



```
15 2jju_A Signal regulatory prote 76.8
                                                 6.8 0.0002
                                                                24.6
                                                                        5.2
                                                                                    3-82
                                                                                               1-82
                                                                                                      (127)
  16 2ywz A NEW antigen receptor va 76.0
                                                  12 0.00035
                                                                22.7
                                                                        6.4
                                                                              71
                                                                                     6-82
                                                                                               1-74
                                                                                                      (111)
  17 1dlf L Anti-dansvl immunoglobu
                                        74.7
                                                  12 0.00034
                                                                22.4
                                                                        5.7
                                                                              72
                                                                                    5-82
                                                                                               1-84
                                                                                                      (113)
  18 4hgm A Shark V-NAR: IG-fold, h
                                        74.6
                                                 8.4 0.00024
                                                                23.9
                                                                        5.1
                                                                              71
                                                                                     6-82
                                                                                               1-74
                                                                                                      (112)
  19 3u6r L Antibody 1:7 (light cha
                                                      0.0003
                                                                23.9
                                                                              71
                                                                                     6-82
                                                                                               1-78
                                                                                                      (143)
                                                   11 0.00033
                                                                                               1-74
  20 2coq A NEW antigen receptor va
                                        74.1
                                                                22.5
                                                                        5.5
                                                                              71
                                                                                     6-82
                                                                                                      (108)
                                                                                                      (134)
  21 3bik_B Programmed cell death p
                                        73.1
                                                   16 0.00046
                                                                22.7
                                                                        6.5
                                                                              77
                                                                                     2-82
                                                                                               6-91
  22 2dia A Filamin-B; beta-sandwic
                                        72.6
                                                  20 0.00056
                                                                23.5
                                                                        7.8
                                                                              75
                                                                                     3 - 79
                                                                                              11-85
                                                                                                      (113)
  23 4aj0 A Germinal LINE lambda 3
                                        70.9
                                                   12 0.00034
                                                                22.3
                                                                        5.0
                                                                              72
                                                                                     5-82
                                                                                               1-78
                                                                                                      (107)
72
                                                                                               1-79
  24 2d7t L Anti polyhydroxybutyrat
                                        70.6
                                                   14 0.00041
                                                                22.7
                                                                                     5-82
                                                                        5.5
                                                                                                      (116)
  25 3moq_A NEW antigen receptor va
                                                      0.0006
                                                                              71
                                                                                               1-74
                                                                                                      (126)
  26 4unu_A MCG, IG lambda chain V-
                                                                                               1-82
                                                   17
                                                      0.0005
                                                                21.6
                                                                        5.5
                                                                              73
                                                                                     4-82
                                                                                                      (111)
  27 3bp6 A Programmed cell death p
                                        69.3
                                                   18 0.00052
                                                                21.7
                                                                        6.6
                                                                              72
                                                                                     7-82
                                                                                               1-81
                                                                                                      (117)
  28 3rgh A Filamin-A: cell adhesio
                                                   22 0.00063
                                        69.0
                                                                22.6
                                                                        6.4
                                                                              75
                                                                                     3 - 79
                                                                                               8-82
                                                                                                      (100)
                                                   18 0.00051
                                                                21.4
                                                                        5.9
  29 1jhl L IGG1-kappa D11.15 FV (1
                                                                              72
                                                                                               1-79
                                        68.6
                                                                                     5-82
                                                                                                      (108)
  30 1i8k A Epidermal growth factor
                                                      0.0005
                                                                21.4
                                                                        5.3
                                                                                     5-82
                                                                                               1-79
                                                                                                      (107)
                                                   18 0.00053
                                                                                              15-79
  31 1qfw M FV, antibody (anti beta
                                                                21.4
                                                                        5.4
                                                                              59
                                                                                    18-82
                                                                                                      (108)
  32 3r8b_B G5-8, enterotoxin type
                                        67.1
                                                  21 0.00062
                                                                21.8
                                                                        5.8
                                                                              74
                                                                                    4-82
                                                                                               4-87
                                                                                                      (125)
                                                                                                      (119)
33 2e27 L Anti-ciquatoxin antibod
                                        66.3
                                                  19 0.00055
                                                                22.2
                                                                        5.4
                                                                              74
                                                                                     3-82
                                                                                               1-81
  34 2yc1 B Single chain antibody f
                                                   18 0.00052
                                                                              75
                                                                                    2-82
                                                                                              13-94
                                        66.3
                                                                23.6
                                                                        5.5
                                                                                                      (146)
  35 1mqk_L Antibody 7E2 FV fragmen
                                        66.2
                                                  20 0.00057
                                                                21.9
                                                                        5.5
                                                                              72
                                                                                     5-82
                                                                                               1-79
                                                                                                      (120)
  36 2dmc A Filamin-B; beta-sandwic
                                                 4.6 0.00013
                                                                27.0
                                                                                    15-78
                                                                                              26-87
                                                                                                      (116)
                                                                              79
  37 4kjy_B High-affinity sirpa var
                                                   21
                                                      0.0006
                                                                22.5
                                                                                     3-82
                                                                                               5-86
                                                                                                      (133)
  38 2d7p_A Filamin-C; beta-sandwic
                                                   32 0.00093
                                                                22.6
                                                                        6.5
                                                                              74
                                                                                     3-79
                                                                                              11-84
                                                                                                      (112)
                                        63.6
  39 4hbc L Antigen binding fragmen
                                        63.3
                                                  21 0.00059
                                                                24.0
                                                                        5.5
                                                                              72
                                                                                    5-82
