```
>sp|Q00010|COAT_BYDV1           94: ILKSYHLYKITNVKVEFKSHASASTVGAmFIELDTwCSQSTLg    184,    1.4e-09   1.83e-11
>gi|533390|gp|U06865|           91: ILKSYHdYAITNVqIfYRSHASSETeGA1FIELDnSCTQSALA    172,   1.13e-08   1.29e-10
>gi|533393|gp|U06866|           91: ILKSYHdYAITNVqVfYRSHASSETeGA1FIELDnSCTQSALg    163,   5.16e-08   5.71e-10
>gi|511649|gp|L34672|    !   7  104: VAANWSKYSLLSVTYTYLPSCPSTTSGSIHMGFQYDMADTLPV    341,         0   1.61e-26
>sp|P15183|COAT_CNV C    !   8  140: IAANFDQYKFNSLRFEYVPLVNTTTNGRVALYFDKDSEDPGPD    340,         0   1.15e-26
>gi|755719|gp|X85215|    !   9  144: IAANFDQYTFNSVTLHYVPLCATTETGRVAMYFDKDSEDLEPA    339,         0    1.1e-26
>gi|231078|pdb|4SBV|A    !  10  104: VAQNWSKYAWVAIRYTYLPSCPTTTSGAIHMGFQYDMADTLPV    331,         0   5.23e-26
>sp|P22959|COAT_TNVA     !  13  125: IADLYSKYRWLSCEIIYIPKCPTTTSGSIAMAFTYDRNDAAPT    331,         0   5.23e-26
>pir|S05457|S05457 co    !  11  144: LASNFDQYMFNTLRLQYVPMCASTETGRVAIYFDKDSQDLEPV    330,         0   6.66e-26
>gi|230755|pdb|2TBV|A    !  12  148: LASNFDQYSFNSVVLDYVPLCGTTEVGRVALYFDKDSQDPEPA    325,         0   2.54e-25
>gi|310363|gp|L20835|    !   1   96: ILKAYHEYKITSVLLQFITEASSTSSGSIAYELDPHCKYSEIQ    317,         0   2.67e-24
>sp|P06663|COAT_TCV C    !  14  122: EAAQYEKYRFTSLRFRYSPMSPSTTGGKVALAFDRDAAKPPPN    315,         0   4.45e-24
>sp|P22955|COAT_RCNMV    !  18   92: EAANYDMYRLKKLTLRYVPLVTVQNSGRVAMIWDPDSQDSAPQ    309,         0   2.47e-23
>pir|JQ2190|JQ2190 P3    !  17  124: IAASYEKYKFTSLRFRYSSTCPTSTGGKVALAFERDAANPLPD    305,         0   7.62e-23
>sp|P19899|COAT_MNSV     !  15  141: QAQLYDMYRFTRLRITYIPTTGSTSTGRVSLLWDRDSQDPLPI    304,         0   9.75e-23
>sp|P27210|COAT_TNVD     !  16  117: IADLYSKWRWISCSVVYIPKCPTSTQGSVVMAIVYDAQDTVPT    302,         0    1.6e-22
>sp|P19126|COAT_BLRV     !  26   92: ILKAYHEYNITNVELAYITEASSTSSGSIAYELDPHLKNTTIQ    299,         0   3.24e-22
>gi|323232|gp|L10356|    !   2   97: ILKAYHEYKITNCVLQFITEASSTAAGSISYELDPHCKSSSLT    298,         0    3.3e-22
>gi|289519|gp|L12757|    !   3   67: ILKAYHEYKITKIILEFISEASSTQSGSIAYELDPHNKLSTLA    298,         0    3.3e-22
>gi|304452|gp|L18870|    !  19   94: EAANYDLYRFAKLRLSYVHDTNATVSGRVSLMWDRDSQDVPPN    287,         0   5.72e-21
>sp|P09509|COAT_BWYVG    !   4   98: ILKAYHEYKISMVILEFVSEASSQNSGSIAYELDPHCKLNSLS    285,         0   9.49e-21
>sp|P04383|COAT_CARMV    !  20  123: LATNFNKYRITALTVKYSPACSFETNGRVALGFNDDASDTPPT    281,         0   2.63e-20
>pir|S32327|S32327 co    !  21   38: RTVGTWLRSWLSVRYTYIPSCPSSTAGSIHMGFQYDMADTVPV    272,         0   2.31e-19
>gi|727424|gp|U23142|    !  22   47: LARCYSMWKPTRWDVVYLPEVSATVAGSIEMCFLYDYADTIPS    270,         0   3.71e-19
>gi|58786|gp|X56050|B    !   5   95: ILKSYHRYKITSVRVEFKSHASATTAGAIFIELDTACKQSALA    258,   4.44e-16   6.33e-18
>sp|P11642|COAT_MCMV     !  23   94: QSQMWNTIVFNSVRITWETFTADTTSGYISMAFLSDYMLSIPT    216,   3.4e-12   4.89e-14
>sp|P29153|COAT_PEAMV    !   6   82: NLAAYQKYRIVWLKVVYQSEAAATDRGCIAYHVDTSTTKKAAD    211,   9.1e-12   1.25e-13
>gi|496315|gp|D30814|    !  24   95: AARIFQRYAVETLEFEIQPMCPANTGGGYVAGFLPDPTDNDHT    196,   1.58e-10    2.1e-11
>sp|Q04611|VST2_HEVMY    !  25  178: EASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPT    182,   1.99e-09   2.49e-11

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Fig. 8. MoST results for the conserved motif in the capsid proteins of small spherical viruses—detection of a related segment in the HEV capsid protein.

tant motifs. Labor-consuming hierarchical alignment procedures, typically with a significant contribution from visual inspection, have been most important in delineating the relationships between these proteins. Although these expert approaches still play a significant role, especially when the first representative of new group of viruses is sequenced, most of the results now can be achieved using more automatic and statistically better-justified methods.

We deliberately left out the issue of phylogenetic interpretation of sequence similarities. Because, in many cases, the proteins to be analyzed share only limited sequence similarity, it is crucial that the correct alignment of the sequences is, achieved prior to construction of the trees. With the conserved blocks delineated by statistically reliable methods, like those described above, phylogenies can be inferred by a variety of different methods and algorithms. Another vast area that requires a separate discussion is sequence–structure relationship. With an increasing number of tertiary structures of proteins and viral capsids resolved, structure-based alignments are becoming more and more important in establishing functional and evolutionary relationships between viruses. Detailed knowledge of capsid protein topology is also of increasing importance for the purpose of design of plant virus-based expression vectors that can be used for peptide display (49,50). Methods of homology modeling are currently rapidly developing, and one may anticipate that this type of analysis will dominate the field in the future.