A

```
BLASTP 1.4.8MP [19-Dec-94] [Build 13:14:38 Apr 24 1995]

Reference:  Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers,
and David J. Lipman (1990).  Basic local alignment search tool.  J. Mol. Biol.
215:403-10.

Query=  COAT_TMV
        (158 letters)

Database:  Non-redundant PDB+SwissProt+SPupdate+PIR+GenPept+GPupdate
           148,485 sequences; 43,480,653 total letters.
Searching.....................................................done

                                                                    Smallest
                                                                      Sum
                                                             High  Probability
Sequences producing High-scoring Segment Pairs:              Score  P(N)       N

sp|P03572|COAT_TMVO     COAT PROTEIN. >pir|B91925|VCTMOO c...   802  8.1e-106  1
sp|P03571|COAT_TMVOM    COAT PROTEIN. >pir|A91925|VCTMOM c...   797  3.9e-105  1
sp|P03573|COAT_TMVER    COAT PROTEIN.                           793  1.4e-104  1
sp|P03574|COAT_TMV06    COAT PROTEIN.                           790  3.6e-104  1
.....
sp|P03578|COAT_ORSV     COAT PROTEIN.                           356  5.2e-78   2
.....
sp|P19521|COAT_CGMVS    COAT PROTEIN.                           285  6.0e-35   1
.....
sp|P09318|PRL2_OREMO    PROLACTIN II PRECURSOR (PRL-177).        65  0.64      1
.....
gp|X82625|BMMVP1P2_1    RNA2 polyprotein [Barley mild mosa...    51  0.65      2
.....
sp|P03302|POLG_POL3L    GENOME POLYPROTEIN (COAT PROTEINS ...    45  0.81      3
.....
sp|Q05142|COAT_NVMV     COAT PROTEIN (CAPSID PROTEIN) (ORF...    62  0.93      1

>sp|P19521|COAT_CGMVS COAT PROTEIN.
          Length = 160

 Score = 285 (129.8 bits), Expect = 6.0e-35, P = 6.0e-35
 Identities = 58/153 (37%), Positives = 92/153 (60%)

Query:      1 SYSITTPSQFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSEVWKPSPQVTV 60
              +Y+  TPS+ +  S+++     L+N    + G  FQTQ  R   +   S +       +
Sbjct:      1 AYNPITPSKLIAFSASYVPVRTLLNFLVASQGTAFQTQAGRDSFRESLSALPSSVVDINS 60

Query:     61 RFPDSDFKVYRYNAVLDPLVTALLGAFDTRNRIIEVENQANPTTAETLDATRRVDDATVA 120
              RFPD+ F  +    VL P+  +LL + DTRNR+IEV + +NPTTAE+L+A +R DDA+ A
Sbjct:     61 RFPDAGFYAFLNGPVLRPIFVSLLSSTDTRNRVIEVVDPSNPTTAESLNAVKRTDDASTA 120

Query:    121 IRSAINNLIVELIRGTGSYNRSSFESSSGLVWT 153
              R+ I+NLI  + +G   Y+R+SFE++  +VW+
Sbjct:    121 ARAEIDNLIESISKGFDVYDRASFEAAFSVVWS 153
```

Fig. 4. BLAST searches with general and special-purpose sequence databases. **(A)** An excerpt of the BLAST output with the TMV capsid protein sequence as a query (designated as sbjct) and the NR database. **(B)** An excerpt of the BLAST output with the TMV capsid protein sequence as a query and the database of virus capsid protein sequences.