



## results of **BLAST**

### **BLASTX 2.2.6 [Apr-09-2003]**

#### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

RID: 1051070402-016438-11005

**Query=** gi|29826277:21477-25244 SARS coronavirus, complete genome  
(3768 letters)

**Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF  
1,415,660 sequences; 455,667,871 total letters

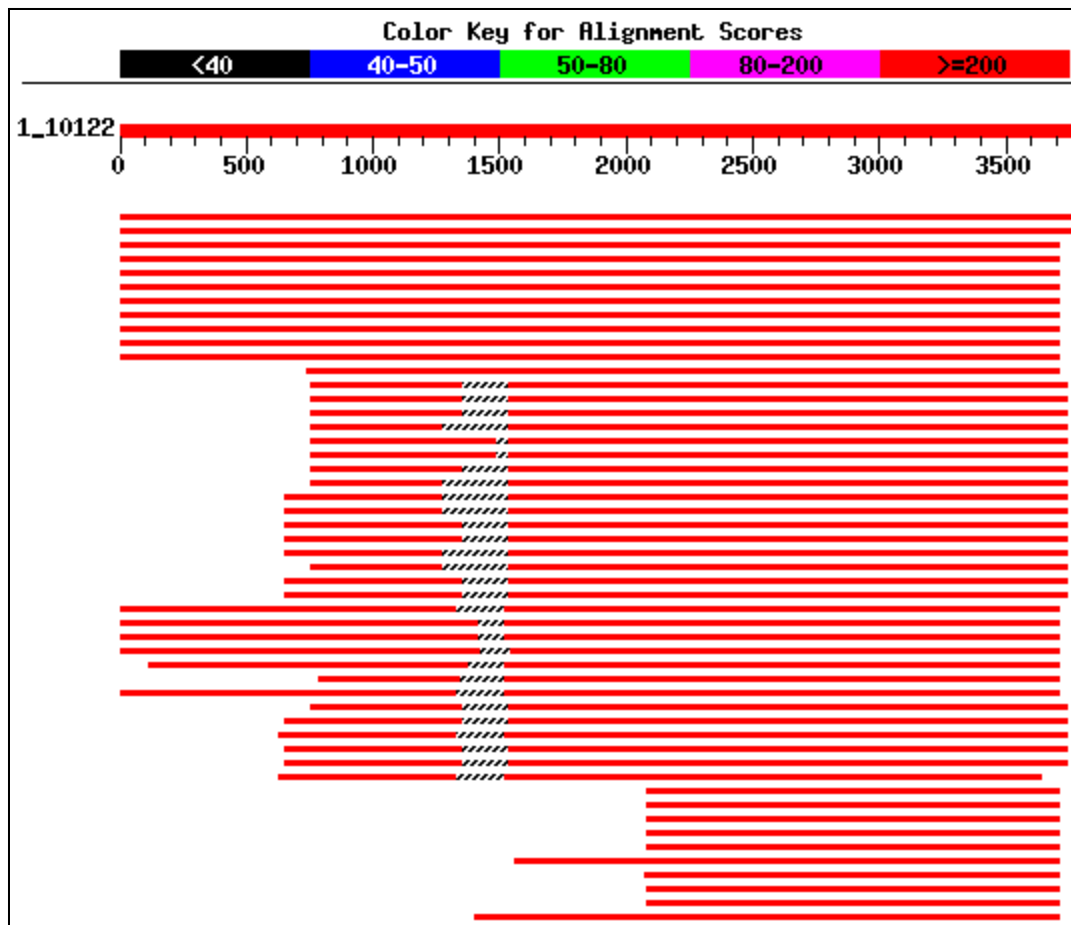
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

### [Distribution of 129 Blast Hits on the Query Sequence](#)

Mouse-over to show defline and scores. Click to show alignments

---



Sequences producing significant alignments:	Score	E
	(bits)	Value
<a href="#">gi 29836496 ref NP_828851.1 </a> putative E2 glycoprotein precu...	<a href="#">2462</a>	0.0
<a href="#">gi 30023954 gb AAP13567.1 </a> putative E2 glycoprotein precurs...	<a href="#">2456</a>	0.0
<a href="#">gi 547041 gb AAB30950.1 </a> S=viral surface peplomer {monoclon...	<a href="#">536</a>	e-150
<a href="#">gi 138178 sp P11225 VGL2_CVMJH</a> E2 glycoprotein precursor (S...	<a href="#">535</a>	e-150
<a href="#">gi 7769344 gb AAF69334.1 AF208066_5</a> spike glycoprotein prec...	<a href="#">521</a>	e-146
<a href="#">gi 74849 pir VGIH59</a> E2 glycoprotein precursor - murine hep...	<a href="#">516</a>	e-144
<a href="#">gi 7769355 gb AAF69344.1 AF208067_5</a> spike glycoprotein prec...	<a href="#">515</a>	e-144
<a href="#">gi 28916168 gb AAO59467.1 </a> hybrid spike protein [RNA transc...	<a href="#">515</a>	e-144
<a href="#">gi 9629814 ref NP_045300.1 </a> E2 glycoprotein precursor [Muri...	<a href="#">515</a>	e-144
<a href="#">gi 1352862 sp P11224 VGL2_CVMA5</a> E2 glycoprotein precursor (...)	<a href="#">514</a>	e-144
<a href="#">gi 5565844 gb AAD45229.1 AF107212_1</a> spike glycoprotein [mur...	<a href="#">504</a>	e-141
<a href="#">gi 6179903 gb AAF05704.1 </a> spike protein [murine hepatitis v...	<a href="#">501</a>	e-140
<a href="#">gi 138171 sp P25192 VGL2_CVBLY</a> E2 glycoprotein precursor (S...	<a href="#">463</a>	e-128
<a href="#">gi 6706916 gb AAF25499.1 AF058942_3</a> spike glycoprotein [bov...	<a href="#">463</a>	e-128
<a href="#">gi 74857 pir VGIHLY</a> E2 glycoprotein precursor - bovine cor...	<a href="#">461</a>	e-128
<a href="#">gi 6706938 gb AAF25519.1 AF058944_3</a> spike glycoprotein [bov...	<a href="#">461</a>	e-128
<a href="#">gi 15081547 ref NP_150077.1 </a> spike structural protein [Bovi...	<a href="#">461</a>	e-128
<a href="#">gi 138169 sp P25190 VGL2_CVBF</a> E2 glycoprotein precursor (Sp...	<a href="#">460</a>	e-128
<a href="#">gi 6706927 gb AAF25509.1 AF058943_3</a> spike glycoprotein [bov...	<a href="#">460</a>	e-128
<a href="#">gi 18033975 gb AAL57308.1 </a> spike structural protein [bovine...	<a href="#">460</a>	e-128
<a href="#">gi 138172 sp P15777 VGL2_CVBM</a> E2 glycoprotein precursor (Sp...	<a href="#">459</a>	e-127
<a href="#">gi 1352861 sp P25193 VGL2_CVBQ</a> E2 glycoprotein precursor (S...	<a href="#">457</a>	e-127
<a href="#">gi 138174 sp P25194 VGL2_CVBV</a> E2 glycoprotein precursor (Sp...	<a href="#">457</a>	e-127

<a href="#">gi 74856 pir VGIHVA</a>	E2 glycoprotein precursor - bovine cor...	<a href="#">457</a>	e-127
<a href="#">gi 74853 pir VGIHQU</a>	E2 glycoprotein precursor - bovine cor...	<a href="#">457</a>	e-127
<a href="#">gi 628284 pir S44241</a>	surface protein - human coronavirus >...	<a href="#">456</a>	e-126
<a href="#">gi 138170 sp P25191 VGL2_CVBL9</a>	E2 glycoprotein precursor (S...	<a href="#">456</a>	e-126
<a href="#">gi 628283 pir S44240</a>	surface protein - human coronavirus >...	<a href="#">454</a>	e-126
<a href="#">gi 561672 gb AAA87063.1</a>	S glycoprotein [murine hepatitis v...	<a href="#">454</a>	e-126
<a href="#">gi 465382 sp Q02385 VGL2_CVMJC</a>	E2 glycoprotein precursor (S...	<a href="#">453</a>	e-126
<a href="#">gi 138176 sp P22432 VGL2_CVM4</a>	E2 glycoprotein precursor (Sp...	<a href="#">452</a>	e-125
<a href="#">gi 561670 gb AAA87062.1</a>	S glycoprotein [murine hepatitis v...	<a href="#">452</a>	e-125
<a href="#">gi 9719318 gb AAF97738.1 AF207551_3</a>	spike protein [rat sial...	<a href="#">452</a>	e-125
<a href="#">gi 2662177 dbj BAA23719.1</a>	spike glycoprotein [Murine hepat...	<a href="#">451</a>	e-125
<a href="#">gi 1825483 gb AAC56567.1</a>	spike protein [murine hepatitis v...	<a href="#">442</a>	e-122
<a href="#">gi 549302 sp P36334 VGL2_CVHOC</a>	E2 glycoprotein precursor (S...	<a href="#">441</a>	e-122
<a href="#">gi 476773 pir A37474</a>	surface glycoprotein S - human corona...	<a href="#">439</a>	e-121
<a href="#">gi 23295760 gb AAL80031.1</a>	spike glycoprotein [porcine hema...	<a href="#">435</a>	e-120
<a href="#">gi 9653289 gb AAB27260.2</a>	surface glycoprotein S [Human cor...	<a href="#">432</a>	e-119
<a href="#">gi 420564 pir S29998</a>	surface protein - human coronavirus >...	<a href="#">432</a>	e-119
<a href="#">gi 21734849 gb AAM77000.1 AF481863_2</a>	spike glycoprotein [po...	<a href="#">430</a>	e-119
<a href="#">gi 481036 pir S37664</a>	peplomeric polyprotein precursor - av...	<a href="#">374</a>	e-102
<a href="#">gi 58987 emb CAA41065.1</a>	peplomeric polyprotein precursor [...	<a href="#">369</a>	e-100
<a href="#">gi 13378217 gb AAK18745.1</a>	spike glycoprotein, S2 subunit [...	<a href="#">365</a>	4e-99
<a href="#">gi 6425133 gb AAF08315.1</a>	spike protein precursor [Avian in...	<a href="#">362</a>	3e-98
<a href="#">gi 1321872 emb CAA60684.1</a>	spike protein [Avian infectious ...	<a href="#">356</a>	1e-96
<a href="#">gi 28274446 gb AAO34396.1</a>	spike glycoprotein [Avian infect...	<a href="#">354</a>	5e-96
<a href="#">gi 27803884 gb AAO22155.1</a>	spike glycoprotein [Avian infect...	<a href="#">353</a>	9e-96
<a href="#">gi 13448694 gb AAK27168.1</a>	spike glycoprotein [Avian infect...	<a href="#">351</a>	5e-95
<a href="#">gi 138189 sp P12650 VGL2_IBVK</a>	E2 glycoprotein precursor (Sp...	<a href="#">350</a>	1e-94
<a href="#">gi 13377887 gb AAK20887.1 AF334685_1</a>	spike glycoprotein S2 ...	<a href="#">349</a>	2e-94
<a href="#">gi 7595821 gb AAF64465.1 AF239985_1</a>	spike glycoprotein prec...	<a href="#">349</a>	2e-94
<a href="#">gi 58958 emb CAA28431.1</a>	spike protein (AA 1-1153) [Avian i...	<a href="#">346</a>	2e-93
<a href="#">gi 138190 sp P12651 VGL2_IBVM</a>	E2 glycoprotein precursor (Sp...	<a href="#">346</a>	2e-93
<a href="#">gi 4972612 gb AAD34713.1 AF094816_1</a>	spike glycoprotein prec...	<a href="#">346</a>	2e-93
<a href="#">gi 21886636 dbj BAC05493.1</a>	peplomer protein [feline infect...	<a href="#">345</a>	2e-93
<a href="#">gi 13377889 gb AAK20888.1 AF334686_1</a>	spike glycoprotein S2 ...	<a href="#">345</a>	2e-93
<a href="#">gi 806410 gb AAC54067.1</a>	spike protein precursor >gi 205839...	<a href="#">345</a>	3e-93
<a href="#">gi 8980678 gb AAF82270.1 AF239273_1</a>	spike glycoprotein, S2 ...	<a href="#">345</a>	4e-93
<a href="#">gi 138185 sp P05135 VGL2_IBV6</a>	E2 glycoprotein precursor (Sp...	<a href="#">344</a>	6e-93
<a href="#">gi 7542520 gb AAF63482.1 AF239270_1</a>	spike glycoprotein S2 s...	<a href="#">344</a>	6e-93
<a href="#">gi 8980674 gb AAF82268.1 AF239271_1</a>	spike glycoprotein, S2 ...	<a href="#">344</a>	6e-93
<a href="#">gi 11038442 gb AAF99709.2 AF288146_1</a>	spike glycoprotein S2 ...	<a href="#">344</a>	6e-93
<a href="#">gi 4972610 gb AAD34711.1 AF094814_1</a>	spike glycoprotein prec...	<a href="#">344</a>	7e-93
<a href="#">gi 13377885 gb AAK20886.1 AF334684_1</a>	spike glycoprotein S2 ...	<a href="#">344</a>	7e-93
<a href="#">gi 138187 sp P12722 VGL2_IBVD2</a>	E2 glycoprotein precursor (S...	<a href="#">343</a>	1e-92
<a href="#">gi 8980684 gb AAF82273.1 AF239276_1</a>	spike glycoprotein, S2 ...	<a href="#">343</a>	1e-92
<a href="#">gi 12585455 gb AAF82279.2 AF239282_1</a>	truncated spike glycop...	<a href="#">343</a>	1e-92
<a href="#">gi 13492237 gb AAK28144.1 AF335553_1</a>	spike glycoprotein pre...	<a href="#">343</a>	1e-92
<a href="#">gi 13492241 gb AAK28146.1 AF335555_1</a>	spike glycoprotein pre...	<a href="#">343</a>	1e-92
<a href="#">gi 4972614 gb AAD34715.1 AF094818_1</a>	spike glycoprotein prec...	<a href="#">343</a>	1e-92
<a href="#">gi 13492239 gb AAK28145.1 AF335554_1</a>	spike glycoprotein pre...	<a href="#">343</a>	1e-92
<a href="#">gi 4972615 gb AAD34716.1 AF094819_1</a>	spike glycoprotein prec...	<a href="#">343</a>	2e-92
<a href="#">gi 7595819 gb AAF64464.1 AF239984_1</a>	spike glycoprotein prec...	<a href="#">342</a>	2e-92
<a href="#">gi 4972613 gb AAD34714.1 AF094817_1</a>	spike glycoprotein prec...	<a href="#">342</a>	3e-92
<a href="#">gi 7595817 gb AAF64463.1 AF239983_1</a>	spike glycoprotein prec...	<a href="#">342</a>	3e-92
<a href="#">gi 7595815 gb AAF64462.1 AF239982_1</a>	spike glycoprotein prec...	<a href="#">342</a>	3e-92
<a href="#">gi 8980676 gb AAF82269.1 AF239272_1</a>	spike glycoprotein, S2 ...	<a href="#">342</a>	4e-92
<a href="#">gi 773177 gb AAC42112.1</a>	spike protein	<a href="#">341</a>	5e-92
<a href="#">gi 7542518 gb AAF63481.1 AF239269_1</a>	spike glycoprotein S2 s...	<a href="#">341</a>	6e-92
<a href="#">gi 12585342 gb AAF82271.2 AF239274_1</a>	truncated spike glycop...	<a href="#">340</a>	8e-92
<a href="#">gi 15011416 gb AAK77543.1 AF394180_1</a>	spike glycoprotein S2 ...	<a href="#">340</a>	8e-92
<a href="#">gi 8980682 gb AAF82272.1 AF239275_1</a>	spike glycoprotein, S2 ...	<a href="#">340</a>	1e-91

<a href="#">gi 12408749 gb AAF82277.2 AF239280.1</a>	spike glycoprotein, S2...	<a href="#">340</a>	1e-91
<a href="#">gi 21886634 dbj BAC05492.1</a>	peplomer protein [feline infect...	<a href="#">340</a>	1e-91
<a href="#">gi 9626538 ref NP_040831.1</a>	spike protein [Avian infectious...	<a href="#">340</a>	1e-91
<a href="#">gi 93907 pir S14940</a>	E2 glycoprotein precursor - avian infe...	<a href="#">340</a>	1e-91
<a href="#">gi 975637 dbj BAA06805.1</a>	peplomer protein [Feline infectio...	<a href="#">338</a>	3e-91
<a href="#">gi 481035 pir S37663</a>	peplomeric polyprotein precursor - av...	<a href="#">338</a>	3e-91
<a href="#">gi 8980690 gb AAF82276.1 AF239279.1</a>	spike glycoprotein, S2 ...	<a href="#">337</a>	7e-91
<a href="#">gi 14253130 emb CAC39300.1</a>	S protein [Avian infectious bro...	<a href="#">336</a>	2e-90
<a href="#">gi 138182 sp P24413 VGL2_CVPRM</a>	E2 GLYCOPROTEIN PRECURSOR (S...	<a href="#">322</a>	2e-86
<a href="#">gi 138181 sp P27655 VGL2_CVPR8</a>	E2 GLYCOPROTEIN PRECURSOR (S...	<a href="#">321</a>	7e-86
<a href="#">gi 540805 pir S41453</a>	spike protein - canine coronavirus >g...	<a href="#">321</a>	7e-86
<a href="#">gi 1155077 emb CAA56778.1</a>	Spike glycoprotein [Feline coron...	<a href="#">320</a>	1e-85
<a href="#">gi 13604338 gb AAK32191.1</a>	spike glycoprotein [Human corona...	<a href="#">320</a>	1e-85
<a href="#">gi 3660558 dbj BAA33439.1</a>	Spike protein [Canine coronavirus]	<a href="#">319</a>	2e-85
<a href="#">gi 332875 gb AAA46905.1</a>	S protein [Porcine respiratory cor...	<a href="#">319</a>	2e-85
<a href="#">gi 13604336 gb AAK32190.1</a>	spike glycoprotein [Human corona...	<a href="#">318</a>	3e-85
<a href="#">gi 13604332 gb AAK32188.1</a>	spike glycoprotein [Human corona...	<a href="#">318</a>	6e-85

Alignments

>[gi|29836496|ref|NP\\_828851.1](#) putative E2 glycoprotein precursor; putative spike coronavirus]  
 Length = 1255

Score = 2462 bits (6381), Expect = 0.0  
 Identities = 1214/1255 (96%), Positives = 1214/1255 (96%)  
 Frame = +1

```

Query: 1      MFIFLLFLTLTSGSDDLDRCTTFDDVQAPNYTQHTSSMRGVVYPDEIFRSDTLYLTQDLFL 180
              MFIFLLFLTLTSGSDDLDRCTTFDDVQAPNYTQHTSSMRGVVYPDEIFRSDTLYLTQDLFL
Sbjct: 1      MFIFLLFLTLTSGSDDLDRCTTFDDVQAPNYTQHTSSMRGVVYPDEIFRSDTLYLTQDLFL 60

Query: 181    PFYSNVTGFHTINHTFGNPVVPFKDGIYFAATEKSNVVRGWVFGSTMNNKXXXXXXXXXXXXX 360
              PFYSNVTGFHTINHTFGNPVVPFKDGIYFAATEKSNVVRGWVFGSTMNNK
Sbjct: 61     PFYSNVTGFHTINHTFGNPVVPFKDGIYFAATEKSNVVRGWVFGSTMNNKSQSVIIINNS 120

Query: 361    XXXXXRACNFELCDNPFFAVSKPMGTQHTMIIFDNAFNCTFEYISDAFSLDVSEKSGNFK 540
              RACNFELCDNPFFAVSKPMGTQHTMIIFDNAFNCTFEYISDAFSLDVSEKSGNFK
Sbjct: 121   TNVVIRACNFELCDNPFFAVSKPMGTQHTMIIFDNAFNCTFEYISDAFSLDVSEKSGNFK 180

Query: 541    HLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSP 720
              HLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSP
Sbjct: 181   HLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSP 240

Query: 721    AQDIWGTSAAYFVGYLKPTTFMCLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIY 900
              AQDIWGTSAAYFVGYLKPTTFMCLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIY
Sbjct: 241   AQDIWGTSAAYFVGYLKPTTFMCLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIY 300

Query: 901    QTSNFRVVPDGVVRFNPITNLCPFGEVFNATKFPVSVYAWERKKISNCVADYSVLYNSTF 1080
              QTSNFRVVPDGVVRFNPITNLCPFGEVFNATKFPVSVYAWERKKISNCVADYSVLYNSTF
Sbjct: 301   QTSNFRVVPDGVVRFNPITNLCPFGEVFNATKFPVSVYAWERKKISNCVADYSVLYNSTF 360

Query: 1081  FSTFKCYGVSATKLNLDLCSNVYADSFVVKGDDVVRQIAPGQTGVIADYNYKLPDDFMGCV 1260
              FSTFKCYGVSATKLNLDLCSNVYADSFVVKGDDVVRQIAPGQTGVIADYNYKLPDDFMGCV
  
```

Sbjct: 361 FSTFKCYGVSATKLNLDLCSNVYADSFVVKGDDVVRQIAPGQTGVIADYNYKLPDDFMGCV 420

Query: 1261 LAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPPALNCYWPLND 1440  
 LAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPPALNCYWPLND

Sbjct: 421 LAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPPALNCYWPLND 480

Query: 1441 YGFYTTTTGIGYQPYRVVVLVLSFELLNAPATVCGPKLSTDLIKQCVNFNFNGLTGTGVLTTP 1620  
 YGFYTTTTGIGYQPYRVVVLVLSFELLNAPATVCGPKLSTDLIKQCVNFNFNGLTGTGVLTTP

Sbjct: 481 YGFYTTTTGIGYQPYRVVVLVLSFELLNAPATVCGPKLSTDLIKQCVNFNFNGLTGTGVLTTP 540

Query: 1621 SSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDISPACAFGGVSVITPGTNASSEVAVLYQD 1800  
 SSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDISPACAFGGVSVITPGTNASSEVAVLYQD

Sbjct: 541 SSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDISPACAFGGVSVITPGTNASSEVAVLYQD 600

Query: 1801 VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSEYCDIPIGAGICASY 1980  
 VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSEYCDIPIGAGICASY

Sbjct: 601 VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSEYCDIPIGAGICASY 660

Query: 1981 HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDC 2160  
 HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDC

Sbjct: 661 HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDC 720

Query: 2161 NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG 2340  
 NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG

Sbjct: 721 NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG 780

Query: 2341 GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGL 2520  
 GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGL

Sbjct: 781 GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGL 840

Query: 2521 TVLPPLLTDDMIAAYTAALVSXXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYE 2700  
 TVLPPLLTDDMIAAYTAALVS LQIPFAMQMAYRFNGIGVTQNVLYE

Sbjct: 841 TVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYE 900

Query: 2701 NQKQIANQFNKAISQIQESLTTTSTALGKQLQDVVNQNAQALNTLVKQLSSNFGAISSVLN 2880  
 NQKQIANQFNKAISQIQESLTTTSTALGKQLQDVVNQNAQALNTLVKQLSSNFGAISSVLN

Sbjct: 901 NQKQIANQFNKAISQIQESLTTTSTALGKQLQDVVNQNAQALNTLVKQLSSNFGAISSVLN 960

Query: 2881 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK 3060  
 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK

Sbjct: 961 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK 1020

Query: 3061 RVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVN 3240  
 RVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVN

Sbjct: 1021 RVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVN 1080

Query: 3241 GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKN 3420  
 GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKN

Sbjct: 1081 GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKN 1140

Query: 3421 HTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL 3600  
 HTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL

Sbjct: 1141 HTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL 1200

Query: 3601 GFIAGLIAIVMVTIXXXXXXXXXXXXXKGCSCGSCCKFDEDDSEPVLKGVKLHYT 3765  
 GFIAGLIAIVMVTI KGCSCGSCCKFDEDDSEPVLKGVKLHYT

Sbjct: 1201 GFIAGLIAIVMVTILLCCMTSCCSCLKGCSCGSCCKFDEDDSEPVLKGVKLHYT 1255

>[gi|30023954|gb|AAP13567.1](#) putative E2 glycoprotein precursor [SARS coronavirus]  
 Length = 1255

Score = 2456 bits (6366), Expect = 0.0  
 Identities = 1211/1255 (96%), Positives = 1212/1255 (96%)  
 Frame = +1

```

Query: 1      MFIFLLFLTLTSGSDLRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL 180
             MFIFLLFLTLTSGSDLRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL
Sbjct: 1      MFIFLLFLTLTSGSDLRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL 60

Query: 181    PFYNSVTGFHTINHTFGNPVVPFKDGIYFAATEKSNVVRGWVFGSTMNNKXXXXXXXXXX 360
             PFYNSVTGFHTINHTF NPVVPFKDGIYFAATEKSNVVRGWVFGSTMNNK
Sbjct: 61     PFYNSVTGFHTINHTFDNPVVPFKDGIYFAATEKSNVVRGWVFGSTMNNKSQSVIIINNS 120

Query: 361    XXXXXRACNFELCDNPFPAVSKPMGTQHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK 540
             RACNFELCDNPFPAVSKPMGTQHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK
Sbjct: 121    TNVVIRACNFELCDNPFPAVSKPMGTQHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK 180

Query: 541    HLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFNTLKPFIKPLPLGINITNFRAILTAFSP 720
             HLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFNTLKPFIKPLPLGINITNFRAILTAFSP
Sbjct: 181    HLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFNTLKPFIKPLPLGINITNFRAILTAFSP 240

Query: 721    AQDIWGTSAAAAYFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIY 900
             AQD WGTSAAAAYFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIY
Sbjct: 241    AQDTWGTSAAAAYFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIY 300

Query: 901    QTSNFRVVPDGVVRFNPITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLVYNSTF 1080
             QTSNFRVVPDGVVRFNPITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLVYNSTF
Sbjct: 301    QTSNFRVVPDGVVRFNPITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLVYNSTF 360

Query: 1081   FSTFKCYGVSATKLNLDLCSNVYADSFVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCV 1260
             FSTFKCYGVSATKLNLDLCSNVYADSFVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCV
Sbjct: 361    FSTFKCYGVSATKLNLDLCSNVYADSFVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCV 420

Query: 1261   LAWNTRNIDATSTGNINYKYRYLRHGKLRPFERDISNVPFSPDGKCTPPALNCYWPLND 1440
             LAWNTRNIDATSTGNINYKYRYLRHGKLRPFERDISNVPFSPDGKCTPPALNCYWPLND
Sbjct: 421    LAWNTRNIDATSTGNINYKYRYLRHGKLRPFERDISNVPFSPDGKCTPPALNCYWPLND 480

Query: 1441   YGFYTTTIGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTTP 1620
             YGFYTTTIGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTTP
Sbjct: 481    YGFYTTTIGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTTP 540

Query: 1621   SSKRFQPFQFGRDVSDFTDSVRDPKTSEILDISPFCFAGGVSVITPGTNASSEVAVLYQD 1800
             SSKRFQPFQFGRDVSDFTDSVRDPKTSEILDISP+FGGVSVITPGTNASSEVAVLYQD
Sbjct: 541    SSKRFQPFQFGRDVSDFTDSVRDPKTSEILDISPFCFAGGVSVITPGTNASSEVAVLYQD 600

Query: 1801   VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAHEVDTSYECDIPIGAGICASY 1980
             VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAHEVDTSYECDIPIGAGICASY
Sbjct: 601    VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAHEVDTSYECDIPIGAGICASY 660

Query: 1981   HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNTTIAIPTNFSISITTEVMPVSMAKTSVDC 2160
             HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNTTIAIPTNFSISITTEVMPVSMAKTSVDC
Sbjct: 661    HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNTTIAIPTNFSISITTEVMPVSMAKTSVDC 720

Query: 2161   NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG 2340
             NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG
Sbjct: 721    NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG 780

Query: 2341   GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGL 2520
    
```

Sbjct: 781 GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGL 840

Query: 2521 TVLPPLLTTDDMIAAYTAALVSXXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYE 2700  
 TVLPPLLTTDDMIAAYTAALVS LQIPFAMQMAYRFNGIGVTQNVLYE

Sbjct: 841 TVLPPLLTTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYE 900

Query: 2701 NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN 2880  
 NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN

Sbjct: 901 NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN 960

Query: 2881 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK 3060  
 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK

Sbjct: 961 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK 1020

Query: 3061 RVDFCGKGYHLMSFPQAAPHGTVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVN 3240  
 RVDFCGKGYHLMSFPQAAPHGTVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVN

Sbjct: 1021 RVDFCGKGYHLMSFPQAAPHGTVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVN 1080

Query: 3241 GTSWFITQRNFFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKN 3420  
 GTSWFITQRNFFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKN

Sbjct: 1081 GTSWFITQRNFFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKN 1140

Query: 3421 HTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL 3600  
 HTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL

Sbjct: 1141 HTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL 1200

Query: 3601 GFIAGLIAIVMVTIXXXXXXXXXXXXXXXXXKGACSCGSCCKFDEDDSEPVLKGVKLHYT 3765  
 GFIAGLIAIVMVTI KGACSCGSCCKFDEDDSEPVLKGVKLHYT

Sbjct: 1201 GFIAGLIAIVMVTILLCCMTSCCCLGKACSCGSCCKFDEDDSEPVLKGVKLHYT 1255

>[gi|547041|gb|AAB30950.1](#) S=viral surface peplomer {monoclonal antibody resistar hepatitis virus MHV, Wb 1, MAR 11F/1, Peptide Mutant, 1235 aa]  
 Length = 1235

Score = 536 bits (1381), Expect = e-150  
 Identities = 404/1307 (30%), Positives = 600/1307 (45%), Gaps = 71/1307 (5%)  
 Frame = +1

Query: 1 MFIFLLFLTLTSGSDLRCTTFDDVQAPNYTQHTSSM-----RGVYYP-DEI 138  
 +F+F+L L G D F +Q NY + +S RG YY D +

Sbjct: 2 LFVFILLLLPSCGLGYIGD----FRCIQTVNYNGNNASAPSISTEAVDVSKGRGTYVLDREV 57

Query: 139 FRSDTLYLTQDLFLPF----YSNV--TGFHTINHTFGNP--VIPFKDGIYFAATE-KSNV 291  
 + + TL LT + P Y N+ TG +T++ T+ P + F DGI+ K+N

Sbjct: 58 YLNATLLLTG--YYPVDGSNYRNLALTGTNTLSLTFWKPPFLSEFNDGIFAKVQNLKTNT 115

Query: 292 VRGW-----VFGSTMNNKXXXXXXXXXXXXXXXXXRACNFELCDNPFPAVSKPMGTQTHT 450  
 G V GS N C + +C P+ KP

Sbjct: 116 PTGATSYFPTIVIGSLFGNTSYTVVLEPYNNIIMASVCTYTTICQLPY-TPCKP----- 167

Query: 451 MIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFYVY---KGYQPIDVVR 621  
 N + + DV K R F F +LY + +G

Sbjct: 168 -----NTNGNRVIGFWHTDVKPPICLLK--RNFTFNVNAPWLYFHFYQQGGTFYAYYA 218

Query: 622 DLPSGFNTLKIPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYD 801  
 D PS L F + +G +T + + +P T Y+V L ++ ++

Sbjct: 219 DKPSATTFL---FSVYIGDILTQYFVLPFICTPTAG--STLRPLYWVTPLLKRQYLFNFN 273

Query: 802 ENGTITDAVDCSQNPLAELKCSVKSF EIDKGIYQTSNFRVVPVSGDVVR-FPNITNLCPCFG 978  
 E G IT AVDC+ + ++E+KC +S G+Y S + V P G V R PN+ + C

Sbjct: 274 EKGVITSAVDCASSYISEIKCKTQSLLPSTGVYDLSGYTVQPVGVVYRRVPLPD-CKIE 332

Query: 979 EVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLCFSNVYADS 1158  
 E A PS WER+ NC + S L + C + A+K+ +CF +V D

Sbjct: 333 EWLTAKSVPSPNLNWERRTFQNCNFNLSLLRYVQAESLSCNNIDASKVYGMCFGVSVVDK 392

Query: 1159 FVVKGDDVVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHG 1338  
 F + + G +G + NYK+ C L ++ + T NYN R+G

Sbjct: 393 FAIPRSRQIDLQIGNSGFLQTANYKIDTAATSCQLYYSLPKNNVT-INNYNPSSWNRRYG 451

Query: 1339 KLRPFERDISNVPFSPDGKPCPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLFSFELLNA 1518  
 + +ND R + + LLN

Sbjct: 452 -----FKVND-----RCQIFANILLNG 468

Query: 1519 --PATVCGPKL---STDLIKNQCVNFNFNGLTGTGVLTTP-SSKRFQPFQFGRDVSDFTD 1680  
 T C L +T++ CV ++ G+TG GV + + +Q DV+ +

Sbjct: 469 INSGTTCSTDLQLPNTTEVATGVCVRYDLYGITGQGVFKEVKADYYNSWQALLYDVNGNLN 528

Query: 1681 SVRDPKTSEILDISPFAFGGVSIVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWR 1860  
 RD T++ I C G VS + E A+LY+++NC+ V T + + P

Sbjct: 529 GFRDLTTNKTYTIRSCYSGRVSAAYH--KEAPEPALLYRNINCSYVFTNNISREENPL-- 584

Query: 1861 IYSTGNNVFQQTQAGCLIGAEHV--DTSYECDIPIGAGICASYHTVSLLR---STSQK--S 2019  
 N F + GC++ A++ + CD+ +GAG+C Y R ST + +

Sbjct: 585 -----NYFDSYLGCVVNADNRTDEALPNCDLRMGAGLCVDYKSRARRRSVSTGYRLTT 638

Query: 2020 IVAYTMSLGADSSIAYSN-NTIAIPTNFISISITTEVMPVSMAKTSVDCNMYICGDSTECA 2196  
 Y L DS + + IPTNF+I E + + K ++DC ++CGD+ C

Sbjct: 639 FEPYMPMLVNDVSVQSVGGLYEMQIPTNFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACR 698

Query: 2197 NLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQ 2358  
 L++YGSFC +N L+ + D +V + + Q + G NFS

Sbjct: 699 QQLVEYGSFCDNVNAILNEVNNLLDNMQLQVASALMQGVTISSRLPDGISGPIDDINFSP 758

Query: 2359 ILP-----DPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQ 2505  
 +L P RS IEDLLF+KV L+D GF++ Y C G RDL+C Q

Sbjct: 759 LLGCIGSTCAEDGNGPSAIRGRSAIEDLLFDKVKLSDVGFVEAYNNCTGGQEVRLDLCVQ 818

Query: 2506 KFNGLTVLPPLLTDMMIAAYTAALVXXXXXXXXXXXXXXXXXQLIPFAMQMAYRFNGIGVTQ 2685  
 FNG+ VLPP+L++ I+ YTA + +PF++ + YR NG+GVT

Sbjct: 819 SFNGIKVLPPVLSSESQISGYTAGATAAAMFPWTAAG----VPFSLNVQYRINGLGVTM 874

Query: 2686 NVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAI 2865  
 NVL ENQK IA+ FN A+ IQE T++ALGK+Q VVN NA+ALN L+ QLS+ FGAI

Sbjct: 875 NVLSENQKMIASAFNNALGAIQEGFDATNSALGKIQSVVNANAEALNNLLNQLSNRFGAI 934

Query: 2866 SSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECV 3045  
 S+ L +IL+RLD VEA+ QIDRLI GRL +L Y+++QL + I+ SA A K++ECV

Sbjct: 935 SASLQEILTRLDAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKFSAAQAIEKVNCEV 994

Query: 3046 LGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPRE 3222  
 Q+ R+++FCG G H++S Q AP+G+ F+H +YVP+ + +P +C G + P+

Sbjct: 995 KSQTTRINFCGNGNHILSLVQNAPYGLCFIHFSYVPTSFKTANVSPGLCISGDRGLAPKA 1054

Query: 3223 GVFVFNQTSWFITQRNFFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEEL 3402  
 G FV + W T N++ P+ IT N+ V +C V + P L FKEEL

