |-----|

```

Score = 137 (71.8 bits), Expect = 4.3e-40, P(5) = 4.3e-40
Identities = 17/21 (80%), Positives = 20/21 (95%)

Query: 2530 BSPVGVZPLLNEHTFCAGLSK 2550
+SPVGV+P+LNEHTFCAG SK
Sbjct: 248 KSPVGVQPILNEHTFCAGMSK 268

Score = 134 (70.2 bits), Expect = 2.0e-19, P(3) = 2.0e-19
Identities = 18/20 (90%), Positives = 20/20 (100%)

Query: 3180 HNLTSGATLLNEZWLLTTAK 3199
HNLTSGATL+NE+WLLTTAK
Sbjct: 106 HNLTSGATLINEQWLLTTAK 125

Score = 122 (64.1 bits), Expect = 4.3e-40, P(5) = 4.3e-40
Identities = 14/17 (82%), Positives = 17/17 (100%)

Query: 2160 BVMPCLCLPSZDYAEVGR 2176
+VMP+CLPS+DYAEVGR
Sbjct: 184 RVMPICLPSKDYAEVGR 200

Score = 107 (56.4 bits), Expect = 4.3e-40, P(5) = 4.3e-40
Identities = 13/17 (76%), Positives = 16/17 (94%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
+VVLHPDYS VD+GL+K
Sbjct: 158 KVVLPDYSKVDIGLIK 174

Score = 88 (46.7 bits), Expect = 8.1e-33, P(5) = 8.1e-33
Identities = 11/14 (78%), Positives = 12/14 (85%)

Query: 3937 BCLPHYEGSTVPEK 3950
+C HYEGSTVPEK
Sbjct: 231 KCVQHYEGSTVPEK 244

Score = 88 (46.7 bits), Expect = 2.7e-17, P(4) = 2.7e-17
Identities = 11/13 (84%), Positives = 12/13 (92%)

Query: 1431 BSCAVAEYGVYVK 1443
+SC VAEYGVYVK
Sbjct: 302 KSCTVAEYGVYVK 314

Score = 86 (45.7 bits), Expect = 1.5e-24, P(4) = 1.5e-24

Identities = 10/12 (83%), Positives = 12/12 (100%)

Query: 745 BYVMLPVPADZDK 756
+YVMLPVPAD+DK
Sbjct: 220 KYVMLPVPADQDK 231

Score = 73 (39.1 bits), Expect = 4.3e-40, P(5) = 4.3e-40
Identities = 10/12 (83%), Positives = 11/12 (91%)

Query: 401 BNFLFLGHTDDAK 412
+NLFLGH DDAK
Sbjct: 125 KNFLFLGHKDDAK 136

Score = 71 (38.1 bits), Expect = 2.4e-22, P(4) = 2.4e-22
Identities = 9/12 (75%), Positives = 11/12 (91%)

Query: 1085 BNSNFNYSELLK 1096
+NSNFN+ ELLK
Sbjct: 209 RNSNFNFTELLK 220

Score = 66 (35.5 bits), Expect = 1.6e-23, P(4) = 1.6e-23
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 194 BMGYVSGWGR 203
+GYVSGWGR
Sbjct: 200 RIGYVSGWGR 209

Score = 59 (31.9 bits), Expect = 4.3e-40, P(5) = 4.3e-40
Identities = 6/9 (66%), Positives = 9/9 (100%)

Query: 1 BNPVDZVZR 9
+NPVD+V+R
Sbjct: 76 KNPVDQVQR 84

Score = 56 (30.4 bits), Expect = 0.71, P(2) = 0.51
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 4311 BSSFPWZAK 4319
+SFPW+AK
Sbjct: 93 KGSFPWQAK 101

^ = [sp|P19007|HPT_RABIT](#) Haptoglobin precursor
Length = 347

	0	70	140	210	280		347
sp P19007 HPT_RABIT							
Local hits (HSPs)		—	—	—	—	—	—

Score = 131 (68.7 bits), Expect = 3.8e-33, P(5) = 3.8e-33
Identities = 16/21 (76%), Positives = 19/21 (90%)

Query: 2530 BSPVGZVZPLLNEHTFCAGLSK 2550
+PVGVP+P+LNEHTFCAG SK
Sbjct: 266 KNPVGVPILNEHTFCAGMSK 286

Score = 115 (60.5 bits), Expect = 3.8e-33, P(5) = 3.8e-33
Identities = 13/17 (76%), Positives = 16/17 (94%)

Query: 2160 BVMPCLCLPSZDYAEVGR 2176
+VMP+CLPS+DY EVGR
Sbjct: 202 RVMPICLPSKDYTEVGR 218

Score = 110 (58.0 bits), Expect = 5.8e-13, P(3) = 5.8e-13
Identities = 15/20 (75%), Positives = 17/20 (85%)

Query: 3180 HNLTSGATLLNEZWLLTTAK 3199
HNL GATL+ E+WLLTTAK
Sbjct: 124 HNLVTGATLISEQWLLTTAK 143

Score = 100 (52.9 bits), Expect = 3.8e-33, P(5) = 3.8e-33
Identities = 12/17 (70%), Positives = 16/17 (94%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
+VVLHP+YS VD+GL+K
Sbjct: 176 KVVLPHPNYSEVDIGLIK 192

Score = 88 (46.7 bits), Expect = 5.2e-15, P(4) = 5.2e-15
Identities = 11/13 (84%), Positives = 12/13 (92%)

Query: 1431 BSCAVAEYGVYVK 1443
+SC VAEYGVYVK
Sbjct: 320 KSCTVAEYGVYVK 332

Score = 86 (45.7 bits), Expect = 2.4e-21, P(4) = 2.4e-21
Identities = 10/12 (83%), Positives = 12/12 (100%)

Query: 745 BYVMLPVDZDK 756
+YVMLPVD+DK
Sbjct: 238 KYVMLPVDQDK 249

Score = 77 (41.1 bits), Expect = 3.4e-25, P(5) = 3.4e-25
Identities = 9/13 (69%), Positives = 11/13 (84%)

Query: 3937 BCLPHYEGSTVPE 3949
+C+ HYE STVPE
Sbjct: 249 KCIQHYENSTVPE 261

Score = 66 (35.5 bits), Expect = 2.4e-21, P(4) = 2.4e-21
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 194 BMGYVSGWGR 203
+ GYVSGWGR
Sbjct: 218 RVGYVSGWGR 227

Score = 56 (30.4 bits), Expect = 11., P(2) = 0.99998
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 4311 BSSFPWZAK 4319
+ SFPW+AK
Sbjct: 111 KGSFPWQAK 119

Score = 55 (29.9 bits), Expect = 3.8e-33, P(5) = 3.8e-33
Identities = 7/11 (63%), Positives = 10/11 (90%)

Query: 401 BNLFLGHTDDA 411
+NLFL HT++A
Sbjct: 143 KNLFLNHTENA 153

Score = 53 (28.9 bits), Expect = 1.6e-16, P(4) = 1.6e-16
Identities = 7/12 (58%), Positives = 8/12 (66%)

Query: 1130 BNSNFNYSZNLK 1141
+NSNF Y LK
Sbjct: 227 RNSNFTYTDHLK 238

Score = 51 (27.8 bits), Expect = 3.8e-33, P(5) = 3.8e-33
Identities = 5/9 (55%), Positives = 8/9 (88%)

Query: 1 BNPVDZVZR 9
+ PVD+V+R
Sbjct: 94 KHPVDQVQR 102

^ = [sp|P00738|HPT_HUMAN](#) Haptoglobin precursor
Length = 406

	0	90	180	270	360		
						406	
sp P00738 HPT_HUMAN		-----					
Local hits (HSPs)			-	-	-	-	

Score = 137 (71.8 bits), Expect = 3.5e-31, P(5) = 3.5e-31
Identities = 17/21 (80%), Positives = 20/21 (95%)

Query: 2530 BSPVGVZPLLNEHTFCAGLSK 2550
+SPVGV+P+LNEHTFCAG SK
Sbjct: 325 KSPVGVQPILNEHTFCAGMSK 345

Score = 128 (67.2 bits), Expect = 1.5e-14, P(3) = 1.5e-14
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 3180 HNLTSGATLLNEZWLTTAK 3199
HNL T GATL+NE+WLLTTAK
Sbjct: 183 HNLTTGATLINEQWLLTTAK 202

Score = 122 (64.1 bits), Expect = 3.5e-31, P(5) = 3.5e-31
Identities = 14/17 (82%), Positives = 17/17 (100%)

