

B

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: coat
 91 sequences; 36,464 total letters.
 Searching.....done

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Sum Probability P(N)	N
COAT_TMV	717	7.5e-97	1
COAT_NVMV	62	0.0021	1
COAT_SBWMV	38	0.19	2
COAT_TNVA	47	0.27	1
VGNM_APMV	37	0.90	2
COAT_MNSV	40	0.96	1
COAT_WCMVO	39	0.98	1
COAT_CNV	39	0.99	1
COAT_CRV	38	0.998	1
COAT_IPCV	37	0.9996	1
COAT_SHVX	37	0.9997	1
POLG_PYFV1	37	0.9998	1

>COAT_NVMV
 Length = 174

 Score = 62 (28.1 bits), Expect = 0.0021, P = 0.0021
 Identities = 10/32 (31%), Positives = 20/32 (62%)

Query: 121 IRSAINNLIVELIRGTGSYNRSSFESSGLVW 152
 +R+A++ + L+ G Y R++ E+ G+VW
 Sbjct: 131 LRTALSQMEKALVNGESLYTRTTIENKLGIVW 162

>COAT_SBWMV
 Length = 176

 Score = 38 (17.2 bits), Expect = 0.21, Sum P(2) = 0.19
 Identities = 8/29 (27%), Positives = 16/29 (55%)

Query: 95 EVENQANPTTAETLDATRRVDDATVAIRS 123
 +VEN+ T +TL + V + + +R+
 Sbjct: 122 QVENEEQQQTDQTLAISNAVAELMIFVRT 150

Score = 35 (15.9 bits), Expect = 0.21, Sum P(2) = 0.19
 Identities = 6/14 (42%), Positives = 8/14 (57%)

Query: 139 YNRSSFESSGLVW 152
 Y + SFE+ L W
 Sbjct: 159 YTQDSFEAKYNLKW 172

sequences using the CLUS program (34) and a cutoff score of 60. Each cluster at Fig. 5 is defined by the minimal score observed between a pair of sequences within this cluster. Most of the clusters appear to contain a single virus group.