Sbjct: 1055 GYFVQDNGEWKFTGSNYYYPEPITDKNSVVMISCAVNYTKAPEVFLNNSIPNLPDFKEEL 1114  
 Query: 3403 DKYFKNHTS--PDVDLGDISGINASVVNIQKEIDRLNEVAKNLSLIDLQELGKYEQYI 3576  
 DK+FKN TS PD+ L D +N + +++ E++R+ + K LNES I+L+E+G YE Y+  
 Sbjct: 1115 DKWFKNQTSIAPDLSL-DFEKLNVTFDLTYEMNRIQDAIKKLNESYINLKEVGTYEMYV 1173  
 Query: 3577 KWPWYVVLGFIAGLIAIVMVTIXXXXXXXXXXXXXXKAC---SCGSCC 3708  
 KWPWYVWL LI + V + G+C CGSCC  
 Sbjct: 1174 KWPWYVWL-----LIGLAGVAVCVLLFFICCTGCGSCCFRCKGSCC 1215

>[gi|138178](#)|[sp|P11225|VGL2\\_CVMJH](#) E2 glycoprotein precursor (Spike glycoprotein) (  
 [Contains: Spike protein S1 (90B); Spike protein S2  
 (90A)]  
[gi|74850|pir|VGIHMJ](#) E2 glycoprotein precursor - murine hepatitis virus (strain J  
[gi|58980|emb|CAA28484.1](#) surface projection glycoprotein [Murine hepatitis virus]  
 Length = 1235

Score = 535 bits (1377), Expect = e-150  
 Identities = 403/1307 (30%), Positives = 600/1307 (45%), Gaps = 71/1307 (5%)  
 Frame = +1

Query: 1 MFIFLLFLTLTSGSDDLDRCTTFDDVQAPNYTQHTSSM-----RGVYYP-DEI 138  
 +F+F+L L G D F +Q NY + +S RG YY D +  
 Sbjct: 2 LFVFILLLLPSCGLGYIGD----FRCIQTVNYNGNNASAPSISTEAVDVSKGRGTYYVLDREV 57  
 Query: 139 FRSDTLTYLTQDLFLPF----YSNV--TGFHTINHTFGNP--VIPFKDGIYFAATE-KSNV 291  
 + + TL LT + P Y N+ TG +T++ T+ P + F DGI+ K+N  
 Sbjct: 58 YLNATLLLTG--YYPVDGSNYRNLALTGTNTLSLTFWFKPPFLSEFNDGIFAKVQNLKNT 115  
 Query: 292 VRGW-----VFGSTMNNKXXXXXXXXXXXXXXXXXACNFELCDNPFPAVSKPMGTQHT 450  
 G V GS N C + +C P+ KP  
 Sbjct: 116 PTGATSYFPTIVIGSLFGNTSYTVVLEPYNNIIMASVCTYTTICQLPY-TPCKP----- 167  
 Query: 451 MIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFYVY---KGYQPIDVVR 621  
 N + + DV K R F F +LY + +G  
 Sbjct: 168 -----NTNGNRVIGFWHTDVKPPICLLK--RNFTFNVNAPWLYFHFYQQGGTFYAYYA 218  
 Query: 622 DLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYD 801  
 D PS L F + +G +T + + +P T A Y+V L ++ ++  
 Sbjct: 219 DKPSATTFL---FSVYIGDILTQYFVLPFICTPTAG--STLAPLYWVTPLLKRQYLFNFN 273  
 Query: 802 ENGTITDAVDCSQNPLAELKCSVKSFEDKGIYQTSNFRVVPVSGDVVR-FPNITNLCPCFG 978  
 E G IT AVDC+ + ++E+KC +S G+Y S + V P G V R PN+ + C  
 Sbjct: 274 EKGVITSAVDCASSYISEIKCKTQSLLPSTGVYDLSGYTVQPVGVVYRRVPLPD-CKIE 332  
 Query: 979 EVFNATKFPVSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLCFSNVYADS 1158  
 E A PS WER+ NC + S L + C + A+K+ +CF +V D  
 Sbjct: 333 EWLTAKSVPSPLNWERRTFQNCNFNLSLLRYVQAESLSCNNIDASKVYGMCFGVSVVDK 392  
 Query: 1159 FVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNINYKYRYLRHG 1338  
 F + + G +G + NYK+ C L ++ + T NYN R+G  
 Sbjct: 393 FAIPRSRQIDLQIGNSGFLQTANYKIDTAATSCQLYYSLPKNNVT-INNYNPSSWNRRYG 451  
 Query: 1339 KLRPFERDISNVPFSPDGKPCPPALNCYWPLNDYGFYTTTIGIGYQPYRVVLSFELLNA 1518  
 + +ND R + + LLN  
 Sbjct: 452 -----FKVND-----RCQIFANILLNG 468  
 Query: 1519 --PATVCGPKL---STDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFTD 1680

Sbjct: 469 T C L +T++ CV ++ G+TG GV + + +Q DV+ +  
 INSGTTCSTDLQLPNTTEVATGVCVRYDLYGITGQGVFKEVKADYYNSWQALLYDVNGNLN 528

Query: 1681 SVRDPKTSEILDISPFAFGGVSIVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWR 1860  
 RD T++ I C G VS + E A+LY+++NC+ V T + + P

Sbjct: 529 GFRDLTTNKTYTIRSCYSGRVSAAYH--KEAPEPALLYRNINCSYVFTNNISREENPL-- 584

Query: 1861 IYSTGNNVFQQTQAGCLIGAEHV--DTSYECDIPIGAGICASYHTVSLLR---STSQK--S 2019  
 N F + GC++ A++ + C++ +GAG+C Y R ST + +

Sbjct: 585 -----NYFDSYLGCVVNADNRTDEALPNCNLRMGAGLCVDYSKSRARRRSVSTGYRLTT 638

Query: 2020 IVAYTMSLGADSSIAYSN-NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECA 2196  
 Y L DS + + IPTNF+I E + + K ++DC ++CGD+ C

Sbjct: 639 FEPYMPMLVNDQSVQSVGGLYEMQIPTNFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACR 698

Query: 2197 NLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQ 2358  
 L++YGSFC +N L+ + D +V + + Q + G NFS

Sbjct: 699 QQLVEYGSFCDNVNAILNEVNLLDNMQQLQVASALMQGVTISSRLPDGISGPIDDINFSP 758

Query: 2359 ILP-----DPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQ 2505  
 +L P RS IEDLLF+KV L+D GF++ Y C G RDL+C Q

Sbjct: 759 LLGCIGSTCAEDGNGPSAIRGRSAIEDLLFDKVKLSDVGFVEAYNNCTGGQEVRLDLCVQ 818

Query: 2506 KFNGTLVLPPLLTDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQ 2685  
 FNG+ VLPP+L++ I+ YTA + +PF++ + YR NG+GVT

Sbjct: 819 SFNGIKVLPVLSSESQISGYTAGATAAAMFPWTAAG----VPFSLNVQYRINGLGVTM 874

Query: 2686 NVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAI 2865  
 NVL ENQK IA+ FN A+ IQE T++ALGK+Q VVN NA+ALN L+ QLS+ FGAI

Sbjct: 875 NVLSENQKMIASAFNNALGAIQEGFDATNSALGKIQSVVNANAEALNNLLNQLSNRFGAI 934

Query: 2866 SSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECV 3045  
 S+ L +IL+RLD VEA+ QIDRLI GRL +L Y+++QL + I+ SA A K++ECV

Sbjct: 935 SASLQEILTRLDAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKFSAAQAIEKVNNECV 994

Query: 3046 LGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPRE 3222  
 Q+ R++FCG G H++S Q AP+G+ F+H +YVP+ + +P +C G + P+

Sbjct: 995 KSQTTTRINFCGNGNHILSLVQNPYGLCFIHFSYVPTSFKTANVSPGLCISGDRGLAPKA 1054

Query: 3223 GVFVFNQTSWFITQRNFFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEEL 3402  
 G FV + W T N++ P+ IT N+ +C V + P L FKEEL

Sbjct: 1055 GYFVQDNGEWKFTGSNYYYPEPITDKNSVAMISCAVNYTKAPEVFLNNSIPNLPDFKEEL 1114

Query: 3403 DKYFKNHTS--PDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYI 3576  
 DK+FKN TS PD+ L D +N + +++ E++R+ + K LNES I+L+E+G YE Y+

Sbjct: 1115 DKWFKNQTSIAPDLSL-DFEKLNVTFLDLTYEMNRIQDAIKKLNESYINLKEVGTYEMYV 1173

Query: 3577 KWPWYVWLGFIAGLIAIVMVTIXXXXXXXXXXXXXXKGC---SCGSCC 3708  
 KWPWYVWL LI + V + G+C CGSCC

Sbjct: 1174 KWPWYVWL-----LIGLAGVAVCVLLFFICCTGCGSCCFRKCSCC 1215

>[gi|7769344](#) | [gb|AAF69334.1](#) | [AF208066\\_5](#) spike glycoprotein precursor [murine hepati  
 Length = 1321

Score = 521 bits (1342), Expect = e-146  
 Identities = 404/1347 (29%), Positives = 616/1347 (45%), Gaps = 111/1347 (8%)  
 Frame = +1

Query: 1 MFIFLLFLTLTSGSDLD-RCTTF-----DDVQAPNYTQHT---SSMRGVYYP-DEIFRSD 150  
 +F+F+LFL G D RC +V AP+ + T S G YY D ++ +  
 Sbjct: 2 LFVFIILFLPSCGLGYIGDFRCIQLVNSNGANVSAPSISTETVEVSQGLGTYYYVLDREVYVLA 61

Query: 151 TLYLTQDLFLPFYSN-----VTGFHTINHTFGNP--VIPFKDGIYFAATE-KSNVVRGW 303  
 TL LT + P + +TG ++++ ++ P + F DGI+ K++ G  
 Sbjct: 62 TLLLTG--YYPVDGSKFRNFALTGTNSVLSWFPQPPYLSQFNDGIFAKVQNLKTSTPSGA 119

Query: 304 -----VFGSTMNNKXXXXXXXXXXXXXXXXXACNFELCDNPFVAVSKPMGTQTHMIFD 462  
 V GS C + +C P+ +  
 Sbjct: 120 TAYFPTIVIGSLFGYTSYTVVIEPYNGVIMASVCQYTICQLPYTDCKPNTNGNKLIGFWH 179

Query: 463 NAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFVYKGYQPIDVVRDLPSGFN 642  
 + F+L+V+ + F F G Y Y D PS  
 Sbjct: 180 TDVKPPICVLKRNFTLVNADAFYFH-----FYQHGGTFYAYYA-----DKPSATT 225

Query: 643 TLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITD 822  
 L F + +G +T + + +P T A Y+V L ++ +++ G IT  
 Sbjct: 226 FL---FSVYIGDILTQYYVLPFICNPTAG--STFAPRYWVTPLVKRQYLFNFNQKGVITS 280

Query: 823 AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVRFPNITNL--CPFGEVFNAT 996  
 AVDC+ + +E+KC +S G+Y+ S + V P G V R + NL C E A  
 Sbjct: 281 AVDCASSYTSEIKCKTQSMPLSTGVYELSGYTVQPVGVVYR--RVANLPACNIEEWLTAR 338

Query: 997 KFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGD 1176  
 PS WERK NC + S L + C + A+K+ CF ++ D F V  
 Sbjct: 339 SVPSPLNWERKTFQNCNFNLSLLRYVQAESLFCNNMDASKVYGRFCGSI SVDKFAVPRS 398

Query: 1177 DVRQIAPGQTGVIADYNYKLPDDFMGCVLAW----NTRNIDATSTGNYNKYRYLRHGKL 1344  
 + G +G + NYK+ C L + N I+ + ++N +Y + G  
 Sbjct: 399 RQVDLQLGNSGFLQTANYKIDTAATSCQLHYTLPKNNVTINNHNPSWNRRYGFNDAGVF 458

Query: 1345 RPFERDI-----SNVPFS-PD-GKPCTP----- 1407  
 + D+ S P + PD PCT  
 Sbjct: 459 GKNQHDVVYAQQCFTVRSSYCPCAPDIVSPCTTQTKPKSAFVNVGDHCEGLGVLEDNCG 518

Query: 1408 ---PALNCYWPLNDY-GFYTTTGIGYQPYRVVLSFELLNA--PATVCGPKL---STDLI 1560  
 P C N + G+ T + R + + LLN T C L +T+++  
 Sbjct: 519 NADPHKGCICANNSFIGWSHDTCLVND--RCQIFANILLNGINSHTTCSIDLQLPNTEVV 576

Query: 1561 KNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFTDSDVRDPKTSEILDISPCAFG 1737  
 CV ++ G+TG GV + + +Q DV+ + RD T++ I C G  
 Sbjct: 577 TGICVKYDLYGITGQGVFKEVKADYYSWQTLLYDVNGNLNGFRDLTTNKTYTIRSCYSG 636

Query: 1738 GVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNVVFQTQAGCLIGA 1917  
 VS + E A++Y+++NC+ V + + + P N F + GC++ A  
 Sbjct: 637 RVSAAFH--KDAPEPALIYRNINCSYVFSNNISREENPL-----NYFDSYLGCVVNA 686

Query: 1918 EHV--DTSYECDIPIGAGICASYHTVSLLRSTSQK-----SIVAYTMSLGADSSIAYSN- 2073  
 ++ + CD+ +G+G+C +Y T RS+ + +T+ + DS +  
 Sbjct: 687 DNRTDEALPNCDLRMGSLCVNYSTSHRARSSVSTGYKLTTFEPFTVRIVNDSVESVDGL 746

Query: 2074 NTIAIPTNFSISITTEVMPVSMAKTSDCNMYICGDSTECANLLLQYGSFCTQLNRALSG 2253  
 + IPTNF+I+ E + K ++DC ++CG T C L++YGSFC +N L  
 Sbjct: 747 YELQIPTNFTIASHQEFVQTRSPKVTIDCAAFVCGGHTACRQQLVEYGSFCNINAILGE 806

Query: 2254 IAAEQDRNTREVFAQVKQ--MYKTPTLKYFGG----FNFSQILP-----DPLKPTK 2388  
 + D +V + + Q + GG NFS +L T  
 Sbjct: 807 VNNLIDTMQLQVASALIQQVTLSSRLSDGIGGQIDDINFSPLLGCLGSDCGEVTMAAQTG 866

Query: 2389 RSFIEDLLFNKVTLDAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYT 2568  
 RS IED+LF+KV L+D GF++ Y C G RDL+C Q FNG+ VLPP+L+++ I+ YT  
 Sbjct: 867 RSAIEDVLFDKVKLSDVGFVEAYNNCTGGQEVDRLLCVQSFNGIKVLPVLSNQISGYT 926

Query: 2569 A-ALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQ 2745  
 A A VS +PF++ + YR NG+GVT NVL ENQK IA+ FN AI  
 Sbjct: 927 AGATVSAMFPWSAAAG-----VPFSLSVQYRINGLGVTMNVLSNQKMIASAFNNAIGA 980

Query: 2746 IQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQI 2925  
 IQE T++AL K+Q VVN NA+ALN L+ QLS+ FGAIS+ L +ILSRLD +EA+ QI  
 Sbjct: 981 IQEGFAATNSALAKMQFVVNANAALNLLNQLSNRFGAISASLQEILSRLDALEAQAQI 1040

Query: 2926 DRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFP 3105  
 DRLI GRL +L YV++QL ++ SA A K++ECV QS R++FCG G H++S  
 Sbjct: 1041 DRLINGRLTALNAYVSKQLSDMTLVKVSAAQAIEKVNCEVKSQSSRINFCGNGNHILSLV 1100

Query: 3106 QAAPHGVVFLHVTVYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRNFFSP 3282  
 Q AP+G+ F+H +YVP+ +P +C G + P+ G FV + W T N++ P  
 Sbjct: 1101 QNAPYGLYFIHFSYVPTSFTTANVSPGLCISGDRGLAPKAGYFVQDDGEWKFTGSNYYYP 1160

Query: 3283 QIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS--PDVDLGDIS 3456  
 + IT N+ V +C + P L FKEELDK+FKN TS PD+ L D  
 Sbjct: 1161 EPITDKNSVVMSSCAANYTKAPEVFLNTSIPNLPDFKEELDKWFKNQTSIAPDLSL-DFE 1219

Query: 3457 GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMV 3636  
 +N +++++ E++R+ + K LNES I+L+++G YE Y+KWPWYVWL LI + V  
 Sbjct: 1220 KLNVTLLDLTDEMNRIQDAIKKLNESYINLKDVGTYEMYVKWPWYVWL-----LIGLAGV 1274

Query: 3637 TIXXXXXXXXXXXXXXGAC---SCGSCC 3708  
 + G+C CG+CC  
 Sbjct: 1275 AVCVLLFFICCTGCGSCCFKCKGNCC 1301

>[gi|74849|pir||VGIH59](#) E2 glycoprotein precursor - murine hepatitis virus (strair  
 Length = 1324

Score = 516 bits (1329), Expect = e-144  
 Identities = 401/1348 (29%), Positives = 611/1348 (45%), Gaps = 112/1348 (8%)  
 Frame = +1

Query: 1 MFIFLLFLTLTSGSDLD-RCTTF-----DDVQAPNYTQHT---SSMRGVYYP-DEIFRSD 150  
 +F+F+LFL G D RC +V AP+ + T S G YY D ++ +  
 Sbjct: 2 LFVFILFLPSCGLGYIGDFRCIQLVNSNGANVSAPSISTETVEVSQGLGTYVYVLDREVYVLA 61

Query: 151 TLYLTQDLFLPFYSN-----VTGFHTINHTFGNP--VIPFKDGIYFAATE-KSNVVRGW 303  
 TL LT + P + +TG +++++ ++ P + F DGI+ K++ G  
 Sbjct: 62 TLLLTG--YYPVDGSKFRNLALTGTNSVLSWFPQPPYLNQFNDGIFAKVQNLKTSTPSGA 119

Query: 304 -----VFGSTMNNKXXXXXXXXXXXXXXXXXACNFELCDNPFVAVSKPMGTQTHMIFD 462  
 V GS C + +C P+ +  
 Sbjct: 120 TAYFPTIVIGSLFGYTSYTVVIEPYNGVIMASVCQYTICQLPYTDCKPNTNGNKLIGFWH 179

Query: 463 NAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGLYVYKGYQPIDVVRDLPSGFN 642  
 + F+L+V+ + F F G Y Y D PS  
 Sbjct: 180 TDVKPPICVLKRNFTLVNADAFYFH-----FYQHGGTFYAYYA-----DKPSATT 225

Query: 643 TLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITD 822  
 L F + +G +T + + +P T A Y+V L ++ +++ G IT  
 Sbjct: 226 FL---FSVYIGDILTQYYVLPFICNPTAG--STFAPRYWVTPLVKRQYLFNFNQKGVITS 280

Query: 823 AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVRFNPITNL--CPFGEVFNAT 996  
 AVDC+ + +E+KC +S G+Y+ S + V P G V R + NL C E A  
 Sbjct: 281 AVDCASSYTSEIKCKTQSMLPSTGVYELSGYTVQPVGVVYR--RVANLPACNIEEWLTAR 338

Query: 997 KFPSVYAWERKKISNCVADYSVLNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGD 1176  
 PS WERK NC + S L + C + A+K+ CF ++ D F V  
 Sbjct: 339 SVPSPLNWERKTFQNCNFNLSLLRYVQAESLFCNNIDASKVYGRFCFGSISVDKFAVPRS 398

Query: 1177 DVRQIAPGQGTGVIADYNYKLPDDFMGCVLAW----NTRNIDATSTGNINYKYRYLRHGKL 1344  
 + G +G + NYK+ C L + N I+ + ++N +Y + G  
 Sbjct: 399 RQVDLQLGNSGFLQTANYKIDTAATSCQLHYTLPKNNVTINNHNPSWNRRYGFNDAGVF 458

Query: 1345 RPFERDI-----SNVPFS-PD-GKPCTP----- 1407  
 + D+ S P + PD PCT  
 Sbjct: 459 GKNQHDVVYAQQCFTVRSSYCPCAPDIVSPCTTQTKPKSAFVNVGDHCEGLGVLEDNCG 518

Query: 1408 ---PALNCYWPLNDY-GFYTTTIGIGYQPYRVVLSFELLNA--PATVCGPKL---STDLI 1560  
 P C N + G+ T + R + + LLN T C L +T+++  
 Sbjct: 519 NADPHKGCICANNSFIGWSHDTCLVND--RCQIFANILLNGINSGTTCCSTDLQLPNTTEVV 576

Query: 1561 KNQCVNFNFNGLTGTGVLTP-SSKRFQPFQQFGRDVSDFTDSDVRDPKTSEILDISPCAFG 1737  
 CV ++ G+TG GV + + +Q DV+ + RD T++ I C G  
 Sbjct: 577 TGICVKYDLYGITGQGVFKEVKADYVNSWQTLTYDVNGNLNGFRDLTTNKTYTIRSCYSG 636

Query: 1738 GVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNVVFQTQAGCLIGA 1917  
 VS + E A+LY+++NC+ V + + + P N F + GC++ A  
 Sbjct: 637 RVSAAFH--KDAPEPALLYRNINCSYVFSNNISREENPL-----NYFDSYLGCVVNA 686

Query: 1918 EHV--DTSYECDIPIGAGICASYHTVSLR--RSTSQ----KSIVAYTMSLGADSSIAYSN- 2073  
 ++ + CD+ +GAG+C Y RS S + YT L DS +  
 Sbjct: 687 DNRTDEALPNCDLRMGAGLCVDYKSRRAHRSVSTGYRLTTFEPYTPMLVNDVSVQSVVDGL 746

Query: 2074 NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSG 2253  
 + IPTNF+I E + K ++DC ++CGD+T C L++YGSFC +N L+  
 Sbjct: 747 YEMQIPTNFTIGHHEEFIQTRSPKVTIDCAAFVCGDNTACRQQLVEYGSFCVNVNAILNE 806

Query: 2254 IAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQILP-----DPLKP 2382  
 + D +V ++ Q + G NFS +L P  
 Sbjct: 807 VNNLLDNMQQLQVASALMQGVTISSRLPDGISGPIDDINFSPLLGCIGSTCAEDGNGPSAI 866

Query: 2383 TKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAA 2562  
 RS IEDLLF+KV L+D GF++ Y C G RDL+C Q FNG+ VLPP+L++ I+  
 Sbjct: 867 RGRSAIEDLLFDKVKLSDVGFVEAYNNTGGQEVDRLLCVQSFNGIKVLPVLSSESQISG 926

Query: 2563 YTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTVQNVLYENQKQIANQFNKAIS 2742  
 YT + +PF++ + YR NG+GVT NVL ENQK IA+ FN A+  
 Sbjct: 927 YTTGATAAAMFPPWSAAAG----VPFSLSVQYRINGLVGTMNVLSENQKMIASAFNNALG 982

Query: 2743 QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQ 2922  
 IQ+ T++ALGK+Q VVN NA+ALN L+ QLS+ FGAIS+ L +IL+RL+ VEA+ Q  
 Sbjct: 983 AIQDGFDATNSALGKIQSVVNANAEALNLLNQLSNRFGAISASLQEIILTRLEAVEAKAQ 1042

Query: 2923 IDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHLMSF 3102  
 IDRLI GRL +L Y+++QL + I+ SA A K++ECV Q+ R++FCG G H++S  
 Sbjct: 1043 IDRLINGRLTALNAYISKQLSDSTLIKVSAAQAIEKVNCEVKSQTTRINFCGNGNHILSL 1102

Query: 3103 PQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRNFFS 3279  
 Q AP+G+ F+H +YVP +P +C G + P+ G FV + W T +++  
 Sbjct: 1103 VQNAPYGLYFIHFSYVPISTTANVSPGLCISGDRGLAPKAGYFVQDDGEWKFTGSSYYY 1162

Query: 3280 PQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS--PDVDLGDI 3453  
 P+ IT N+ + +C V + P FKEELDK+FKN TS PD+ L D  
 Sbjct: 1163 PEPITDKNSVIMSSCAVNYTKAPEVFLNTSIPNPPDFKEELDKWFKNQTSIAPDLSL-DF 1221

Query: 3454 SGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVM 3633  
 +N +++++ E++R+ + K LNES I+L+E+G YE Y+KWPWYVWL LI +  
 Sbjct: 1222 EKLNVTLTLLDLYEMNRIQDAIKKLNESYINLKEVGTYEMVYKWPWYVWL-----LIGLAG 1276

Query: 3634 VTIXXXXXXXXXXXXXXKGAC---SCGSCC 3708  
 V + G+C CG+CC  
 Sbjct: 1277 VAVCVLLFFICCTGCGSCCFKKCGNCC 1304

>gi|7769355|gb|AAF69344.1|AF208067\_5 spike glycoprotein precursor [murine hepati  
 Length = 1324

Score = 515 bits (1326), Expect = e-144  
 Identities = 400/1348 (29%), Positives = 611/1348 (45%), Gaps = 112/1348 (8%)  
 Frame = +1

Query: 1 MFIFLLFLTLTSGSDDL-RCTTF-----DDVQAPNYTQHT---SSMRGVYYP-DEIFRSD 150  
 +F+F+LFL G D RC +V AP+ + T S G YY D ++ +  
 Sbjct: 2 LFFVILFLPSCSLGYIGDFRCIQLVNSNGANVSAPSISTETVEVSQGLGTYVLDLDRVYLN 61

Query: 151 TLYLTQDLFLPFYSN-----VTGFHTINHTFGNP--VIPFKDGIYFAATE-KSNVVRGW 303  
 TL LT + P + +TG +++++ ++ P + F DGI+ K++ G  
 Sbjct: 62 TLLLTG--YYPVDGSKFRNLALTGTNSVLSLWFPYLSQFNDGIFAKVQNLKTSTPSGA 119

Query: 304 -----VFGSTMNNKXXXXXXXXXXXXXXXXXACNFELCDNPFVAVSKPMGTQTHMIFD 462  
 V GS C + +C P+ +  
 Sbjct: 120 TAYFPTIVIGSLFGYTSYTVVIEPYNGVIMASVCQYTICQLPYTDCKPNTNGNKLIGFWH 179

Query: 463 NAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFVYVYKGYQPIDVVRDLPSGFN 642  
 + F+L+V+ + F F G Y Y D PS  
 Sbjct: 180 TDVKPPICVLKRNFTLNVNADAFYFH-----FYQHGGTFYAYYA-----DKPSATT 225

Query: 643 TLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITD 822  
 L F + +G +T+ + +P T A Y+V L ++ +++ G IT  
 Sbjct: 226 FL---FSVYIGDILTQYYVLPFICNPTAG--STFAPRYWVTPLVKRQYLFNFNQKGVITS 280

Query: 823 AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVRFPNITNL--CPFGEVFNAT 996  
 AVDC+ + +E+KC +S G+Y+ S + V P G V R + NL C E A  
 Sbjct: 281 AVDCASSYTSEIKCKTQSMPLPSTGVYELSGYTVQPVGVVYR--RVANLPACNIEEWLTAR 338

Query: 997 KFPSVYAWERKKISNCVADYSVLNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGD 1176  
 PS WERK NC + S L + C + A+K+ CF ++ D F V  
 Sbjct: 339 SVPSPLNWERKTFQNCNFNLSLLRYVQAESLFCNNMDASKVYGRFCFSGSISVDKFAVPRS 398

Query: 1177 DVRQIAPGQTGVIADYNYKLPDDFMGCVLAW----NTRNIDATSTGNINYKYRYLRHGKL 1344  
 + G +G + NYK+ C L + N I+ + ++N +Y + G  
 Sbjct: 399 RQVDLQLGNSGFLQTANYKIDTAATSCQLHYTLPKNNVTINNHNPSWNRRYGFNDAGVF 458

Query: 1345 RPFERDI-----SNVPFS-PD-GKPCTP----- 1407  
 + D+ S P + PD PCT  
 Sbjct: 459 GKNQHDVVYAQQCFVTRSSYCPCAPDIVSPCTTQTKPKSAFVNVDHCEGLGVLEDNCG 518

Query: 1408 ---PALNCYWPLNDY-GFYTTTIGIGYQPYRVVLSFELLNA--PATVCGPKL---STDLI 1560  
 P C N + G+ T + R + + LLN T C L +T+++

Sbjct: 519 NADPHKGCICANNSFIGWSHDTCLVND--RCQIFANILLNGINS GTTCSTDLQLPNTTEVV 576

Query: 1561 KNQCVNFNFNGLTGTGVLTP--SSKRFQPFQQFGRDVSDFTDSDVRDPKTSEILDISPCAFG 1737  
 CV ++ G+TG GV + + +Q DV+ + RD T++ I C G

Sbjct: 577 TGICVKYDLYGITGQGVFKEVKADYNSWQTLLEYDVGNGNLNGFRDLTTNKTYTIRSCYSG 636

Query: 1738 GVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNVVFQTQAGCLIGA 1917  
 VS + E A++Y+++NC+ V + + + P N F + GC++ A

Sbjct: 637 RVSAAFH--KDAPEPALIYRNINCSYVFSNNISREENPL-----NYFDSYLGCVVNA 686

Query: 1918 EHV--DTSYECDIPIGAGICASYHTVSL--RSTSQ----KSIVAYTMSLGADSSIAYSN- 2073  
 ++ + CD+ +GAG+C Y RS S + YT L DS +

Sbjct: 687 DNRTDEALPNCDLRMGAGLCVDYSKSRRAHRSVSTGYRLTTFEPYTPMLVNSVQSV DGL 746

Query: 2074 NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSG 2253  
 + IPTNF+I E + K ++DC ++CGD+T C L++YGSFC +N L+

Sbjct: 747 YEMQIPTNFTIGHHEEFIQTRSPKVTIDCAAFCVCGDNTACRQQLVEYGSFCVNVNAILNE 806

Query: 2254 IAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQILP-----DPLKP 2382  
 + D +V + + Q + G NFS +L P

Sbjct: 807 VNNLLDNMQQLQVASALMQGVTISSRLPDGISGPIDDINFSPLLGCIGSTCAEDGNGPSAI 866

Query: 2383 TKRSFIEDLLFNKVTLDAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAA 2562  
 RS IEDLLF+KV L+D GF++ Y C G RDL+C Q FNG+ VLPP+L++ I+

Sbjct: 867 RGRSAIEDLLFDKVKLSDVGFVEAYNNCTGGQEVDRLLCVQSFNGIKVLPVLSSESQISG 926

Query: 2563 YTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTVQNVLYENQKQIANQFNKAIS 2742  
 YT + +PF++ + YR NG+GVT NVL ENQK IA+ FN A+

Sbjct: 927 YTTGATAAAMFPPWSAAAG----VPFSLSVQYRINGLGVTMNVLSENQKMIASAFNNALG 982

Query: 2743 QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQ 2922  
 IQ+ T++ALGK+Q VVN NA+ALN L+ QLS+ FGAIS+ L +IL+RL+ VEA+ Q

Sbjct: 983 AIQDGFDATNSALGKIQSVVNANAEALNLLNQLSNRFGAISASLQEILTRLEAVEAKAQ 1042

Query: 2923 IDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF 3102  
 IDRLI GRL +L Y+++QL + I+ SA A K++ECV Q+ R++FCG G H++S

Sbjct: 1043 IDRLINGRLTALNAYISKQLSDSTLIKVSAAQAIKVNNECVKSQNTTRINFCGNGNHILSL 1102

Query: 3103 PQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRNFFS 3279  
 Q AP+G+ F+H +YVP +P +C G + P+ G FV + W T +++

Sbjct: 1103 VQNAPYGLYFIHFSYVPISFTTANVSPGLCISGDRGLAPKAGYFVQDDGEWKFTGSSYYY 1162

Query: 3280 PQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS--PDVDLGDI 3453  
 P+ IT N+ + +C V + P FKEELDK+FKN TS PD+ L D

Sbjct: 1163 PEPITDKNSVIMSSCAVNYTKAPEVFLNTSIPNPPDFKEELDKWFKNQTSIAPDLSL-DF 1221

Query: 3454 SGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVM 3633  
 +N +++++ E++R+ + K LNES I+L+E+G YE Y+KWPWYVWL LI +

Sbjct: 1222 EKLNVTLLDLTYEMNRIQDAIKKLNESYINLKEVGTYEMYVKWPWYVWL-----LIGLAG 1276

Query: 3634 VTIXXXXXXXXXXXXXXGAC---SCGSCC 3708  
 V + G+C CG+CC

Sbjct: 1277 VAVCVLLFFICCCTGCGSCCFKKCGNCC 1304

>[gi|28916168|gb|AAO59467.1](#) hybrid spike protein [RNA transcription vector pBRD] Length = 1324

Score = 515 bits (1326), Expect = e-144

Identities = 400/1349 (29%), Positives = 611/1349 (45%), Gaps = 113/1349 (8%)  
 Frame = +1

Query: 1 MFIFLLFLTLTSGSDLD-RCTTF-----DDVQAPNYTQHT---SSMRGVYYP-DEIFRSD 150  
 +F+F+LFL G D RC +V AP+ + T S G YY D ++ +  
 Sbjct: 2 LFVVFILFLPSCLGYGDFRCIQLVNSNGANVSAPSISTETVEVSQQLGTYVLDLDRVYLN 61

Query: 151 TLYLTQDLFLPFYSN-----VTGFHTINHTFGNP--VIPFKDGIYFAATE-KSNVVRGW 303  
 TL LT + P + + G ++++ ++ P + F DGI+ K++ G  
 Sbjct: 62 TLLLTG--YYPVDGSKFRNLALRGTNSVLSWFPQPPYLNQFNDGIFAKVQNLKTSTPSGA 119

Query: 304 -----VFGSTMNNKXXXXXXXXXXXXXXXXXRRACNFELCDNPFPAVSKPMGTQHTMIFD 462  
 V GS C + +C P+ +  
 Sbjct: 120 TAYFPTIVIGSLFGYTSYTVVIEPYNGVIMASVCQYTICQLPYTDCKPNTNGNKLIGFWH 179

Query: 463 NAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGLYVYKGYQPIDVVRDLPSGFN 642  
 + F+L+V+ + F F G Y Y D PS  
 Sbjct: 180 TDVKPPICVLKRNFTLNVNADAFYFH-----FYQHGGTFYAYYA-----DKPSATT 225

Query: 643 TLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITD 822  
 L F + +G +T+ + +P T A Y+V L ++ +++ G IT  
 Sbjct: 226 FL---FSVYIGDILTQYVYVLPFICNPTAG--STFAPRYWVTPLVKRQYLFNFNQKGVITS 280

Query: 823 AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVRFPNITNL--CPFGEVFNAT 996  
 AVDC+ + +E+KC +S G+Y+ S + V P G V R + NL C E A  
 Sbjct: 281 AVDCASSYTSEIKCKTQSMPLSTGVYELSGYTVQPVGVVYR--RVANLPACNIEEWLTAR 338

Query: 997 KFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGD 1176  
 PS WERK NC + S L + C + A+K+ CF ++ D F V  
 Sbjct: 339 SVPSPLNWERKTFQNCNFNLSLLRYVQAESLFCNNIDASKVYGRFCFSGSISVDKFAVPRS 398

Query: 1177 DVRQIAPGQTGVIADYNYKLPDDFMGCVLAW----NTRNIDATSTGNINYKYRYLRHGKL 1344  
 + G +G + NYK+ C L + N I+ + ++N +Y + G  
 Sbjct: 399 RQVDLQLGNSGFLQTANYKIDTAATSCQLHYTLPKNNVTINNHNPSWNRRYGFNDAGVF 458

Query: 1345 RPFERDI-----SNVPFS-PD-GKPCTP----- 1407  
 + D+ S P + PD PCT  
 Sbjct: 459 GKNQHDVVYAQQCFTVRSSYCPCAQPDI VSPCTTQTKPKSAFVNVDHCEGLGVLEDNCG 518

Query: 1408 ---PALNCYWPLNDY-GFYTTTGIGYQPYRVVLSFELLNA--PATVCGPKL---STDLI 1560  
 P C N + G+ T + R + + LLN T C L +T+++  
 Sbjct: 519 NADPHKGCICANNSFIGWSDTCLVND--RCQIFANILLNGINSGTTCSTDLQLPNTTEVV 576