Query: 2160 BVMPCLCLPSZDYAEVGR 2176
+VMP+CLPS+DYAEVGR
Sbjct: 261 RVMPICLPSKDYAEVGR 277

Score = 99 (52.4 bits), Expect = 3.5e-31, P(5) = 3.5e-31
Identities = 12/17 (70%), Positives = 16/17 (94%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
+VVLHP+YS VD+GL+K
Sbjct: 235 KVVLPNYSQVDIGLIK 251

Score = 95 (50.3 bits), Expect = 2.0e-12, P(4) = 2.0e-12
Identities = 12/13 (92%), Positives = 13/13 (100%)

Query: 1431 BSCAVAEYGVYVK 1443
+SCAVAEYGVYVK
Sbjct: 379 KSCAVAEYGVYVK 391

Score = 87 (46.2 bits), Expect = 7.8e-24, P(5) = 7.8e-24
Identities = 11/13 (84%), Positives = 12/13 (92%)

Query: 3938 CLPHYEGSTVPEK 3950
C+ HYEGSTVPEK
Sbjct: 309 CIRHYEGSTVPEK 321

Score = 79 (42.1 bits), Expect = 1.4e-18, P(4) = 1.4e-18
Identities = 9/11 (81%), Positives = 11/11 (100%)

Query: 745 BYVMLPVADZD 755
+YVMLPVAD+D
Sbjct: 297 KYVMLPVADQD 307

Score = 66 (35.5 bits), Expect = 1.4e-18, P(4) = 1.4e-18
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 194 BMGYVSGWGR 203
+ GYVSGWGR
Sbjct: 277 RVGYVSGWGR 286

Score = 48 (26.3 bits), Expect = 3.5e-31, P(5) = 3.5e-31
Identities = 6/11 (54%), Positives = 9/11 (81%)

Query: 401 BNLFLGHTDDA 411
+NLFL H ++A
Sbjct: 202 KNLFLNHSENA 212

Score = 40 (22.2 bits), Expect = 6.6e-13, P(4) = 6.6e-13
Identities = 5/12 (41%), Positives = 7/12 (58%)

Query: 1130 BNSNFNYSZNLK 1141
+N NF + LK
Sbjct: 286 RNANFKFTDHLK 297

Score = 35 (19.7 bits), Expect = 3.5e-31, P(5) = 3.5e-31
Identities = 4/9 (44%), Positives = 7/9 (77%)

Query: 1 BNPVDZVZR 9
+NP + V+R
Sbjct: 153 KNPANPVQR 161

[^](#) = [sp|Q8SPS7|HPT_PIG](#) Haptoglobin precursor
Length = 347

	0	70	140	210	280		347
sp Q8SPS7 HPT_PIG							
Local hits (HSPs)		-----					

Score = 142 (74.3 bits), Expect = 3.7e-28, P(5) = 3.7e-28
Identities = 18/21 (85%), Positives = 21/21 (100%)

Query: 2530 BSPVGVZPLLNEHTFCAGLSK 2550
+SPVGV+P+LNEHTFCAGLSK
Sbjct: 266 KSPVGVQPILNEHTFCAGLSK 286

Score = 136 (71.3 bits), Expect = 7.2e-18, P(3) = 7.2e-18
Identities = 19/25 (76%), Positives = 22/25 (88%)

Query: 3201 BMNGTHNLTSGATLLNEZWLTTAK 3225
+M HNLTSGATL+NE+WLLTTAK
Sbjct: 119 KMISHHNLTSGATLINEQWLLTTAK 143

Score = 96 (50.8 bits), Expect = 3.7e-28, P(5) = 3.7e-28
Identities = 11/16 (68%), Positives = 14/16 (87%)

Query: 2160 BVMPCLCLPSZDYAEVG 2175
+VMP+CLPS+DY VG
Sbjct: 202 RVMPICLPSKDYVNVG 217

Score = 80 (42.7 bits), Expect = 1.1e-22, P(4) = 1.1e-22
Identities = 9/12 (75%), Positives = 12/12 (100%)

Query: 745 BYVMLPVADZDK 756
+YVMLPVAD++K
Sbjct: 238 KYVMLPVADQEK 249

Score = 79 (42.1 bits), Expect = 3.7e-28, P(5) = 3.7e-28
Identities = 10/17 (58%), Positives = 14/17 (82%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
+V+ HPD S VD+GL+K
Sbjct: 176 KVIFHPDNSTVDIGLIK 192

Score = 76 (40.6 bits), Expect = 1.8e-18, P(5) = 1.8e-18
Identities = 10/14 (71%), Positives = 11/14 (78%)

Query: 3937 BCLPHYEGSTVPEK 3950
+C YEGSTVPEK
Sbjct: 249 KCVQYYEGSTVPEK 262

Score = 65 (35.0 bits), Expect = 2.2e-11, P(4) = 2.2e-11
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 1431 BSCAVAEYGVYV 1442
+SC AEYGVYV
Sbjct: 320 KSCRTAEYGVYV 331

Score = 62 (33.5 bits), Expect = 1.1e-22, P(4) = 1.1e-22
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 196 GYVSGWGR 203
GYVSGWGR
Sbjct: 220 GYVSGWGR 227

Score = 59 (31.9 bits), Expect = 3.7e-28, P(5) = 3.7e-28
Identities = 6/9 (66%), Positives = 9/9 (100%)

Query: 1 BNPVDZVZR 9
+NPVD+V+R
Sbjct: 94 KNPVDQVQR 102

Score = 56 (30.4 bits), Expect = 0.79, P(2) = 0.54
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 4311 BSSFPWZAK 4319
+ SFPW+AK
Sbjct: 111 KGSFPWQAK 119

Score = 42 (23.3 bits), Expect = 3.7e-28, P(5) = 3.7e-28
Identities = 7/12 (58%), Positives = 9/12 (75%)

Query: 401 BNLF LGHTDDAK 412
+NL LGH +D K
Sbjct: 143 KNLRLGHKNDTK 154

Score = 40 (22.2 bits), Expect = 8.0e-17, P(4) = 8.0e-17
Identities = 6/12 (50%), Positives = 8/12 (66%)

Query: 1085 BNSNFNYSELLK 1096
+N N N+ E LK
Sbjct: 227 RNANLNFTEHLK 238

^ = [sp|Q61646|HPT_MOUSE](#) Haptoglobin precursor
Length = 347

	0	70	140	210	280		
						347	
sp Q61646 HPT_MOUSE		-----					
Local hits (HSPs)		-----					

Score = 133 (69.7 bits), Expect = 1.2e-24, P(5) = 1.2e-24
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 2641 SPVGVZPLLNEHTFCAGVTK 2660
SPVGV+P+LNEHTFCAG TK
Sbjct: 267 SPVGVQPILNEHTFCAGLTK 286

Score = 106 (55.9 bits), Expect = 3.2e-12, P(3) = 3.2e-12
Identities = 15/25 (60%), Positives = 19/25 (76%)

Query: 3201 BMNGTHNLTSGATLLNEZWLTTAK 3225
+M H LT GATL+ ++WLLTTAK
Sbjct: 119 KMISRHLTTGATLISDQWLLTTAK 143

Score = 88 (46.7 bits), Expect = 1.2e-24, P(5) = 1.2e-24
Identities = 11/17 (64%), Positives = 14/17 (82%)

Query: 2160 BVMPCLCLPSZDYAEVGR 2176
+VMP+CLPS+DY GR
Sbjct: 202 RVMPICLPSKDYIAPGR 218

Score = 88 (46.7 bits), Expect = 5.2e-15, P(4) = 5.2e-15
Identities = 11/12 (91%), Positives = 12/12 (100%)

Query: 1431 BSCAVAEYGVYV 1442
+SCAVAEYGVYV
Sbjct: 320 KSCAVAEYGVYV 331

Score = 86 (45.7 bits), Expect = 1.2e-21, P(4) = 1.2e-21
Identities = 10/12 (83%), Positives = 12/12 (100%)

Query: 745 BYVMLPVADZDK 756
+YVMLPVAD+DK

Sbjct: 238 KYVMLPVPADQDK 249

Score = 81 (43.2 bits), Expect = 1.2e-24, P(5) = 1.2e-24
Identities = 11/17 (64%), Positives = 15/17 (88%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
+VVLHP+ S VD+GL+K

Sbjct: 176 KVVLPNHSVVDIGLIK 192

