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82 entries involved in 174 pairs with S = 60

Score: 747
1 ( 5):      2 component geminiviruses
Score: 899
2 ( 4):      Comoviruses
Score: 210
3 ( 12):     Tombusviruses, sobemoviruses, dianthoviruses,
machloviruses, necroviruses, carmoviruses
Score: 266
4 ( 8):     Potexviruses, carlaviruses
Score: 352
5 ( 2):     Potyviruses, bymoviruses
Score: 506
6 ( 3):     Phytoreoviruses
Score: 183
7 ( 6):     Caulimoviruses, badnaviruses
Score: 507
8 ( 2):     Cucumoviruses
Score: 354
9 ( 3):     Tymoviruses
Score: 290
10 ( 5):    Luteoviruses, enamoviruses
Score: 373
11 ( 3):    Bromoviruses
Score: 380
12 ( 2):    Tospoviruses
Score: 162
13 ( 5):    1 component geminiviruses
Score: 135
14 ( 3):    Nepoviruses
Score: 126
15 ( 3):    Tobraviruses, hordeiviruses, IPCV
Score: 175
16 ( 2):    Trichoviruses, capilloviruses
Score: 98
17 ( 2):    Satellite viruses
Score: 91
18 ( 3):    Rhabdoviruses
Score: 87
19 ( 2):    Sequiviruses
Score: 75
20 ( 2):    Closteroviruses
Score: 62
21 ( 2):    Tobamoviruses, NVMV
Score: 60
22 ( 2):    Iilarviruses, idaeoviruses
20 groups   77 sequences

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Fig. 5. Clustering of the viral capsid proteins on the basis of BLASTP scores. Virus groups comprising a cluster are separated by commas, and each cluster is preceded by the minimal BLASTP score for a pair of two sequences within the cluster.

However, it is notable that several groups of small spherical viruses are in the same cluster, as are tobnaviruses and hordeiviruses. Attempts to use a lower cutoff resulted in erroneous results, with clusters based on spurious hits (not shown).