Query: 1561 KNQCVNFNFNGLTGTGVLP-SSKRFQPFQFGRDVSDFTDSDVRDPKTSEILDISPCAFG 1737  
 CV ++ G+TG GV + + +Q DV+ + RD T++ I C G  
 Sbjct: 577 TGICVKYDLYGITGQGVFKEVKADYNSWQTLTYDVGNGLNDFRDLTTNKTYTIRSCYSG 636

Query: 1738 GVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGA 1917  
 VS + E A+LY+++NC+ V + + + P N F + GC++ A  
 Sbjct: 637 RVSAAFH--KDAPEPALLYRNINCSYVFSNNISREENPL-----NYFDSYLGCVVNA 686

Query: 1918 EHV--DTSYECDIPIGAGICASYHTVSLR-RSTSQ----KSIVAYTMSLGADSSIAYSN- 2073  
 ++ + CD+ +GAG+C Y RS S + YT L DS +  
 Sbjct: 687 DNRTDEALPNCDLRMGAGLCVDYKSRRAHRSVSTGYRLTTFEPYTPMLVNDVSVQSV DGL 746

Query: 2074 NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSG 2253  
 + IPTNF+I E + K ++DC ++CGD+T C L++YGSFC +N L+  
 Sbjct: 747 YEMQIPTNFTIGHHEEFIQTRSPKVTIDCAAFVCGDNTACRQQLVEYGSFCVNVNAILNE 806

Query: 2254 IAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQILP-----DPLKP 2382

```

+   D   +V + + Q   +   G       NFS +L           P
Sbjct: 807 VNNLLDNMQLVASALMQGVTISSRLPDGISGPIDDINFSPLLGCIGSTCAEDGNGPSAI 866

Query: 2383 TKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAA 2562
          RS IEDLLF+KV L+D GF++ Y C G   RDL+C Q FNG+ VLPP+L++ I+
Sbjct: 867 RGRSAIEDLLFDKVKLSDVGFVEAYNNCTGGQEVDRLLCVQSFNGIKVLPVLSSESQISG 926

Query: 2563 YTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTONVLYENQKQIANQFNKAIS 2742
          YT   +                               +PF++ + YR NG+GVT NVL ENQK IA+ FN A+
Sbjct: 927 YTTGATAAAMFPPWSAAAG----VPFSLSVQYRINGLGVTMNVLSENQKMIASAFNNALG 982

Query: 2743 QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQ 2922
          IQ+   T++ALGK+Q VVN NA+ALN L+ QLS+ FGAIS+ L +IL+RL+ VEA+ Q
Sbjct: 983 AIQDGFDATNSALGKIQSVVNANAEALNNLLNQLSNRFGAISASLQEILTRLEAVEAKAQ 1042

Query: 2923 IDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF 3102
          IDRLI GRL +L Y+++QL + I+ SA A K++ECV Q+ R++FCG G H++S
Sbjct: 1043 IDRLINGRLTALNAYISKQLSDSTLIKVSAAQAIIEKVNCEVKSQTTTRINFCGNGNHILSL 1102

Query: 3103 PQAAPHGVVFLHVTVYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRNFFS 3279
          Q AP+G+ F+H +YVP           +P +C G + P+ G FV + W T +++
Sbjct: 1103 VQNAPYGLYFIHFSYVPI SFTTANVSPGLCISGDRGLAPKAGYFVQDDGEWKFTGSSYYY 1162

Query: 3280 PQIITDNTFVSGNCDVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS--PDVDLGDI 3453
          P+ IT N+ + +C V           + P   FKEELDK+FKN TS PD+ L D
Sbjct: 1163 PEPITDKNSVIMSSCAVNYTKAPEVFLNTSIPNPPDFKEELDKWFKNQTSIAPDLSL-DF 1221

Query: 3454 SGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVM 3633
          +N +++++ E++R+ + K LNES I+L+E+G YE Y+KWPWYVWL + GL+ +
Sbjct: 1222 EKLNVTLTLDLTYEMNRIQDAIKKLNESYINLKEVGTYEMYVWKPWYVWL--LIGLVVVF 1279

Query: 3634 VTIXXXXXXXXXXXXXXXXXKGACSC----GSCC 3708
          + +                               G C C   GSCC
Sbjct: 1280 IPLLLFCCFST-----GCCGICGLGSCC 1303

```

[gi|9629814|ref|NP\\_045300.1](#) E2 glycoprotein precursor [Murine hepatitis virus]  
[gi|2641129|gb|AAB86819.1](#) E2 glycoprotein precursor [murine hepatitis virus]  
 Length = 1324

Score = 515 bits (1326), Expect = e-144  
 Identities = 401/1348 (29%), Positives = 611/1348 (45%), Gaps = 112/1348 (8%)  
 Frame = +1

```

Query: 1   MFIFLLFLTTLTSGSDDL-DCTTF-----DDVQAPNYTQHT---SSMRGVYYP-DEIFRSD 150
          +F+F+LFL   G D RC           +V AP+ + T S G YY D ++ +
Sbjct: 2   LFVVFILFLPSCLGYGDFRCIQLVNSNGANVSAPSISTETVEVSQGLGTYVVLDRVYLNA 61

Query: 151 TLYLTQDLFLPFYSN-----VTGFHTINHTFGNP--VIPFKDGIYFAATE-KSNVVRGW 303
          TL LT + P +           +TG +++++ ++ P + F DGI+ K++ G
Sbjct: 62 TLLLTLG--YYPVDGSKFRNLALTGTNSVLSLWFPYLSQFNDGIFAKVQNLKTSTPSGA 119

Query: 304 -----VFGSTMNNKXXXXXXXXXXXXXXXXXACNFELCDNPFPAVSKPMGTQTHMIFD 462
          V GS                               C + +C P+ +
Sbjct: 120 TAYFPTIVIGSLFGYTSYTVVIEPYNGVIMASVCQYTIICLLPYTDCKPNTNGNKLIGFWH 179

Query: 463 NAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFVYVYKGYQPIDVVRDLPSGFN 642
          + F+L+V+ + F           F G Y Y D PS
Sbjct: 180 TDVKPPICVLKRNFTLNVNADAFYFH-----FYQHGGTFYAYYA-----DKPSATT 225

```

Query: 643 TLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGTTID 822  
 L F + +G +T+ + +P T A Y+V L ++ +++ G IT  
 Sbjct: 226 FL---FSVYIGDILTQYYVLPFICNPTAG--STFAPRYWVTPLVKRQYLFNFNQKGVITS 280

Query: 823 AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVRFPNITNL--CPFGEVFNAT 996  
 AVDC+ + +E+KC +S G+Y+ S + V P G V R + NL C E A  
 Sbjct: 281 AVDCASSYTSEIKCKTQSMLPSTGVYELSGYTVQPVGVVYR--RVANLPACNIEEWLTAR 338

Query: 997 KFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNRYADSFVVKGD 1176  
 PS WERK NC + S L + C + A+K+ CF ++ D F V  
 Sbjct: 339 SVPSPLNWERKTFQNCNFNLSLLRYVQAESLFCNNIDASKVYGRFCGFSISVDKFAVPRS 398

Query: 1177 DVRQIAPGQTGVIADYNYKLPDDFMGCVLAW----NTRNIDATSTGNYNKYRYLRHGKL 1344  
 + G +G + NYK+ C L + N I+ + ++N +Y + G  
 Sbjct: 399 RQVDLQLGNSGFLQTANYKIDTAATSCQLHYTLPKNNVTINNHNPSWNRRYGFNDAGVF 458

Query: 1345 RPFERDI-----SNVPFS-PD-GKPCTP----- 1407  
 + D+ S P + PD PCT  
 Sbjct: 459 GKNQHDVVYAQQCFTVRSSYCPCAPDIVSPCTTQTKPKSAFVNVGDHCEGLGVLEDNCG 518

Query: 1408 ---PALNCYWPLNDY-GFYTTTIGIGYQPYRVVLSFELLNA--PATVCGPKL---STDLI 1560  
 P C N + G+ T + R + + LLN T C L +T+++  
 Sbjct: 519 NADPHKGCICANNSFIGWSHDTCLVND--RCQIFANILLNGINSGTTCSTDLQLPNTTEVV 576

Query: 1561 KNQCVNFNFNGLTGTGVLTTP-SSKRFQPFQQFGRDVSDFTDSDVRDPKTSEILDISPCAFG 1737  
 CV ++ G+TG GV + + +Q DV+ + RD T++ I C G  
 Sbjct: 577 TGICVKYDLYGITGQGVFKEVKADYNSWQTLTYDVGNGNLNGFRDLTTNKTYTIRSCYSG 636

Query: 1738 GVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNVVFQTQAGCLIGA 1917  
 VS + E A+LY+++NC+ V + + + P N F + GC++ A  
 Sbjct: 637 RVSAAFH--KDAPEPALLYRNINCSYVFSNNISREENPL-----NYFDSYLGCVVNA 686

Query: 1918 EHV--DTSYECDIPIGAGICASYHTVSLR-RSTSQ----KSIVAYTMSLGADSSIAYSN- 2073  
 ++ + CD+ +GAG+C Y RS S + YT L DS +  
 Sbjct: 687 DNRTDEALPNCDLRMGAGLCVDYKSRRADRSVSTGYRLTTFEPYTPMLVNDVSVQSVGDGL 746

Query: 2074 NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSG 2253  
 + IPTNF+I E + K ++DC ++CGD+T C L++YGSFC +N L+  
 Sbjct: 747 YEMQIPTNFTIGHHEEFIQTRSPKVTIDCAAFVCGDNTACRQQLVEYGSFCVNVNAILNE 806

Query: 2254 IAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQILP-----DPLKP 2382  
 + D +V + + Q + G NFS +L P  
 Sbjct: 807 VNNLLDNMQLVASALMQGVTISSRLPDGISGPIDDINFSPLLGCIGSTCAEDGNGPSAI 866

Query: 2383 TKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAA 2562  
 RS IEDLLF+KV L+D GF++ Y C G RDL+C Q FNG+ VLPP+L++ I+  
 Sbjct: 867 RGRSAIEDLLFDKVKLSDVGVFEAYNNCTGGQEVDRLLCVQSFNGIKVLPVLSSESQISG 926

Query: 2563 YTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTONVLYENQKQIANQFNKAIS 2742  
 YT + +PF++ + YR NG+GVT NVL ENQK IA+ FN A+  
 Sbjct: 927 YTTGATAAAMFPPWSAAAG----VPFSLSVQYRINGLVGVTMNVLSENQKMIASAFNNALG 982

Query: 2743 QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQ 2922  
 IQ+ T++ALGK+Q VVN NA+ALN L+ QLS+ FGAI+ L +IL+RL+ VEA+ Q  
 Sbjct: 983 AIQDGFDFATNSALGKIQSVVNANAEALNNLLNQLSNRFGAISASLQEILTRLEAVEAKAQ 1042

Query: 2923 IDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF 3102  
 IDRLI GRL +L Y+++QL + I+ SA A K++ECV Q+ R+++FCG G H++S  
 Sbjct: 1043 IDRLINGRLTALNAYISKQLSDSTLIKVSAAQAIIEKVNCEVKSQTTRINFCGNGNHILSL 1102

Query: 3103 PQAAPHGVVFLHVITYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTWSFITQRNFFS 3279  
 Q AP+G+ F+H +YVP +P +C G + P+ G FV + W T +++  
 Sbjct: 1103 VQNAPYGLYFIHFSYVPISTTANVSPGLCISGDRGLAPKAGYFVQDDGEWKFTGSSYYY 1162

Query: 3280 PQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS--PDVDLGDI 3453  
 P+ IT N+ + +C V + P FKEELDK+FKN TS PD+ L D  
 Sbjct: 1163 PEPITDKNSVIMSSCAVNYTKAPEVFLNTSIPNPPDFKEELDKWFKNQTSIAPDLSL-DF 1221

Query: 3454 SGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVM 3633  
 +N +++++ E++R+ + K LNES I+L+E+G YE Y+KWPWYVWL LI +  
 Sbjct: 1222 EKLNVTLLDLTYEMNRIQDAIKKLNESYINLKEVGTYEMVYKWPWYVWL-----LIGLAG 1276

Query: 3634 VTIXXXXXXXXXXXXXXXXXKAC---SCGSCC 3708  
 V + G+C CG+CC  
 Sbjct: 1277 VAVCVLLFFICCTGCGSCCFKKCGNCC 1304

>[gi|1352862|sp|P11224|VGL2\\_CVMA5](#) E2 glycoprotein precursor (Spike glycoprotein)  
 [Contains: Spike protein S1 (90B); Spike protein S2 (90A)]  
[gi|331845|gb|AAA46455.1|](#) membrane associated glycoprotein E2 precursor [murine he  
 virus]  
 Length = 1324

Score = 514 bits (1323), Expect = e-144  
 Identities = 400/1348 (29%), Positives = 610/1348 (45%), Gaps = 112/1348 (8%)  
 Frame = +1

Query: 1 MFIFLLFLTLTSGSDLD-RCTTF-----DDVQAPNYTQHT---SSMRGVYYP-DEIFRSD 150  
 +F+F+LFL G D RC +V AP+ + T S G YY D ++ +  
 Sbjct: 2 LFVVFILFLPSCGLGYIGDFRCIQLVNSNGANVSAPSISTETVEVSQGLGTYVLDLDRVYLN 61

Query: 151 TLYLTQDLFLPFYSN-----VTGFHTINHTFGNP--VIPFKDGIYFAATE-KSNVVRGW 303  
 TL LT + P + + G +++++ ++ P + F DGI+ K++ G  
 Sbjct: 62 TLLLGTG--YYPVDGSKFRNLALRGTNSVLSWFPQPPYLNQFNDGIFAKVQNLKTSTPSGA 119

Query: 304 -----VFGSTMNNKXXXXXXXXXXXXXXXXXRACNFELCDNPFVAVSKPMGTQHTMIFD 462  
 V GS C + +C P+ +  
 Sbjct: 120 TAYFPTIVIGSLFGYTSYTVVIEPYNGVIMASVCQYTICQLPYTDCKPNTNGNKLIGFWH 179

Query: 463 NAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFN 642  
 + F+L+V+ + F F G Y Y D PS  
 Sbjct: 180 TDVKPPICVLKRNFTLNVNADAFYFH-----FYQHGGTFYAYYA-----DKPSATT 225

Query: 643 TLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITD 822  
 L F + +G +T + + +P T A Y+V L ++ +++ G IT  
 Sbjct: 226 FL---FSVYIGDILTQYYVLPFICNPTAG--STFAPRYWVTPLVKRQYLFNFNQKGVITS 280

Query: 823 AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVRFNPITNL--CPFGEVFNAT 996  
 AVDC+ + +E+KC +S G+Y+ S + V P G V R + NL C E A  
 Sbjct: 281 AVDCASSYTSEIKCKTQSMPLSTGVYELSGYTVQPVGVVYR--RVANLPACNIEEWLTAR 338

Query: 997 KFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLCFSNVYADSFVVKGD 1176  
 PS WERK NC + S L + C + A+K+ CF ++ D F V  
 Sbjct: 339 SVPSPLNWERKTFQNCNFNLSLLRYVQAESLFCNNIDASKVYGRFCFSGSISVDKFAVPRS 398

Query: 1177 DVRQIAPGQTGVIADYNYKLPDDFMGCVLAW----NTRNIDATSTGNINYKYRYLRHGKL 1344  
 + G +G + NYK+ C L + N I+ + ++N +Y + G

Sbjct: 399 RQVDLQLGNSGFLQQTANYKIDTAATSCQLHYTLPKNNVTINNHNPSWNRRYGFNDAGVF 458

Query: 1345 RPFERDI-----SNVPFS-PD-GKPCTP----- 1407  
 + D+ S P + PD PCT

Sbjct: 459 GKNQHADVVAQQCFTVRSSYCPCAPDIVSPCTTQTKPKSAFVNVGDHCEGLGVLEDNCG 518

Query: 1408 ---PALNCYWPLNDY-GFYTTTGIGYQPYRVVLSFELLNA--PATVCGPKL---STDLI 1560  
 P C N + G+ T + R + + LLN T C L +T+++

Sbjct: 519 NADPHKGCICANNSFIGWSHDTCLVND--RCQIFANILLNGINSGTTCSTDLQLPNTTEVV 576

Query: 1561 KNQCVNFNFNGLTGTGVLTP-SSKRFQPFQQFGRDVSDFTDVSRDPKTSEILDISPCAFG 1737  
 CV ++ G+TG GV + + +Q DV+ + RD T++ I C G

Sbjct: 577 TGICVKYDLYGITGQGVFKEVKADYNSWQTLTYDVGNGLNNGFRDLTTNKTYTIRSCYSG 636

Query: 1738 GVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGA 1917  
 VS + E A+LY+++NC+ V + + + P N F + GC++ A

Sbjct: 637 RVSAAFH--KDAPEPALLYRNINCSYVFSNNISREENPL-----NYFDSYLGCVVNA 686

Query: 1918 EHV--DTSYECDIPIGAGICASYHTVSLR-RSTSQ----KSIVAYTMSLGADSSIAYSN- 2073  
 ++ + CD+ +GAG+C Y RS S + YT L DS +

Sbjct: 687 DNRTDEALPNCDLRMGAGLCVDYKSRRAHRSVSTGYRLTTFEPYTPMLVNDVSVQSV DGL 746

Query: 2074 NTIAIPTNFSISITTEVMPVSMAKTSVDCNMVICGDSTECANLLLQYGSFCTQLNRALSG 2253  
 + IPTNF+I E + K ++DC ++CGD+T C L++YGSFC +N L+

Sbjct: 747 YEMQIPTNFTIGHHEEFIQTRSPKVTIDCAAFVCGDNTACRQQLVEYGSFCVNVNAILNE 806

Query: 2254 IAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQILP-----DPLKP 2382  
 + D +V + + Q + G NFS +L P

Sbjct: 807 VNNLLDNMQLVASALMQGVTISSRLPDGISGPIDDINFSPLLGCIGSTCAEDGNGPSAI 866

Query: 2383 TKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAA 2562  
 RS IEDLLF+KV L+D GF++ Y C G RDL+C Q FNG+ VLPP+L++ I+

Sbjct: 867 RGRSAIEDLLFDKVKLSDVGFVEAYNNCTGGQEVDRLLCVQSFNGIKVLPVLSSESQISG 926

Query: 2563 YTAALVSXXXXXXXXXXXXXXXXLQIPFAMQAMAYRFNGIGVTQNVLYENQKQIANQFNKAIS 2742  
 YT + +PF++ + YR NG+GVT NVL ENQK IA+ FN A+

Sbjct: 927 YTTGATAAAMFPPWSAAAG----VPFSLSVQYRINGLVGVTMNVLSNQKMIASAFNNALG 982

Query: 2743 QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQ 2922  
 IQ+ T+++ALGK+Q VVN NA+ALN L+ QLS+ FGAIS+ L +IL+RL+ VEA+ Q

Sbjct: 983 AIQDGF DATNSALGKIQSVVNANAEALNLLNQLSNRFGAISASLQEILTRLEAVEAKAQ 1042

Query: 2923 IDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMFS 3102  
 IDRLI GRL +L Y+++QL + I+ SA A K++ECV Q+ R++FCG G H++S

Sbjct: 1043 IDRLINGRLTALNAYISKQLSDSTLIKVSAAQAIKVNCEVKSQTTRINFCGNGNHILSL 1102

Query: 3103 PQAAPHGVVFLHVTVYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTTSWFITQRNFFS 3279  
 Q AP+G+ F+H +YVP +P +C G + P+ G FV + W T +++

Sbjct: 1103 VQNAPYGLYFIHFSYVPI SFTTANVSPGLCISGDRGLAPKAGYFVQDDGEWKFTGSSYYY 1162

Query: 3280 PQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS--PDVDLGDI 3453  
 P+ IT N+ + +C V + P FKEELDK+FKN TS PD+ L D

Sbjct: 1163 PEPITDKNSVIMSSCAVNYTKAPEVFLNTSIPNPPDFKEELDKWFKNQTSIAPDLSL-DF 1221

Query: 3454 SGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVM 3633  
 +N +++++ E++R+ + K LNES I+L+E+G YE Y+KWPWYVWL LI +

Sbjct: 1222 EKLNVTLLDLTYEMNRIQDAIKKLNESYINLKEVGTYEMYVKWPWYVWL-----LIGLAG 1276

Query: 3634 VTIXXXXXXXXXXXXXXKAC---SCGSCC 3708  
 V + G+C CG+CC

Sbjct: 1277 VAVCVLLFFICCTGCGSCCFKKCGNCC 1304

>[gi|5565844|gb|AAD45229.1|AF107212\\_1](#) spike glycoprotein [murine hepatitis virus]  
 Length = 1223

Score = 504 bits (1298), Expect = e-141  
 Identities = 399/1307 (30%), Positives = 591/1307 (45%), Gaps = 71/1307 (5%)  
 Frame = +1

```

Query: 1 MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSM-----RGVYYP-DEI 138
      +F+F+L L G D F +Q NY + +S RG YY D +
Sbjct: 2 LFVFIILLPSCGLGYIGD----FRCIQTVNYNGNNASAPSISTEAVDVSKGRGTYVLDLDRV 57

Query: 139 FRSDTLYLTQDLFLPF----YSNV--TGFHTINHTFGNP--VIPFKDGIYFAATE-KSNV 291
      + + TL LT + P Y N+ TG +T++ T+ P + F DGI+ K+N
Sbjct: 58 YLNATLLLTG--YYPVDGSNYRNLALTGTNTLSLTFWKPPFLSEFNDGIFAKVQNLKNTNT 115

Query: 292 VRGW-----VFGSTMNNKXXXXXXXXXXXXXXXXXRRACNFELCDNPFPAVSKPMGTQHT 450
      G V GS N C + +C P+ KP
Sbjct: 116 PTGATSYFPTIVIGSLFGNTSYTVVLEPYNNIIMASVCTYTICQLPY-TPCKP----- 167

Query: 451 MIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFYVY--KGYQPIDVVR 621
      N + + DV K R F F +LY + +G
Sbjct: 168 -----NTNGNRVIGFWHTDVKPPICLLK--RNFTFNVNAPWLYFHFYQQGGTFYAYYA 218

Query: 622 DLPSGFNTLKPFIKLPKLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPPTTFMLKYD 801
      D PS L F + +G +T + + +P T A Y+V L ++ ++
Sbjct: 219 DKPSATTFL---FSVYIGDILTQYFVLPFICTPTAG--STLAPLYWVTPLLKRQYLFNFN 273

Query: 802 ENGTITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVR-FPNITNLCPCFG 978
      E G IT AVDC+ + ++E+KC +S G+Y S + V P G V R PN+ + C
Sbjct: 274 EKGVITSAVDCASSYISEIKCKTQSLLPSTGVYDLGTYVQVGVVYRRVPLPD-CKIE 332

Query: 979 EVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADS 1158
      E A PS WER+ NC + S L + C N++ S VY
Sbjct: 333 EWLTAKSVPSPLNWERRTFQNCNFNLSLLRYVQAESLSC-----NNIDASKVYGM 384

Query: 1159 FVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNINYKYRYLRHG 1338
      F G ++ + +P +R ID GN +
Sbjct: 385 F-----GSVSVDKFAIP-----RSRQIDL-QIGNSGFL----- 411

Query: 1339 KLRPFERDISNVPFSPDGKPCPPALNCYWPLNDYGFYTTTIGIGYQPYRVVLSFELLNA 1518
      +N C L P N+ T Y P ++ LLN
Sbjct: 412 -----QTANYKIDTAATSCQ---LYYSLPKNN-----VTINNYNPSSQIFANILLNG 456

Query: 1519 --PATVCGPKL---STDLIKQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFTD 1680
      T C L +T++ CV ++ G+TG GV + + +Q DV+ +
Sbjct: 457 INSGTTCSTDLQLPNTTEVATGVCVRYDLYGITGQGVFKEVKADYYNSWQALLYDVNGNLN 516

Query: 1681 SVRDPKTSEILDISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWR 1860
      RD T++ I C G VS + E A+LY+++NC+ V T + + P
Sbjct: 517 GFRDLTTNKTYTIRSCYSGRVSAAYH--KEAPEPALLYRNINCSYVFTNNISREENPL-- 572

Query: 1861 IYSTGNNVFQTQAGCLIGAEHV--DTSYECDIPIGAGICASYHTVSLLR---STSQK--S 2019
      N F + GC++ A++ + C++ +GAG+C Y R ST + +
Sbjct: 573 -----NYFDSYLGCVVNADNRTDEALPNCNLRMGAGLCVDYSKSRARRSVSTGYRLTT 626

Query: 2020 IVAYTMSLGADSSIAYSN-NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECA 2196
    
```

Y L DS + + IPTNF+I E + + K ++DC ++CGD+ C  
 Sbjct: 627 FEPYMPMLVNDQSVQSVGGLYEMQIPTNFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACR 686  
 Query: 2197 NLLLQYGSFCTQLNRLSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQ 2358  
 L++YGSFC +N L+ + D +V + + Q + G NFS  
 Sbjct: 687 QQLVEYGSFCDNVNAILNEVNNLLDNMQLQVASALMQGVTISSRLPDGISGPIDDINFSP 746  
 Query: 2359 ILP-----DPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQ 2505  
 +L P RS IEDLLF+KV L+D GF++ Y C G RDL+C Q  
 Sbjct: 747 LLGCIGSTCAEDGNGPSAIRGRSAIEDLLFDKVKLSDVGFVEAYNNCTGGQEVRLDLCVQ 806  
 Query: 2506 KFNGLTVLPPLLTDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQ 2685  
 FNG+ VLPP+L++ I+ YTA + +PF++ + YR NG+GVT  
 Sbjct: 807 SFNGIKVLPPVLSSESQISGYTAGATAAAMFPWTAAG----VPFSLNVQYRINGLGVTM 862  
 Query: 2686 NVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAI 2865  
 NVL ENQK IA+ FN A+ IQE T++ALGK+Q VVN NA+ALN L+ QLS+ FGAI  
 Sbjct: 863 NVLSENQKMIASAFNNALGAIQEGFDATNSALGKIQSVVNANAALNNLLNQLSNRFGAI 922  
 Query: 2866 SSVLNDILSRLDKVEAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECV 3045  
 S+ L +IL+RLD VEA+ QIDRLI GRL +L Y+++QL + I+ SA A K++ECV  
 Sbjct: 923 SASLQEILTRLDAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKFSAAQAIKVNNECV 982  
 Query: 3046 LGQSKRVDFCGKGYHLSFQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPRE 3222  
 Q+ R++FCG G H++S Q AP+G+ F+H +YVP+ + +P +C G + P+  
 Sbjct: 983 KSQTTTRINFCGNGNHILSLVQNPYGLCFIHFSYVPTSFKTANVSPGLCISGDRGLAPKA 1042  
 Query: 3223 GVFVFNQTSWFITQRNFFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEEL 3402  
 G FV + W T N++ P+ IT N+ +C V + P L FKEEL  
 Sbjct: 1043 GYFVQDNGEWKFTGSNYYYPEPITDKNSVAMISCAVNYTKAPEVFLNNSIPNLPDFKEEL 1102  
 Query: 3403 DKYFKNHTS--PDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYI 3576  
 DK+FKN TS PD+ L D +N + +++ E++R+ + K LNES I+L+++G YE Y+  
 Sbjct: 1103 DKWFKNQTSIAPDLSL-DFEKLNVTFDLTDEMNRIQDAIKKLNESYINLKDVGTYEMYV 1161  
 Query: 3577 KWPWYVWLGFIAGLIAIVMVTIXXXXXXXXXXXXXKGC---SCGSCC 3708  
 KWPWYVWL LI + V + G+C CGSCC  
 Sbjct: 1162 KWPWYVWL-----LIGLAGVAVCVLLFFICCTGCGSCCFKCGSCC 1203

>gi|6179903|gb|AAF05704.1| spike protein [murine hepatitis virus]  
 Length = 1361

Score = 501 bits (1291), Expect = e-140  
 Identities = 348/1116 (31%), Positives = 515/1116 (46%), Gaps = 125/1116 (11%)  
 Frame = +1

Query: 736 GTSAAAYFVGYLKPTTFMLKYDENGITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNF 915  
 G + Y+V L ++ +++ G IT AVDC+ + +E+KC +S G+Y + +  
 Sbjct: 252 GVFSPOYVWVTPLVKRQYLFNFNQKGVITSVAVDCASSYTSEIKCKTQSMNPSTGVYDLTGY 311  
 Query: 916 RVPVSGDVVRFNPITNL--CPFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFST 1089  
 V P G V R + NL C + A PS WERK NC + S L +  
 Sbjct: 312 TVQPVGVVYR--RVRNLPDCKIEDWLTAKTVPSPLNWERKTFQNCNFNLSLLRFVQAES 369  
 Query: 1090 FKCYGVSATKLNLDLCSNVYADSFVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCVL-- 1263  
 C + A+K+ +CF +V D F + + G +G + +NYK+ C L  
 Sbjct: 370 LSCSNIDASKVYGMCFGSVSIDKFAIPNRRRVDLQLGNSGFLQSFNYKIDTRATSCQLYY 429

Query: 1264 -----AWNTRN--IDATSTGNYNYKYRY-----LRHGKLRP 1350  
 +WN R D + GN + Y + P

Sbjct: 430 SLAQNNVTVINHNPSWNRRYGFNDVATFGNGKHDVAYAEACYTVGASYCPCANPSIVSP 489

Query: 1351 FERD---ISNVPFSPDGKPCPPALNCYW-----PLNDYGF-----YTTTGIGYQ 1476  
 +D +N P + C P AL PL Y + G+G

Sbjct: 490 CTQDKPKAANCPVGTRNRECNPALGSLNLFKCDCTCNPSPLTTYDLRCLQARSMLGVGDH 549

Query: 1477 PYRVVLSFELLNAPATVCGPKLSTDLIKNQCV-----NFNFNGL----- 1596  
 + VL + + C K+ C+ NF NG+

Sbjct: 550 CEGLGVLEDKCGGSNTCNCSDAFVGVWAKDSCLSNGYCHIFSNFVLNGINS GTTCSTDLQ 609

Query: 1597 -----TGTGVLTP-SSKRFQPFQFGRDVSDFTDSDVRDPKTSEILD 1716  
 TG GV + + +Q DV+ + RD T++

Sbjct: 610 LPNTEVIIGVCVKYDLYGITGQGVFKEVKADYYNSWQNLLYDVNGNLNGFRDIVTNKTYL 669

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTTQ 1896  
 I C G VS + E A+LY+++ C V + + TP N F +

Sbjct: 670 IRSCYSGRVSAAY--HQDAPEPALLYRNLKCDYVFNNNISREETPL-----NYFDSY 719

Query: 1897 AGCLIGAHEH-VDTSEY-CDIPIGAGICASY---HTVSLLRSTSQK--SIVAYTMSLGADS 2055  
 GC++ A++ + S + CD+ +G+G+C ++ H ST K + +T+S+ DS

Sbjct: 720 LGCVVNADNSTEQSVDACDLRMGSLCVNFSLAHRARRSVSTGYKLTTTFEPFTVSIVNDS 779

Query: 2056 SIAYSN-NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQ 2232  
 + + + IPTNF+I+ E + K ++DC ++CGD T C L++YGSFC

Sbjct: 780 AESVGGLYEMQIPTNFTIASHQEFIQTRSPKVTIDCAAFVCGDYTACRQQLIEYGSFCDN 839

Query: 2233 LNRALSGI-----AAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQ 2358  
 +N L + R + Q+ + +P L G SQ

Sbjct: 840 INAILGEVNNLIDTMQLQVASALIQGVTLSSRLADGISGQIDDINFSPLLGCLG----SQ 895

Query: 2359 ILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPL 2538  
 + RS IEDLLF+KV L+D GF++ Y C G RDL+C Q FNG+ VLPP+

Sbjct: 896 CSEGTMAAQGRSTIEDLLFDKVKLSDVGFVEAYNNCTGGQEVRLDLCVQSFNGIKVLPV 955

Query: 2539 LTDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIA 2718  
 L+++ I+ YTA + +PF++ + YR NG+GVT NVL ENQK IA

Sbjct: 956 LSENQISGYTAGATASSMFPWSAAAG----VPFSLSVQYRINGLGVTMNVLSENQKMIA 1011

Query: 2719 NQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRL 2898  
 + FN AI IQE T++AL K+Q VVN NA+ALN L+ QLS+ FGAIS+ L +ILSRL

Sbjct: 1012 SAFNNAIGAIQEGFDATNSALAKIQSVVNANAEALNNLLNQLSNRFGAISASLQEILSRL 1071

Query: 2899 DKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCG 3078  
 D +EA+ QIDRLI GRL +L YV++QL I+ SA A K++ECV QS R++FCG

Sbjct: 1072 DALEAQAQIDRLINGRLTALNAYVSKQLSDMTLIKVSAAQAVEKVNCEVKSQSPRINFCG 1131

Query: 3079 KGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWF 3255  
 G H++S Q AP+G+ F+H +YVP+ + +C G + P+ G FV + W

Sbjct: 1132 NGNHILSLVQNAPYGLYFIHFSYVPTSFTTANVSTGLCISGDRGLAPKAGYFVQDNGEWK 1191

Query: 3256 ITQRNFFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS-- 3429  
 T N++ P+ I N+ V +C V + P L FKEELDK+FKN TS

Sbjct: 1192 FTGSNYYYPEPINDKNSVVMSSCAVNYTKAPEVFLNTSLPNLPDFKEELDKWFKNQTSVA 1251

Query: 3430 PDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFI 3609  
 PD+ L D +N + +++ E++R+ E K LNES I+L+E+G YE Y+KWPWYVWL

Sbjct: 1252 PDLSL-DFEKLNVTFDLDSGEMNRIQEAIKKLNESYINLKEVGTYEMYVKWPWYVWL--- 1307

Query: 3610 AGLIAIVMVTIXXXXXXXXXXXXXKAC---SCGSCC 3708  
 LI + V + G+C CG+CC  
 Sbjct: 1308 --LIGLAGVAVCVLLFFICCTGCGSCCFKRCGNCC 1341

>gi|138171|sp|P25192|VGL2\_CVBLY E2 glycoprotein precursor (Spike glycoprotein) (  
 [Contains: Spike protein S1 (90B); Spike protein S2  
 (90A)]  
 Length = 1363

Score = 463 bits (1191), Expect = e-128  
 Identities = 277/758 (36%), Positives = 405/758 (53%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQ 1896  
 I C G VS SSE A+L++++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAHEVDTS--YECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A++ +S CD+ +G+G C Y T R + + Y + ++  
 Sbjct: 731 LGCVVNADNSTSSAVQTCDLTVGSGYCVDYSTK---RRSRAITTYRFTNFEPFTVNSV 787

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSF 2223  
 N++ I IP+ F+I E + +S K ++DC+ ++CGD C + L++YGSF  
 Sbjct: 788 NDSLEPVGGLYEIQIPSEFTIGNMEEFIQISSPKVTIDCSAFVCGDYAACKSQLVEYGSF 847

Query: 2224 CTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQIL----PDP 2373  
 C +N L+ + D +V + T G NFS +L D  
 Sbjct: 848 CDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDINFPVLGCLGSDC 907

Query: 2374 LKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDM 2553  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+++  
 Sbjct: 908 NKVSSRSAIEDLLFSKVKLSDVGFVEAYNNCTGGAEIRDLCVQSYNGIKVLPPLLSENQ 967

Query: 2554 IAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNK 2733  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN FN  
 Sbjct: 968 ISGYTLAATSASLFPWSAAAG----VPHYLVQYRINGIGVTMDVLSQNQKLIANAFNN 1023

Query: 2734 AISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 2913  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRLD +EA  
 Sbjct: 1024 ALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISSSLQEILSRLDALEA 1083

Query: 2914 EVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHL 3093  
 + QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H+  
 Sbjct: 1084 QAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGNGNHI 1143

Query: 3094 MSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRN 3270  
 +S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T  
 Sbjct: 1144 ISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGSG 1203

Query: 3271 FFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGD 3450  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL  
 Sbjct: 1204 YYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPDL-S 1262

Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630

+ IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + GL +  
 Sbjct: 1263 LDYINVTFLDLQDEMNRLLQEAIKVLNQSYINLKDIGTYEYVVKWPWYVWL--LIGLAGVA 1320  
 Query: 3631 MVTIXXXXXXXXXXXXXXXXXKGCSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K  
 Sbjct: 1321 MLVLLFFICCTGCGTSCFKKCGGCCDDYTGHQELVIK 1358

Score = 98.2 bits (243), Expect = 9e-19  
 Identities = 54/204 (26%), Positives = 95/204 (46%), Gaps = 5/204 (2%)  
 Frame = +1

Query: 754 YFVGYLKPTTFMLKYDENGITDAVDCSQNPLAELKCSVKSF EIDKGIYQTSNFRVVPSPG 933  
 Y+V L ++L ++++G I +AVDC + ++E+KC S G+Y+ + + V P  
 Sbjct: 260 YWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIA 319  
 Query: 934 DVVR-FPNITNLCPFGEVFNATKFPVSYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS 1110  
 DV R PN+ + C N PS WERK SNC + S L + +F C +  
 Sbjct: 320 DVYRRIPNLPD-CNIEAWLNDKSVPSPLNWERKTFSNCFNMSSLMSFIQADSFTCNNID 378  
 Query: 1111 ATKLNLDLCSNVYADSFVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TR 1278  
 A K+ +CFS++ D F + + G G + +NY++ C L +N  
 Sbjct: 379 AAKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAAANV 438  
 Query: 1279 NIDATSTGNYNYKYRYLRHGKLRP 1350  
 ++ + +N ++ + +P  
 Sbjct: 439 SVSRFNPSTWNRFRGFTEQSVFKP 462

[gi|6706916|gb|AAF25499.1|AF058942\\_3](#) spike glycoprotein [bovine coronavirus]  
 Length = 1363

Score = 463 bits (1191), Expect = e-128  
 Identities = 277/758 (36%), Positives = 405/758 (53%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFTDSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680  
 Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQQTQ 1896  
 I C G VS SSE A+L++++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLSRQLQPI-----NYFDSY 730  
 Query: 1897 AGCLIGAEHVDTS--YECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A++ +S CD+ +G+G C Y T R + + Y + ++  
 Sbjct: 731 LGCVVNADNSTSSAVQTCDLTVGSGYCVDYSTK---RRSRRAITTYRFTNFEPFTVNSV 787  
 Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSF 2223  
 N++ I IP+ F+I E + +S K ++DC+ ++CGD C + L++YGSF  
 Sbjct: 788 NDSLEPVGGLYEIQIPSEFTIGNMEEFIQISSPKVTIDCSAFVCGDYAACKSQLVEYGSF 847  
 Query: 2224 CTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQIL----PDP 2373  
 C +N L+ + D +V + T G NFS +L D  
 Sbjct: 848 CDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFVDDINFSPVLGCLGSDC 907  
 Query: 2374 LKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDM 2553  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+++

Sbjct: 908 NKVSSRSAIEDLLFSKVKLSDVGFVEAYNNCTGGAEIRDLICVQSYNGIKVLPPLLESENQ 967

Query: 2554 IAAytaalvsxxxxxxxxxxxxxxxxlqipfamqmayrfngigvtqnvlyenqkqianqfnk 2733  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN FN

Sbjct: 968 ISGYTLAATSASLFPWSAAAG----VPFYLVNQYRINGIGVTMDVLSQNQKLIANAFNN 1023

Query: 2734 AISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 2913  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRLD +EA

Sbjct: 1024 ALDAIQEGFDATNSALVKIQAVVNANAALNLLQQLSNRFGAISSSLQEILSRLDALEA 1083

Query: 2914 EVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHL 3093  
 + QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H+

Sbjct: 1084 QAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGNGNHI 1143

Query: 3094 MSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRN 3270  
 +S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T

Sbjct: 1144 ISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGSG 1203

Query: 3271 FFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKNHTSPDVDLGD 3450  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL

Sbjct: 1204 YYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPDL-S 1262

Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + GL +

Sbjct: 1263 LDYINVTFLDLQDEMNRLEAIKVLNQSYINLKDIGTYEYVVKWPWYVWL--LIGLAGVA 1320

Query: 3631 MVTIXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K

Sbjct: 1321 MLVLLFFICCTGCGTSCFKKCGGCCDDYTGHQELVIK 1358

Score = 98.2 bits (243), Expect = 9e-19  
 Identities = 54/204 (26%), Positives = 95/204 (46%), Gaps = 5/204 (2%)  
 Frame = +1

Query: 754 YFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVPSG 933  
 Y+V L ++L ++++G I +AVDC + ++E+KC S G+Y+ + + V P

Sbjct: 260 YWVTPLTSKQYLLAFNQDGVIFNAVDCSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIA 319

Query: 934 DVVR-FPNITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS 1110  
 DV R PN+ + C N PS WERK SNC + S L + +F C +

Sbjct: 320 DVYRRIPNLPD-CNIEAWLNDKSVPSPLNWERKTFSNCFNMSSLMSFIQADSFTCNNID 378

Query: 1111 ATKLNLCFSNVYADSFVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TR 1278  
 A K+ +CFS++ D F + + G G + +NY++ C L +N

Sbjct: 379 AAKIYGCMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANV 438

Query: 1279 NIDATSTGNINYKYRYLRHGKLRP 1350  
 ++ + +N ++ + +P

Sbjct: 439 SVSRFNPSTWNRFRFGFTEQSVFKP 462

>[gi|74857|pir||VGIHLY](#) E2 glycoprotein precursor - bovine coronavirus (strain LY-  
 Length = 1363

Score = 461 bits (1187), Expect = e-128  
 Identities = 276/758 (36%), Positives = 404/758 (53%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+

Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQQTQ 1896  
 I C G VS SSE A+L++++ C V + QL P N F +

Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNVVFNNTLRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAEHVDTS--YECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A++ +S CD+ +G+G C Y T R + + Y + ++

Sbjct: 731 LGCVVNADNSTSSAVQTCDLTVGSGYCVDYSTK---RRSRAITTYGRFTNFEPFTVNSV 787

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSF 2223  
 N++ I IP+ F+I E + +S K ++DC+ ++CGD C + L++YGSF

Sbjct: 788 NDSLEPVGGLYEIQIPSEFTIGNMEEFIQISSPKVTIDCSAFVCGDYAACKSQLVEYGSF 847

Query: 2224 CTQLNRALSGIAAEQDRNTREVFQAQVKQMYKTPTLKYFG-----GFNFSQIL----PDP 2373  
 C +N L+ + D +V + T G NFS +L D

Sbjct: 848 CDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDINFSVPLGCLGSDC 907

Query: 2374 LKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDM 2553  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+++

Sbjct: 908 NKVSSRSAIEDLLFSKVKLSVDVGFVEAYNCTGGAEIRDLCVQSYNGIKVLPPLLESENQ 967

Query: 2554 IAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTVQNVLYENQKQIANQFNK 2733  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN FN

Sbjct: 968 ISGYTLAATSASLFPWSAAAG---VPFYLVNQYRINGIGVTMDVLSQNQKLIANAFNN 1023

Query: 2734 AISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 2913  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRLD +EA

Sbjct: 1024 ALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISSSLQEILSRLDALEA 1083

Query: 2914 EVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHL 3093  
 + QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H+

Sbjct: 1084 QAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGNGNHI 1143

Query: 3094 MSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRN 3270  
 +S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T

Sbjct: 1144 ISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGSG 1203

Query: 3271 FFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKNHTSPDVDLGD 3450  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL

Sbjct: 1204 YYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPDL-S 1262

Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +

Sbjct: 1263 LDYINVTFLDLQDEMNRLEAIAIKVLNQSYINLKDIGTYEYVVKWPWYVWL--LIGFAGVA 1320

Query: 3631 MVTIXXXXXXXXXXXXXXXXXKACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K

Sbjct: 1321 MLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIK 1358

Score = 98.2 bits (243), Expect = 9e-19  
 Identities = 54/204 (26%), Positives = 95/204 (46%), Gaps = 5/204 (2%)  
 Frame = +1

Query: 754 YFVGYLKPPTTFMLKYDENGITDAVDCSQNPLAELKCSVKSF EIDKGIYQTSNFRVVPSPG 933

Y+V L ++L ++++G I +AVDC + ++E+KC S G+Y+ + + V P  
 Sbjct: 260 YWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIA 319

Query: 934 DVVR-FPNITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS 1110  
 DV R PN+ + C N PS WERK SNC + S L + +F C +  
 Sbjct: 320 DVYRRIPNLPD-CNIEAWLNDKSVPSPLNWERKTFSNCFNMSSLMSFIQADSFTCNNID 378

Query: 1111 ATKLNLDLCSNVYADSFVVKGDDVQRQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TR 1278  
 A K+ +CFS++ D F + + G G + +NY++ C L +N  
 Sbjct: 379 AAKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSCQLYLNLPAAANV 438

Query: 1279 NIDATSTGNVNYKYRYLRHGKLRP 1350  
 ++ + +N ++ + +P  
 Sbjct: 439 SVSRFNPSTWNRFRGFTEQSVFKP 462

>[gi|6706938](#)|[gb|AAF25519.1](#)|[AF058944\\_3](#) spike glycoprotein [bovine coronavirus]  
 Length = 1363

Score = 461 bits (1187), Expect = e-128  
 Identities = 279/759 (36%), Positives = 405/759 (53%), Gaps = 24/759 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVDRPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQ 1896  
 I C G VS SSE A+L++++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAEHVDTSY--ECDIPIGAGICASYHTVSLLRSTSQKSIVA-----YTMSL 2043  
 GC++ A++ +S CD+ +G+G C Y T + S++SI +T++  
 Sbjct: 731 LGCVVNADNSTSSVVQTCDLTVGSGYCVDYST----KRRSRRSITTGYRFTNFEPFTVNS 786

Query: 2044 GADSSIAYSN-NTIAIPTNFSISITTEVMPVSMKTSVDCNMYICGDSTECANLLLQYGS 2220  
 DS I IP+ F+I E + S K ++DC+ ++CGD C + L++YGS  
 Sbjct: 787 VNSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGS 846

Query: 2221 FCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQIL----PD 2370  
 FC +N L+ + D +V + T G NFS +L D  
 Sbjct: 847 FCDNINAILTEVNELLDTTQLQVANS LMNGVTLSTKLKDGVNFNVDINFSVPLGCLGSD 906

Query: 2371 PLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDD 2550  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+++  
 Sbjct: 907 CNKVSSRSAIEDLLFSKVKLSDVGFVEAYNNCTGGAEIRDLICVQSYNGIKVLPPLLSSEN 966

Query: 2551 MIAAYTAALVSXXXXXXXXXXXXXXXXXQIPFAMQMAAYRFNGIGVTQNVLYENQKQIANQFN 2730  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN FN  
 Sbjct: 967 QISGYTLAATSASLFPWSAAAG----VPFYLVNQYRINGIGVTMDVLSQNQKLIANAFN 1022

Query: 2731 KAISQIQESLTTTSTALGKLDVVNQNQAALNTLVKQLSSNFGAISSVLNDILSRDLKVE 2910  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRDL +E  
 Sbjct: 1023 NALGAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISSSLQEILSRDLDALE 1082

Query: 2911 AEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYH 3090  
 A+ QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H  
 Sbjct: 1083 AQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNNECVKSQSSRINFCGNGNH 1142

Query: 3091 LMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTTSWFITQR 3267  
 ++S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T  
 Sbjct: 1143 IISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGS 1202

Query: 3268 NFFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLG 3447  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL  
 Sbjct: 1203 GYYYPEPITGNNVVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPDL- 1261

Query: 3448 DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAI 3627  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +  
 Sbjct: 1262 SLDYINVTFLDLQDEMNRLQEAIKVLNQSYINLKDITGYEYVVKWPWYVWL--LIGFAGV 1319

Query: 3628 VMVTIXXXXXXXXXXXXXXKACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K  
 Sbjct: 1320 AMLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIK 1358

Score = 97.8 bits (242), Expect = 1e-18  
 Identities = 52/174 (29%), Positives = 85/174 (48%), Gaps = 1/174 (0%)  
 Frame = +1

Query: 754 YFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVPSG 933  
 Y+V L ++L ++++G I +AVDC + ++E+KC S G+Y+ + + V P  
 Sbjct: 260 YWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIA 319

Query: 934 DVVR-FPNITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS 1110  
 DV R PN+ + C N PS WERK SNC + S L + +F C +  
 Sbjct: 320 DVYRRIPNLPD-CNIEAWLNDKSVPSPLNWERKTFSNCFNMSSLMSFIQADSFTCNNID 378

Query: 1111 ATKLNLDLCSNVYADSFVVKGDDVQRQIAPGQTGVIADYNYKLPDDFMGCVLAWN 1272  
 A K+ +CFS++ D F + + G G + +NY++ C L +N  
 Sbjct: 379 AAKIYGMCFSSITIDKFAIPNGRKVLDLQLGNLGYLQSFNYRIDTTATSCQLYYN 432

>[gi|15081547|ref|NP\\_150077.1](#) spike structural protein [Bovine coronavirus]  
[gi|15077811|gb|AAK83356.1](#) spike structural protein [bovine coronavirus]  
 Length = 1363

Score = 461 bits (1185), Expect = e-128  
 Identities = 279/759 (36%), Positives = 405/759 (53%), Gaps = 24/759 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLNLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQ 1896  
 I C G VS SSE A+L++++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAHEVDTSY--ECDIPIGAGICASYHTVSLLRSTSQKSIVA-----YTMSL 2043  
 GC++ A++ +S CD+ +G+G C Y T + S++SI +T++  
 Sbjct: 731 LGCVVNADNSTSSVVQTCDLTVGSGYCVDYST----KRRSRRSITTGYRFTNFEPFTVNS 786

Query: 2044 GADSSIAYSN-NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGS 2220  
 DS I IP+ F+I E + S K ++DC+ ++CGD C + L++YGS  
 Sbjct: 787 VNSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGS 846

Query: 2221 FCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTTLKYFG-----GFNFSQIL----PD 2370  
 FC +N L+ + D +V + T G NFS +L D  
 Sbjct: 847 FCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFVDDINFSPVLGCLGSD 906

Query: 2371 PLKPTKRSFIEDLLFNKVTLDAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDD 2550  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+++  
 Sbjct: 907 CNKVSSRSAIEDLLFSKVKLSDVGFVEAYNNCTGGAEIRDLICVQSYNGIKVLPPLLSSEN 966

Query: 2551 MIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTVQNVLYENQKQIANQFN 2730  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN FN  
 Sbjct: 967 QISGYTLAATSASLFPWSAAAG----VPFYLVNQYRINGIGVTMDVLSQNQKLIANAFN 1022

Query: 2731 KAISQIQESLTTTSTALGKLDQVVNQNQAALNTLVKQLSSNFGAISSVLNDILSRDLKVE 2910  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRDL +E  
 Sbjct: 1023 NALGAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISSSLQEILSRDLDALE 1082

Query: 2911 AEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYH 3090  
 A+ QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H  
 Sbjct: 1083 AQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGNGNH 1142

Query: 3091 LMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTWSFITQR 3267  
 ++S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T  
 Sbjct: 1143 IISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMTGS 1202

Query: 3268 NFFSPQIITDNTFVSGNCDVVGIIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVLG 3447  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL  
 Sbjct: 1203 GYYYPEPITGNVVMSTCAVNYTKAPDVMLNISTPNLPYFKEELDQWFKNQTSVAPDL- 1261

Query: 3448 DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAI 3627  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +  
 Sbjct: 1262 SLDYINVTFLDLQDEMNRLEAIKVLNQSINLKDITGYEYVYKWPWYVWL--LIGFAGV 1319

Query: 3628 VMVTIXXXXXXXXXXXXXXXXXKACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K  
 Sbjct: 1320 AMLVLLFFICCTGCGTSCFKKCGGCCDDYTGHQELVIK 1358

Score = 98.2 bits (243), Expect = 9e-19  
 Identities = 68/264 (25%), Positives = 112/264 (42%), Gaps = 22/264 (8%)  
 Frame = +1

Query: 754 YFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVPSG 933  
 Y+V L ++L ++++G I +AVDC + ++E+KC S G+Y+ + + V P  
 Sbjct: 260 YWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIA 319

Query: 934 DVVR-FPNITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS 1110  
 DV R PN+ + C N PS WERK SNC + S L + +F C +  
 Sbjct: 320 DVYRRIPNLPD-CNIEAWLNKSVSPNLNWERKTFNSCNFNMSLMSFIQAYSFTCNNID 378

Query: 1111 ATKLNDLCFSNVYADSFVVKGDDVQRQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TR 1278  
 A K+ +CFS++ D F + + G G + +NY++ C L +N  
 Sbjct: 379 AAKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAAV 438

Query: 1279 NIDATSTGNINYKYRYLRHGKLRP-----FERDISNVPFSPDGKPCPTP 1407  
 ++ + +N ++ + +P F+ + P DG C  
 Sbjct: 439 SVSRFNPSTWNRFRGFTEQSVFKPQPAGVFTDHDVVYAQHCFKASTNFCPCCKLDGSLCVG 498

Query: 1408 PALNCYWPLNDYGFYTTTGIGYQP 1479  
 P D G Y T+GIG P

Sbjct: 499 NG-----PGIDAG-YKTSGIGTCP 516

>[gi|138169|sp|P25190|VGL2\\_CVBF](#) E2 glycoprotein precursor (Spike glycoprotein) (F [Contains: Spike protein S1 (90B); Spike protein S2 (90A)])

[gi|74854|pir||VGIHF1](#) E2 glycoprotein precursor - bovine coronavirus (strain F15)

[gi|221137|dbj|BAA00631.1|](#) spike glycoprotein precursor [Bovine coronavirus]  
Length = 1363

Score = 460 bits (1183), Expect = e-128  
Identities = 277/762 (36%), Positives = 403/762 (52%), Gaps = 27/762 (3%)  
Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRF-QPFQQFGRDVSDFDTSVRDPKTSEILD 1716  
K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEANATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQ 1896  
I C G VS SSE A+L++++ C V + QL P N F +  
Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAEHVDTS--YECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYS 2070  
GC++ A++ S CD+ +G+G C Y ST ++S+ A T + ++  
Sbjct: 731 LGCVVNADNSTASAVQTCDLTVGSGYCVDY-----STKRRSVRAITTYRFTNFEPFT 783

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQ 2211  
N+ I IP+ F+I E + S K ++DC+ ++CGD C + L++  
Sbjct: 784 VNSVNSDLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDCAACKSQLVE 843

Query: 2212 YGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPT-LKYFGGFNFSQILPDPL---- 2376  
YGSFC +N L+ + D +V + T LK FN I P+  
Sbjct: 844 YGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDINFSVPLGCL 903

Query: 2377 -----KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLL 2541  
K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL  
Sbjct: 904 GSECNKVSSRSAIEDLLFSKVKLSVDVGFVEAYNNCTGGAEIRDLCVQSYNGIKVLPPLL 963

Query: 2542 TDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIAN 2721  
+++ I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN  
Sbjct: 964 SENQISGYTLAATSASLFPPWSAAAG----VFPYLVNQYRINGIGVTMDVLSQNQKLIAN 1019

Query: 2722 QFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLD 2901  
FN A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRLD  
Sbjct: 1020 AFNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISSSLQEILSRLD 1079

Query: 2902 KVEAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGK 3081  
+EA+ QIDRLI GR +L YV+QQL + ++ SA A K++ECV QS R++FCG  
Sbjct: 1080 ALEAQRQIDRLINGRFTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGN 1139

Query: 3082 GYHLMSFPQAAPHGVVFLHVITYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFI 3258  
G H++S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W  
Sbjct: 1140 GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWFM 1199

Query: 3259 TQRNFFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDV 3438  
T ++ P+ IT +N V C V + + + P L FKEELD++FKN TS  
Sbjct: 1200 TGSGYYYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAP 1259

Query: 3439 DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGL 3618

DL + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G  
 Sbjct: 1260 DL-SLDYINVTFLDLQDEMNRLLQEAIKLLNQSYINLKDIGTYEYVVKWPWYVWL--LIGF 1316

Query: 3619 IAIVMVTIXXXXXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 + M+ + CG CC E V+K  
 Sbjct: 1317 AGVAMLVLLFFICCTGCGTSCFKKCGGCCDDYTGHQELVIK 1358

Score = 97.8 bits (242), Expect = 1e-18  
 Identities = 52/174 (29%), Positives = 85/174 (48%), Gaps = 1/174 (0%)  
 Frame = +1

Query: 754 YFVGYLKPTTFMLKYDENGITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVPSG 933  
 Y+V L ++L ++++G I +AVDC + ++E+KC S G+Y+ + + V P  
 Sbjct: 260 YWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIA 319

Query: 934 DVVR-FPNITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS 1110  
 DV R PN+ + C N PS WERK SNC + S L + +F C +  
 Sbjct: 320 DVYRRIPNLPD-CNIEAWLNDKSVPSPLNWERKTFSNCFNMSSLMSFIQADSFTCNNID 378

Query: 1111 ATKLNLDLCSNVYADSFVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCVLAWN 1272  
 A K+ +CFS++ D F + + G G + +NY++ C L +N  
 Sbjct: 379 AAKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYN 432

>[gi|6706927](#)|[gb|AAF25509.1](#)|[AF058943\\_3](#) spike glycoprotein [bovine coronavirus]  
 Length = 1363

Score = 460 bits (1183), Expect = e-128  
 Identities = 279/759 (36%), Positives = 404/759 (53%), Gaps = 24/759 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQ 1896  
 I C G VS SSE A+L+++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNFKCNVFNNTLSRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAHEVDTSY--ECDIPIGAGICASYHTVSLLRSTSQKSIVA-----YTMSL 2043  
 GC++ A++ +S CD+ +G+G C Y T + S++SI +T++  
 Sbjct: 731 LGCVVNADNSTSSVVQTCDLTVGSGYCVDYST----KRRSRRSITTYRFTNFEPFTVNS 786

Query: 2044 GADSSIAYSN-NTIAIPTNFSISITTEVMPVSMKTSVDCNMYICGDSTECANLLLQYGS 2220  
 DS I IP+ F+I E + S K ++DC+ ++CGD C + L++YGS  
 Sbjct: 787 VNSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGS 846

Query: 2221 FCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQIL----PD 2370  
 FC +N L+ + D +V + T G NFS +L D  
 Sbjct: 847 FCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDINFSVPLVGLGSD 906

Query: 2371 PLKPTKRSFIEDLLFNKVTLDAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTTDD 2550  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+++  
 Sbjct: 907 CNKVSSRSAIEDLLFSKVKLSDVGFVEAYNNCTGGAEIRDLCVQSYNGIKVLPPLLSEN 966

Query: 2551 MIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFN 2730  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN FN

Sbjct: 967 QISGYTLAATSASLFPWSAAAG----VPFYLVNQYRINGIGVTMDVLSQNQKLIANAFN 1022

Query: 2731 KAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVE 2910  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRDL +E

Sbjct: 1023 NALGAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISSSLQEILSRDLDALE 1082

Query: 2911 AEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYH 3090  
 A+ QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H

Sbjct: 1083 AQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFCGNGNH 1142

Query: 3091 LMSFPQAAPHGVVFLHVTVYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTWSFITQR 3267  
 ++S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T

Sbjct: 1143 IISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGS 1202

Query: 3268 NFFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVLG 3447  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL

Sbjct: 1203 GYYYPEPITGNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPDL- 1261

Query: 3448 DISGINASVNNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAI 3627  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +

Sbjct: 1262 SLDYINVTFLDLQDEMNRLEAIKVLNQSYINLKDIGTYEYVYKWPWYVWL--LIGFAGV 1319

Query: 3628 VMVTIXXXXXXXXXXXXXXXXXKGACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K

Sbjct: 1320 AMLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIK 1358

Score = 98.2 bits (243), Expect = 9e-19  
 Identities = 54/204 (26%), Positives = 95/204 (46%), Gaps = 5/204 (2%)  
 Frame = +1

Query: 754 YFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVPSG 933  
 Y+V L ++L ++++G I +AVDC + ++E+KC S G+Y+ + + V P

Sbjct: 260 YWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIA 319

Query: 934 DVVR-FPNITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS 1110  
 DV R PN+ + C N PS WERK SNC + S L + +F C +

Sbjct: 320 DVYRRIPNLPD-CNIEAWLNDKSVPSPLNWERKTFSNCFNMSSLMSFIQADSFTCNNID 378

Query: 1111 ATKLNLDLCSNVYADSFVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TR 1278  
 A K+ +CFS++ D F + + G G + +NY++ C L +N

Sbjct: 379 AAKIYGMCFSSITIDKFAIPNGRKVDLQGLNGLYLQSFNYRIDTTATSCQLYYNLPAANV 438

Query: 1279 NIDATSTGNVNYKYRYLRHGKLRP 1350  
 ++ + +N ++ + +P

Sbjct: 439 SVSRFNPSTWNRFRGFTEQSVFKP 462

[>gi|18033975|gb|AAL57308.1](#) spike structural protein [bovine coronavirus]  
 Length = 1363

Score = 460 bits (1183), Expect = e-128  
 Identities = 278/759 (36%), Positives = 404/759 (53%), Gaps = 24/759 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+

Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTO 1896  
 I C G VS SSE A+L++++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNLSRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAHEVDTSY--ECDIPIGAGICASYHTVSLLRSTSQKSIVA-----YTMSL 2043  
 GC++ A++ +S CD+ +G+G C Y T + S++SI +T++  
 Sbjct: 731 LGCVVNADNSTSSVVQTCDLTVGSGYCVDYST----KRRSRRSITTGYRFTNFEPFTVNS 786

Query: 2044 GADSSIAYSN-NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGS 2220  
 DS I IP+ F+I E + S K ++DC+ ++CGD C + L++YGS  
 Sbjct: 787 VNDSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGS 846

Query: 2221 FCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQIL----PD 2370  
 FC +N L+ + D +V + T G NFS +L D  
 Sbjct: 847 FCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFVDDINFSPVLGCLGSD 906

Query: 2371 PLKPTKRSFIEDLLFNKVTLDAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDD 2550  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+++  
 Sbjct: 907 CNKVSSRSAIEDLLFSKVKLSDVGFVEAYNNCTGGAEIRDLCVQSYNGIKVLPPLLSSEN 966

Query: 2551 MIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMA YRFGIGVTQNVLYENQKQIANQFN 2730  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN FN  
 Sbjct: 967 QISGYTLAATSASLFPWSAAAG----VPFYLNQYRINGIGVTMDVLSQNQKLIANAFN 1022

Query: 2731 KAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVE 2910  
 A+ IQE T++AL K+Q VVN NA+ LN L++QLS+ FGAISS L +ILSRDL +E  
 Sbjct: 1023 NALGAIQEGFDATNSALVKIQAVVNANAETLNNLLQQLSNRFGAISSSLQEILSRDALE 1082

Query: 2911 AEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYH 3090  
 A+ QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H  
 Sbjct: 1083 AQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFCGNGNH 1142

Query: 3091 LMSFPQAAPHGVVFLHVTVYVPSQERNFTTAPAIC-HEGKAYFPREGVVFVNGTSWFITQR 3267  
 ++S Q AP+G+ F+H +YVP++ +P +C G+ P+ G FV +W T  
 Sbjct: 1143 IISLVQNPAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGGRGIAPKSGYFVNVNNTWMFTGS 1202

Query: 3268 NFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKNHTSPDVLG 3447  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL  
 Sbjct: 1203 GYYYPEPITGNVVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPDL- 1261

Query: 3448 DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAI 3627  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +  
 Sbjct: 1262 SLDYINVTFLDLQDEMNRLQEAIKVLNQSYINLKDITGYEYVYKWPWYVWL--LIGFAGV 1319

Query: 3628 VMVTIXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K  
 Sbjct: 1320 AMLVLLFFICCTGCGTSCFKKCGGCCDDYTGHELVK 1358

Score = 98.6 bits (244), Expect = 7e-19  
 Identities = 68/264 (25%), Positives = 112/264 (42%), Gaps = 22/264 (8%)  
 Frame = +1

Query: 754 YFVGYLKPPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVPSG 933  
 Y+V L ++L ++++G I +AVDC + ++E+KC S G+Y+ + + V P  
 Sbjct: 260 YWVTPLTQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTSLSIAPSTGVYELNGYTVQPIA 319

Query: 934 DVVR-FPNITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS 1110

DV R PN+ + C N PS WERK SNC + S L + +F C +  
 Sbjct: 320 DVYRRIPNLPD-CNIEAWLNDKSVPSPLNWERKTFSNCFNMSSLMSFIQADSFTCNNID 378

Query: 1111 ATKLNLDLCSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TR 1278  
 A K+ +CFS++ D F + + G G + +NY++ C L +N  
 Sbjct: 379 AAKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANV 438

Query: 1279 NIDATSTGNVNYKYRYLRHGKLRP-----FERDISNVPFSPDGKPCPTP 1407  
 ++ + +N ++ + +P F+ + P DG C  
 Sbjct: 439 SVSRFNPSTWNRFRGFTEQSVFKPQPAGVFTDHDVVYAQHCFKAPTDFCCKLDGSLCVG 498

Query: 1408 PALNCYWPLNDYGFYTTTGIGYQP 1479  
 P D G Y T+GIG P  
 Sbjct: 499 NG-----PGIDAG-YKTSIGTGP 516

>[gi|138172|sp|P15777|VGL2\\_CVBM](#) E2 glycoprotein precursor (Spike glycoprotein) (I  
 [Contains: Spike protein S1 (90B); Spike protein S2  
 (90A)]

[gi|74852|pir||VGIHNM](#) E2 glycoprotein precursor - bovine coronavirus (strain Mebus  
[gi|323362|gb|AAA66399.1|](#) spike protein precursor [bovine coronavirus]  
 Length = 1363

Score = 459 bits (1180), Expect = e-127  
 Identities = 276/758 (36%), Positives = 403/758 (53%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTTQ 1896  
 I C G VS SSE A+L++++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAEHVDTSY--ECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A++ +S CD+ +G+G C Y T R + + Y + ++  
 Sbjct: 731 LGCVVNADNSTSSVVQTCDLTVGSGYCVDYSTK---RRSRAITTYRFTTTFEPFTVNSV 787

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSDCNMYICGDSTECANLLLQYGSF 2223  
 N++ I IP+ F+I E + S K ++DC+ ++CGD C + L++YGSF  
 Sbjct: 788 NDSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSF 847

Query: 2224 CTQLNRALSGLIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQIL----PDP 2373  
 C +N L+ + D +V + T G NFS +L D  
 Sbjct: 848 CDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDINFPVLGCLGSDC 907

Query: 2374 LKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDM 2553  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+ +  
 Sbjct: 908 NKVSSRSAIEDLLFSKVKLSDVGFVEAYNNTGGAEIRDLICVQSYNGIKVLPPLLSVNQ 967

Query: 2554 IAAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNK 2733  
 I+ YT A S + +PF + + YR NGIGVT +VL +NQK IAN FN  
 Sbjct: 968 ISGYTLAATSASLFPPLSAA----VGVPFYLVNRYRINGIGVTMDVLSQNQKLIANAFNN 1023

Query: 2734 AISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 2913  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRLD +EA  
 Sbjct: 1024 ALDAIQEGFDATNSALVKIQAVVNANAALNLLQQLSNRFGAISSSLQEILSRLDALEA 1083

Query: 2914 EVQIDRLITGRQLQSLQTYVTTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHL 3093  
 + QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H+  
 Sbjct: 1084 QAQIDRLINGRLTALNVYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFCGNGNHI 1143

Query: 3094 MSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRN 3270  
 +S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T  
 Sbjct: 1144 ISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGSG 1203

Query: 3271 FFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKNHTSPDVDLGD 3450  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL  
 Sbjct: 1204 YYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLHDFKEELDQWFKNQTSVAPDL-S 1262

Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +  
 Sbjct: 1263 LDYINVTFLDLQDEMNRQLQEAIKVLNQSYINLKDIGTYEYVVKWPWYVWL--LIGFAGVA 1320

Query: 3631 MVTIXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K  
 Sbjct: 1321 MLVLLFFICCCTGCGTSCFKICGGCCDDYTGHQELVIK 1358

Score = 99.4 bits (246), Expect = 4e-19  
 Identities = 58/209 (27%), Positives = 99/209 (47%), Gaps = 1/209 (0%)  
 Frame = +1

Query: 649 KPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAAYFVGYLKPTTFMLKYDENGITITDAV 828  
 K +F + LG +++++ + S A + Y+V L ++L ++++G I +AV  
 Sbjct: 231 KFLFNVYLGTVLSHYVYVPLTLCSSAMTL-----EYWVTPLTTSKQYLLAFNQDGVIFNAV 284

Query: 829 DCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPDGVVR-FPNITNLCPFGEVFNATKFP 1005  
 DC + ++E+KC S G+Y+ + + V P DV R PN+ + C N P  
 Sbjct: 285 DCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVRRIPNLPD-CNIEAWLNKDSVP 343

Query: 1006 SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLFCFSNVYADSFVVKGDDVR 1185  
 S WERK SNC + S L + +F C + A K+ +CFS++ D F +  
 Sbjct: 344 SPLNWERKTFSNCFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPNGRKV 403

Query: 1186 QIAPGQTGVIADYNYKLPDDFMGCVLAWN 1272  
 + G G + +NY++ C L +N  
 Sbjct: 404 DLQLGNLGYLQSFNYRIDTTATSCQLYYN 432

[gi|1352861|sp|P25193|VGL2\\_CVBQ](#) E2 glycoprotein precursor (Spike glycoprotein) ( [Contains: Spike protein S1 (90B); Spike protein S2 (90A)] )  
[gi|221139|dbj|BAA00557.1](#) S peplomer polypeptide precursor [Bovine coronavirus]  
[gi|17529675|gb|AAL40400.1|AF220295\\_5](#) spike glycoprotein [bovine coronavirus]  
 Length = 1363

Score = 457 bits (1177), Expect = e-127  
 Identities = 276/758 (36%), Positives = 403/758 (53%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQ 1896



Query: 1006 SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADSFFVVKGDDVR 1185  
 S WERK SNC + S L + +F C + A K+ +CFS++ D F +  
 Sbjct: 344 SPLNWERKTFSNCFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPNGRKV 403

Query: 1186 QIAPGQTGVIADYNYKLPDDFMGCVLAWN 1272  
 + G G + +NY++ C L +N  
 Sbjct: 404 DLQLGNLGYLQSFNYRIDTTATSCQLYYN 432

>[gi|138174](#)|[sp|P25194|VGL2\\_CVBV](#) E2 glycoprotein precursor (Spike glycoprotein) (I  
 [Contains: Spike protein S1 (90B); Spike protein S2  
 (90A)]  
[gi|454810|gb|AAA42908.1](#) spike glycoprotein [bovine coronavirus]  
 Length = 1363

Score = 457 bits (1177), Expect = e-127  
 Identities = 276/758 (36%), Positives = 402/758 (53%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQQTQ 1896  
 I C G VS SSE A+L++++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLSRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAEHVDTSY--ECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A++ +S CD+ +G+G C Y T R + + Y + ++  
 Sbjct: 731 LGCVVNADNSTSSVVQTCDLTVGSGYCVDYSTK---RRSRAITTYGRFTNFEPFTVNSV 787

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSF 2223  
 N++ I IP+ F+I E + S K ++DC+ ++CGD C + L++YGSF  
 Sbjct: 788 NDSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSF 847

Query: 2224 CTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQIL----PDP 2373  
 C +N L+ + D +V + T G NFS +L D  
 Sbjct: 848 CDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDINFSPLVGLGSDC 907

Query: 2374 LKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDMM 2553  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+ +  
 Sbjct: 908 NKVSSRSAIEDLLFSKVKLSDVGFVEAYNCTGGAEIRDLCVQSYNGIKVLPPLLSVNQ 967

Query: 2554 IAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNK 2733  
 I+ YT A S +PF + + YR NGIGVT +VL +NOK IAN FN  
 Sbjct: 968 ISGYTLAATSASLFPWSAAAG----VPFYLNQYRINGIGVTMDVLSQNQKLIANAFNN 1023