Score = 76 (40.6 bits), Expect = 2.6e-16, P(5) = 2.6e-16
Identities = 10/14 (71%), Positives = 11/14 (78%)

Query: 3937 BCLPHYEGSTVPEK 3950
+C HYE STVPEK

Sbjct: 249 KCVVHYENSTVPEK 262

Score = 66 (35.5 bits), Expect = 1.2e-21, P(4) = 1.2e-21
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 194 BMGYVSGWGR 203
+ GYVSGWGR

Sbjct: 218 RVGYVSGWGR 227

Score = 56 (30.4 bits), Expect = 11., P(2) = 0.99998
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 4311 BSSFPWZAK 4319
+ SFPW+AK

Sbjct: 111 KGSFPWQAK 119

Score = 51 (27.8 bits), Expect = 1.2e-24, P(5) = 1.2e-24
Identities = 5/9 (55%), Positives = 8/9 (88%)

Query: 1 BNPVDZVZR 9
+ PVD+V+R

Sbjct: 94 KHPVDQVQR 102

Score = 41 (22.7 bits), Expect = 1.2e-24, P(5) = 1.2e-24
Identities = 6/11 (54%), Positives = 8/11 (72%)

Query: 401 BNLFLGHTDDA 411
+NLFL H + A

Sbjct: 143 KNLFLNHSETA 153

Score = 33 (18.7 bits), Expect = 6.7e-14, P(4) = 6.7e-14
Identities = 5/12 (41%), Positives = 8/12 (66%)

Query: 1085 BNSNFNYSELLK 1096
+N NF + + LK

Sbjct: 227 RNANFRFTDRLK 238

[^ = sp|O35086|HPT_MESAU](#) Haptoglobin precursor
Length = 346

	0	70	140	210	280		346
sp O35086 HPT_MESAU							
Local hits (HSPs)		-----					

Score = 127 (66.7 bits), Expect = 6.7e-24, P(5) = 6.7e-24
Identities = 16/21 (76%), Positives = 19/21 (90%)

Query: 2640 BSPVGZPPLLNEHTFCAGVTK 2660
+S VGV+P+LNEHTFCAG TK

Sbjct: 265 KSSVGVQPILNEHTFCAGMTK 285

Score = 95 (50.3 bits), Expect = 6.7e-11, P(3) = 6.7e-11
Identities = 13/20 (65%), Positives = 16/20 (80%)

Query: 3180 HNLTSGATLLNEZWLTTAK 3199

H L GATL+ ++WLLTTAK
Sbjct: 123 HELITGATLISDQWLLTTAK 142

Score = 89 (47.3 bits), Expect = 6.8e-16, P(4) = 6.8e-16
Identities = 11/13 (84%), Positives = 12/13 (92%)

Query: 1431 BSCAVAEYGVYVK 1443
+SC VAEYGVYVK
Sbjct: 319 KSCSVAEYGVYVK 331

Score = 88 (46.7 bits), Expect = 6.7e-24, P(5) = 6.7e-24
Identities = 11/17 (64%), Positives = 14/17 (82%)

Query: 2160 BVMPCLCLPSZDYAEVGR 2176
+VMP+CLPS+DY GR
Sbjct: 201 RVMPICLPSKDYIAPGR 217

Score = 79 (42.1 bits), Expect = 1.7e-21, P(4) = 1.7e-21
Identities = 9/11 (81%), Positives = 11/11 (100%)

Query: 745 BYVMLPVADZD 755
+YVMLPVAD+D
Sbjct: 237 KYVMLPVADQD 247

Score = 78 (41.6 bits), Expect = 1.7e-21, P(4) = 1.7e-21
Identities = 9/10 (90%), Positives = 10/10 (100%)

Query: 194 BMGYVSGWGR 203
+MGYVSGWGR
Sbjct: 217 RMGYVSGWGR 226

Score = 78 (41.6 bits), Expect = 9.4e-17, P(5) = 9.4e-17
Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 3938 CLPHYEGSTVPEK 3950
C HYEGSTVPEK
Sbjct: 249 CMLHYEGSTVPEK 261

Score = 69 (37.0 bits), Expect = 6.7e-24, P(5) = 6.7e-24
Identities = 9/17 (52%), Positives = 14/17 (82%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
+VV+HP+ S VD+G +K
Sbjct: 175 KVVHPNRSVVDIGVIK 191

Score = 56 (30.4 bits), Expect = 11., P(2) = 0.99998
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 4311 BSSFPWZAK 4319
+ SFPW+AK
Sbjct: 110 KGSFPWQAK 118

Score = 54 (29.4 bits), Expect = 6.7e-24, P(5) = 6.7e-24
Identities = 7/11 (63%), Positives = 9/11 (81%)

Query: 401 BNLFLGHTDDA 411
+NLFL H +DA
Sbjct: 142 KNLFLNHSEDA 152

Score = 51 (27.8 bits), Expect = 6.7e-24, P(5) = 6.7e-24
Identities = 5/9 (55%), Positives = 8/9 (88%)

Query: 1 BNPVDZVZR 9
+ PVD+V+R
Sbjct: 93 KHPVDQVQR 101

Score = 33 (18.7 bits), Expect = 9.0e-15, P(4) = 9.0e-15
Identities = 5/12 (41%), Positives = 8/12 (66%)

Query: 1085 BNSNFNYSELLK 1096
+N NF + + LK

Sbjct: 226 RNANFRFTDRLK 237

^ = [sp|P50417|HPT_ATEGE](#) Haptoglobin precursor
Length = 347

	0	70	140	210	280		
						347	
sp P50417 HPT_ATEGE		-----					
Local hits (HSPs)		-----					

Score = 128 (67.2 bits), Expect = 1.0e-13, P(3) = 1.0e-13
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 3180 HNLTSGATLLNEZWLLTTAK 3199
HNL T GATL+NE+WLLTTAK

Sbjct: 124 HNLTTGATLINEQWLLTTAK 143

Score = 123 (64.6 bits), Expect = 1.1e-27, P(5) = 1.1e-27
Identities = 16/21 (76%), Positives = 19/21 (90%)

Query: 2530 BSPVGVZPLLNEHTFCAGLSK 2550
+SPVG +P+LNEHTFCAG SK

Sbjct: 266 KSPVQQPILNEHTFCAGMSK 286

Score = 122 (64.1 bits), Expect = 1.1e-27, P(5) = 1.1e-27
Identities = 14/17 (82%), Positives = 17/17 (100%)

Query: 2160 BVMPCLCLPSZDYAEVGR 2176
+VMP+CLPS+DYAEVGR

Sbjct: 202 RVMPICLPSKDYAEVGR 218

Score = 87 (46.2 bits), Expect = 1.1e-27, P(5) = 1.1e-27
Identities = 11/17 (64%), Positives = 15/17 (88%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
+VVL P+YS VD+GL+K

Sbjct: 176 KVVLYPNYSQVDIGLIK 192

Score = 87 (46.2 bits), Expect = 2.1e-10, P(4) = 2.1e-10
Identities = 11/13 (84%), Positives = 12/13 (92%)

Query: 1431 BSCAVAEYGVYVK 1443
+SC VAEYGVYVK

Sbjct: 320 KSCGVAEYGVYVK 332

Score = 80 (42.7 bits), Expect = 2.1e-21, P(5) = 2.1e-21
Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 3938 CLPHYEGSTVPEK 3950
C HYEGSTVPEK

Sbjct: 250 CVKH YEGSTVPEK 262

Score = 71 (38.1 bits), Expect = 1.2e-15, P(4) = 1.2e-15
Identities = 8/10 (80%), Positives = 10/10 (100%)

Query: 745 BYVMLPVADZ 754
+YVMLPVAD+

Sbjct: 238 KYVMLPVADQ 247

Score = 66 (35.5 bits), Expect = 1.2e-15, P(4) = 1.2e-15
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 194 BMGYVSGWGR 203
+ GYVSGWGR

Sbjct: 218 RVGYVSGWGR 227

Score = 48 (26.3 bits), Expect = 1.1e-27, P(5) = 1.1e-27
Identities = 6/11 (54%), Positives = 9/11 (81%)

Query: 401 BNLFLGHTDDA 411

+NLFL H ++A
 Sbjct: 143 KNLFLNHSENA 153

 Score = 40 (22.2 bits), Expect = 3.8e-11, P(4) = 3.8e-11