Query: 2734 AISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 2913  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRLD +EA  
 Sbjct: 1024 ALDAIQEGFDATNSALVKIQAVVNANAALNLLQQLSNRFGAISSSLQEILSRLDALEA 1083

Query: 2914 EVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHL 3093  
 + QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H+  
 Sbjct: 1084 QAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGNGNHI 1143

Query: 3094 MSFPQAAPHGVVFLHVTVYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRN 3270  
 +S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T  
 Sbjct: 1144 ISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGSG 1203

Query: 3271 FFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGD 3450  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL  
 Sbjct: 1204 YYYPEPITGNNVVVMSTCAVNYTKAPDVMLNISTPNLHDFKEELDQWFKNQTSVAPDL-S 1262

Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +  
 Sbjct: 1263 LDYINVTFLDLQDEMNRQLQEAIKVLNQSYINLKDIGTYEYVVKWPWYVWL--LIGFAGVA 1320

Query: 3631 MVTIXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K  
 Sbjct: 1321 MLVLLFFICCCTGCGTSCFKICGGCCDDYTGHQELVIK 1358

Score = 99.4 bits (246), Expect = 4e-19  
 Identities = 61/240 (25%), Positives = 110/240 (45%), Gaps = 6/240 (2%)  
 Frame = +1

Query: 649 KPIFKLPLGINITNFRAI-LTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITITDA 825  
 K +F + LG ++++ + LT +S Y+V L ++L ++++G I +A  
 Sbjct: 231 KFLFNVYLGTVLSHYVYVPLTLCYS-----AMTLEYWVTPLTQYLLAFNQDGVIFNA 283

Query: 826 VDQSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVR-FPNITNLCPFGEVFNATKF 1002  
 VDC + ++E+KC S G+Y+ + + V P DV R PN+ + C N  
 Sbjct: 284 VDCKSDFMSEIKCKTSLIAPSTGVYELNGYTVQPIADVYRRIPNLPD-CNIEAWLNDKSV 342

Query: 1003 PSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLFCFSNVYADSFVVKGDDV 1182  
 PS WERK SNC + S L + +F C + A K+ +CFS++ D F +  
 Sbjct: 343 PSPLNWERKTFSNCFNMSSLMSFIQADSFTCNIEAAKIYGMCFSSITIDKFAIPNGRK 402

Query: 1183 RQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TRNIDATSTGNVNYKYRYLRHGKLRP 1350  
 + G G + +NY++ C L +N ++ + +N ++ + +P  
 Sbjct: 403 VDLQLGNLGYLQSFNYRIDTTAASCQLYINLPAANVSVSRFNPSTWNRFRGFTEQSVFKP 462

>[gi|74856|pir||VGIHVA](#) E2 glycoprotein precursor - bovine coronavirus (strain vac  
 Length = 1363

Score = 457 bits (1177), Expect = e-127  
 Identities = 276/758 (36%), Positives = 402/758 (53%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNGLTGTGLTLP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTTQ 1896  
 I C G VS SSE A+L++++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAHEVDTSY--ECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A++ +S CD+ +G+G C Y T R + + Y + ++  
 Sbjct: 731 LGCVVNADNSTSSVVQTCDLTVGSGYCVDYSTK---RRSRAITTYRFTNFEPFTVNSV 787

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSF 2223  
 N++ I IP+ F+I E + S K ++DC+ ++CGD C + L++YGSF  
 Sbjct: 788 NDSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSF 847

Query: 2224 CTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQIL----PDP 2373  
 C +N L+ + D +V + T G NFS +L D  
 Sbjct: 848 CDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDG VNFVDDINFSPVLGCLGSDC 907

Query: 2374 LKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDM 2553  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+ +  
 Sbjct: 908 NKVSSRSAIEDLLFSKVKLSDVGFVEAYNCTGGAEIRDLCVQSYNGIKVLPPLLSVNQ 967

Query: 2554 IAAytaalvsxxxxxxxxxxxxxxxxlqipfamqmayrfngigvtqnvlyenqkqianqfnk 2733  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN FN  
 Sbjct: 968 ISGYTLAATSASLFPWSAAAG----VPFYLVNQYRINGIGVTMDVLSQNQKLIANAFNN 1023

Query: 2734 AISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 2913  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRLD +EA  
 Sbjct: 1024 ALDAIQEGFDATNSALVKIQAVVNANAEALNLLQQLSNRFGAISSSLQEILSRLDALEA 1083

Query: 2914 EVQIDRLITGRLOSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHL 3093  
 + QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H+  
 Sbjct: 1084 QAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGNGNHI 1143

Query: 3094 MSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRN 3270  
 +S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T  
 Sbjct: 1144 ISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGSG 1203

Query: 3271 FFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGD 3450  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL  
 Sbjct: 1204 YYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLHDFKEELDQWFKNQTSVAPDL-S 1262

Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +  
 Sbjct: 1263 LDYINVTFLDLQDEMNRLEAIAIKVLNQSINLKDIGTYEYVVKWPWYVWL--LIGFAGVA 1320

Query: 3631 MVTIXXXXXXXXXXXXXXXXXKACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K  
 Sbjct: 1321 MLVLLFFICCCTGCGTSCFKICGGCCDDYTGHQELVIK 1358

Score = 99.4 bits (246), Expect = 4e-19  
 Identities = 61/240 (25%), Positives = 110/240 (45%), Gaps = 6/240 (2%)  
 Frame = +1

Query: 649 KPIFKLPLGINITNFRAI-LTAFSPAQDIWGTSAAAYFVGYLKPTTFMLKYDENGITITDA 825  
 K +F + LG +++++ + LT +S Y+V L ++L ++++G I +A  
 Sbjct: 231 KFLFNVYLGTVLSHYVVLPLTCYS-----AMTLEYVWTPLTSKQYLLAFNQDGVIFNA 283

Query: 826 VDQSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVR-FPNITNLCPFGEVFNATKF 1002  
 VDC + ++E+KC S G+Y+ + + V P DV R PN+ + C N  
 Sbjct: 284 VDCKSDFMSEIKCKTSLSIAPSTGVYELNGYTVQPIADVYRRIPNLPD-CNIEAWLNDKSV 342

Query: 1003 PSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGDDV 1182  
 PS WERK SNC + S L + +F C + A K+ +CFS++ D F +  
 Sbjct: 343 PSPLNWERKTFSNCFNMSSLMFSFIQADSFTCNNIDA AKIYGMCFSSITIDKFAIPNGRK 402

Query: 1183 RQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TRNIDATSTGNINYKYRYLRHGKLRP 1350  
 + G G + +NY++ C L +N ++ + +N ++ + +P  
 Sbjct: 403 VDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSRFNPSTWNRFRFGFTEQSVFKP 462

>gi|74853|pir||VGIHQU E2 glycoprotein precursor - bovine coronavirus (strain Que  
 Length = 1363

Score = 457 bits (1177), Expect = e-127  
 Identities = 276/758 (36%), Positives = 403/758 (53%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYLTRNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQQTQ 1896  
 I C G VS SSE A+L++++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAHEVDTSY--ECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A++ +S CD+ +G+G C Y T R + + Y + ++  
 Sbjct: 731 LGCVVNADNSTSSVVQTCDLTVGSGYCVDYSTK---RRSRAITTYGRFTNFEPFTVNSV 787

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSF 2223  
 N++ I IP+ F+I E + S K ++DC+ ++CGD C + L++YGSF  
 Sbjct: 788 NDSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSF 847

Query: 2224 CTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPT-LKYFGGFNFSQILPDPL----- 2376  
 C +N L+ + D +V + T LK FN I P+  
 Sbjct: 848 CDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDINFSVPLGCLGSAC 907

Query: 2377 -KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVPPLLTDDM 2553  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+ +  
 Sbjct: 908 NKVSSRSAIEDLLFSKVKLSDVGFVEAYNNCTGGAEIRDLICVQSYNGIKVLPPLLSVNQ 967

Query: 2554 IAAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTVQNVLYENQKQIANQFNK 2733  
 I+ YT A S + +PF + + YR NGIGVT +VL +NQK IAN FN  
 Sbjct: 968 ISGYTLAATSASLFPPLSAA---VGVPFYLVNQQYRINGIGVTMDVLSQNQKLIANAFNN 1023

Query: 2734 AISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 2913  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRLD +EA  
 Sbjct: 1024 ALDAIQEGFDATNSALVKIQAVVNANAEALNLLQQLSNRFGAISSSLQEILSRLDALEA 1083

Query: 2914 EVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHL 3093  
 + QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H+  
 Sbjct: 1084 QAQIDRLINGRLTALNVYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGNGNHI 1143

Query: 3094 MSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRN 3270  
 +S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T  
 Sbjct: 1144 ISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGSG 1203

Query: 3271 FFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGD 3450  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL  
 Sbjct: 1204 YYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLHDFKEELDQWFKNQTSVAPDL-S 1262

Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +  
 Sbjct: 1263 LDYINVTFLDLQDEMNRLEAIAIKVLNQSINLKDIGTYEYVVKWPWYVWL--LIGFAGVA 1320

Query: 3631 MVTIXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K  
 Sbjct: 1321 MLVLLFFICCCTGCGTSCFKICGGCCDDYTGHQELVIK 1358

Score = 99.4 bits (246), Expect = 4e-19  
 Identities = 58/209 (27%), Positives = 99/209 (47%), Gaps = 1/209 (0%)  
 Frame = +1

Query: 649 KPFIKPLPLGINITNFRAILTAFSPAQDIWGTSAAAAYFVGYLKPTTFMLKYDENGITIDAV 828  
 K +F + LG +++++ + SA + Y+V L ++L ++++G I +AV  
 Sbjct: 231 KFLFNVYLGTVLSHYVYVPLTCCSSAMTL-----EYWVTPLTTSKQYLLAFNQDGVIFNAV 284

Query: 829 DCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVR-FPNITNLCPFGEVFNATKFP 1005  
 DC + ++E+KC S G+Y+ + + V P DV R PN+ + C N P  
 Sbjct: 285 DCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLDP-CNIEAWLNDKSV 343

Query: 1006 SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLFCFSNVYADSFVVKGDVDR 1185  
 S WERK SNC + S L + +F C + A K+ +CFS++ D F +  
 Sbjct: 344 SPLNWERKTFSNCFNMSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPNGR 403

Query: 1186 QIAPGQTGVIADYNYKLPDDFMGCVLAWN 1272  
 + G G + +NY++ C L +N  
 Sbjct: 404 DLQLGNLGYLQSFNYRIDTTATSCQLYYN 432

>[gi|628284|pir||S44241](http://gi|628284|pir||S44241) surface protein - human coronavirus  
[gi|475894|emb|CAA83661.1](http://gi|475894|emb|CAA83661.1) surface protein [Human coronavirus OC43]  
 Length = 1363

Score = 456 bits (1174), Expect = e-126  
 Identities = 274/758 (36%), Positives = 401/758 (52%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNAPYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQ 1896  
 I C G VS SSE A+L++++ C V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLSRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAEHVDTS--YECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A++ S CD+ +G+G C Y T R + + Y + ++  
 Sbjct: 731 LGCVVNADNSTASAVQTCDLTVGSGYCVDYSTK---RRSRAITTYGRFTNFEPFTVNSV 787

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSF 2223  
 N++ I IP+ F+I E + S K ++DC+ ++CGD C + L++YGSF  
 Sbjct: 788 NDSLEHVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDCAACKSQLVEYGSF 847

Query: 2224 CTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPT-LKYFGGFNFSQILPDPL----- 2376  
 C +N L+ + D +V + T LK FN + P+  
 Sbjct: 848 CDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDVNFSPVLGCLGSEC 907

Query: 2377 -KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTD 2553  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+D+  
 Sbjct: 908 NKVSSRSAIEDLLFSKVRSLSDVGFVEAYNNTGGAGIRDLCVQSYNGIKVLPPLLSDNQ 967

Query: 2554 IAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNK 2733  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN FN  
 Sbjct: 968 ISGYTLAATSANLFPWSAAAG---VPFYLVNQYRINGIGVTMDVLSQNQKLIANAFNN 1023

Query: 2734 AISQIQESLTTTSTALGKQLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 2913

A+ IQE T++AL K+Q VVN +A+ALN L++QLS+ FGAISS L +ILSRLD +EA  
 Sbjct: 1024 ALDAIQEGFDATNSALVKIQAVVNADAEALNNLLQQLSNRFGAISSSLQEILSRLDALEA 1083

Query: 2914 EVQIDRLITGRLQSLQTYVTTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHL 3093  
 + QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H+  
 Sbjct: 1084 QAQIDRLINGRLTALDAYVSQQLSDSTLVKFSAAQAMEKVNNECVKSQSSRINFVCGNGNHI 1143

Query: 3094 MSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRN 3270  
 +S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T  
 Sbjct: 1144 ISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGSR 1203

Query: 3271 FFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKNHTSPDVLDGD 3450  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN T DL  
 Sbjct: 1204 YYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTLVAPDL-S 1262

Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +  
 Sbjct: 1263 LDYINVTFLDLQDEMNRLEAIKVLNQSYINLKDIGTYEYVVKWPWYVWL--LIGFAGVA 1320

Query: 3631 MVTIXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K  
 Sbjct: 1321 MLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIK 1358

Score = 97.8 bits (242), Expect = 1e-18  
 Identities = 52/174 (29%), Positives = 85/174 (48%), Gaps = 1/174 (0%)  
 Frame = +1

Query: 754 YFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSF EIDKGIYQTSNFRVPSG 933  
 Y+V L ++L +++G I +AVDC + ++E+KC S G+Y+ + + V P  
 Sbjct: 260 YWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIA 319

Query: 934 DVVR-FPNITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS 1110  
 DV R PN+ + C N PS WERK SNC + S L + +F C +  
 Sbjct: 320 DVYRRIPNLPD-CNIEAWLNDKSVPSPLNWERKTFSNCFNMSSLMSFIQADSFTCNNID 378

Query: 1111 ATKLNLDLCSNVYADSFVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCVLAWN 1272  
 A K+ +CFS++ D F + + G G + +NY++ C L +N  
 Sbjct: 379 AAKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYN 432

[gi|138170|sp|P25191|VGL2\\_CVBL9](#) E2 glycoprotein precursor (Spike glycoprotein) (  
 [Contains: Spike protein S1 (90B); Spike protein S2  
 (90A)]  
[gi|74855|pir|VGIHL9](#) E2 glycoprotein precursor - bovine coronavirus (strain L9)  
[gi|323356|gb|AAA42907.1|](#) spike glycoprotein [bovine coronavirus]  
 Length = 1363

Score = 456 bits (1173), Expect = e-126  
 Identities = 275/758 (36%), Positives = 401/758 (52%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFTDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNAPYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTO 1896  
 I C G VS SSE A+L++++ C V + QL P N F +

Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNTLSRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAHEVDTSY--ECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A++ +S CD+ +G+G C Y T R + + Y + ++

Sbjct: 731 LGCVVNADNSTSSVVQTCDLTVGSGYCVDYSTK---RRSRAITTTGYRFTNFEPFTVNSV 787

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSF 2223  
 N++ I IP+ F+I E + S K ++DC+ ++CGD C + L++YGSF

Sbjct: 788 NDSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSF 847

Query: 2224 CTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQIL----PDP 2373  
 C +N L+ + D +V + T G NFS +L D

Sbjct: 848 CDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFVDDINFSPVLGCLGSDC 907

Query: 2374 LKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDM 2553  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+ +

Sbjct: 908 NKVSSRSAIEDLLFSKVKLSDVGFVEAYNNTGGAEIRDLICVQSYNGIKVLPPLLSVNQ 967

Query: 2554 IAAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNK 2733  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN FN

Sbjct: 968 ISGYTLAATSASLFPPWSAAAG----VPFYLVNQQYRINGIGVTMDVLSQNQKLIANAFNN 1023

Query: 2734 AISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 2913  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAISS L +ILSRLD +EA

Sbjct: 1024 ALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISSLQEILSRLDALEA 1083

Query: 2914 EVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHL 3093  
 + QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H+

Sbjct: 1084 QAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGNGNHI 1143

Query: 3094 MSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRN 3270  
 +S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T

Sbjct: 1144 ISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGSG 1203

Query: 3271 FFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKNHTSPDVDLGD 3450  
 ++ P+ IT +N V C + + + P L FKEELD++FKN TS DL

Sbjct: 1204 YYPEPITGNNVVMSTCAANYTKAPDVMLNISTPNLHDFKEELDQWFKNQTSVAPDL-S 1262

Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +

Sbjct: 1263 LDYINVTFLDLQDEMNRLEAIAIKVLNQSINLKDIGTYEYVYKWPWYVWL--LIGFAGVA 1320

Query: 3631 MVTIXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K

Sbjct: 1321 MLVLLFFICCCTGCGTSCFKICGGCCDDYTGHQELVIK 1358

Score = 99.0 bits (245), Expect = 5e-19  
 Identities = 59/239 (24%), Positives = 109/239 (45%), Gaps = 5/239 (2%)  
 Frame = +1

Query: 649 KPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITITDAV 828  
 K +F + LG ++++ + + A + Y+V L ++L ++++G I +AV

Sbjct: 231 KFLFNVYLGTVLSHYVYVPLTNCNSAMTL-----EYWVTPLTTSKQYLLAFNQDGVIFNAV 284

Query: 829 DCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVR-FPNITNLCPFGEVFNATKFP 1005  
 DC + ++E+KC S G+Y+ + + V P DV R PN+ + C N P

Sbjct: 285 DCKSDFMSEIKCKTSLIAPSTGVYELNGYTVQPIADVRRIPNLPD-CNIEAWLNDKSVP 343

Query: 1006 SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGDVDR 1185  
 S WERK SNC + S L + +F C + A K+ +CFS++ D F +  
 Sbjct: 344 SPLNWERKTFSNCFNMSCLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPNGRKV 403

Query: 1186 QIAPGQTGVIADYNYKLPDDFMGCVLAWN----TRNIDATSTGNYNYKYRYLRHGKLRP 1350  
 + G G + +NY++ C L +N ++ + +N ++ + +P  
 Sbjct: 404 DLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAAANVSVSRFNPSTWNRRFGFTEQSVFKP 462

[gi|628283|pir||S44240](#) surface protein - human coronavirus  
[gi|475892|emb|CAA83660.1](#) surface protein [Human coronavirus OC43]  
 Length = 1363

Score = 454 bits (1168), Expect = e-126  
 Identities = 274/758 (36%), Positives = 402/758 (53%), Gaps = 23/758 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFTDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+TG G+ ++ + +Q D + RD T+  
 Sbjct: 621 KSNTDIILGVCVNYDLYGITGQIFVEVNAPYYNSWQNLLYDSNGNLYGFRDYLTNRTFM 680

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQQTQ 1896  
 I C G VS SSE A+L++++ C+ V + QL P N F +  
 Sbjct: 681 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCSYVFNNTLSRQLQPI-----NYFDSY 730

Query: 1897 AGCLIGAHEVDTSY--ECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A++ +S CD+ +G+G C Y T R + + Y + ++  
 Sbjct: 731 LGCVVNADNSTSSVVQTCDLTVGSGYCVDYSTK---RRSRRAITTYRFTNFEPFTVNSV 787

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSSVDCNMYICGDSTECANLLLQYGSF 2223  
 N++ I IP+ F+I E + S K ++DC+ ++CGD C + L++YGSF  
 Sbjct: 788 NDSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSF 847

Query: 2224 CTQLNRALSGIAAEQDRNTREVFQAQVKQMYKTPT-LKYFGGFNFSQILPDPL----- 2376  
 C +N L+ + D +V + T LK FN I P+  
 Sbjct: 848 CDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDINFPVLGCLGSAC 907

Query: 2377 -KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDM 2553  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ VLPPLL+ +  
 Sbjct: 908 NKVSSRSAIEDLLFSKVKLSDVGFVEAYNNTGGAEIRDLCVQSYNGIKVLPPLLSVNQ 967

Query: 2554 IAAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNK 2733  
 I+ YT A S +PF + + YR NGIGVT +VL +NQK IAN F+  
 Sbjct: 968 ISGYTLAATSASLFPPWSAAAG----VPFYLVNQQYRINGIGVTMDVLSQNQKLIANAFSN 1023

Query: 2734 AISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 2913  
 A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAI S L +ILSRLD +EA  
 Sbjct: 1024 ALDAIQEGFDATNSALVKIQAVVNANAALNLLQQLSNRFGAIGSSLQEILSRLDALEA 1083

Query: 2914 EVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHL 3093  
 + QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG G H+  
 Sbjct: 1084 QAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGNGNHI 1143

Query: 3094 MSFPQAAPHGVVFLHVITYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFITQRN 3270  
 +S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W T  
 Sbjct: 1144 ISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFTGSG 1203

Query: 3271 FFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKNHTSPDVDLGD 3450  
 ++ P+ IT +N V C V + + + P L FKEELD++FKN TS DL

Sbjct: 1204 YYYPEPITGNNVVVMSTCAVNYTKAPDVMLNISTPNLHDFKEELDQWFKNQTSVAPDL-S 1262  
 Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630  
 + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL + G +  
 Sbjct: 1263 LDYINVTFLDLQDEMNRQLQEAIKVLNQSINLKDIGTYEYVVKWPWYVWL--LIGFAGVA 1320  
 Query: 3631 MVTIXXXXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 M+ + CG CC E V+K  
 Sbjct: 1321 MLVLLFFICCTGCGTSCFKICGGCCDDYTGHQELVIK 1358

Score = 98.6 bits (244), Expect = 7e-19  
 Identities = 59/239 (24%), Positives = 109/239 (45%), Gaps = 5/239 (2%)  
 Frame = +1

Query: 649 KPIFKLPLGINITNFRAILTAFAQDIWGTSAAYFVGYLKPTTFMLKYDENGITITDAV 828  
 K +F + LG ++++ + + A + Y+V L ++L ++++G I +AV  
 Sbjct: 231 KFLFNVYLGTVLSHYYVLP LPTCN SAMTL-----EYWVTPLTSKQYLLAFNQDGVIFNAV 284  
 Query: 829 DCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVP SGDVVR-FPNITNLC PFGEVFNATKFP 1005  
 DC + ++E+KC S G+Y+ + + V P DV R PN+ + C N P  
 Sbjct: 285 DCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVRRIPNLPD-CNIEAWLNDKSVP 343  
 Query: 1006 SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDL CFSNVYADSFVVKGDVVR 1185  
 S WERK SNC + S L + +F C + A K+ +CFS++ D F +  
 Sbjct: 344 SPLNWERKTFSNCFNMSSLSFIQADSFTCNNIDA AKIYGMCFSSITIDKFAIPNGRKV 403  
 Query: 1186 QIAPGQTGVIADYNYKLPDDFMGCVLAWN----TRNIDATSTGNINYKYRYLRHGKLRP 1350  
 + G G + +NY++ C L +N ++ + +N ++ + +P  
 Sbjct: 404 DLQLGNLGYLQSFNYRIDTTATSCQLYINLPAANVSVSRFNPSTWNRFRFGFTEQSVFKP 462

>[gi|561672|gb|AAA87063.1](#) S glycoprotein [murine hepatitis virus]  
 Length = 1361

Score = 454 bits (1167), Expect = e-126  
 Identities = 276/764 (36%), Positives = 405/764 (53%), Gaps = 36/764 (4%)  
 Frame = +1

Query: 1525 TVCGPKL---STDLIKQCVNFNFNGLTGTGVLTLP-SSKRFQPFQFGRDVSDFTDSDVRD 1692  
 T C L +T+++ CV++ G+TG GV + + +Q DV+ + RD  
 Sbjct: 602 TTCSTDLQLPNTEVVTGVCVKYDLYGITGQGVFKEVKADYYNSWQNLLYDVNGNLNGFRD 661  
 Query: 1693 PKTSEILDISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYST 1872  
 T++ I C G VS + E A+LY+++ C V + + TP  
 Sbjct: 662 IVTNKTYLIRSCYSGRVSAAYH--QDAPEPALLYRNLKCDYVFNNNISREETPL----- 713  
 Query: 1873 GNNVFQTQAGCLIGA EH-VDTSEY-CDIPIGAGICASYHTVSLLR---STSQK--SIVAY 2031  
 N F + GC++ A++ + S + CD+ +G+G+C +Y T R ST K + +  
 Sbjct: 714 --NYFDSYLGCVVNADNSTEPQSVDACDLRMGSGLCVNYSTTHRARRSVSTGYKLTTTFEPF 771  
 Query: 2032 TMSLGADSSIAYSN-NTIAIPTNFISISITTEVMPVSMAKTSVDCNMYICGDSTECANLLL 2208  
 T+S+ DS + + IPTNF+I+ E + K ++DC ++CGD T C L+  
 Sbjct: 772 TVSIVNDSVESVGGLYEMQIPTNF TIASHQEFIQTRSPKVTIDCAAFVCGDYTACRQQLI 831  
 Query: 2209 QYGSFCTQLNRALSGI-----AAEQDRNTREVFAQVKQMYKTPTLKY 2334  
 +YGSFC +N L + R + Q+ + +P L  
 Sbjct: 832 EYGSFCDNINAILGEVNNLIDTMQLQVASALIQGVTLSSRLADGISGQIDDINFSPLLGC 891

Query: 2335 FGGFNFSQILPDLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFN 2514  
 G SQ + RS IEDLLF+KV L+D GF++ Y C G RDL+C Q FN  
 Sbjct: 892 LG----SQCSEGTMAAQGRSTIEDLLFDKVKLSDVGFVEAYNNCTGGQEVDRLLCVQSFN 947

Query: 2515 GLTVLPPLLTDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVL 2694  
 G+ VLPP+L+++ I+ YTA + +PF++ + YR NG+GVT NVL  
 Sbjct: 948 GIKVLPVLSENQISGYTAGATASSMFPWSAAAG----VPFSLSVQYRINGLVGVTMNVL 1003

Query: 2695 YENQKQIANQFNKAISQIQESLTTTSTALGKLDVNVNQAALNTLVKQLSSNFGAISSV 2874  
 ENQK IA+ FN AI IQE T++AL K+Q VVN NA+ALN L+ QLS+ FGAIS+  
 Sbjct: 1004 SENQKMIASAFNNAIGAIQEGFDATNSALAKIQSVVNANAEALNNLLNQLSNRFGAISAS 1063

Query: 2875 LNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQ 3054  
 L +ILSRLD +EA+ QIDRLI GRL +L YV++QL I+ SA A K++ECV Q  
 Sbjct: 1064 LQEILSRLDALEAQAQIDRLINGRLTALNAYVSKQLSDMTLIKVSAAQAIEKVNCECVKSQ 1123

Query: 3055 SKRVDFCGKGYHLMSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVF 3231  
 S R++FCG G H++S Q AP+G+ F+H +YVP+ +P +C G + P+ G F  
 Sbjct: 1124 SPRINFCGNGNHILSLVQNPYGLYFIHFSYVPTSFTTANVSPGLCISGDRGLAPKAGYF 1183

Query: 3232 VFNGTSWFITQRNFFSPQIITTDNTFVSGNCDVIGIINNTVYDPLQPELDSFKEELDKY 3411  
 V + W N++ P+ IT N+ + +C V + P L FKEELDK+  
 Sbjct: 1184 VQDDGEWKFIGSNYYYPEPITDKNSVIMSSCAVNYTRAPEVFLNTSIPNLPDFKEELDKW 1243

Query: 3412 FKNHTS--PDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP 3585  
 FKN TS PD+ L D +N + +++ E++R+ + K LNES I+L+E+G YE Y+KWP  
 Sbjct: 1244 FKNQTSVAPDLSL-DFEKLNVTFDLTDEMNR IQDAIKKLNESYINLKEVGTYEMYVKWP 1302

Query: 3586 WYVWLGFIAGLIAIVMVTIXXXXXXXXXXXXXXXXXKGAC---SCGSCC 3708  
 WYVWL LI + V + G+C CG+CC  
 Sbjct: 1303 WYVWL-----LIGLAGVAVCVLLFFICCTGCGSCCFKKCGNCC 1341

Score = 100 bits (248), Expect = 2e-19  
 Identities = 108/474 (22%), Positives = 186/474 (39%), Gaps = 32/474 (6%)  
 Frame = +1

Query: 1 MFIFLLFLTTLTSGSDLD-RC-----TTFDDVQAPNYTQHTSSMR---GVYYP-DEIFRSD 150  
 +F+F+L L G D RC T + AP+ + + G YY D ++ +  
 Sbjct: 2 LFVFIILLPSCGLGYIGDFRCINLVNTDTSNASAPSVSTEVVDVSKGIGTYVLDLDRVYVYLN 61

Query: 151 TLYLTQDLFLPFYSN-----VTGFHTIN-HTFGNPVIP-FKDGIFYAATE-KSNVVRGW 303  
 TL LT + P S+ +TG +T++ + + +P + F DGI+ K+++ R  
 Sbjct: 62 TLLLGTG--YYPVDSSNYRNLALTGTNTLSLNWYKSPFLSEFNDGIFAKVKNL KASLPRDS 119

Query: 304 V-----FGSTMNNKXXXXXXXXXXXXXXXXXACNFELCDNPFPAVSKPMGTQHTMIFD 462  
 V GS N C + +C P+ G +  
 Sbjct: 120 VSYFPTIVIGSNFVNTSYTVVLEPYNGIIMASICQYAICQLPYTDCKPNTGGNKLIGFWH 179

Query: 463 NAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFNKNDGFLYVYKGYQPIDVVRDLPSGFN 642  
 + F+ +V+ + F F + G Y Y D+ S  
 Sbjct: 180 TDLKSPVCILKRNFTFNVAE-----WLYFHFYQGGTFYAYYA-----DVSSATT 225

Query: 643 TLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPPTTFMLKYDENGITID 822  
 L F + +G +T+ + +P G + Y+V L ++ +++ G IT  
 Sbjct: 226 FL---FSMYIGDVLTYQYFVLPFMCTPTTS--GVFSPQYWVTPVVKRQYLFNFNQRGVITS 280

Query: 823 AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVRFNPITNL--CPFGEVFNAT 996

AVDC+ + +E+KC +S G+Y + + V P G V R + NL C + A  
 Sbjct: 281 AVDCASSYTSEIKCKTQSMNPSTGVYDLTGYTVQPVGLVYR--RVRNLPDCKIEDWLTAK 338

Query: 997 KFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLCFSNVYADSFVVKGD 1176  
 PS WERK NC + S L + C + A+K+ +CF +V D F +  
 Sbjct: 339 TVPSPLNWERKTFQNCNFNLSLLRFVQAESLSCSNIDASKVYGMCFGVSVIDKFAIPNR 398

Query: 1177 DVRQIAPGQTGVIADYNYKLPDDFMGC----VLAWNTRNIDATSTGNYNKYRY 1326  
 + G +G + +NYK+ C LA N ++ + ++N +Y +  
 Sbjct: 399 RRVDLQLGNSGFLQSFNYKIDTRATSCQLYSLAQNNVTVNNHNPSSWNRRYGF 452

>[gi|465382](#)|[sp|Q02385](#)|[VGL2\\_CVMJC](#) E2 glycoprotein precursor (Spike glycoprotein) ( [Contains: Spike protein S1 (90B); Spike protein S2 (90A)] )  
[gi|320217](#)|[pir](#)|[|JQ1534](#) E2 glycoprotein precursor - murine hepatitis virus (strain [gi|222140](#)|[dbj](#)|[BAA01085.1](#))  
 cl-2 S protein precursor [Murine hepatitis virus]  
 Length = 1376

Score = 453 bits (1166), Expect = e-126  
 Identities = 277/763 (36%), Positives = 406/763 (53%), Gaps = 35/763 (4%)  
 Frame = +1

Query: 1525 TVCGPKL---STDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVDR 1692  
 T C L +T++ CV ++ G+TG GV + + +Q DV+ + RD  
 Sbjct: 614 TTCSTDLQLPNTEVATGVVRYDLYGITGQGVFKEVKADYYNSWQALLYDVNGNLNGFRD 673

Query: 1693 PKTSEILDISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYST 1872  
 T++ I C G VS + E A+LY+++NC+ V T + + P  
 Sbjct: 674 LTTNKTYTIRSCYSGRVSAAYH--KEAPEPALLYRNINCSYVFTNNISREENPL----- 725

Query: 1873 GNNVFQTQAGCLIGAEHV--DTSYECDIPIGAGICASYHTVSLLR---STSQK--SIVAY 2031  
 N F + GC++ A++ + CD+ +GAG+C Y R ST + + Y  
 Sbjct: 726 --NYFDSYLGCVVNADNRPDEALPNCDLRMGAGLCVDYKSRARRRSVSTGYRLTTTFEPY 783

Query: 2032 TMSLGADSSIAYSNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLL 2208  
 L DS + + IPTNF+I E + + K ++DC ++CGD+ C L+  
 Sbjct: 784 MPMLVNDVSVQSVGGLYEMQIPTNFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACRQQLV 843

Query: 2209 QYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQILP- 2367  
 +YGSFC +N L+ + D +V + + Q + G NFS +L  
 Sbjct: 844 EYGSFCDNVNAILNEVNNLLDNMQLQVASALMQGVTISSRLPDGISGPIDDINFSPLLGC 903

Query: 2368 -----DPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNG 2517  
 P RS IEDLLF+KV L+D GF++ Y C G RDL+C Q FNG  
 Sbjct: 904 IGSTCAEDGNGPSAMRGRSAIEDLLFDKVKLSDVGFVEAYNNCTGGQEVRLDLCVQSFNG 963

Query: 2518 LTVLPPLLTDDMIAAYTAALVXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLY 2697  
 + VLPP+L++ I+ YTA + +PF++ + YR NG+GVT NVL  
 Sbjct: 964 IKVLPPVLSESQISGYTAGATAAAMFPPTAAAG---VPFSLNVQYRINGLGVTMNVLS 1019

Query: 2698 ENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVL 2877  
 ENQK IA+ FN A+ IQE T++ALGK+Q VVN NA+ALN L+ QLS+ FGAIS+ L  
 Sbjct: 1020 ENQKMIASAFNNALGAIQEGFDATNSALGKIQSVVNANAEALNNLLNQLSNRFGAISASL 1079

Query: 2878 NDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQS 3057  
 +IL+RLD+VEA+ QIDRLI GRL +L Y+++QL + I+ SA A K++ECV Q+  
 Sbjct: 1080 QEILTRLDRVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKFSAAQAIEKVNNECVKSQT 1139

Query: 3058 KRVDFCGKGYHLMSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGV FV 3234  
 R++FCG G H++S Q AP+G+ F+H +YVP+ + +P +C G + P+ G FV  
 Sbjct: 1140 TRINFCGNGNHILSLVQNAPYGLCFIHFSYVPTSFKTANVSPGLCISGDRGLAPKAGYFV 1199

Query: 3235 FNGTSWFITQRNFFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYF 3414  
 + W T N++ P+ IT N+ V +C V + P L FKEELDK+F  
 Sbjct: 1200 QDNGEWKFTGSNYYYPEPITDKNSVVMISCAVNYTKAPEVFLNNSIPNLPDFKEELDKWF 1259

Query: 3415 KNHTS--PDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPW 3588  
 KN TS PD+ L D +N + +++ E++R+ + K LNES I+L+E+G YE Y+KWPW  
 Sbjct: 1260 KNQTSIAPDLSL-DFEKLNVTFLDLTYEMNRIQDAIKKLNESYINLKEVGTYEMVVKWPW 1318

Query: 3589 YVWLGFIAGLIAIVMVTIXXXXXXXXXXXXXXKGC---SCGSCC 3708  
 YVWL LI + V + G+C CGSCC  
 Sbjct: 1319 YVWL-----LIGLAGVAVCVLLFFICCTGCGSCCFRKCGSCC 1356

Score = 110 bits (274), Expect = 2e-22  
 Identities = 125/512 (24%), Positives = 195/512 (38%), Gaps = 42/512 (8%)  
 Frame = +1

Query: 1 MFIFLLFLTTLTSGSDLDRCTTFDDVQAPNYTQHTSSMR-----GVYYP-DEI 138  
 +F+F+LFL G D F +Q NY + +S G YY D +  
 Sbjct: 2 LFFVILFLPSCGLGYIGD----FRCIQTVNYNGNNASAPSISTEAVDVSKGLGTYVLDLV 57