 Identities = 5/12 (41%), Positives = 7/12 (58%)

Query: 1130 BNSNFNYSZNLK 1141
 +N NF + LK
 Sbjct: 227 RNANFKFTDHLK 238

 Score = 35 (19.7 bits), Expect = 1.1e-27, P(5) = 1.1e-27
 Identities = 4/9 (44%), Positives = 7/9 (77%)

Query: 1 BNPVDZVZR 9
 +NP + V+R
 Sbjct: 94 KNPANPVQR 102

^ = [sp|Q60574|HPT_MUSCR](#) Haptoglobin precursor
 Length = 347

	0	70	140	210	280		
						347	
sp Q60574 HPT_MUSCR		-----					
Local hits (HSPs)		-----					

Score = 133 (69.7 bits), Expect = 2.4e-24, P(5) = 2.4e-24
 Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 2641 SPVGVZPLLNEHTFCAGVTK 2660
 SPVGV+P+LNEHTFCAG TK
 Sbjct: 267 SPVGVQPILNEHTFCAGLTK 286

Score = 106 (55.9 bits), Expect = 1.2e-11, P(3) = 1.2e-11
 Identities = 15/25 (60%), Positives = 19/25 (76%)

Query: 3201 BMNGTHNLTSGATLLNEZWLTTAK 3225
 +M H LT GATL+ ++WLLTTAK
 Sbjct: 119 KMISRHLTTGATLISDQWLLTTAK 143

Score = 91 (48.3 bits), Expect = 2.4e-24, P(5) = 2.4e-24
 Identities = 11/17 (64%), Positives = 14/17 (82%)

Query: 2160 BVMPCLCLPSZDYAEVGR 2176
 +VMP+CLPS+DY GR
 Sbjct: 202 RVMPICLPSKDYVAPGR 218

Score = 88 (46.7 bits), Expect = 5.2e-15, P(4) = 5.2e-15
 Identities = 11/12 (91%), Positives = 12/12 (100%)

Query: 1431 BSCAVAEYGVYV 1442
 +SCAVAEYGVYV
 Sbjct: 320 KSCAVAEYGVYV 331

Score = 86 (45.7 bits), Expect = 1.2e-21, P(4) = 1.2e-21
 Identities = 10/12 (83%), Positives = 12/12 (100%)

Query: 745 BYVMLPVADZDK 756
 +YVMLPVAD+DK
 Sbjct: 238 KYVMLPVADQDK 249

Score = 76 (40.6 bits), Expect = 2.4e-24, P(5) = 2.4e-24
 Identities = 10/17 (58%), Positives = 15/17 (88%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
 +V+LHP+ S VD+GL+K
 Sbjct: 176 KVILHPNHSVVDIGLIK 192

Score = 72 (38.6 bits), Expect = 1.9e-15, P(5) = 1.9e-15
 Identities = 10/14 (71%), Positives = 11/14 (78%)

Query: 3937 BCLPHYEGSTVPEK 3950
 +C HYE STVPEK
 Sbjct: 249 KCVVHYEKSTVPEK 262

Score = 66 (35.5 bits), Expect = 1.2e-21, P(4) = 1.2e-21
 Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 194 BMGYVSGWGR 203
 + GYVSGWGR
 Sbjct: 218 RVGYVSGWGR 227

Score = 56 (30.4 bits), Expect = 11., P(2) = 0.99998
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 4311 BSSFPWZAK 4319
 + SFPW+AK
 Sbjct: 111 KGSFPWQAK 119

Score = 51 (27.8 bits), Expect = 2.4e-24, P(5) = 2.4e-24
 Identities = 5/9 (55%), Positives = 8/9 (88%)

Query: 1 BNPVDZVZR 9
 + PVD+V+R
 Sbjct: 94 KHPVDQVQR 102

Score = 41 (22.7 bits), Expect = 2.4e-24, P(5) = 2.4e-24
 Identities = 6/11 (54%), Positives = 8/11 (72%)

Query: 401 BNLF LGHTDDA 411
 +NLFL H + A
 Sbjct: 143 KNLF LN HSETA 153

^ = [sp|P06866|HPT_RAT](#) Haptoglobin precursor
 Length = 347

	0	70	140	210	280		
						347	
sp P06866 HPT_RAT		-----					
Local hits (HSPs)		- - - - -					

Score = 115 (60.5 bits), Expect = 1.1e-21, P(5) = 1.1e-21
 Identities = 15/19 (78%), Positives = 17/19 (89%)

Query: 2642 PVGVZPLLNEHTFCAGVTK 2660
 PVGV+P+LN HTFCAG TK
 Sbjct: 268 PVGVQPILNKHTFCAGLTK 286

Score = 99 (52.4 bits), Expect = 1.9e-09, P(3) = 1.9e-09
 Identities = 14/24 (58%), Positives = 18/24 (75%)

Query: 3201 BMNGTHNLTSGATLLNEZWLTTA 3224
 +M H LT GATL+ ++WLLTTA
 Sbjct: 119 KMISRHGLTTGATLISDQWLLTTA 142

Score = 95 (50.3 bits), Expect = 6.5e-17, P(4) = 6.5e-17
 Identities = 12/13 (92%), Positives = 13/13 (100%)

Query: 1431 BSCA VA EYGVYVK 1443
 +SCA VA EYGVYVK
 Sbjct: 320 KSCA VA EYGVYVK 332

Score = 91 (48.3 bits), Expect = 1.1e-21, P(5) = 1.1e-21
 Identities = 11/17 (64%), Positives = 14/17 (82%)

Query: 2160 BVMP LCLPSZDYAEVGR 2176
 +VMP+CLPS+DY GR
 Sbjct: 202 KVMPICLPSKDYVAPGR 218

Score = 80 (42.7 bits), Expect = 7.3e-20, P(4) = 7.3e-20
 Identities = 9/12 (75%), Positives = 12/12 (100%)

Query: 745 BYVMLPVPADZDK 756
 +YVMLPVPAD++K
 Sbjct: 238 KYVMLPVPADQEK 249

Score = 78 (41.6 bits), Expect = 7.3e-20, P(4) = 7.3e-20
 Identities = 9/10 (90%), Positives = 10/10 (100%)

Query: 194 BMGYVSGWGR 203
 +MGYVSGWGR
 Sbjct: 218 RMGYVSGWGR 227

Score = 74 (39.6 bits), Expect = 1.1e-21, P(5) = 1.1e-21
 Identities = 11/17 (64%), Positives = 15/17 (88%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
 +VVLHP+ S VD+GL+K
 Sbjct: 176 KVVLPERSVVDIGLIK 192

Score = 64 (34.5 bits), Expect = 2.6e-14, P(5) = 2.6e-14
 Identities = 9/14 (64%), Positives = 10/14 (71%)

Query: 3967 BCPLHYEGSSLPEK 3980
 +C LHYE S PEK
 Sbjct: 249 KCELHYEKSTVPEK 262

Score = 56 (30.4 bits), Expect = 11., P(2) = 0.99998
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 4311 BSSFPPWZAK 4319
 + SFPW+AK
 Sbjct: 111 KGSFPWQAK 119

Score = 51 (27.8 bits), Expect = 1.1e-21, P(5) = 1.1e-21
 Identities = 5/9 (55%), Positives = 8/9 (88%)

Query: 1 BNPVDZVZR 9
 + PVD+V+R
 Sbjct: 94 KHPVDQVQR 102

Score = 43 (23.8 bits), Expect = 1.1e-21, P(5) = 1.1e-21
 Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 402 NLFLGHTDDA 411
 NLFL H ++A
 Sbjct: 144 NLFLNHSENA 153

^ = [sp|P00739|HPTR_HUMAN](#) Haptoglobin-related protein precursor
 Length = 348

	0	70	140	210	280	348	
sp P00739 HPTR_HUMAN							
Local hits (HSPs)		-----					

Score = 129 (67.7 bits), Expect = 1.1e-27, P(5) = 1.1e-27
 Identities = 16/21 (76%), Positives = 19/21 (90%)

Query: 2530 BSPVGVZPLLNEHTFCAGLSK 2550
 +SPVGV+P+LNEHTFC G SK
 Sbjct: 267 KSPVGVQPILNEHTFCVGMASK 287

Score = 128 (67.2 bits), Expect = 1.3e-10, P(3) = 1.3e-10
 Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 3180 HNLTSGATLLNEZWLTTAK 3199
 HNL T GATL+NE+WLLTTAK
 Sbjct: 125 HNLTTGATLINEQWLLTTAK 144

Score = 116 (61.0 bits), Expect = 1.1e-27, P(5) = 1.1e-27

Identities = 13/17 (76%), Positives = 17/17 (100%)

Query: 2160 BVMPCLCLPSZDYAEVGR 2176
 +VMP+CLPS++YAEVGR
 Sbjct: 203 RVMPICLPSKNYAEVGR 219

Score = 95 (50.3 bits), Expect = 2.1e-10, P(4) = 2.1e-10
 Identities = 12/13 (92%), Positives = 13/13 (100%)

Query: 1431 BSCAVAEYGVYVK 1443
 +SCAVAEYGVYVK
 Sbjct: 321 KSCAVAEYGVYVK 333

Score = 87 (46.2 bits), Expect = 1.1e-27, P(5) = 1.1e-27
 Identities = 11/17 (64%), Positives = 15/17 (88%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
 +VVLHP+Y VD+GL+K
 Sbjct: 177 KVVLPHPNYHQVDIGLIK 193

Score = 71 (38.1 bits), Expect = 2.4e-15, P(4) = 2.4e-15
 Identities = 8/10 (80%), Positives = 10/10 (100%)

Query: 745 BYVMLPVADZ 754
 +YVMLPVAD+
 Sbjct: 239 KYVMLPVADQ 248

Score = 59 (31.9 bits), Expect = 1.7e-17, P(5) = 1.7e-17
 Identities = 8/11 (72%), Positives = 9/11 (81%)

Query: 3938 CLPHYEGSTVP 3948
 C+ HYEGST P
 Sbjct: 251 CITHYEGSTCP 261

Score = 58 (31.4 bits), Expect = 2.4e-15, P(4) = 2.4e-15
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 194 BMGYVSGWG 202
 + GYVSGWG
 Sbjct: 219 RVGYVSGWG 227

Score = 48 (26.3 bits), Expect = 1.1e-27, P(5) = 1.1e-27
 Identities = 6/11 (54%), Positives = 9/11 (81%)

Query: 401 BNFLFGHTDDA 411
 +NLFL H ++A
 Sbjct: 144 KNLFLNHSENA 154

Score = 35 (19.7 bits), Expect = 1.1e-27, P(5) = 1.1e-27
 Identities = 4/9 (44%), Positives = 7/9 (77%)

Query: 1 BNPVDZVZR 9
 +NP + V+R
 Sbjct: 95 KNPANPVQR 103

^ = [sp|Q62558|HPT_MUSSA](#) Haptoglobin precursor
 Length = 347

	0	70	140	210	280		
						347	
sp Q62558 HPT_MUSSA		-----					
Local hits (HSPs)		-----					

Score = 122 (64.1 bits), Expect = 5.6e-21, P(6) = 5.6e-21
 Identities = 16/19 (84%), Positives = 18/19 (94%)

Query: 2531 SPVGVZPLLNEHTFCAGLS 2549
 SPVGV+P+LNEHTFC GLS
 Sbjct: 267 SPVGVQPILNEHTFCVGLS 285

Score = 106 (55.9 bits), Expect = 2.0e-09, P(4) = 2.0e-09
Identities = 15/25 (60%), Positives = 19/25 (76%)

Query: 3201 BMNGTHNLTSGATLLNEZWLLTTAK 3225
+M H LT GATL+ ++WLLTTAK
Sbjct: 119 KMISRHLTTGATLISDQWLLTTAK 143

Score = 91 (48.3 bits), Expect = 5.6e-21, P(6) = 5.6e-21
Identities = 11/17 (64%), Positives = 14/17 (82%)

Query: 2160 BVMPCLCLPSZDYAEVGR 2176
+VMP+CLPS+DY GR
Sbjct: 202 RVMPICLPSKDYVAPGR 218

Score = 88 (46.7 bits), Expect = 1.1e-11, P(4) = 1.1e-11
Identities = 11/12 (91%), Positives = 12/12 (100%)

Query: 1431 BSCAVAEYGVYV 1442
+SCAVAEYGVYV
Sbjct: 320 KSCAVAEYGVYV 331

Score = 86 (45.7 bits), Expect = 2.3e-16, P(5) = 2.3e-16
Identities = 10/12 (83%), Positives = 12/12 (100%)

Query: 745 BYVMLPVADZDK 756
+YVMLPVAD+DK
Sbjct: 238 KYVMLPVADQDK 249

Score = 81 (43.2 bits), Expect = 5.6e-21, P(6) = 5.6e-21
Identities = 11/17 (64%), Positives = 15/17 (88%)

Query: 1831 BVVLHPDYSNVDLGLLK 1847
+VVLHP+ S VD+GL+K
Sbjct: 176 KVVVLHPNHSVVDIGLIK 192

Score = 76 (40.6 bits), Expect = 2.1e-14, P(6) = 2.1e-14
Identities = 10/14 (71%), Positives = 11/14 (78%)

Query: 3937 BCLPHYEGSTVPEK 3950
+C HYE STVPEK
Sbjct: 249 KCVVHYENSTVPEK 262

Score = 59 (31.9 bits), Expect = 2.3e-16, P(5) = 2.3e-16
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 194 BMGYVSGWGR 203
+ GY SGWGR
Sbjct: 218 RVGYLSGWGR 227

Score = 41 (22.7 bits), Expect = 5.6e-21, P(6) = 5.6e-21
Identities = 6/11 (54%), Positives = 8/11 (72%)

Query: 401 BNLFLGHTDDA 411
+NLFL H + A
Sbjct: 143 KNLFLNHSETA 153

Score = 35 (19.7 bits), Expect = 5.6e-21, P(6) = 5.6e-21
Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 4503 EDSWZA 4508
ED W A
Sbjct: 307 EDTWXA 312

Score = 35 (19.7 bits), Expect = 5.6e-21, P(6) = 5.6e-21
Identities = 4/9 (44%), Positives = 7/9 (77%)

Query: 1 BNPVDZVZR 9
+ PV +V+R
Sbjct: 94 KHPVVQVQR 102

[^ = sp|Q91507|VSP1_TRIMU](#) Microfibrase 1 precursor
Length = 257

	0	60	120	180	240	257	
sp Q91507 VSP1_TRIMU		-----					
Local hits (HSPs)		-	-				

Score = 66 (35.5 bits), Expect = 42., P(2) = 1.00000
Identities = 10/13 (76%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
G TLLNE W LTA
Sbjct: 50 GGTLNNEEWVLTAA 62

Score = 35 (19.7 bits), Expect = 42., P(2) = 1.00000
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 2539 LNEHTF 2544
+NEH F
Sbjct: 33 INEHPF 38

[^ = sp|Q91508|VSP2_TRIMU](#) Microfibrase 2 precursor (Trimubin)
Length = 257

	0	60	120	180	240	257	
sp Q91508 VSP2_TRIMU		-----					
Local hits (HSPs)		-	-				

Score = 66 (35.5 bits), Expect = 42., P(2) = 1.00000
Identities = 10/13 (76%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
G TLLNE W LTA
Sbjct: 50 GGTLNNEEWVLTAA 62

Score = 35 (19.7 bits), Expect = 42., P(2) = 1.00000
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 2539 LNEHTF 2544
+NEH F
Sbjct: 33 INEHPF 38

[^ = sp|Q9DG84|VSP7_TRIMU](#) Serpentokallikrein-2 precursor
Length = 257

	0	60	120	180	240	257	
sp Q9DG84 VSP7_TRIMU		-----					
Local hits (HSPs)		-	-				

Score = 66 (35.5 bits), Expect = 42., P(2) = 1.00000
Identities = 9/13 (69%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
G TL+NE W LTA
Sbjct: 50 GGTLNNEEWVLTAA 62

Score = 35 (19.7 bits), Expect = 42., P(2) = 1.00000
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 2539 LNEHTF 2544
+NEH F
Sbjct: 33 INEHPF 38

[^ = sp|Q91511|VSP5_TRIMU](#) Microfibrase 5 precursor
Length = 257