Query: 139 FRSDTLYLTQDLFLPF----YSNV--TGFHTINHTFGNP--VIPFKDGIYFAATE-KSNV 291  
 + + TL LT + P Y N+ TG +T++ T+ P + F DGI+ K+N  
 Sbjct: 58 YLNATLLLTG--YYPVDGSNYRNLALTGTNTLSLTWFKPPFLSEFNDGIFAKVQNLKTNT 115

Query: 292 VRGW-----VFGSTMNNKXXXXXXXXXXXXXXXXXRACNFELCDNPFPAVSKPMGTQHT 450  
 G V GS N C + +C P+ KP  
 Sbjct: 116 PTGATSYFPTIVIGSLFGNTSYTVVLEPYNNIIMASVCTYTICQLPY-TPCKP----- 167

Query: 451 MIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFNKNDGFLYVY---KGYQPIDVVR 621  
 N + + DV K R F F +LY + +G  
 Sbjct: 168 -----NTNGNRVIGFWHTDVKPPICLLK--RNFTFNVNAPWLYFHFYQQGGTFYAYYA 218

Query: 622 DLPSGFNTLKPFIKFLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPPTTFMLKYD 801  
 D PS L F + +G +T + + +P T Y+V L ++ ++  
 Sbjct: 219 DKPSATTFL---FSVYIGDILTQYFVLPFICTPTAG--STLLPLYWVTPLLKRQYLFNFN 273

Query: 802 ENGTITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVR-FPNITNLCPFG 978  
 E G IT AVDC+ + ++E+KC +S G+Y S + V P G V R PN+ + C  
 Sbjct: 274 EKGVITSAVDCASSYISEIKCKTQSLLPSTGVYDLSGYTVQPVGVVYRRVPLPD-CKIE 332

Query: 979 EVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADS 1158  
 E A PS WER+ NC + S L + C + A+K+ +CF +V D  
 Sbjct: 333 EWLTAKSVPSPNLWERRTFQNCNFNLSLLRYVQAESLSCNNIDASKVYGMCFGSVSVDK 392

Query: 1159 FVVKGDDVQRQIAPGQTGVIADYNYKLPDDFMGCVLAW----NTRNIDATSTGNINYKYRY 1326  
 F + + G +G + NYK+ C L + N I+ + ++N +Y +  
 Sbjct: 393 FAIPRSRQIDLQIGNSGFLQTANYKIDTAATSCQLYSLPKNNVTINNYNPSSWNRRYGF 452

Query: 1327 LRHGKLRPFERDISNVP----FSPDGKPCPTP 1410  
 G + D++ P PC P  
 Sbjct: 453 NDAGVFGKSKHDVAYAQQCFIVRPSYCPCAQP 484

>[gi|138176|sp|P22432|VGL2\\_CVM4](#) E2 glycoprotein precursor (Spike glycoprotein) (I  
 [Contains: Spike protein S1 (90B); Spike protein S2  
 (90A)]  
[gi|74851|pir|VGIHJ2](#) E2 glycoprotein precursor - murine hepatitis virus (strain w  
 MHV-4)  
[gi|234140|gb|AAB19590.1](#) E2 [murine hepatitis virus strain 4]  
[gi|331847|gb|AAA46456.1](#) E2 glycoprotein [murine hepatitis virus]  
 Length = 1376

Score = 452 bits (1162), Expect = e-125  
 Identities = 277/763 (36%), Positives = 405/763 (53%), Gaps = 35/763 (4%)  
 Frame = +1

Query: 1525 TVCGPKL---STDLIKNCQVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRD 1692  
 T C L +T++ CV ++ G+TG GV + + +Q DV+ + RD  
 Sbjct: 614 TTCSTDLQLPNTEVATGVCVRYDLYGITGQGVFKEVKADYYNSWQALLYDVNGNLNGFRD 673

Query: 1693 PKTSEILDISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYST 1872  
 T++ I C G VS + E A+LY+++NC+ V T + + P  
 Sbjct: 674 LTTNKTYTIRSCYSGRVSAAYH--KEAPEPALLYRNINCSYVFTNNISREENPL----- 725

Query: 1873 GNNVFQTQAGCLIGAEHV--DTSYECDIPIGAGICASYHTVSLLR---STSQK--SIVAY 2031  
 N F + GC++ A++ + CD+ +GAG+C Y R ST + + Y  
 Sbjct: 726 --NYFDSYLGCVVNADNRTDEALPNCDLRMGAGLCVDYSKSRARRSVSTGYRLTTFEPY 783

Query: 2032 TMSLGADSSIAYSN-NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLL 2208  
 L DS + + IPTNF+I E + + K ++DC ++CGD+ C L+  
 Sbjct: 784 MPMLVNDVSVQSVGGLYEMQIPTNFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACRQQLV 843

Query: 2209 QYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQILP- 2367  
 +YGSFC +N L+ + D +V + + Q + G NFS +L  
 Sbjct: 844 EYGSFCDNVNAILNEVNNLLDNMQLQVASALMQGVTISSRLPDGISGPIDDINFSPLLGC 903

Query: 2368 -----DPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNG 2517  
 P RS IEDLLF+KV L+D GF++ Y C G RDL+C Q FNG  
 Sbjct: 904 IGSTCAEDGNGPSAIRGRSAIEDLLFDKVKLSDVGVFEAYNNCTGGQEVRLDLCVQSFNG 963

Query: 2518 LTVLPPLLTDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLY 2697  
 + VLPP+L++ I+ YTA + +PF++ + YR NG+GVT NVL  
 Sbjct: 964 IKVLPPVLSESQISGYTAGATAAAMFPWTAAG---VPFSLNVQYRINGLGVTMNVLS 1019

Query: 2698 ENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVL 2877  
 ENQK IA+ FN A+ IQE T++ALGK+Q VVN NA+ALN L+ QLS+ FGAIS+ L  
 Sbjct: 1020 ENQKMIASAFNNALGAIQEGFDATNSALGKIQSVVNANAEALNNLLNQLSNRFGAISASL 1079

Query: 2878 NDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQS 3057  
 +IL+RLD VEA+ QIDRLI GRL +L Y+++QL + I+ SA A K++ECV Q+  
 Sbjct: 1080 QEILTRLDAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKFSAAQAIEKVNNECVKSQT 1139

Query: 3058 KRVDFCGKGYHLMSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGV FV 3234  
 R+++FCG G H++S Q AP+G+ F+H +YVP+ + +P +C G + P+ G FV  
 Sbjct: 1140 TRINFCGNGNHILSLVQNAPYGLCFIHFSYVPTSFKTANVSPGLCISGDRGLAPKAGYFV 1199

Query: 3235 FNGTSWFITQRNFFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYF 3414  
 + W T N++ P+ IT N+ V +C V + P L FKEELDK+F  
 Sbjct: 1200 QDNGEWKFTGSNYYYPEPITDKNSVVMISCAVNYTKAPEVFLNNSIPNLPDFKEELDKWF 1259

Query: 3415 KNHTS--PDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPW 3588  
 KN TS PD+ L D +N + +++ E++R+ + K LNES I+L+E+G YE Y+KWPW  
 Sbjct: 1260 KNQTSIAPDLSL-DFEKLNVTFLDLTYEMNRIQDAIKKLNESYINLKEVGTIEMVYKWPW 1318

Query: 3589 YVWLGFIAGLIAIVMVTIXXXXXXXXXXXXXKGC---SCGSCC 3708  
 YVWL LI + V + G+C CGSCC  
 Sbjct: 1319 YVWL-----LIGLAGVAVCVLLFFICCTGCGSCCFRKCSCC 1356

Score = 107 bits (268), Expect = 1e-21  
 Identities = 124/512 (24%), Positives = 194/512 (37%), Gaps = 42/512 (8%)  
 Frame = +1

Query: 1 MFIFLLFLTLTSGSDLRCTTFDDVQAPNYTQHTSSMR-----GVYYP-DEI 138  
 +F+F+L L G D F +Q NY + +S G YY D +  
 Sbjct: 2 LFVFILLLLPSCGLGYIGD----FRCIQTVNYNGNNASAPSISTEAVDVSKGLGTYYVLDVR 57

Query: 139 FRSDTLYLTQDLFLPF----YSNV--TGFHTINHTFGNP--VIPFKDGIYFAATE-KSNV 291  
 + + TL LT + P Y N+ TG +T++ T+ P + F DGI+ K+N  
 Sbjct: 58 YLNATLLLTG--YYPVDGNSYRNLALTGTNTLSLTWFKPPFLSEFNDGIFAKVQNLKTNT 115

Query: 292 VRGW-----VFGSTMNNKXXXXXXXXXXXXXXXXXACNFELCDNPFVAVSKPMGTQHT 450  
 G V GS N C + +C P+ KP  
 Sbjct: 116 PTGATSYFPTIVIGSLFGNTSYTVVLEPYNNIIMASVCTYTICQLPY-TPCKP----- 167

Query: 451 MIFDNFNFCTFEYISDAFSLDVSEKSGNFKHLREFVFNKNDGFLYVY---KGYQPIDVVR 621  
 N + + DV K R F F +LY + +G  
 Sbjct: 168 -----NTNGNRVIGFWHTDVKPPICLLK--RNFTFNVNAPWLYFHFYQQGGTFYAYYA 218

Query: 622 DLPSGFNTLKP IFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYD 801  
 D PS L F + +G +T + + +P T Y+V L ++ ++  
 Sbjct: 219 DKPSATTFL---FSVYIGDILTQYFVLPFICTPTAG--STLLPLYWVTPLLKRQYLFNFN 273

Query: 802 ENGTITDAVDCSQNPLAELKCSVKSF EIDKGIYQTSNFRVVPVSGDVVR-FPNITNLCDFG 978  
 E G IT AVDC+ + ++E+KC +S G+Y S + V P G V R PN+ + C  
 Sbjct: 274 EKGVITSAVDCASSYISEIKCKTQSLLPSTGVYDLSGYTVQPVGVVYRRVPLPD-CKIE 332

Query: 979 EVFNATKFPVSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADS 1158  
 E A PS WER+ NC + S L + C + A+K+ +CF +V D  
 Sbjct: 333 EWLTAKSVPSPLNWERRTFQNCNFNLSLLRYVQAESLSCNNIDASKVYGMCFGSVSDK 392

Query: 1159 FVVKGDVDRQIAPGQTGVIADYNYKLPDDFMGCVLAW----NTRNIDATSTGNINYKYRY 1326  
 F + + G +G + NYK+ C L + N I+ + ++N +Y +  
 Sbjct: 393 FAIPRSRQIDLQIGNSGFLQTANYKIDTAATSCQLYISLPKNNVTINNYNPSSWNRRYGF 452

Query: 1327 LRHGKLRPFERDISNV----PFSPDGKPCPTPP 1410  
 G + D++ P PC P  
 Sbjct: 453 NDAGVFGKSKHDVAYAQQCFTVRPSYCPCAQP 484

[gi|561670|gb|AAA87062.1](#) S glycoprotein [murine hepatitis virus]  
 Length = 1376

Score = 452 bits (1162), Expect = e-125  
 Identities = 277/763 (36%), Positives = 406/763 (53%), Gaps = 35/763 (4%)  
 Frame = +1

Query: 1525 TVCGPKL---STDLIKNCVNFNFNGLTGTGVLTP--SSKRFQPFQFGRDVSDFTDSVRD 1692  
 T C L +T++ CV ++ G+TG GV + + +Q DV+ + RD  
 Sbjct: 614 TTCSTDLQLPNTEVATGVCVRYDLYGITGQGVFKEVKADYYNSWQTLTYDVNGNLNGFRD 673

Query: 1693 PKTSEILDISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYST 1872  
 T++ I C G VS + E A+LY+++NC+ V + + + P  
 Sbjct: 674 LTTNKTYTIRSCYSGRVSAAYH--KDAPEPALLYRNINCSYVFSNNISREENPL----- 725

Query: 1873 GNNVFQTQAGCLIGAE-HVDTSY-ECDIPIGAGICASYHTVSLLR---STSQK--SIVAY 2031  
 N F + GC++ A+ H D + D+ +GAG+C Y R ST + + Y  
 Sbjct: 726 --NYFDSYLGCVVNADNHTDEALPNRDLRMGAGLCVDYSKSRARRSVSTGYRLTTTFEPY 783

Query: 2032 TMSLGADSSIAYSNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLL 2208  
 T L DS + + IPTNF+I E + + K ++DC ++CGD+T C L+  
 Sbjct: 784 TPMLVNDVSVQSVGGLYEMQIPTNFTTIGHHEEFIQIRAPKVTIDCAAFVCGDNTACRQQLV 843

Query: 2209 QYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLK YFG-----GFNFSQILP- 2367  
 +YGSFC +N L+ + D +V + + Q + G NFS +L  
 Sbjct: 844 EYGSFCDNVNAILNEVNNLLDNMQLQVASALMQGVTISSRLPDGISGPIDNINFSPLLG 903

Query: 2368 -----DPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNG 2517  
 P RS IEDLLF+KV L+D GF++ Y C G RDL+C Q FNG  
 Sbjct: 904 IGSTCAEDGNGPSAIRGRSAIEDLLFDKVKLSDVGFVEAYNNCTGGQEVRLDLCVQSFNG 963

Query: 2518 LTVLPPLLTDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLY 2697  
 + VLPP+L++ I+ YT + +PF++ + YR NG+GVT NVL  
 Sbjct: 964 IKVLPPVLSESQISGYTTGATAAAMFPWSAAAG---VPFSLNVQYRINGLGVTMNVLS 1019

Query: 2698 ENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVL 2877  
 ENQK IA+ FN A+ IQE T++ALGK+Q VVN NA+ALN L+ QLS+ FGAI+ L  
 Sbjct: 1020 ENQKMIASAFNNALGAIQEGFDATNSALGKIQSVVNANAEALNNLLNQLSNRFGAISASL 1079

Query: 2878 NDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQS 3057  
 +IL+RLD VEA+ QIDRLI GRL +L Y+++QL + I+ SA A K++ECV Q+  
 Sbjct: 1080 QEILTRLDAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKFSAAQAIEKVNCEVKSQT 1139

Query: 3058 KRVDFCGKGYHLMSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGV FV 3234  
 R+++FCG G H++S Q AP+G+ F+H +YVP+ +P +C G + P+ G FV  
 Sbjct: 1140 TRINFCGNGNHILSLVQNPYGLYFIHFSYVPTSFTTANVSPGLCISGDRGLAPKAGYFV 1199

Query: 3235 FNGTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYF 3414  
 + W T +++ P+ IT N+ V +C V + + P L FKEELDK+F  
 Sbjct: 1200 QDDGEWKFTGSSYYYPEPITDKNSVVMSSCSVNYTKAPEVLLNSSIPNLPDFKEELDKWF 1259

Query: 3415 KNHTS--PDVDLGDISGINASVUNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPW 3588  
 KN TS PD+ L D +N + +++ E++R+ E K LNES I+L+E+G YE Y+KWPW  
 Sbjct: 1260 KNQTSIAPDLSL-DFEKLNVTFLDLSDEMNR IQEAIKKNL NESYINLKEVGTYEMYVKWPW 1318

Query: 3589 YVWLGFIAGLIAIVMVTIXXXXXXXXXXXXXXKGC---SCGSCC 3708  
 YVWL LI + V + G+C CG+CC  
 Sbjct: 1319 YVWL-----LIGLAGVAVCVLLFFICCTGCGSCCFKCKGNCC 1356

Score = 103 bits (256), Expect = 3e-20  
 Identities = 104/440 (23%), Positives = 169/440 (38%), Gaps = 22/440 (5%)  
 Frame = +1

Query: 115 GVYYP-DEIFRSDTLYLTLQDLFLPF----YSNV--TGFHTINHTFGNP--VIPFKDGIYF 267  
 G YY D ++ + TL LT + P Y N+ TG +T++ T+ P + F DGI+  
 Sbjct: 49 GTYYVLDREVYLNATLLLTG--YYPVDGSNYRNLALTGTNTVSLTWFKPPFLSEFNDGIFA 106

Query: 268 AATE-KSNVVRGW-----VFGSTMNNKXXXXXXXXXXXXXXXXXACNFELCDNPF FAVS 423  
 K+N+ G V GS N C + +C P+

Sbjct: 107 KVHNLKTNMPTGATSYFPTIVIGSLFGNTSYTVVLEPYNNIIMASVCTYTTICQLPYTPCK 166

Query: 424 KPMGTQHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFVYVYKGYQ 603  
 + + + F+ DV+ F F + G Y Y

Sbjct: 167 PNTNGNSVIGFWHTDVKPPICLLKRNFDFVNAD-----WLYFHFYQGGTFYAYYA-- 218

Query: 604 PIDVVRDLPSGFNTLKPFIKFLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTT 783  
 D S L F + +G +T + + +P A Y+V L

Sbjct: 219 -----DKASATTFL---FSVYIGDILTQYFVLPFICTPTAG--SILAPRYWVTPLVKRQ 267

Query: 784 FMLKYDENGTTITDAVDCSQNPLAELKCSVKSF EIDKGIYQTSNFRVVP SGDVVR-FPNIT 960  
 ++ ++E G IT AVDC+ + +E+KC +S G+Y S + V P G V R PN+

Sbjct: 268 YLFNFNEKGVITS AVDCASSYTSEIKCKTQSLSPSTGVYDL SGYTVQPVGVVYRRVPLP 327

Query: 961 NLCPFGEVFNATKFP SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLN DLCSF 1140  
 + C E A PS WER+ NC + S L + C + A+K+ +CF

Sbjct: 328 D-CKIEEWLTA KSVPSPLNWERRTFQNCN FNLSLLRYVRAESLSCNNIDASKVYGMCFG 386

Query: 1141 NVYADSFVVKGD D V R Q I A P G Q T G V I A D Y N Y K L P D D F M G C V L A W ---NTRNIDATSTGNY 1308  
 +V D F + + G +G + NYK+ C L + N I+ + ++

Sbjct: 387 SVSVDKFAIPRSRQIDLQVGN S G F L Q T A N Y K I D T A A T S C Q L Y Y S L P K N N V T I N N Y N P S S W 446

Query: 1309 NYKYRYLRHGKLRPFERDIS 1368  
 N +Y + G + D++

Sbjct: 447 NRRYGFNDAGVFGKKQHDVA 466

>gi|9719318|gb|AAF97738.1|AF207551\_3 spike protein [rat sialodacryoadenitis corc  
 Length = 1360

Score = 452 bits (1162), Expect = e-125  
 Identities = 278/749 (37%), Positives = 403/749 (53%), Gaps = 28/749 (3%)  
 Frame = +1

Query: 1546 STDLIKNOQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFTDSVRDPKTSEILDIS 1722  
 +T+++ CV ++ G TG GV + + +Q DV+ + RD T++ +

Sbjct: 611 NTEVVTGVCVKYDLYGSTGQGVFKEVKADYYNSWQNL LYDVNGNLNGFRDIVTNKTYLLR 670

Query: 1723 PCAFGGVS VITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAG 1902  
 C G VS + E A+LY+++ C V + + TP N F + G

Sbjct: 671 SCYSGRVSAAYH--QDAPEPALLYRNLKCDYVFNNNISREETPL-----NYFDSYLG 720

Query: 1903 CLIGA EH-VDTSYE-CDIPIGAGICASYHTVSLLR---STSQK--SIVAYTMSLGADSSI 2061  
 C+I A++ + S + CD+ +G+G+C +Y R ST K + +T+S+ DS

Sbjct: 721 CVINADNSTEQSVDACDLRMGSLCVNYSIAHRARRSVSTGYKLTTTFEPFTVSIVNDSVE 780

Query: 2062 AYSN-NTIAIPTNFSISITTEVMPVSM AKTSVDCNMYICGDSTECANLLLQYGSFCTQLN 2238  
 + + IPTNF+I+ E + K ++DC ++CGD T C L+ YGSFC +N

Sbjct: 781 SVGGLYEMQIPTNFTIASHQEFIQTRSPKVTIDCAAFVCGDYTACRQQLVDYGSFCDNIN 840

Query: 2239 RALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQIL----PDPLKPTK 2388  
 L + D +V + + Q + G NFS +L D + TK

Sbjct: 841 AILGEVNNLIDTMQLQVASALIQGVTLSSRLADGISGQIDDINFSPLLGCLGSDCSEGTK 900

Query: 2389 ----RSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTD DMI 2556  
 RS IED+LF+KV L+D GF++ Y C G RDL+C Q FNG+ VLPP+L++ I

Sbjct: 901 AAQGRSAIEDVLFDKVKLS D V G F V E S Y N N C T G G Q E V R D L L C V Q S F N G I K V L P P V L S E S Q I 960

Query: 2557 AAYTAALVSXXXXXXXXXXXXXXXXX LQIPFAMQ MAYRFNGIGVTQNVLYENQKQIANQFNKA 2736

+ YTA + +PFA+ + YR NG+GVT NVL ENQK IA+ FN A  
 Sbjct: 961 SGYTAGATASAMFPPWSAAAG----VPFALSVQYRINGLGVTMNVLSENQKMIASSFNNA 1016

Query: 2737 ISQIQESLTTTSTALGKLDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAE 2916  
 I IQE T++AL K+Q VVN NA+ALN L+ QLS+ FGAIS+ L +ILSRLD +EA+  
 Sbjct: 1017 IGAIQEGFDATNSALAKIQSVVNANAEALNNLLNQLSNRFGAISASLQEILSRLDALEAQ 1076

Query: 2917 VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM 3096  
 QIDRLI GRL +L YV++QL I+ SA A K++ECV QS R++FCG G H++  
 Sbjct: 1077 AQIDRLINGRLTALNAYVSKQLSDMTLIKVSAAQAIEKVNCEVKSQSPRINFCGNGNHIL 1136

Query: 3097 SFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTWSWFITQRNF 3273  
 S Q AP+G+ F+H +YVP+ +P +C G + P+ G FV + W T N+  
 Sbjct: 1137 SLVQNAPYGLYFIHFSYVPTSFTTVNVSPGLCISGDRGLAPKAGYFVQDHGEWKFTGSNY 1196

Query: 3274 FSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVLG-D 3450  
 + P+ IT N+ V +C V + L FKEELDK+FKN TS DL D  
 Sbjct: 1197 YYPESITDKNSVVMSSCAVNYTKAPEVFLNTSITNLPDFKEELDKWFKNQTSIVPDLSD 1256

Query: 3451 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIV 3630  
 I +N + +++ E++R+ + KNLNES I+L+E+G YE Y+KWPWYVWL LI +  
 Sbjct: 1257 IGKLNVTFLDLSYEMNRIQDAIKNLNESYINLKEIGTYEMYVKWPWYVWL-----LIGLA 1311

Query: 3631 MVTIXXXXXXXXXXXXXXGAC---SCGSCC 3708  
 V + G+C CG+CC  
 Sbjct: 1312 GVAVCVLLFFICCTGCGSCCFKCKGNCC 1340

Score = 107 bits (268), Expect = 1e-21  
 Identities = 121/522 (23%), Positives = 199/522 (38%), Gaps = 48/522 (9%)  
 Frame = +1

Query: 1 MFIFLLFLTTLTSGSDDL-RC-----TTFDDVQAPNYTQHT---SSMRGVYYP-DEIFRSD 150  
 +F+FL L G D RC T + +AP+ + S G YY D ++ +  
 Sbjct: 2 LFVFLTLTLLPSCGLGYIGDFRCINLVNTRISNARAPSVSTEVVDVSKGLGTYVVLDRVYLN 61

Query: 151 TLYLTQDLFLP----FYSNVT--GFHTINHTFGNP--VIPFKDGIYFAATE-KSNVVRGW 303  
 TL LT + P Y N+ G +T++ + P + F DGIY K+++ G  
 Sbjct: 62 TLLLTLG--YYPVDGSMYRNMALMGTNTLSLWFEPPFLSEFNDGIYAKVKNLKASLPIGS 119

Query: 304 -----VFGSTMNNKXXXXXXXXXXXXXXXXXRACNFELCDNPFVAVSKPMGTQTHMIFD 462  
 + GS N C + +C P G T +  
 Sbjct: 120 ASYFPTIIIGSNFVNTSYTVVLEPYNGIIMASICQYTICQLPHTDCKPNTGGNTLIGFWH 179

Query: 463 NAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFN 642  
 + F+ +V+ + F F + G Y Y D+ S  
 Sbjct: 180 TDLRPPVCILKRNFVFNVAE-----WLYFHFYQQGGTFYAYYA-----DVSSATT 225

Query: 643 TLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITD 822  
 L F +G +T+ + SP G S+ Y+V L ++ +++ G IT  
 Sbjct: 226 FL---FSSYIGAVLTQYFVLPYMCSPPTS--GVSSPYWVTPLVKRQYLFNFNQKGIITS 280

Query: 823 AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVRFNPITNL--CPFGEVFNAT 996  
 AVDC+ + +E+KC +S + G+Y S + V P G V R + NL C E A  
 Sbjct: 281 AVDCASSYTSEIKCKTQSMNPNTGVYDLSGYTVQPVGLVYR--RVRNLPDCKIEEWLAAN 338

Query: 997 KFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGD 1176  
 PS WERK NC + S L + C + A+K+ +CF ++ D F +  
 Sbjct: 339 TVPSPLNWERKTFQNCNFNLSLLRFVQAESLSCSNIDASKVYGMCFGSISIDKFAIPNS 398

Query: 1177 DVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDAT----STGNYNYKYRYLRHGKL 1344  
 + G++G++ +NYK+ C L ++ + T + ++N +Y +  
 Sbjct: 399 RRVDLQLGKSGLLQSFNYKIDTRATSCQLYYSLSAQDNVTVINHNPSWNRRYGFNDVATF 458

Query: 1345 RPFERDIS-----NVPFSPDGKPCPT-----PPALNC 1422  
 E D++ + P KP T P + NC  
 Sbjct: 459 HSGEHDVAYAEACFTVYGASYCPCAKPSTVYSCVTVGKPKSANC 500

>[gi|2662177|dbj|BAA23719.1](http://gi|2662177|dbj|BAA23719.1) spike glycoprotein [Murine hepatitis virus]  
 Length = 1360

Score = 451 bits (1160), Expect = e-125  
 Identities = 275/764 (35%), Positives = 400/764 (52%), Gaps = 36/764 (4%)  
 Frame = +1

Query: 1525 TVCGPKL---STDLIKNCQVNFNFNGLTGTGVLTP-SSKRFQPFQQFGRDVSDFTDSDVRD 1692  
 T C L +T+++ CV ++ G+TG GV + + +Q DV+ + RD  
 Sbjct: 601 TTCSMDLQLPNTEVVVTGICVKYDLYGITGQGVFKEVKADYYNSWQNLQDYNVNGNLNGFRD 660

Query: 1693 PKTSEILDISPFAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYST 1872  
 T++ C G VS + E A+LY+++ C V + TP  
 Sbjct: 661 IVTNKTYLTRSCYSGRVSAAYH--QGAPEPALLYRNLKCDYVFNNNIFREETPL----- 712

Query: 1873 GNNVFQTQAGCLIGAHEVDTSY--ECDIPIGAGICASYHTVSLLR---STSQK--SIVAY 2031  
 N F + GC++ A++ CD+ +G+G+C +Y T R ST K + +  
 Sbjct: 713 --NYFDSYLGCVVNADNTEQAVDACDLRMGSLGCVNYSTAHRRARPVSTGYKLTTFEPF 770

Query: 2032 TMSLGADSSIAYSN-NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLL 2208  
 T+S+ DS + + IPTNF+I+ E + K ++DC ++CGD T C L+  
 Sbjct: 771 TVSIVNDSVESVGLYEMQIPTNFTIASHQEFIQTRAPKVTIDCAAFVCGDYTTTCRQQLV 830

Query: 2209 QYGSFCTQLNRALSGI-----AAEQDRNTREVFAQVKQMYKTPTLKY 2334  
 +YGSFC +N L + R + Q+ + +P L  
 Sbjct: 831 EYGSFCDNINAILGEVNNLIDTMQLQVASALIQQVTLSSRLADGISGIDDINFSPLLG 890

Query: 2335 FGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFN 2514  
 G SQ + RS +EDLLF+KV L+D GF++ Y C G RDL+C Q FN  
 Sbjct: 891 LG----SQCSEGTMAAQGRSTVEDLLFDKVKLSVGFVEAYNNCTGGQEVRLDLCVQSFN 946

Query: 2515 GLTVLPPLLTDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVL 2694  
 G+ VLPP+L+++ ++ YTA + +PF++ + YR NG+GVT NVL  
 Sbjct: 947 GIKVLPVLSVQYRINGLVGVTMNVL 1002

Query: 2695 YENQKQIANQFNKAISQIQESLTTTSTALGKLDVVNQNAQALNTLVKQLSSNFGAISSV 2874  
 ENQK IA+ FN AI IQE T++AL K+Q VVN NA+ALN L+ QLS+ FGAIS+  
 Sbjct: 1003 SENQKMIASAFNNAIGAIQEGFDATNSALAKIQSVVNANAEALNNLLNQLSNRFGAISAS 1062

Query: 2875 LNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQ 3054  
 L +ILSRLD +EA+ QIDRLI GRL +L YV++QL I+ SA A K++ECV Q  
 Sbjct: 1063 LQEILSRLDALEAQAQIDRLINGRLTALNAYVSKQLSDMTLIKVSAAQAIEKVNCEVKSQ 1122

Query: 3055 SKRVDFCGKGYHLMSFPQAAPHGVVFLHVTVYVPSQERNFTTAPAICHEG-KAYFPREGVF 3231  
 S R++FCG G H++S Q AP+G+ FLH +YVP+ +P +C G + P+ G F  
 Sbjct: 1123 SPRINFCGNGNHILSLVQNAPYGLYFLHFSYVPTSFTTANVSPGLCISGDRGLAPKAGYF 1182

Query: 3232 VFNGTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKY 3411  
 V + W T N++ P+ IT N+ V +C V + L FKEELDK+

Sbjct: 1183 VQDDGEWKFTGSNYYYEPITDKNSVVMSSCAVNYTKAPEVFLNTSISINLPDFKEELDKW 1242  
 Query: 3412 FKNHTS--PDVDLGDISGINASVUNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP 3585  
 FKN TS PD+ L D +N + +++ E++R+ E K LNES I+L+E+G YE Y+KWP  
 Sbjct: 1243 FKNQTSVAPDLSL-DFEKLNVTFDLDSDEMNR IQEAIKKNL NESYINLKEIGTYEMYVKWP 1301  
 Query: 3586 WYVWLGFIAGLIAIVMVTIXXXXXXXXXXXXXXK GAC---SCGSCC 3708  
 WYVWL LI + V + G+C CG+CC  
 Sbjct: 1302 WYVWL-----LIGLAGVAVCVLLFFICCTGCGSCCFKKCGNCC 1340

Score = 91.7 bits (226), Expect = 8e-17  
 Identities = 53/187 (28%), Positives = 86/187 (45%), Gaps = 2/187 (1%)  
 Frame = +1

Query: 784 FMLKYDENGTTITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVP SGDVVRFPNITN 963  
 ++ +++ GTIT AVDC+ + +E+KC +S + G+Y S + V P G V R + N  
 Sbjct: 267 YLFNFNQKGTITS AVDCASSYTSEIKCKTQSMNPNTGVYDLSGYTVQPVGLVYR--RVRN 324  
 Query: 964 L--CPFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCF 1137  
 L C + A PS WERK NC + S L + C + A K+ +CF  
 Sbjct: 325 LPDCRIEDWLA AKTVPSPLNWERKTFQNCN FNLSLLRLVQAGSLSCSNIDA AKVYGMCF 384  
 Query: 1138 SNVYADSFVVKGDDVVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYK 1317  
 ++ D F + + G +G + +NYK+ C L ++ + T N+N  
 Sbjct: 385 GSMSIDKFAIPNSRRVDLQLGNSGFLQSFNYKIDTRATSCQLYSLAQSNVT-VNNHNPS 443  
 Query: 1318 YRYLRHG 1338  
 R+G  
 Sbjct: 444 SWNRRYG 450

>[gi|1825483|gb|AAC56567.1](#) spike protein [murine hepatitis virus]  
[gi|6625763|gb|AAF19386.1|AF201929\\_4](#) spike glycoprotein precursor [murine hepatitis virus]  
[gi|7739598|gb|AAF68923.1|AF207902\\_5](#) spike glycoprotein precursor [murine hepatitis virus]  
 Length = 1361

Score = 442 bits (1138), Expect = e-122  
 Identities = 273/762 (35%), Positives = 404/762 (53%), Gaps = 34/762 (4%)  
 Frame = +1

Query: 1525 TVCGPKL---STDLIKNCQVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVVD 1692  
 T C L +T+++ CV ++ G+TG G+ + + +Q DV+ RD  
 Sbjct: 602 TTCSMDLQLPNTTEVVTGVCVKYDLYGITGQIFKEVKADYYHSWQNLLYDVNGNLIGFRD 661  
 Query: 1693 PKTSEILDISP C AFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYST 1872  
 ++ I C G VS + E A+LY+++ C V + + TP  
 Sbjct: 662 FVANKSYTIRSCYSGRVSAAYH--QDAPEPALLYRNLKCDYVFNNNISREETPL----- 713  
 Query: 1873 GNNVFQTQAGCLIGA EHV--DTSYECDIPIGAGICASYHTVSLLRSTSQK-----SIVAY 2031  
 N F + GC++ A++ + CD+ +G+G+C +Y T RS+ + +  
 Sbjct: 714 --NYFDSYLGCVVNADNSTEEAVDACDLRMGSGLCVNYSTSHRARSSVSTGYKLTTTFEPF 771  
 Query: 2032 TMSLGADSSIAYSN-NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLL 2208  
 T+ + DS + + IPTNF+I+ E + K ++DC ++CG T C L+  
 Sbjct: 772 TVRIVNDSVESVDGLYELQIPTNFTIASHQEFVQTRSPKVTIDCAAFVCGGHTACRQQLV 831  
 Query: 2209 QYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQ--MYKTPTLKYFGG----FNFSQILP- 2367

+YGSFC +N L + D +V + + Q + GG NFS +L  
 Sbjct: 832 EYGSFCDNINAILGEVNNLIDTMQLQVASALIQGVTLSSRLSDGIGGQIDDINFSPLLGC 891

Query: 2368 -----DPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLT 2523  
 T RS IED+LF+KV L+D GF++ Y C G RDL+C Q FNG+  
 Sbjct: 892 LGSDCGEVTMAAQGTGRSAIEDVLFDKVKLSVDFVEAYNNCTGGQEVRLDLCVQSFNGIK 951

Query: 2524 VLPPLLTDMMIAAYTA-ALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYE 2700  
 VLPP+L+++ I+ YTA A VS +PF++ + YR NG+GVT NVL E  
 Sbjct: 952 VLPPVLSENQISGYTAGATVSAMFPWSAAAG-----VPFSLSVQYRINGLVGTMNVLSE 1005

Query: 2701 NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN 2880  
 NQK IA+ FN AI IQE T+++AL K+Q VVN NA+ALN L+ QLS+ FGAIS+ L  
 Sbjct: 1006 NQKMIASAFNNAIGAIQEGFAATNSALAKMQFVVNANAALNLLNQLSNRFGAISASLQ 1065

Query: 2881 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK 3060  
 +ILSRLD +EA+ QIDRLI GRL +L YV++QL ++ SA A K++ECV QS  
 Sbjct: 1066 EILSRLDALEAQAQIDRLINGRLTALNAYVSKQLSDMTLVKVSAAQAIEKVNCECVKSQSS 1125

Query: 3061 RVDFCGKGYHLSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFV 3237  
 R+++FCG G H++S Q AP+G+ F+H +YVP+ +P +C G + P+ G FV  
 Sbjct: 1126 RINFCGNGNHILSLVQNPYGLYFIHFSYVPTSFTTANVSPGLCISGDRGLAPKAGYFVQ 1185

Query: 3238 NGTSWFITQRNFFSPQIITDNTFVSGNCDVVGIIINNTVYDPLQPELDSFKEELDKYFK 3417  
 + W T N++ P+ IT N+ V +C + P L FKEELDK+FK  
 Sbjct: 1186 DDGEWKFTGSNYYYPEPITDKNSVVMSSCAANYTKAPEVFLNTSIPNLPDFKEELDKWFK 1245