```

                0          60          120          180          240
                |          |          |          |          |
sp|Q91511|VSP5_TRIMU | _____|257
Local hits (HSPs)   |          -          -

```

Score = 66 (35.5 bits), Expect = 42., P(2) = 1.00000
Identities = 9/13 (69%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
G TL+NE W LTA
Sbjct: 50 GGTLNNEEWVLTAA 62

Score = 35 (19.7 bits), Expect = 42., P(2) = 1.00000
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 2539 LNEHTF 2544
+NEH F
Sbjct: 33 INEHPF 38

^ = [sp|Q91509|VSP3_TRIMU](#) Mucrofibrase 3 precursor
Length = 257

```

                0          60          120          180          240
                |          |          |          |          |
sp|Q91509|VSP3_TRIMU | _____|257
Local hits (HSPs)   |          -          -

```

Score = 66 (35.5 bits), Expect = 42., P(2) = 1.00000
Identities = 10/13 (76%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
G TLLNE W LTA
Sbjct: 50 GGTLNNEEWVLTAA 62

Score = 35 (19.7 bits), Expect = 42., P(2) = 1.00000
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 2539 LNEHTF 2544
+NEH F
Sbjct: 33 INEHPF 38

^ = [sp|Q9I8X0|VSP3_AGKAC](#) Venom serine proteinase Dav-KN precursor
Length = 257

```

                0          60          120          180          240
                |          |          |          |          |
sp|Q9I8X0|VSP3_AGKAC | _____|257
Local hits (HSPs)   |          -          -

```

Score = 66 (35.5 bits), Expect = 42., P(2) = 1.00000
Identities = 10/13 (76%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
G TLLNE W LTA
Sbjct: 50 GGTLNNEEWVLTAA 62

Score = 35 (19.7 bits), Expect = 42., P(2) = 1.00000
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 2539 LNEHTF 2544
+NEH F
Sbjct: 33 INEHPF 38

^ = [sp|O13062|VSPC_TRIGA](#) Venom serine proteinase 2C precursor
Length = 257

```

                0          60          120          180          240

```

sp|O13062|VSPC_TRIGA | | | | | | 257
 Local hits (HSPs) | | | | | |

Score = 66 (35.5 bits), Expect = 42., P(2) = 1.00000
 Identities = 9/13 (69%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLTA 3821
 G TL+NE W LTA
 Sbjct: 50 GGTLINEEWVLT 62

Score = 35 (19.7 bits), Expect = 42., P(2) = 1.00000
 Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 2539 LNEHTF 2544
 +NEH F
 Sbjct: 33 INEHPF 38

^ = [sp|Q91510|VSP4_TRIMU](#) Microfibrase 4 precursor
 Length = 257

0 60 120 180 240 | 257
 | | | | |
 sp|Q91510|VSP4_TRIMU | | | | | |
 Local hits (HSPs) | | | | | |

Score = 66 (35.5 bits), Expect = 42., P(2) = 1.00000
 Identities = 9/13 (69%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLTA 3821
 G TL+NE W LTA
 Sbjct: 50 GGTLINEEWVLT 62

Score = 35 (19.7 bits), Expect = 42., P(2) = 1.00000
 Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 2539 LNEHTF 2544
 +NEH F
 Sbjct: 33 INEHPF 38

^ = [sp|P16295|FA9_CAVPO](#) Coagulation factor IX (Christmas factor)
 Length = 285

0 60 120 180 240 | 285
 | | | | |
 sp|P16295|FA9_CAVPO | | | | | |
 Local hits (HSPs) | | | | | |

Score = 60 (32.4 bits), Expect = 1.e+02, P(2) = 1.00000
 Identities = 6/13 (46%), Positives = 9/13 (69%)

Query: 3809 GATLLNEZWLTA 3821
 G + NE+W+ TA
 Sbjct: 85 GGSIVNEKWIVTA 97

Score = 39 (21.7 bits), Expect = 1.e+02, P(2) = 1.00000
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 170 BMGYV 174
 +MGYV
 Sbjct: 20 RMGYV 24

^ = [sp|Q9UKQ9|KLK9_HUMAN](#) Kallikrein 9 precursor (Kallikrein-like protein 3)
 (KLK-L3)
 Length = 250

0 50 100 150 200 250 | 250
 | | | | |

sp|Q9UKQ9|KLK9_HUMAN | _____
 Local hits (HSPs) | _____

Score = 66 (35.5 bits), Expect = 6.0, P = 0.997
 Identities = 9/13 (69%), Positives = 11/13 (84%)

Query: 3809 GATLLNEZWLLTA 3821
 GATL+ + WLLTA
 Sbjct: 49 GATLISDRWLLTA 61

^ = [sp|P03953|CFAD_MOUSE](#) Complement factor D precursor (C3 convertase activator)
 (Properdin factor D) (Adipsin) (28 kDa protein, adipocyte)
 Length = 259

	0	60	120	180	240	
						259
sp P03953 CFAD_MOUSE	_____					
Local hits (HSPs)	_____					

Score = 65 (35.0 bits), Expect = 8.8, P = 0.9999
 Identities = 9/13 (69%), Positives = 11/13 (84%)

Query: 3887 GATLLNEZWLLSA 3899
 G TLL+E+W LSA
 Sbjct: 52 GGTLLEQWVLSA 64

^ = [sp|Q26422|LFC_CARRO](#) Limulus clotting factor C precursor (FC)
 Length = 1019

	0	210	420	630	840	
						1019
sp Q26422 LFC_CARRO	_____					
Local hits (HSPs)	_____					

Score = 65 (35.0 bits), Expect = 36., P = 1.00000
 Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
 G LLNE+W+ TA
 Sbjct: 795 GGSLLNEKWIVTA 807

^ = [sp|P28175|LFC_TACTR](#) Limulus clotting factor C precursor (FC)
 Length = 1019

	0	210	420	630	840	
						1019
sp P28175 LFC_TACTR	_____					
Local hits (HSPs)	_____					

Score = 65 (35.0 bits), Expect = 36., P = 1.00000
 Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
 G LLNE+W+ TA
 Sbjct: 795 GGSLLNEKWIVTA 807

^ = [sp|P16296|FA9_RAT](#) Coagulation factor IX (Christmas factor)
 Length = 282

	0	60	120	180	240	
						282
sp P16296 FA9_RAT	_____					
Local hits (HSPs)	_____					

Score = 64 (34.5 bits), Expect = 14., P = 1.00000
 Identities = 6/13 (46%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
 G ++NE+W+ TA
 Sbjct: 82 GGAIINEKWIVTA 94

[^ = sp|P16294|FA9_MOUSE](#) Coagulation factor IX precursor (Christmas factor)
 Length = 459

	0	100	200	300	400		
						459	
sp P16294 FA9_MOUSE		-----					
Local hits (HSPs)							

Score = 64 (34.5 bits), Expect = 23., P = 1.00000
 Identities = 6/13 (46%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
 G ++NE+W+ TA
 Sbjct: 251 GGAIINEKWIVTA 263

[^ = sp|P44507|GRK_HAEIN](#) Glycerate kinase
 Length = 378

	0	80	160	240	320		
						378	
sp P44507 GRK_HAEIN		-----					
Local hits (HSPs)							

Score = 61 (33.0 bits), Expect = 54., P = 1.00000
 Identities = 9/11 (81%), Positives = 9/11 (81%)

Query: 977 YVMLPVADGGE 987
 YV LP ADGGE
 Sbjct: 36 YVKLPMADGGE 46

[^ = sp|P23524|GRK2_ECOLI](#) Glycerate kinase 2
 Length = 381

	0	80	160	240	320		
						381	
sp P23524 GRK2_ECOLI		-----					
Local hits (HSPs)							

Score = 61 (33.0 bits), Expect = 55., P = 1.00000
 Identities = 9/11 (81%), Positives = 9/11 (81%)

Query: 977 YVMLPVADGGE 987
 YV PVADGGE
 Sbjct: 36 YVSPVADGGE 46

[^ = sp|Q9UL52|DES1_HUMAN](#) Serine protease DESC1 precursor
 Length = 422

	0	90	180	270	360		
						422	
sp Q9UL52 DES1_HUMAN		-----					
Local hits (HSPs)							

Score = 61 (33.0 bits), Expect = 61., P = 1.00000
 Identities = 9/13 (69%), Positives = 10/13 (76%)

Query: 3887 GATLLNEZWLLSA 3899
 GATL+N WL SA
 Sbjct: 217 GATLINATWLVS A 229

[^ = sp|P39808|YVYG_BACSU](#) Hypothetical protein yvyG
 Length = 160

```

                0          40          80          120          160
                |          |          |          |          |
sp|P39808|YVYG_BACSU | _____|
Local hits (HSPs)   |          |          |          |          |

```

Score = 60 (32.4 bits), Expect = 31., P = 1.00000
 Identities = 6/12 (50%), Positives = 9/12 (75%)

Query: 1130 BNSNFNYSZNLK 1141
 + NFNYS+ +K
 Sbjct: 133 KENNFNYSKSIK 144

^ = [sp|P32038|CFAD_RAT](#) Complement factor D precursor (C3 convertase activator)
 (Properdin factor D) (Adipsin) (Endogenous vascular elastase)
 Length = 263

```

                0          60          120          180          240
                |          |          |          |          |
sp|P32038|CFAD_RAT | _____|
Local hits (HSPs)   |          |          |          |          |

```

Score = 60 (32.4 bits), Expect = 53., P = 1.00000
 Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 3887 GATLLNEZWLLSA 3899
 G TL +E+W LSA
 Sbjct: 52 GGTLVDEQWVLSA 64

^ = [sp|P16293|FA9_PIG](#) Coagulation factor IX (Christmas factor)
 Length = 271

```

                0          60          120          180          240
                |          |          |          |          |
sp|P16293|FA9_PIG | _____|
Local hits (HSPs)   |          |          |          |          |

```

Score = 60 (32.4 bits), Expect = 55., P = 1.00000
 Identities = 6/13 (46%), Positives = 9/13 (69%)

Query: 3809 GATLLNEZWLLTA 3821
 G ++NE+W TA
 Sbjct: 71 GGSIIINEKWVVT A 83

^ = [sp|P16292|FA9_RABIT](#) Coagulation factor IX (Christmas factor)
 Length = 275