Query: 3418 NHTS--PDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWY 3591  
 N TS PD+ L D +N +++++ E++R+ + K LNES I+L+++G YE Y+KWPWY  
 Sbjct: 1246 NQTSIAPDLSL-DFEKLNVTLTLLDLDLDEMNRIQDAIKKLNESYINLKDVGTYEMYVWKPWY 1304

Query: 3592 VWLGFIAGLIAIVMVTIXXXXXXXXXXXXXXXXXKAC---SCGSCC 3708  
 VWL LI + V + G+C CG+CC  
 Sbjct: 1305 VWL-----LIGLAGVAVCVLLFFICCCCTGCGSCCFKKCGNCC 1341

Score = 101 bits (251), Expect = 1e-19  
 Identities = 109/474 (22%), Positives = 183/474 (38%), Gaps = 32/474 (6%)  
 Frame = +1

Query: 1 MFIFLLFLTTLTSGSDLD-RC-----TTFDDVQAPNYTQHTSSMR---GVYYP-DEIFRSD 150  
 +F+FL L + G D RC T + AP+ + + G YY D ++ +  
 Sbjct: 2 LFFVFLTLPLSSLYIGDFRCIQLVNTDTSNASAPSVSTEVVDVSKGIGTYVVLDRVYLN 61

Query: 151 TLYLTQDLFLP----FYSNV--TGFHTINHTFGNP--VIPFKDGIYF-----AATEKSN 288  
 TL LT + P Y N+ TG +TI+ + P + F DGI+ A+ K +  
 Sbjct: 62 TLLLTG--YYPVDGSMYRNMAALTGINTISLWYKPPFLSEFNDGIFAKVKNLKASLPKDS 119

Query: 289 V--VRGWVFGSTMNNKXXXXXXXXXXXXXXXXXRACNFELCDNPFPAVSKPMGTQHTMIFD 462  
 + + GS C + +C P+ G +  
 Sbjct: 120 ISYFPTIIIGSNFVTTSYTVVLEPYNGIIMASICQYTICQLPYTDCKPNTGGNKLIGFWH 179

Query: 463 NAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFVYVYKGYQPIDVVRDLPSGFN 642  
 + F+ +V+ + F F + G Y Y D+ S  
 Sbjct: 180 TELKSPVCILKRNFVFNVAE-----WLYFHFYQGGTFYAYYA-----DVSSATT 225

Query: 643 TLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITD 822  
 L F + +G +T + + + G + Y+V L ++ +++ G IT  
 Sbjct: 226 FL---FSMYIGDVLTYQ--FVLPYMCTLTTTGVFSPQYWVTPLVKRQYLFNFNQKGIITS 280

Query: 823 AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVRFNPITNL--CPFGEVFNAT 996  
 AVDC+ + +E+KC +S + G+Y S + V P G V R + NL C E A  
 Sbjct: 281 AVDCASSYTSEIKCKTQSMNPNTGVYDLSGYTVQPVGLVYR--RVRNLPDCKIEEWLTAK 338

Query: 997 KFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGD 1176  
 PS WERK NC D S L + C + A+K+ +CF ++ D F +  
 Sbjct: 339 SVPSPLNWERKTFQNCNFDLSSLLRFVQAESLSCSNIDASKVYGMCFGSISIDKFAIPNR 398

Query: 1177 DVRQIAPGQTGVIADYNYKLPDDFMGC----VLAWNTRNIDATSTGNYNKYRY 1326  
 + G +G + +NYK+ C LA N ++ + ++N +Y +  
 Sbjct: 399 RRVDLQLGNSGFLQSFNYKIDTRATSCQLYYS LAKNNVTVNNHNPSSWNRRYGF 452

>[gi|549302|sp|P36334|VGL2\\_CVHOC](#) E2 glycoprotein precursor (Spike glycoprotein) ([Contains: Spike protein S1 (90B); Spike protein S2 (90A)])  
[gi|476485|pir||JQ2168](#) E2 glycoprotein precursor - human coronavirus (strain OC43)  
[gi|306156|gb|AAA03055.1|](#) spike protein [Human coronavirus OC43]  
 Length = 1353

Score = 441 bits (1134), Expect = e-122  
 Identities = 274/763 (35%), Positives = 399/763 (52%), Gaps = 28/763 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP--SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+ G G+ ++ + +Q D + RD +  
 Sbjct: 611 KANTDIILGVCVNYDLYGILGQGIFVEVNATYYNSWQNLLYDSNGNLYGFRDYIINRTFM 670

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQQTQ 1896  
 I C G VS SSE A+L++++ C V QL P N F +  
 Sbjct: 671 IRSCYSGRVSAAFHAN--SSEPALLFRNIKCNYVFNNSLTRQLQPI-----NYFDSY 720

Query: 1897 AGCLIGAHEVD--TSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A + + CD+ +G+G C Y S +++S A T + ++  
 Sbjct: 721 LGCVVNAYNSTAISVQTCDLTVGSGYCVDY-----SKNRRSRGAITTYRFTNFEPFT 773

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQ 2211  
 N+ I IP+ F+I E + S K ++DC ++CGD C + L++  
 Sbjct: 774 VNSVNSLEPVGGLYEIQIPSEFTIGNMVEFIQTSSPKVTIDCAAFVCGDYAACKSQLVE 833

Query: 2212 YGSFCTQLNRALSGLIAAEQDRNTREVFAQVKQMYKTPT-LKYFGGFNFSQILPDPL---- 2376  
 YGSFC +N L+ + D +V + T LK FN I P+  
 Sbjct: 834 YGSFCDNINAILTEVNELLDTTQLQVANS LMNGVTLSTKLKDGVNFNVD DINFSPVLGCL 893

Query: 2377 -----KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLL 2541  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q + G+ VLPPLL  
 Sbjct: 894 GSECKASSRSAIEDLLFDKVKLSDVGFVEAYNNTGGAEIRD LICVQSYKGIKVLPPLL 953

Query: 2542 TDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIAN 2721  
 +++ I+ YT A S +PF + + YR NG+GVT +VL +NQK IAN  
 Sbjct: 954 SENQISGYTLAATSASLFPPWTAAG----VPFYLVNQYRINGLGVTMDVLSQNQKLIAN 1009

Query: 2722 QFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLD 2901  
 FN A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAIS+ L +ILSRLD  
 Sbjct: 1010 AFNNALYAIQEGFDATNSALVKIQAVVNANAEALNLLQQLSNRFGAISASLQEILSRLD 1069

Query: 2902 KVEAEVQIDRLITGRLOSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGK 3081  
 +EAE QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG

Sbjct: 1070 ALEAEAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNNECVKSQSSRINFCGN 1129

Query: 3082 GYHLMSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFI 3258  
 G H++S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W

Sbjct: 1130 GNHIISLVQNAPYGLYFIHFSYVPTKYVTARVSPGLCIAGDRGIAPKSGYFVNVNNTWMY 1189

Query: 3259 TQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDV 3438  
 T ++ P+ IT +N V C V + + P L FKEELD++FKN TS

Sbjct: 1190 TGSGYYYYPEPITENNVVVMSTCAVNYTKAPYVMLNTSIPNLPDFKEELDQWFKNQTSVAP 1249

Query: 3439 DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGF- IAG 3615  
 DL + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL +AG

Sbjct: 1250 DL-SLDYINVTFLDLQVEMNRLQEAIKVLNQSYINLKDIGTYEYVVKWPWYVWLLICLAG 1308

Query: 3616 LIAIVMVTIXXXXXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 + +V++ K CG CC E V+K

Sbjct: 1309 VAMLVLLFFICCCTGCGTSCFK---KCGGCCDDYTGYQELVIK 1348

Score = 97.4 bits (241), Expect = 2e-18  
 Identities = 54/204 (26%), Positives = 96/204 (47%), Gaps = 5/204 (2%)  
 Frame = +1

Query: 754 YFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPG 933  
 Y+V L ++L ++++G I +A DC + ++E+KC +S G+Y+ + + V P

Sbjct: 264 YWVTPLTSRQYLLAFNQDGIIFNAEDCMSDFMSEIKCKTQSIAPPTGVYELNGYTVQPIA 323

Query: 934 DVVRF-PNITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS 1110  
 DV R PN+ N C N PS WERK SNC + S L + +F C +

Sbjct: 324 DVYRRKPNLPN-CNIEAWLNDKSVPSPLNWERKTFSNCFNMSSLMSFIQADSFTCNNID 382

Query: 1111 ATKLNDLCFSNVYADSFVVKGDDVQRQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TR 1278  
 A K+ +CFS++ D F + + G G + +NY++ C L +N

Sbjct: 383 AAKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANV 442

Query: 1279 NIDATSTGNYNYKYRYLRHGKLRP 1350  
 ++ + +N ++ ++ +P

Sbjct: 443 SVSRFNPSTWNKRFGFIEDSVFKP 466

>[gi|476773|pir||A37474](http://gi|476773|pir||A37474) surface glycoprotein S - human coronavirus  
 Length = 1362

Score = 439 bits (1128), Expect = e-121  
 Identities = 275/763 (36%), Positives = 397/763 (52%), Gaps = 28/763 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+ G G+ ++ + +Q D + RD T+

Sbjct: 620 KANTDIILGVCVNYDLYGILGQIGIFVEVNATYYNSWQNLLYDSNGNLYGFRDYITNRTFM 679

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTO 1896  
 I C G VS SSE A+L +++ C V QL P N F +

Sbjct: 680 IRSCYSGRVSAAFHAN--SSEPALLSRNIKCNYVFNNLSLTRLQPI-----NYFDSY 729

Query: 1897 AGCLIGAEHVD--TSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC + A + + CD+ +G+G C Y S +++S A T + ++

Sbjct: 730 LGCavnayNSTAISVQTCDLTVGSGYCVDY-----SKNRRSRGAIITTYRFTNFEPFT 782

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQ 2211  
 N+ I IP+ F+I E + S K ++DC ++CGD C + L+

Sbjct: 783 VNSVNSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCAAFVCGDYAACKSQLVG 842

Query: 2212 YGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPT-LKYFGGFNFSQILPDPL---- 2376  
 YGSFC +N L+ + D +V + T LK FN I P+

Sbjct: 843 YGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDINFSPLVGLCL 902

Query: 2377 -----KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLL 2541  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q + G+ VLPPLL

Sbjct: 903 GSECSKASSRSAIEDLLFDKVKLSDVGFVEAYNNTGGAEIRDLICVQSYKGKIVLPPLL 962

Query: 2542 TDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIAN 2721  
 +++ I+ YT A S +PF + + YR NG+GVT +VL +NQK IAN

Sbjct: 963 SENQISGYTLAATSASLFPWTAAG----VPFYLVNQYRINGLGVTMDVLSQNQKLIAN 1018

Query: 2722 QFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLD 2901  
 FN A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAIS+ L +ILSRLD

Sbjct: 1019 AFNNALYAIQEGFDATNSALVKIQAVVNANAALNLLQLSNRFGAISASLQEIILSRLD 1078

Query: 2902 KVEAEVQIDRLITGRQLSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGK 3081  
 +EAE QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG

Sbjct: 1079 ALEAEAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSQSSRINFVCGN 1138

Query: 3082 GYHLMSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFI 3258  
 G H++S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W

Sbjct: 1139 GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWVY 1198

Query: 3259 TQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKEYFKNHTSPDV 3438  
 T ++ P+ IT +N V C V + + P L FKEELD++FKN TS

Sbjct: 1199 TGSGYYPPEPITENNVMSTCAVNYTKAPYVMLNTSIPNLPDFKEELDQWFKNQTSVAP 1258

Query: 3439 DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGF-IAG 3615  
 DL + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL +AG

Sbjct: 1259 DL-SLDYINVTFLDLQVEMNRLQEAIKVLNQSYINLKDIDIGTYEYVVKWPWYVWLLICLAG 1317

Query: 3616 LIAIVMVTIXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 + +V++ K CG CC E V+K

Sbjct: 1318 VAMLVLLFFICCTGCGTSCFK---KCGGCCDDYTGQYELVIK 1357

Score = 95.9 bits (237), Expect = 4e-18  
 Identities = 61/240 (25%), Positives = 113/240 (47%), Gaps = 6/240 (2%)  
 Frame = +1

Query: 649 KPIFKLPLGINITNFRAI-LTAFSPAQDIWGTSAAAYFVGYLKPTTFMLKYDENGITIDA 825  
 K +F + LG+ ++++ + LT S ++ G Y+V L ++L ++++ I +A

Sbjct: 237 KFLFNVYLGMAISHYVYVPLTCSKVKN--GFMTLEYVWVTPTRKQYLLAFNQDIVIFNA 294

Query: 826 VDQSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVRF-PNITNLCPFGEVFNATKF 1002  
 VD + ++E+KC +S G+Y+ + + V P DV R PN+ N C N

Sbjct: 295 VDMKSDFMSEIKCKTQSIAPPTGVYELNGYTVQPIADVYRRKPNLPN-CNIEAWLNDKSV 353

Query: 1003 PSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGDDV 1182  
 PS WERK SNC + S L + +F C + A K+ +CFS++ D F +

Sbjct: 354 PSPLNWERKTFSNCFNMSLMSFIQADSFTCNNIDA AKIYGMCFSSITIDKFAIPNGRK 413

Query: 1183 RQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TRNIDATSTGNINYKYRYLRHGKLRP 1350

+ G G + +NY++ C L +N ++ + +N ++ ++ +P  
 Sbjct: 414 VDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAAVSVSRFNPSTWNKRFGFIEDSVFKP 473

>[gi|23295760|gb|AAL80031.1](#) spike glycoprotein [porcine hemagglutinating enceph  
 Length = 1349

Score = 435 bits (1119), Expect = e-120  
 Identities = 271/767 (35%), Positives = 402/767 (52%), Gaps = 27/767 (3%)  
 Frame = +1

Query: 1525 TVCGPKL---STDLIKNCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRD 1692  
 T C L +T + + CVN++ G+TG G+L ++ + +Q D S RD  
 Sbjct: 599 TTCSTDLQQGNTIITTDVVCVNYDLYGITGQGILIEVNTYYNSWQNLLYDSSGNLYGFRD 658

Query: 1693 PKTSEILDISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDV--STAIHADQLTPAWRIY 1866  
 ++ I C G VS + SSE A+++++ C+ V +T + QL  
 Sbjct: 659 YLSNRTFLIRSCYSGRVSAVFHAN--SSEPALMFRNLKCSHFVFNNTILRQIQLV----- 710

Query: 1867 STGNNVFQQTQAGCLIGAEHVDTSY--ECDIPIGAGICASYHTVSLLRSTSQ-----KS 2019  
 N F + GC++ A + S CD+ +G+G C Y V+ LRS +  
 Sbjct: 711 ----NYFDSYLGCVVNAYNNTASAVSTCDLTVGSGYCVDY--VTALRSRRSFTTGYRFTN 764

Query: 2020 IVAYTMSLGADSSIAYSN-NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECA 2196  
 + +L DS I IP+ F+I E + K ++DC ++CGD C  
 Sbjct: 765 FEPFAANLVNDSIEPVGGLYEIQIPSEFTIGNLEEFIQTRSPKVTIDCATFVCGDYAACR 824

Query: 2197 NLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPT-LKYFGGFNFSQILPDP 2373  
 L +YGSFC +N L+ + D +V + T +K FN I P  
 Sbjct: 825 QQLAEYGSFCENINAILTEVNELLDTTQLQVANS LMNGVTLSTKIKDGINFNVD DINFSP 884

Query: 2374 L-----KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTV 2526  
 + + + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ V  
 Sbjct: 885 VLGCLGSECNRASTRSAIEDLLFDKVKLSDVGVFQAYNNCTGGAEIRD LICVQSYNGIKV 944

Query: 2527 LPPLLTDMMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQ 2706  
 LPPLL+++ I+ YT A + +PF + + YR NG+GVT +VL +NQ  
 Sbjct: 945 LPPLLSENQISGYTLAATAASLFPWTAAG----VPFYLVNQYRINGLGVTMDVLSQSQ 1000

Query: 2707 KQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDI 2886  
 K IA+ FN A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAIS+ L +I  
 Sbjct: 1001 KLIASAFNNALDAIQEGFDATNSALVKIQAVVNANA EALNNLLQQLSNRFGAISASLQEI 1060

Query: 2887 LSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRV 3066  
 LSRLD +EA+ QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R+  
 Sbjct: 1061 LSRLDALEAKAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAIEKVNECVKSQSSRI 1120

Query: 3067 DFCGKGYHLMSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEGK-AYFPREGVVFVNG 3243  
 +FCG G H++S Q AP+G+ F+H +YVP++ +P +C G P+ G F+  
 Sbjct: 1121 NFCGNGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDIGISPKSGYFINVN 1180

Query: 3244 TSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNH 3423  
 SW T +++ P+ IT +N V C V + + + P L FKEEL ++FKN  
 Sbjct: 1181 NSWMFTGSSYYPEPITQNNVVVMSTCAVNYTKAPDLMLNTSTPNLPDFKEELYQWFKNQ 1240

Query: 3424 TSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLG 3603  
 +S DL + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL  
 Sbjct: 1241 SSVAPDL-SLDYINVTFLDLQDEMNRLEAEIKVLNQSYINLKDIDIGTYEYVWKPWYVWL- 1298

Query: 3604 FIAGLIAIVMVTIXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744  
 + GL + M+ + CG CC E V+K  
 Sbjct: 1299 -LIGLAGVAMLVLLFFICCTGCGTSCFKKCGGCCDDYTGHQEFVIK 1344

Score = 95.9 bits (237), Expect = 4e-18  
 Identities = 62/235 (26%), Positives = 110/235 (46%), Gaps = 3/235 (1%)  
 Frame = +1

Query: 631 SGFNTLKPFIKPLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENG 810  
 +GF T K +FKL LG ++++ + + A + Y+V L F+L +D++G  
 Sbjct: 226 TGFVT-KFLFKLYLGTVLSHYYVMPLTCNSALS-----EYWVTPLTTRQFLLAFDQDG 278

Query: 811 TITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVR-FPNITNLCPFGEVF 987  
 + AVDC+ + ++E+ C S G+Y+ + + V P V R P++ N C  
 Sbjct: 279 VLYHAVDCASDFMSEIMCKTSSITPPTGVYELNGYTVQPVATVYRRIPDLPN-CDIEAWL 337

Query: 988 NATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLFCFSNVYADSFVV 1167  
 N+ S WERK SNC + L + +F C + A++L +CF ++ D F +  
 Sbjct: 338 NSKTVSSPLNWERKIFSNCNFMGRMSFIQADSFGCNNIDASRLYGMCFGSIIDKFAI 397

Query: 1168 KGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWN--TRNIDATSTGNYNYKYRY 1326  
 + G++G + +NYK+ C L ++ N+ T ++ RY  
 Sbjct: 398 PNSRKVDLQVGKSGYLQSFNYKIDTAVSSQLYYSLPAANVSVTHYNPSSWNRRY 452

>[gi|9653289](#) | [gb|AAB27260.2](#) | surface glycoprotein S [Human coronavirus OC43]  
 Length = 1361

Score = 432 bits (1112), Expect = e-119  
 Identities = 273/763 (35%), Positives = 396/763 (51%), Gaps = 28/763 (3%)  
 Frame = +1

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFDTSVRDPKTSEILD 1716  
 K +TD+I CVN++ G+ G G+ ++ + +Q D + RD T+  
 Sbjct: 619 KANTDIILGVCVNYDLYGILGQIFVEVNATYYNSWQNLLYDSNGNLYGFRDYITNRTFM 678

Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQ 1896  
 I C G VS SSE A+L +++ C V QL P N F +  
 Sbjct: 679 IRSCYSGRVSAAFHAN--SSEPALLSRNIKCNYVFNNSLTRQLQPI-----NYFDSY 728

Query: 1897 AGCLIGAHEVDTSY--ECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A + + CD+ +G+G C Y S +++S A T + ++  
 Sbjct: 729 LGCVVNAYNSTAIFVQTCDLTVGSGYCVDY-----SKNRRSRGAIITTYRFTNFEPFT 781

Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQ 2211  
 N+ I IP+ F+I E + S K ++DC ++CGD C + L+  
 Sbjct: 782 VNSVNSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCAAFVCGDYAACKSQLVG 841

Query: 2212 YGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPT-LKYFGGFNFSQILPDPL----- 2376  
 YGSFC +N L+ + D +V + T LK FN I P+  
 Sbjct: 842 YGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDINFSPLGCL 901

Query: 2377 -----KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLL 2541  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q + G+ VLPPLL  
 Sbjct: 902 GSECKASSRSAIEDLLFDKVKLSDVGFVEAYNNCTGGAEIRDLICVQSYKGIKVLPLPL 961

Query: 2542 TDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIAN 2721

```

      +++ I+ YT A S                +PF + + YR NG+GVT +VL +NOK IAN
Sbjct: 962 SENQISGYTLAATSASLFPWPWTAAG----VPFYLVNQYRINGLGVTMDVLSQNQKLIAN 1017

Query: 2722 QFNKAISQIQESLTTTSTALGKQLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLD 2901
      FN A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAIS+ L +ILSRLD
Sbjct: 1018 AFNNALYAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISASLQEILSRLD 1077

Query: 2902 KVEAEVQIDRLITGRQLQSLQTYVVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGK 3081
      +EAE QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG
Sbjct: 1078 ALEAEAQIDRLINGRLTALNAYVVSQQLSDSTLVKFSAAQAMEKVNNECVKSQSSRINFVCGN 1137

Query: 3082 GYHLMSFPQAAPHGVVFLHVITYVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFI 3258
      G H++S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W
Sbjct: 1138 GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMI 1197

Query: 3259 TQRNFFSPQIIITDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDV 3438
      T ++ + IT +N V V + + P L FKEELD++FKN TS
Sbjct: 1198 TGSGYYYLEPITENNVVVMSTWAVNYTKAPYVMLNTSIPNLHDFKEELDQWFKNQTSVAP 1257

Query: 3439 DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGF- IAG 3615
      DL + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL +AG
Sbjct: 1258 DL-SLDYINVTFLDLQVEMNRLQEAIKVLNQSINLKDIDGTYEYVYKWPWYVWLLICLAG 1316

Query: 3616 LIAIVMVTIXXXXXXXXXXXXXXXXXXGACSCGSCCKFDEDDSEPVLK 3744
      + +V++ K CG CC E V+K
Sbjct: 1317 VAMLVLLFFICCTGCGTSCFK---KCGGCCDDYTG YQELVIK 1356
    
```

Score = 97.8 bits (242), Expect = 1e-18  
 Identities = 61/240 (25%), Positives = 114/240 (47%), Gaps = 6/240 (2%)  
 Frame = +1

```

Query: 649 KPIFKLPLGINITNFRAI-LTAFSPAQDIWGTSAAAAYFVGYLKPTTFMLKYDENGITITDA 825
      K +F + LG+ ++++ + LT S ++ + Y+V ++L ++++G I +A
Sbjct: 237 KFLFNVYLGMAISHYYVMP L TCNSKVKNGF---TLEYWVTL SLLDQYLLAFNQDGIIFNA 293

Query: 826 VD C SQNPLAELKCSVKSFEIDKGIYQTSNFRVVP SGDVVRF-PNITNLCPFGEVFNATKF 1002
      VDC + ++E+KC +S G+Y+ + + V P DV R PN+ N C N
Sbjct: 294 VDCMSDFMSEIKCKTQSIAPPTGVYELNGYTVQPIADVYRRKPNL PN-CNIEAWLNDKSV 352

Query: 1003 PSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLN DL CFSNVYADSFVVKGD DV 1182
      PS WERK SNC + S L + +F C + A K+ +CFS++ D F +
Sbjct: 353 PSPLNWERKTFSNCFNMSSLMSFIQADSFTCNNIDA AKIYGMCFSSITIDKFAIPNGRK 412

Query: 1183 RQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TRNIDATSTGN YNYKYRYLRHGKLRP 1350
      + G G + +NY++ C L +N ++ + +N ++ ++ +P
Sbjct: 413 VDLQLGNLGYLQSFNYRIDTTATSCQLYLNLP AANVSVSRFNPSTWNKRFGFIEDSVFKP 472
    
```

[>gi|420564|pir||S29998](#) surface protein - human coronavirus  
[gi|62392|emb|CAA79896.1|](#) surface protein [Human coronavirus OC43]  
 Length = 1361

Score = 432 bits (1111), Expect = e-119  
 Identities = 273/763 (35%), Positives = 396/763 (51%), Gaps = 28/763 (3%)  
 Frame = +1

```

Query: 1540 KLSTDLIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDFTDSVRDPKTSEILD 1716
    
```

K +TD+I CVN++ G+ G G+ ++ + +Q D + RD T+  
 Sbjct: 619 KANTDIILGVCVNYDLYGILGQGIFVEVNATYYNSWQNLLYDSNGNLYGFRDYITNRTFM 678  
 Query: 1717 ISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQQTQ 1896  
 I C G VS SSE A+L +++ C V QL P N F +  
 Sbjct: 679 IRSCYSGRVSAAFHAN--SSEPALLSRNIKCNYVFNNLSLTRQLQPI-----NYFDSY 728  
 Query: 1897 AGCLIGAEHVD--TSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYS 2070  
 GC++ A + + CD+ +G+G C Y S +++S A T + ++  
 Sbjct: 729 LGCVVNAYNSTAISVQTCDLTVGSGYCVDY-----SKNRRSRGAITTYGRFTNFEPFT 781  
 Query: 2071 NNT-----IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQ 2211  
 N+ I IP+ F+I E + S K ++DC ++CGD C + L+  
 Sbjct: 782 VNSVNSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCAAFVCGDYAACKSQLVG 841  
 Query: 2212 YGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPT-LKYFGGFNFSQILPDPL---- 2376  
 YGSFC +N L+ + D +V + T LK FN I P+  
 Sbjct: 842 YGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDG VNFVDDINFSPVLGCL 901  
 Query: 2377 -----KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLL 2541  
 K + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q + G+ VLPPLL  
 Sbjct: 902 GSECSKASSRSAIEDLLFDKVKLSDVGFVEAYNNTGGAEIRDLCVQSYKGIKVLPLPL 961  
 Query: 2542 TDDMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIAN 2721  
 +++ I+ YT A S +PF + + YR NG+GVT +VL +NQK IAN  
 Sbjct: 962 SENQISGYTLAATSASLFPWTAAG---VPFYLVNQYRINGLVMTDVLVSNQKLIAN 1017  
 Query: 2722 QFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLD 2901  
 FN A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FGAI+ L +ILSRLD  
 Sbjct: 1018 AFNNALDAIQEGFDATNSALVKIQAVVNANAALNLLQQLSNRFGAISASLQEIILSRLD 1077  
 Query: 2902 KVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGK 3081  
 +EAE QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R++FCG  
 Sbjct: 1078 ALEAEAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNNECVKSQSSRINFVCGN 1137  
 Query: 3082 GYHLMSFPQAAPHGVVFLHVTVVPSQERNFTTAPAICHEG-KAYFPREGVVFVNGTSWFI 3258  
 G H++S Q AP+G+ F+H +YVP++ +P +C G + P+ G FV +W  
 Sbjct: 1138 GNHIISLVQNPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWY 1197  
 Query: 3259 TQRNFFSPQIIITDNTFVSGNCDVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDV 3438  
 T ++ + IT +N V V + + P L FKEELD++FKN TS  
 Sbjct: 1198 TGSGYYYYLEPITENNVVMSTWAVNYTKAPYVMLNTSIPNLPDFKEELDQWFKNQTSVAP 1257  
 Query: 3439 DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGF-IAG 3615  
 DL + IN + +++Q E++RL E K LN+S I+L+++G YE Y+KWPWYVWL +AG  
 Sbjct: 1258 DL-SLDYINVTFLDLQVEMNRLQEAIKVLNQSYINLKDIDIGTYEYVVKWPWYVWLLICLAG 1316  
 Query: 3616 LIAIVMVTIXXXXXXXXXXXXXXXXXKACSCGSCCKFDEDDSEPVLK 3744  
 + +V++ K CG CC E V+K  
 Sbjct: 1317 VAMLVLLFFICCTGCGTSCFK---KCGGCCDDYTGQELVIK 1356

Score = 100 bits (249), Expect = 2e-19  
 Identities = 62/240 (25%), Positives = 115/240 (47%), Gaps = 6/240 (2%)  
 Frame = +1

Query: 649 KPIFKLPLGINITNFRAI-LTAFSPAQDIWGTSAAAYFVGYLKPTTFMLKYDENGITDA 825  
 K +F + LG+ ++++ + LT S ++ + Y+V L ++L ++++G I +A  
 Sbjct: 237 KFLFNVYLGMAISHYYVMP LTCNSKVKNGF---TLEYWVTP LTRSQYLLAFNQDGIIFNA 293

Query: 826 VDCCSQNPLAELKCSVKSF EIDKGIYQTSNFRVVP SGDVVRF-PNITNLC PFGEVFNATKF 1002  
 VDC + ++E+KC +S G+Y+ + + V P DV R PN+ N C N  
 Sbjct: 294 VDCMSDFMSEIKCKTQSIAPPTGVYELNGYTVQPIADVYRRKPNL PN-CNIEAWLNDKSV 352

Query: 1003 PSVYAWERKKISNCVADYSVLN STFFSTFKCYGVSATKLN DL CFSNVYADSFVVKGDDV 1182  
 PS WERK SNC + S L + +F C + A K+ +CFS++ D F +  
 Sbjct: 353 PSPLNWERKTF SNCFNMSSLMSFIQADSFTCNNIDA AKIYGMCFSSITIDKFAIPNGRK 412

Query: 1183 RQIAPGQTGVIADYNYKLPDDFMGCVLAWN----TRNIDATSTGN YNYKYRYLRHGKLRP 1350  
 + G G + +NY++ C L +N ++ + +N ++ ++ +P  
 Sbjct: 413 VDLQLGNLGYLQSFNYRIDTTATSCQLYYNLP AANVSVSRFNPSTWNKRFGFIEDSVFKP 472

>gi|21734849|gb|AAM77000.1|AF481863\_2 spike glycoprotein [porcine hemagglutinati  
 Length = 1349

Score = 430 bits (1106), Expect = e-119  
 Identities = 265/732 (36%), Positives = 394/732 (53%), Gaps = 28/732 (3%)  
 Frame = +1

Query: 1525 TVCGPKL---STD LIKNQCVNFNFNGLTGTGVLTP-SSKRFQPFQFGRDVSDF TDSVRD 1692  
 T C L +T++ + CVN++ G+TG G+L ++ + +Q D S RD  
 Sbjct: 599 TTCSTDLQQGNTNITTDVCVNYDLYGITGQGILIEVNATYYNSWQNL LYDSSGNLYGFRD 658

Query: 1693 PKTSEILDISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVS--TAIHADQLTPAWRIY 1866  
 ++ I C G VS + SSE A+++++ C+ V T + QL  
 Sbjct: 659 YLSNRTFLIRSCYSGRVSAVFHAN--SSEPALMFRNLKCSHFVNYTILRQIQLV----- 710

Query: 1867 STGNNVFQTQAGCLIGAEHVDTSY--ECDIPIGAGICASYHTVSL LRSTSQ-----KS 2019  
 N F + GC++ A + S CD+ +G+G C Y V+ LRS +  
 Sbjct: 711 ----NYFDSYLGCVVNAYNNTASAVSTCDLTVGSGYCVDY--VTALRSRRSFTTGYRFTN 764

Query: 2020 IVAYTMSLGADSSIAYSN-NTIAIPTNF SISITTEVMPVSMAKTSVDCNMYICGDSTECA 2196  
 + +L DS I IP+ F+I E + S K ++DC ++CGD C  
 Sbjct: 765 FEPFAANLVNDSIEPVGGLYEIQIPSEFTIGNLEEFIQTSSPKVTIDCATFVCGDYAACR 824

Query: 2197 NLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG-----GFNFSQ 2358  
 L +YGSFC +N L + D +V + T G NFS  
 Sbjct: 825 QQLAEYGSFCENINAILIEVNELLDTTQLQVANS LMNGVTLSTKIKDGINFNVDDINFSS 884

Query: 2359 IL----PDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTV 2526  
 +L + + + RS IEDLLF+KV L+D GF++ Y C G RDLIC Q +NG+ V  
 Sbjct: 885 VLGCLGSECNRASTRSAIEDLLFDKVKLSDVGFVQAYNNCTGGAEIRD LICVQSYNGIKV 944

Query: 2527 LPPLLTDMMIAAYTAALVSXXXXXXXXXXXXXXXXLQIPFAMQMA YRFNGIGVTQNVLYENQ 2706  
 LPPLL+++ I+ YT+A + +PF + + YR NG+GVT +VL +NQ  
 Sbjct: 945 LPPLLSENQISGYTSAATAASLFPPTAAAG----VPFYLVNQYRINGLGVTMDVLSQNQ 1000

Query: 2707 KQIANQFNKAISIQIESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDI 2886  
 K IA+ FN A+ IQE T++AL K+Q VVN NA+ALN L++QLS+ FG AIS+ L +I  
 Sbjct: 1001 KLIASAFNNALDSIQEGFDATNSALVKIQAVVNANA EALNNLLQQLSNRFGAISASLQEI 1060

Query: 2887 LSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRV 3066  
 LSRLD +EA+ QIDRLI GRL +L YV+QQL + ++ SA A K++ECV QS R+  
 Sbjct: 1061 LSRLDALEAKAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAIEKVN ECVKSQSSRI 1120

Query: 3067 DFCGKGYHLMSFPQAAPHGVVFLHVTVYVPSQERNFTTAPAICHEGK-A YFPREGVVFVNG 3243  
 +FCG G H++S Q AP+G+ F+H +YVP++ +P +C G P+ G F+

Sbjct: 1121 NFCGNGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDIGISPKSGYFINVN 1180  
 Query: 3244 TSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNH 3423  
 SW T ++ P+ IT +N V C V + + + P L FKEEL ++FKN  
 Sbjct: 1181 NSWMFTGSGYYPITQNNVVVMSTCAVNYTKAPDLMLNTSTPNLPDFKEELYQWFKNQ 1240  
 Query: 3424 TSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLG 3603  
 +S DL IN + +++Q E++RL E K LN S I+L+++G YE Y+KWPWYVWL  
 Sbjct: 1241 SSLAPDL-SFDYINVTFLDLQDEMNRLEAIAIKVLNHSYINLKDIGTYEYVWKPWYVWLL 1299  
 Query: 3604 F-IAGLIAIVMV 3636  
 +AG++ +V++  
 Sbjct: 1300 ICLAGVVMLVLL 1311

Score = 95.5 bits (236), Expect = 6e-18  
 Identities = 62/235 (26%), Positives = 109/235 (46%), Gaps = 3/235 (1%)  
 Frame = +1

Query: 631 SGFNTLKPFIKPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENG 810  
 +GF T K +FKL LG +++++ + A + Y+V L F+L +D+++G  
 Sbjct: 226 TGFVT-KFLFKLYLGTVLSHYVVMLPTCDSALS-----EYWVTPLTTRQFLLAFDQDG 278  
 Query: 811 TITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPVSGDVVR-FPNITNLCPFGEVF 987  
 + AVDC+ + ++E+ C S G+Y+ + + V P V R P++ N C  
 Sbjct: 279 VLYHAVDCASDFMSEIMCKTSSITPPTGVYELNGYTVQPVATVYRRIPDLPN-CDIEAWL 337  
 Query: 988 NATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLFCFSNVYADSFVV 1167  
 N+ S WERK SNC + L + +F C + A++L +CF ++ D F +  
 Sbjct: 338 NSKTVSSPLNWERKIFSNCNFMGRMFSFIQADSFGCNNIDASRLYGMCFGISITIDKFAI 397  
 Query: 1168 KGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWN--TRNIDATSTGNYNYKYRY 1326  
 + G++G + +NYK+ C L ++ N+ T ++ RY  
 Sbjct: 398 PNSRKVDLQVGKSGYLQSFNYKIDTAVSSCQLYYSLPAANVSVTHYNPSSWNRRY 452