```

                0          60          120          180          240
                |          |          |          |          |
sp|P16292|FA9_RABIT | _____|
Local hits (HSPs)   |          |          |          |          |

```

Score = 60 (32.4 bits), Expect = 56., P = 1.00000
 Identities = 6/13 (46%), Positives = 9/13 (69%)

Query: 3809 GATLLNEZWLLTA 3821
 G ++NE+W TA
 Sbjct: 75 GGSIIINEKWVVT A 87

^ = [sp|P19540|FA9_CANFA](#) Coagulation factor IX precursor (Christmas factor)
 Length = 452

```

                0          90          180          270          360          450
                |          |          |          |          |          |
sp|P19540|FA9_CANFA | _____|
Local hits (HSPs)   |          |          |          |          |

```

Score = 60 (32.4 bits), Expect = 93., P = 1.00000
 Identities = 6/13 (46%), Positives = 9/13 (69%)

Query: 3809 GATLLNEZWLLTA 3821
 G ++NE+W TA
 Sbjct: 244 GGSIIINEKWVTA 256

[^ = sp|Q95ND7|FA9_PANTR](#) Coagulation factor IX precursor (Christmas factor)
 Length = 461

	0	100	200	300	400	461
sp Q95ND7 FA9_PANTR						
Local hits (HSPs)		_____				

Score = 60 (32.4 bits), Expect = 95., P = 1.00000
 Identities = 6/13 (46%), Positives = 9/13 (69%)

Query: 3809 GATLLNEZWLLTA 3821
 G + NE+W+ TA
 Sbjct: 253 GGSIVNEKWIVTA 265

[^ = sp|P00740|FA9_HUMAN](#) Coagulation factor IX precursor (Christmas factor) (Plasma
 thromboplastin component) (PTC)
 Length = 461

	0	100	200	300	400	461
sp P00740 FA9_HUMAN						
Local hits (HSPs)		_____				

Score = 60 (32.4 bits), Expect = 95., P = 1.00000
 Identities = 6/13 (46%), Positives = 9/13 (69%)

Query: 3809 GATLLNEZWLLTA 3821
 G + NE+W+ TA
 Sbjct: 253 GGSIVNEKWIVTA 265

[^ = sp|P07477|TRY1_HUMAN](#) Trypsin I precursor (Cationic trypsinogen)
 Length = 247

	0	50	100	150	200	247
sp P07477 TRY1_HUMAN						
Local hits (HSPs)		_____				

Score = 59 (31.9 bits), Expect = 71., P = 1.00000
 Identities = 7/13 (53%), Positives = 9/13 (69%)

Query: 3887 GATLLNEZWLLSA 3899
 G L+NE+W SA
 Sbjct: 49 GGSLINEQWVSA 61

[^ = sp|O13058|VSP3_TRIFL](#) Venom serine proteinase 3 precursor
 Length = 257

	0	60	120	180	240	257
sp O13058 VSP3_TRIFL						
Local hits (HSPs)		_____				

Score = 59 (31.9 bits), Expect = 74., P = 1.00000
 Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 3809 GATLLNEZWLLTA 3821
 G TL+N+ W LTA
 Sbjct: 51 GGTLINQEVLTA 63

[^ = sp|P09092|HXA6_MOUSE](#) Homeobox protein Hox-A6 (Hox-1.2) (M5-4)
Length = 232

```

          0          50          100          150          200          |232
sp|P09092|HXA6_MOUSE | _____
Local hits (HSPs)   | _____

```

Score = 58 (31.4 bits), Expect = 94., P = 1.00000
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 608 GAVYGTHGR 616
GAVYG HGR
Sbjct: 147 GAVYGSHGR 155

[^ = sp|P31267|HXA6_HUMAN](#) Homeobox protein Hox-A6 (Hox-1B)
Length = 233

```

          0          50          100          150          200          |233
sp|P31267|HXA6_HUMAN | _____
Local hits (HSPs)   | _____

```

Score = 58 (31.4 bits), Expect = 95., P = 1.00000
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 608 GAVYGTHGR 616
GAVYG HGR
Sbjct: 148 GAVYGSHGR 156

[^ = sp|P48336|YCXF_CYAPA](#) Hypothetical 11.2 kDa protein in YCF23-APCF intergenic region (ORF91)
Length = 91

```

          0          20          40          60          80          |91
sp|P48336|YCXF_CYAPA | _____
Local hits (HSPs)   | _____

```

Score = 57 (30.9 bits), Expect = 48., P = 1.00000
Identities = 5/7 (71%), Positives = 7/7 (100%)

Query: 1266 BYLWNYS 1272
+Y+WNYS
Sbjct: 67 KYIWNYS 73

[^ = sp|Q8KC50|RL31_CHLTE](#) 50S ribosomal protein L31
Length = 75

```

          0          20          40          60          |75
sp|Q8KC50|RL31_CHLTE | _____
Local hits (HSPs)   | _____

```

Score = 55 (29.9 bits), Expect = 79., P = 1.00000
Identities = 6/11 (54%), Positives = 8/11 (72%)

Query: 1813 BPELHPDYSNV 1823
+PE+HP Y V
Sbjct: 2 KPEIHPKYTKV 12

[^ = sp|Q9KTM4|R31B_VIBCH](#) 50S ribosomal protein L31 type B
Length = 85

```

          0          20          40          60          80

```

```

sp|Q9KTM4|R31B_VIBCH | _____ | | | | | | | | 85
Local hits (HSPs)   | _____

```

Score = 55 (29.9 bits), Expect = 92., P = 1.00000
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2015 AGLHPDYSNV 2024
AG+HPDY V
Sbjct: 3 AGIHPDYRKV 12

Parameters:

B=50
E=100
V=50
cpus=1
echofilter
filter=none
hspmax=100
matrix=PAM30MS
nogaps
gres
qtype
sort_by_totalscore
span1
stats

ctxfactor=1.00

Query	Frame	MatID	Matrix name	----- Lambda	As Used K	----- H	----- Lambda	Computed K	----- H
	+0	0	PAM30MS	0.354	0.286	1.79	same	same	same

Query	Frame	MatID	Length	Eff.Length	E	S	W	T	X	E2	S2
	+0	0	4552	4266	78.	60	3	15	20	0.42	33

Statistics:

Query	Frame	MatID	Expected High Score	Observed High Score	HSPs Reportable
	+0	0	70 (35.7 bits)	142 (72.5 bits)	166

Query	Frame	MatID	Neighborhd Words	Word Hits	Excluded Hits	Failed Extensions	Successful Extensions	Overlaps Excluded
	+0	0	37908	145851893	13517254	131946239	388187	285846

Database: /var/local/bio/db/swissprot

Title: swissprot

Posted: 7:17:58 PM EDT May 4, 2004

Created: 7:17:58 PM EDT May 4, 2004

Format: XDF-1

of letters in database: 53,365,827

of sequences in database: 145,079

of database sequences satisfying E: 43

No. of states in DFA: 581 (62 KB)

Total size of DFA: 565 KB (2236 KB)

Time to generate neighborhood: 0.00u 0.00s 0.00t Elapsed: 00:00:00

No. of threads or processors used: 1

Search cpu time: 13.33u 0.09s 13.42t Elapsed: 00:00:15

Total cpu time: 13.34u 0.10s 13.44t Elapsed: 00:00:15

Start: Fri Feb 29 06:27:33 2008 End: Fri Feb 29 06:27:48 2008

Additional Parsing Information

Scoring Table Used 100, 12 peptides

HSP	Score
1	71
2	119
3	149
4	172
5	197
6	239

Color Coding and Additional Parsing Added by:
Jeffrey Oegema, Scionics GmbH
<http://www.scionics.de>



[Your comments](#) are highly appreciated!