>[gi|481036|pir||S37664](#) peplomeric polyprotein precursor - avian infectious bronc  
 (strain D1466) (fragment)  
 Length = 621

Score = 374 bits (961), Expect = e-102  
 Identities = 219/558 (39%), Positives = 303/558 (54%), Gaps = 15/558 (2%)  
 Frame = +1

Query: 2080 IAIPNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIA 2259  
 + IP +F++++T E + M K ++C Y+CG+S +C L QYGS C ++ ++G+A  
 Sbjct: 52 VLIPNSFNLTVTDEYIQTQMOKVQINCIQYVCGNSFQCKQLFQQYGSVCDSIHSIVNGLA 111  
 Query: 2260 AEQDRNTREVFAQVKQM-YKTPTLKYF--GGFNFSQILPDPLKPTKRSFIEDLLFNKVTL 2430  
 + + + ++ K + T + F G FN S ILP +PT RSFIEDLLF+KV  
 Sbjct: 112 QQDNAEMIQFYSSTKPRGFDTNSFSNFSAGDFNISLILPKNGQPTGRSFIEDLLFDKVES 171  
 Query: 2431 ----ADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDMMIAAYTAALVSXXXXX 2598  
 D+ + K LG + +DL+CAQK+NGL VLPP++T +M A YT +LV+  
 Sbjct: 172 LGLPGDSAYQKCTSGPLGFV--KDLVCAQKYNGLLVLPPIITAEMQAMYTISLVA S MAFG 229  
 Query: 2599 XXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTA 2778  
 IPFA Q+ R N +G+TQ VL +NQ++IA FNKA+ +QE + TS A

Sbjct: 230 GITSAGA----IPFATQLQARINHLGITQTVLQKNQEKIAASFNKAMKNVQEGFSATSLA 285

Query: 2779 LGKLQDVVNQNAQALNLTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSL 2958  
 L ++QDVVN+ L + L+ NFGAIS V+ DI +LD +EA Q+DRLITGRL SL

Sbjct: 286 LKQVQDVVNEQGAILQQTMHSLNKNFNGAISHVIQDIYKQLDALEANAQVDRLITGRLSSL 345

Query: 2959 QTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHLMSFPQAAPHGVVFLH 3138  
 + + + A++ LA K++ECV QS R FCG G H+MS PQ AP+G+VFLH

Sbjct: 346 SVLASAKQLEYAKVTQORELAKEKINECVKSQSTRYGFCCGGMHIMSIPQNAPNGMVFLH 405

Query: 3139 VTYVPSQERNFTTAPAIC-----HEGKAYFPREGVVFVNGTWSFITQRNFFSPQIITT 3297  
 TY P N T C G G+FV +++IT R+ ++P+ IT

Sbjct: 406 FTYTPESYVNVTAUVGFCVKSNDNTEYGLVPVTGRGIFVEVNGTYIITSRDMYNPRAITG 465

Query: 3298 DNTFVSGNCDVVIGIINNTVYDPLQPELD-SFKEELDKYFKNHTSPDVDLGDISGINASV 3474  
 + +C IN TV E D F EL K++ N TS D D V

Sbjct: 466 GDVVKLTSCQANYQSINRTVITTFVDEDDDFDNHELKSKWW-NETSRDFPDLQFNYPITPV 524

Query: 3475 VNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTIXXXX 3654  
 +NI EIDR+ EV + LN+SLIDL+ L + YIKWPWYVWL AI +TI

Sbjct: 525 LNISNEIDRIQEVIQGLNDSLIDLETLSILKTYIKWPWYVWL-----AIAFLTIIFIL 577

Query: 3655 XXXXXXXXXXXKACSCGSCC 3708  
 G C C CC

Sbjct: 578 VLCWIFFMTGCCGC--CC 593

>gi|58987|emb|CAA41065.1| peplomeric polyprotein precursor [Avian infectious brc  
 Length = 621

Score = 369 bits (946), Expect = e-100  
 Identities = 217/558 (38%), Positives = 301/558 (53%), Gaps = 15/558 (2%)  
 Frame = +1

Query: 2080 IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIA 2259  
 + IP +F++++T E + M K ++C Y+CG+S +C L QYGS C ++ ++G+A

Sbjct: 52 VLIPNSFNLTVTDEYIQTQMVKVQINCIQYVCGNSFQCKQLFQQYGSVCDSIHSIVNGLA 111

Query: 2260 AEQDRNTREVFAQVKQM-YKTPTLKYF--GGFNFSQILPDPLKPTKRSFIEDLLFNKVTL 2430  
 + + + ++ K + T + F G FN S ILP +PT RSFIEDLLF+KV

Sbjct: 112 QQDNAEMIQFYSSTKPRGFDTNSFSNFSAGDFNISLILPKNGQPTGRSFIEDLLFDKVES 171

Query: 2431 ----ADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSXXXXX 2598  
 D+ + K LG + +DL+CAQK+NGL VLPP++T +M A T +LV+

Sbjct: 172 LGLPGDSAYQKCTSGPLGFV--KDLVCAQKYNGLLVLPPIIITAEMQAMXTISLVASMAFG 229

Query: 2599 XXXXXXXXXXXLQIPFAMQMAYRFNGIGVTONVLYENQKQIANQFNKAISQIQESLTTTSTA 2778  
 IPFA Q+ R N +G+TQ VL +NQ++IA FNKA+ +QE + TS A

Sbjct: 230 GITSAGA----IPFATQLQARINHLGITQTVLQKNQEKIAASFNKAMKNVQEGFSATSLA 285

Query: 2779 LGKLQDVVNQNAQALNLTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSL 2958  
 L ++QDVVN+ L + L+ NFGAIS V+ DI +LD +EA Q+DRLITGRL SL

Sbjct: 286 LKQVQDVVNEQGAILQQTMHSLNKNFNGAISHVIQDIYKQLDALEANAQVDRLITGRLSSL 345

Query: 2959 QTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHLMSFPQAAPHGVVFLH 3138  
 + + + A++ LA K++ECV QS R FCG G H+MS PQ AP+G+V LH

Sbjct: 346 SVLASAKQLEYAKVTQORELAKEKINECVKSQSTRYGFCCGGMHIMSIPQNAPNGMVXLH 405

Query: 3139 VTYVPSQERNFTTAPAIC-----HEGKAYFPREGVVFVNGTWSFITQRNFFSPQIITT 3297

```

          TY P   N T   C           G           G+FV   +++IT R+ ++P+ IT
Sbjct: 406 FTYTPESYVNVTA VVGFCVKSNDNTEYGLVPVTGRGIFVEVNGTYYITSRDMYNPRAITG 465

Query: 3298 DNTFVSGNCDVVIGIINNTVYDPLQPELD-SFKEELDKYFKNHTSPDVLDGDISGINASV 3474
          +   +C           IN TV           E D F EL K++ N TS D   D           V
Sbjct: 466 GDVVKLTSCQANYQSINRTVITTFVDEDDDFDFNHLSKWW-NETSRDFPDLQDFNYTIPV 524

Query: 3475 VNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTIXXXX 3654
          +NI EIDR+ EV + LN+SLIDL+ L   + YIKWPWYVWL           AI +TI
Sbjct: 525 LNISNEIDRIQEVIQGLNDSLIDLETLSILKTYIKWPWYVWL-----AIAFLTIIFIL 577

Query: 3655 XXXXXXXXXXXKGACSCGSCC 3708
          G C C CC
Sbjct: 578 VLCWIFFMTGCCGC--CC 593
    
```

>[gi|13378217|gb|AAK18745.1](#) spike glycoprotein, S2 subunit [Avian infectious brc  
 Length = 630

Score = 365 bits (936), Expect = 4e-99  
 Identities = 214/558 (38%), Positives = 297/558 (53%), Gaps = 15/558 (2%)  
 Frame = +1

```

Query: 2080 IAIPTNFSISITTEVMPVSMAKTSVDCNMYYICGDSTECANLLLQYGSFCTQLNRALSGIA 2259
          + IP +F++++T E +           K ++C Y+CG S +C L QYGS C + ++GIA
Sbjct: 52 VLIPNSFNLTVTDEFIQTFQKIQINCIQYVCGSSIQCKQLFQQYGSVCDNLSIVNGIA 111

Query: 2260 AEQDRNTREVFAQVKQM-YKTPTLKYF--GGFNFSQILPDPLKPTKRSFIEDLLFNKVTL 2430
          + +           ++ K + T + F G FN S +LP +PT RSFIEDLLF+KV
Sbjct: 112 LQDNAEMLHFYSSTKPRGFDTNSFVNFTAGEFNISLVLPKNGQPTGRSFIEDLLFDKVES 171

Query: 2431 ----ADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSXXXXX 2598
          D + K LG + +DL+CAQK+NGL VLPP++T +M A YT +LV+
Sbjct: 172 LGLPGDPAYQKCTSGPLGFV--KDLVCAQKYNGLLVLPPIITAEMQAMYTISLVASMAFG 229

Query: 2599 XXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISSIQIESLTTTSTA 2778
          IPFA Q+ R N +G+TQ VL +NQ++IA FNKA+ +Q+ + TS A
Sbjct: 230 GITSAGA----IPFATQIQARINHLGITQTVLQKNQEKIAASFNKAMKHMQDGFSAATSLA 285

Query: 2779 LGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSL 2958
          L ++QDVVN+ L + L+ NFGAIS V+ DI +LD +EA Q+DR+ITGRL SL
Sbjct: 286 LQQVQDVVNEQGAILQQTMHSLNKNFNGAISHVIQDIYKQLDALEANAQVDRIITGRLSSL 345

Query: 2959 QTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLH 3138
          + + + ++ LA K++ECV QS R FCG+G H+MS PQ AP+G+VFLH
Sbjct: 346 SVLASAKQLEYTKVSQORELAKEKINECVKSQSNRHGFCGEGMHIMSIPQNAPNGIVFLH 405

Query: 3139 VTYVPSQERNFTTAPAIC-----HEGKAYFPREGVVFVNGTTSWFITQRNFFSPQIITT 3297
          TY P N T C G GVF+ +++IT R+ +SP+ IT
Sbjct: 406 FTYTPETAYANVTAVVGFCVKGPNNGTEYGLVPVVGGRGVFIEVNGTYYITGRDMYSPRAITA 465

Query: 3298 DNTFVSGNCDVVIGIINNTVYDPLQPELD-SFKEELDKYFKNHTSPDVLDGDISGINASV 3474
          + +C           IN TV           E D F EL K++ N TS D   D           V
Sbjct: 466 GDVVKLTSCQANYQSINRTVITTFVDEDDDFDFNHLSKWW-NETSRDFPNLDEFNYTIPV 524

Query: 3475 VNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTIXXXX 3654
          +NI EID++ EV + LN+S+IDL+ L   + YIKWPWYVWL           AI TI
Sbjct: 525 LNISNEIDKIQEVIQGLNDSIIDLETLSILKTYIKWPWYVWL-----AIAFATIIFIL 577
    
```

Query: 3655 XXXXXXXXXXXKGACSCGSCC 3708  
                                   G C C CC  
 Sbjct: 578 ILGWVFFMTGCCGC--CC 593

>[gi|6425133|gb|AAF08315.1](#) spike protein precursor [Avian infectious bronchitis]  
 Length = 625

Score = 362 bits (929), Expect = 3e-98  
 Identities = 213/558 (38%), Positives = 296/558 (53%), Gaps = 15/558 (2%)  
 Frame = +1

Query: 2080 IAIPTNFSISITTEVMPVSMAKTSVDCNMYYICGDSTECANLLLQYGSFCTQLNRALSGIA 2259  
           + IP +F++++T E +           K ++C Y+CG S +C L QYGS C + ++GIA  
 Sbjct: 47 VLIPNSFNLTVTDEFIQTFQKIQINCIQYVCGSSIQCKQLFQQYGSVCDNLSIVNGIA 106

Query: 2260 AEQDRNTREVFQAQVKQM-YKTPTLKYF--GGFNFSQILPDPLKPTKRSFIEDLLFNKVTL 2430  
           + +           ++ K + T +   F G FN S +LP +PT RSFIEDLLF+KV  
 Sbjct: 107 LQDNAEMLHFYSSTKPRGFDTNSFVNFTAGEFNISLVLPKNGQPTGRSFIEDLLFDKVES 166

Query: 2431 ----ADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSXXXXX 2598  
           D + K           LG + +DL+CAQK+NGL VLPP++T +M A YT++LV  
 Sbjct: 167 LGLPGDPAYQKCTSGPLGFV--KDLVCAQKYNGLLVLPPIITAEMQAMYTSSLVVSMAFG 224

Query: 2599 XXXXXXXXXXXLQIPFAMQMAYRFNGIGVTVQNVLYENQKQIANQFNKAISQIQESLTTTSTA 2778  
                                   IPFA Q+ R N +G+TQ VL +NQ++IA FNKA+ +Q+ + TS A  
 Sbjct: 225 GITSAGA----IPFATQIQARINHLGITQTVLQKNQEKIAASFNKAMKHMQDGFSAATSLA 280

Query: 2779 LGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSL 2958  
           L ++QDVVN+       L + L+ NFGAIS V+ DI +LD +EA Q+DR+ITGRL SL  
 Sbjct: 281 LQQVQDVVNEQGAILQOTMHSLNKNFGAISHVIQDIYKQLDALEANAQVDRIITGRLSSL 340

Query: 2959 QTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHLSFPQAAPHGVVFLH 3138  
           + + +       ++       LA K++ECV QS R FCG+G H+MS PQ AP+G+VFLH  
 Sbjct: 341 SVLASAKQLEYTKVSQORELAKEKINECVKSQSNRHGFCGEGMHIMSIPQNAPNGIVFLH 400

Query: 3139 VTYVPSQERNFTTAPAIC-----HEGKAYFPREGVVFVNGTWSFITQRNFFSPQIITT 3297  
           TY P       N T       C           G           GVF+       +++IT R+ +SP+ IT  
 Sbjct: 401 FTYTPETYANVTAVVGFCVCKPGNGTEYGLVPVVGGRGVFIEVNGTYIITGRDMYSPRAITA 460

Query: 3298 DNTFVSGNCDVVIGIINNTVYDPLQPELD-SFKEELDKYFKNHTSPDVLDGDISGINASV 3474  
           +       +C           IN TV           E D F EL K++ N S D       D       V  
 Sbjct: 461 GDVVKLTSCQANYQSINRTVITTFVDEDDDFDHELSKWW-NEISRDFPNLDEFNYTIPV 519

Query: 3475 VNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTIXXXX 3654  
           +NI EID++ EV + LN+S+IDL+ L + YIKWPWYVWL           AI TI  
 Sbjct: 520 LNISNEIDKIQEVIQGLNDSIIDLETLSILKTYIKWPWYVWL-----AIAFATIIIFIL 572

Query: 3655 XXXXXXXXXXXKGACSCGSCC 3708  
                                   G C C CC  
 Sbjct: 573 ILGWVFFMTGCCGC--CC 588

>[gi|1321872|emb|CAA60684.1](#) spike protein [Avian infectious bronchitis virus]  
 Length = 1166

Score = 356 bits (914), Expect = 1e-96

Identities = 205/558 (36%), Positives = 297/558 (53%), Gaps = 15/558 (2%)  
 Frame = +1

Query: 2080 IAIPNTFSISITTEVMPVSMAKTSVDCNMVICGDSTECANLLLQYGSFCTQLNRALSGIA 2259  
 + IP +F++++T E + M K ++C Y+CG+S EC L QYG C + ++G+

Sbjct: 588 VLIPDSFNLTVTDEYIQTRMDKVQINCLQYVCGNSIECRKLFQQYGPVCDNILSVVNGVG 647

Query: 2260 AEQDRNTREVFAQVKQM-YKTPTLKYF--GGFNFSQILPDPLKPTKRSFIEDLLFNKVTL 2430  
 +D ++ K Y TP G FN S +L P P RSFIED+LF V

Sbjct: 648 QREDMELLSFYSSTKPRDYNTPLFSNVSTGDFNISLLLTTPSSPNGRSFIEDILFTSVES 707

Query: 2431 ADAGFMKQYGECL-GDIN-ARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSXXXXXXXX 2604  
 +Y +C G + +DL+CA+++NGL VLPP++T DM YT++LV+

Sbjct: 708 VGLPTDAEYKKTAGPLGFVKDLVCAREYNGLLVLPPIITADMQTMYSLVSALGGI 767

Query: 2605 XXXXXXXLQIPFAMQMAYRFNGIGVTONVLYENQKQIANQFNKAISQIQESLTTTSTALG 2784  
 IPFA Q+ R N +G+T ++L +NQ++IA FNKA+ +QE +TS AL

Sbjct: 768 TAAGA----IPFATQLQARINHLGITNSLLLNQEKIAASFNKAMGHMQEGFKSTSLALQ 823

Query: 2785 KLQDVVNQNAQALNLTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQT 2964  
 ++QDVVN+ + L ++ L+ NFGAISSV+ DI +LD ++A+VQ+DR+ITGRL SL

Sbjct: 824 QIQDVVNKQSSILTETMQSLNKNFGAISSVIQDIYQQLDAIQADVQVDRIITGRLSSLSV 883

Query: 2965 YVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHLSFPQAAPHGVVFLHVT 3144  
 + + + LA K++ECV QS R FCG G H+++ PQ AP+G+VF+H T

Sbjct: 884 LASAKQAEYTIIVSQQRQLATQKINECVKSQSNRYSFCGNGRHVLTIPQNAPNGIVFIHFT 943

Query: 3145 YVPSQERNFTTAPAIC-----HEGKAYFPR--EGVVFVNGTWSFITQRNFFSPQIITTDN 3303  
 Y P N T C A P GVF+ S++IT R+ + P+ IT +

Sbjct: 944 YTPESFVNVTAVGFCVNPANASQYAIVPANGRGVFIQVNGSYYITARDMYMPRDITAGD 1003

Query: 3304 TFVSGNCDVVIGIINNTVYDPLQPELD-SFKEELDKYFKN--HTSPDVLGDISGINASV 3474  
 +C +N TV + + D F +EL K++ + H PD D + + V

Sbjct: 1004 IVTLTSCQANYVNVNKTVINTFVEDDDDFDDELKSWWNTKHELPDFDEFNYT---IPV 1060

Query: 3475 VNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTIXXXX 3654  
 +NI EIDR+ E + LN+SLIDL+ L + YIKWPWYVWL AI TI

Sbjct: 1061 LNISNEIDRIQEAIQGLNDSLIDLETLSILKTYIKWPWYVWL-----AIAFATIIFIL 1113

Query: 3655 XXXXXXXXKGCSCGSCC 3708  
 G C C CC

Sbjct: 1114 VLGWVFFMTGCCGC--CC 1129

>[gi|28274446|gb|AAO34396.1](#) spike glycoprotein [Avian infectious bronchitis viru  
 Length = 1164

Score = 354 bits (909), Expect = 5e-96  
 Identities = 246/754 (32%), Positives = 368/754 (48%), Gaps = 39/754 (5%)  
 Frame = +1

Query: 1564 NQCVNFNFNGLTGTGVLTPSSKRFQPFQFGRDVSDFTDTSVRDPKTSEILDISPCAFGGV 1743  
 ++CV +N G G G +T + TDSV + S A GG+

Sbjct: 431 DKCVAYNIYGRVQGQFIT-----NVTDSVAN-----FSYLADGGL 465

Query: 1744 SVITPGTNASSEVAVL-----YQDVN-CTDVSTAIHADQLTPAWRIYSTGNVVFQTQA 1899  
 +++ T+ + +V V+ Y VN C DV+ + S GN V +

Sbjct: 466 AILD--TSGAIDVFFVQGSYGLNYYKVNPCEDVNQQF-----VVSGGNIVGILTS 513

Query: 1900 GCLIGAEHVDTSYECDIP-----IGAGICA----SYHTVSLLRSTSQKSIVAYTMS 2040  
 G+E V+ + + IG ++ SY + S K IV +  
 Sbjct: 514 RNETGSEQVENQFYVKLNTSSHRRRRSIGQNVTSCTPYVSYGRFCIEPDGSLKMIWPEELK 573

Query: 2041 LGADSSIAYSNTTIAIPTNFSISITTEVMPVSMKTSVDCNMYICGDSTECANLLLQYGS 2220  
 + + ++ IP +F++++T E + M K ++C Y+CG+S EC L QYG  
 Sbjct: 574 QFV-APLLNITESVLI PNSFNLTVTDEYIQTRMDKVQINCLQYVCGNSLECRKLFQYGP 632

Query: 2221 FCTQLNRALSGIAAEQDRNTREVFAQVKQM-YKTPTLKYF--GGFNFSQILPDPLKPTKR 2391  
 C + ++ ++ ++D ++ K Y TP L G FN S +L P P+ R  
 Sbjct: 633 VCDNILSVVNSVSQKEDMELLSFYSSSTKPKGYDTPVLSNVSTGEFNISLLLLTPSSPSGR 692

Query: 2392 SFIEDLLFNKVTLADAGFMKQYGEC----LGDINARDLICAQKFNGLTVLPPLLTDDMIA 2559  
 SF+EDLLF V +Y +C LG + +DLICA+++NGL VLPP++T DM  
 Sbjct: 693 SFVEDLLFTSVETVGLPTDAEYKCKTAGPLGTL--KDLICAREYNGLLVLPPIITADMQT 750

Query: 2560 AYTAALVXXXXXXXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAI 2739  
 YTA+LV IPFA Q+ R N +G+ Q++L +NQ++IA FNKAI  
 Sbjct: 751 MYTASLVGAMAFGGITSAAA----IPFATIQIARINHLGIAQSLLMKNQEKIAASFNKAI 806

Query: 2740 SQQIESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEV 2919  
 +QE +TS AL ++QDVVN+ + L + L+ NFGAISSV+ DI ++LD ++A+  
 Sbjct: 807 GHMQEGFRSTSLALQVQDVVNKQSAILTETMNSLNKNFGAISSVIQDIYAQLDAIQADA 866

Query: 2920 QIDRLITGRQLSQTIVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHLMS 3099  
 Q+DRLITGRL SL + + + LA K++ECV QS R FCG G H++S  
 Sbjct: 867 QVDRLITGRLLSVLASAKQSEYIRVSQQRELATQKINCEVKSQSNRYGFCGSGRHLVLS 926

Query: 3100 FPQAAPHGVVFLHVTVVPSQERNFTTAPAIC-----HEGKAYFPREGVVFV---NGTSWF 3255  
 PQ AP+G+VF+H TY P N T C A P G +F NGT ++  
 Sbjct: 927 IPQNA PNGIVFIHFTYTPETFVNVT AIVGFCVNPLNASQY AIVPANGRGIFIQVNGT-YY 985

Query: 3256 ITQRNFFSPQIITDNTFVSGNCDVVIGIINNTVYDPLQPELD-SFKEELDKYFKN--HT 3426  
 IT R+ + P+ IT + +C +N TV + D +F +EL K++ + H  
 Sbjct: 986 ITRDMMYMPRDI TAGDIVTLTSCQANYVNVNKT VITTFVEDDDFNFDDEL SKWVNDTKHG 1045

Query: 3427 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLG 3606  
 PD D D + ++NI EID + V + LN+SLI+L+EL + YIKWPWYVWL  
 Sbjct: 1046 LPDFD--DFN-YTVPILNISGEIDNIQGVIOGLNDSLINLEELSIIKTYIKWPWYVWLAI 1102

Query: 3607 IAGLIAIVMVTIXXXXXXXXXXXXXXXXXKGACSCGSCC 3708  
 +I +++ G C C CC  
 Sbjct: 1103 GF AIIIFILI-----LGWVFFMTGCCGC--CC 1127

>gi|27803884|gb|AAO22155.1| spike glycoprotein [Avian infectious bronchitis viru  
 Length = 1164

Score = 353 bits (907), Expect = 9e-96  
 Identities = 203/559 (36%), Positives = 298/559 (53%), Gaps = 15/559 (2%)  
 Frame = +1

Query: 2077 TIAIPTNFSISITTEVMPVSMKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGI 2256  
 ++ IP +F++++T E + M K ++C Y+CG S EC L QYG C + ++ +  
 Sbjct: 585 SVLIPNSFNLTVTDEYIQTRMDKVQINCLQYVCGSSLECRKLFQYGPVCDNILSVVNSV 644

Query: 2257 AAEQDRNTREVFAQVKQM-YKTPTLKYF--GGFNFSQILPDPLKPTKR SFIEDLLFNKVT 2427  
 + ++D ++ K Y TP L G FN S +L P P+ R SFIEDLLF V  
 Sbjct: 645 SQKEDMELLSFYSSSTKPKGYDTPVLSNVSTGFQFNISLLLLTPSSPSGRSFIEDLLFTSVE 704

Query: 2428 LADAGFMKQYGEC----LGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSXXXX 2595  
 +Y +C LG + +DLICA+++NGL VLPP++T DM YTA+LV  
 Sbjct: 705 TVGLPTDAEYKKCTAGPLGTL--KDLICAREYNGLLVLPPIITADMQMTYASLVGAMAF 762

Query: 2596 XXXXXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAIQIQESLTTTST 2775  
 IPFA Q+ R N +G+TQ++L +NQ++IA FNKAI +QE +TS  
 Sbjct: 763 GGITSAAA----IPFATQIQARINHLGITQSLLMKNQEKIAASFNKAIGHMQEGFRSTSL 818

Query: 2776 ALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQS 2955  
 AL ++QDVVN+ + L + L+ NFGAISSV+ DI ++LD ++A+ Q+DRLITGRL S  
 Sbjct: 819 ALQQVQDVVNKQSAILTETMNALNKNFGAISSVIQDIYAQLDAIQADAQVDRLITGRLSS 878

Query: 2956 LQTYVTQQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHLMSFPQAAPHGVVFL 3135  
 L + + + LA K++ECV QS R FCG G H++S PQ AP+G+VF+  
 Sbjct: 879 LSVLASAKQSEYIRVSQQRELATQKINECVKSQSNRYGFCGSGRHLVLSIPQNAPNGIVFI 938

Query: 3136 HVTYVPSQERNFTTAPAIC-----HEGKAYFPR--EGVVFVNGTTSWFITQRNFFSPQIIT 3294  
 H TY P N T C A P G+F+ S+++T R+ + P+ IT  
 Sbjct: 939 HFTYTPESFVNVTAIVGFCVNPANASQYAIVPANGRGIFIQVNGSYYVTARDMYMPRDI 998

Query: 3295 TDNTFVSGNCDVVIGIINNTVYDPLQPELD-SFKEELDKYFKNHTSPDVLGDISGINAS 3471  
 + +C +N TV + D +F +EL K++ + D D +  
 Sbjct: 999 AGDIVTLTSCQANYVNVNKTVITTFVEDDDFNDFDELKWWNDTKHELPDFEDFN-YTVP 1057

Query: 3472 VVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTIXXX 3651  
 ++NI EID + V + LN+SLI+L+EL + YIKWPWYVWL +I +++  
 Sbjct: 1058 ILNISGEIDHIQGVIOGLNDSLINLEELSIKTYIKWPWYVWLAIGFAIIFILI----- 1112

Query: 3652 XXXXXXXXXXXKGACSCGCC 3708  
 G C C CC  
 Sbjct: 1113 --LGWVFFMTGCCGC--CC 1127

>[gi|13448694|gb|AAK27168.1](#) spike glycoprotein [Avian infectious bronchitis viru  
 Length = 1162

Score = 351 bits (901), Expect = 5e-95  
 Identities = 204/558 (36%), Positives = 296/558 (53%), Gaps = 15/558 (2%)  
 Frame = +1

Query: 2080 IAIPTNFSISITTEVMPVSMAKTSVDCNMYYICGDSTECANLLLQYGSFCTQLNRALSGIA 2259  
 + IP +F++++T E + M K ++C YICG+S EC NL QYG C + + +  
 Sbjct: 584 VLIPNSFNLTVTDEYIQTLMDKVQINCLQYICGNSLECRNLFQQYGPVCDNILSVVNSVG 643

Query: 2260 AEQDRNTREVFAQVKQM-YKTPTLKYF--GGFNFSQILPDPLKPTKRSFIEDLLFNKVTL 2430  
 ++D ++ K + TP L G FN S L P P +RSFIEDLLF V  
 Sbjct: 644 QKEDMELLNFYSSTKPAGFNTPVLSNVSTGEFNISLFLTTPSSPRRRSFIEDLLFTSVES 703

Query: 2431 ADAGFMKQYGECL-GDIN-ARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSXXXXXXXX 2604  
 Y C G + +DL+CA+++NGL VLPP++T +M YT++LV+  
 Sbjct: 704 VGLPTDDAYKNCTAGPLGFLKDLVCAREYNGLLVLPPIITAEMQTLTYTSSLVASMAGGI 763

Query: 2605 XXXXXXXXLQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAIQIQESLTTTSTALG 2784  
 IPFA Q+ R N +G+TQ++L +NQ++IA FNKAI +QE +TS AL  
 Sbjct: 764 TAAGA----IPFATQLQARINHLGITQSLLLLKNQEKIAASFNKAIGHMQEGFRSTSLALQ 819

Query: 2785 KLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQT 2964  
 ++QDVVN+ + L + L+ NFGAISSV+ +I +LD ++A Q+DRLITGRL SL

Sbjct: 820 QIQDVVNKQSAILTETMASLNKNFNGAISSVIQEIYQQLDAIQANAQVDRLITGRLSSLSV 879

Query: 2965 YVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVT 3144  
 + + + LA K++ECV QS R FCG G H+++ PQ AP+G+VF+H +

Sbjct: 880 LASAKQAEYIRVSQQRELATQKINECVKSQSIRYSFCGNGRHVLTIPQNAPNGIVFIHFS 939

Query: 3145 YVPSQERNFTTAPAICHEGK-----AYFPR--EGVFVFNGTSWFITQRNFFSPQIITTDN 3303  
 Y P N T C + A P G+F+ S++IT R+ + P+ IT +

Sbjct: 940 YTPDSFVNVTAIVGFCVKPANASQYAIVPANGRGIFIQVNGSYYITARDMYMPRAITAGD 999

Query: 3304 TFSVGNCDVVIGIINNTVYDPLQPELD-SFKEELDKYFKN--HTSPDVLDGDISGINASV 3474  
 +C V +N TV D F +EL K++ + H PD D + + +

Sbjct: 1000 IVTLTSCQVNYVSVNKTVITTFVDNDDFDNDELKSKWVNDTKHELPDFDKFNYT---VPI 1056

Query: 3475 VNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTIXXXX 3654  
 ++I EIDR+ V + LN+SLIDL++L + YIKWPWYVWL AI TI

Sbjct: 1057 LDIDSEIDRIQGVIQGLNDSLIDLEKLSILKTYIKWPWYVWL-----AIAFATIIFIL 1109

Query: 3655 XXXXXXXXKGCSCGCC 3708  
 G C C CC

Sbjct: 1110 ILGWVFFMTGCCGC--CC 1125

>[gi|138189|sp|P12650|VGL2\\_IBVK](#) E2 glycoprotein precursor (Spike glycoprotein) (F  
 [Contains: Spike protein S1; Spike protein S2]  
[gi|74848|pir||VGIHAK](#) E2 glycoprotein precursor - avian infectious bronchitis viru  
 KB8523)  
[gi|331187|gb|AAA66578.1|](#) spike protein  
 Length = 1162

Score = 350 bits (897), Expect = 1e-94  
 Identities = 205/558 (36%), Positives = 294/558 (52%), Gaps = 15/558 (2%)  
 Frame = +1

Query: 2080 IAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIA 2259  
 + IP +F++++T E + M K ++C YICG+S EC NL QYG C + ++ +

Sbjct: 584 VLIPNSFNLTVTDEYIQTRMDKVQINCLQYICGNSLECRNLFQQYGPVCDNMLSVVNSVG 643

Query: 2260 AEQDRNTREVFAQVKQM-YKTPTLKYF--GGFNFSQILPDPLKPTKRSFIEDLLFNKVTL 2430  
 ++D ++ K + TP L G FN S L P P +RSFIEDLLF V

Sbjct: 644 QKEDMELLNFYSSTKPAGFNTPVLSNVSTGEFNISLFLTTPSSPRRRSFIEDLLFTSVES 703

Query: 2431 ADAGFMKQYGECL-GDIN-ARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSVXXXXXXX 2604  
 Y C G + +DL+CA+++NGL VLPP++T +M YT++LV+

Sbjct: 704 VGLPTDDAYKNCTAGPLGFLKDLVCAREYNGLLVLPPIITAEMQTLTYTSSLVASMAFGGI 763

Query: 2605 XXXXXXXXLQIPFAMQMAYRFNGIGVTVQNVLYENQKQIANQFNKAIHQIQESLTTTSTALG 2784  
 IPFA Q+ R N +G+TQ++L +NQ++IA FNKAI +QE +TS AL

Sbjct: 764 TAAGA----IPFATQLQARINHLGITQSLLLKNQEKIAASFNKAIGHMQEGFRSTSLALQ 819

Query: 2785 KLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQT 2964  
 ++QDVVN+ + L + L+ NFGAISSV+ +I +LD ++A Q+DRLITGRL SL

Sbjct: 820 QIQDVVNKQSAILTETMASLNKNFNGAISSVIQEIYQLDAIQANAQVDRLITGRLSSLSV 879

Query: 2965 YVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVT 3144  
 + + + LA K++ECV QS R FCG G H+++ PQ AP+G+VF+H T

Sbjct: 880 LASAKQAEYIRVSQQRELATQKINECVKSQSTRYSFCGNGRHVLTIPQNAPNGIVFIHFT 939

Query: 3145 YVPSQERNFTTAPAICHEGK-----AYFP--REGVFVFNGTSWFITQRNFFSPQIITTDN 3303

```

          Y P   N T   C +       A P   G+F+   S++IT R+ + P+ IT +
Sbjct: 940  YTPESFVNVT AIVGFCV KPNNASQY AIVPVN GRGIFIQV NDSYYITARDMYMPRHITAGD 999

Query: 3304  T F V S G N C D V V I G I I N N T V Y D P L Q P E L D - S F K E E L D K Y F - - K N H T S P D V D L G D I S G I N A S V 3474
          +C       +N TV           D F +EL K++   + PD D + +   V
Sbjct: 1000  I V T L T S C Q A N Y V S V N K T V I T T F V E N D D F D F D D E L S K W W I E T K Y E L P D F D Q F N Y T - - - I P V 1056

Query: 3475  V N I Q K E I D R L N E V A K N L N E S L I D L Q E L G K Y E Q Y I K W P W Y V W L G F I A G L I A I V M V T I X X X X 3654
          +NI  +ID++ EV K LN+SLIDL+ L   + Y I K W P W Y V W L           A I   T I
Sbjct: 1057  L N I T Y D I D K I E E V I K G L N D S L I D L E T L S I L K T Y I K W P W Y V W L - - - - - - - A I A F A T I I F I L 1109

Query: 3655  X X X X X X X X X K G A C S C G S C C 3708
          G C C   C C
Sbjct: 1110  I L G W V F F M T G C C G C - - C C 1125
    
```

Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 Posted date: Apr 21, 2003 1:41 AM  
 Number of letters in database: 455,667,871  
 Number of sequences in database: 1,415,660

Lambda      K          H  
 0.318      0.135      0.401

Gapped  
 Lambda      K          H  
 0.267      0.0410      0.140

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 2,799,336,456  
 Number of Sequences: 1415660  
 Number of extensions: 57705387  
 Number of successful extensions: 155798  
 Number of sequences better than 10.0: 100  
 Number of HSP's better than 10.0 without gapping: 134220  
 Number of HSP's successfully gapped in prelim test: 0  
 Number of HSP's that attempted gapping in prelim test: 0  
 Number of HSP's gapped (non-prelim): 154572  
 length of database: 455,667,871  
 effective HSP length: 135  
 effective length of database: 264,553,771  
 effective search space used: 296300223520  
 frameshift window, decay const: 50, 0.1  
 T: 12  
 A: 40  
 X1: 16 ( 7.3 bits)  
 X2: 38 (14.6 bits)  
 X3: 64 (24.7 bits)  
 S1: 41 (21.7 bits)



This document was created with Win2PDF available at <http://www.daneprairie.com>.  
The unregistered version of Win2PDF is for evaluation or non-commercial use only.