                                                                                               1-79
                                                                                                      (213)
  40 1p4b L Antibody variable light
                                                   29 0.00084
                                                                                               4-86
                                        63.2
                                                                21.9
                                                                        6.3
                                                                              74
                                                                                     3-82
                                                                                                      (135)
  41 1j05_L T84.66 antibody, anti-C
                                                                                              15-83
                                                   24 0.00068
                                                                20.9
                                                                              59
                                                                                    18-82
                                        63.1
                                                                        5.3
                                                                                                      (111)
  42 4ffy L DENV1-E111 single chain
                                                   18 0.00052
                                                                22.2
                                                                        4.8
                                                                              72
                                                                                     5-82
                                                                                               1-83
                                                                                                      (213)
  43 3r06_A Anti-mouse CD3epsilon a
                                                      0.0006
                                                                24.0
                                                                              59
                                                                                    18-82
                                                                                              15-79
                                        62.8
                                                  21
                                                                        5.4
  44 2d7n A Filamin-C: beta-sandwic
                                        62.3
                                                  28
                                                      0.0008
                                                                22.4
                                                                        5.7
                                                                              60
                                                                                    17-79
                                                                                               6-65
                                                                                                      (93)
                                                        0.001
  45 4wng A TCR variable delta 1 ch
                                        61.9
                                                   35
                                                                22.4
                                                                        6.5
                                                                              76
                                                                                    3-82
                                                                                               1-84
                                                                                                      (207)
                                                  22 0.00062
                                                                22.2
  46 4hgk C Shark V-NAR antibody; I
                                        61.5
                                                                        5.0
                                                                              73
                                                                                    4-82
                                                                                              18-93
                                                                                                      (128)
  47 loaq L Light chain; immune sys
                                                      0.0008
                                                                21.0
                                                                              72
                                                                                     5-82
                                                                                               1-81
                                                                                                      (120)
                                                                        6.4
  48 3hqx_A UPF0345 protein aciad03
                                                  24 0.00069
                                                                                    3-76
                                                                                              17-89
                                                                                                      (111)
                                                                                                      (145
  49 2kzw_A Uncharacterized protein
                                                 6.3 0.00018
                                        60.9
                                                                27.6
                                                                        2.5
                                                                              19
                                                                                    68-87
                                                                                             110-128
  50 leeq A Kappa-4 immunoglobulin
                                        60.8
                                                  22 0.00062
                                                                21.2
                                                                        4.8
                                                                              72
                                                                                    5-82
                                                                                               1-85
                                                                                                      (114)
                                                                                              43-112 (113)
                                                        0.001
                                                                              67
                                                                                    23-90
  51 2dia A Filamin-B; beta-sandwic
                                        60.6
                                                  36
                                                                22.2
                                                                        6.8
  52 2j3s A Filamin-A; cytoskeleton
                                        58.7
                                                   14 0.00039
                                                                28.2
                                                                        4.3
                                                                              62
                                                                                    16-79
                                                                                             113-174 (288)
  53 4uyp_A SCAC, cellulosomal scaf
                                                 5.1 0.00015
                                                                28.8
                                                                        1.7
                                                                              21
                                                                                    19-39
                                                                                              14-41
                                                                                                      (151)
                                                   34 0.00097
  54 2xt1_B Camelid VHH 9; viral pr
                                                                                               1-89
                                        58.7
                                                                21.2
                                                                              78
                                                                                    3-82
                                                                                                      (121)
  55 2k7q_A Filamin-A; IG-like, ABP
                                        57.0
                                                  13 0.00039
                                                                26.6
                                                                        3.8
                                                                              66
                                                                                    12-79
                                                                                               9-74
                                                                                                      (191)
  56 4xt1_C Nanobody 7; GPCR, chemo
                                        56.8
                                                   40 0.0012
                                                                21.5
                                                                        6.9
                                                                              79
                                                                                    2-82
                                                                                               2-90
                                                                                                      (134)
                                                  21 0.00059
                                                                23.5
                                                                              61
                                                                                    17-79
                                                                                              37-97
  57 2e9j A Filamin-B; beta-sandwic
                                        56.7
                                                                        4.4
                                                                                                      (119)
  58 2ccl_A Cellulosomal scaffoldin
                                                  4.4 0.00013
                                                                29.2
                                                                        1.0
                                                                              37
                                                                                               1-45
                                                                                                      (158)
  59 4nzu_L 13PL heavy chain; antib
                                                  32 0.00093
                                                                23.1
                                                                        5.4
                                                                              59
                                                                                    18-82
                                                                                              15-79
                                                                                                      (211)
☐ 60 11k3_L 9D7 light chain; antige
☐ 61 4id1_A Single domain antibody
                                                                              59
                                                                                    18-82
  60 11k3_L 9D7 light chain; antige
                                                  32 0.00092
                                                                23.0
                                                                                              14-78
                                        55.7
                                                                        5.4
                                                                                                      (210)
                                        54.9
                                                  43 0.0012
                                                                21.3
                                                                        6.4
                                                                              76
                                                                                    3-82
                                                                                               1-88
                                                                                                      (136)
                                                                                              66-154
  62 2cdp A Beta-agarase 1; carbohy
                                        54.8
                                                   40
                                                      0.0011
                                                                23.6
                                                                        5.9
                                                                              73
                                                                                    19-92
                                                                                                      (160)
                                                                21.5
  63 4ut7 L Broadly neutralizing hu
                                        54.8
                                                   45
                                                      0.0013
                                                                        6.2
                                                                              74
                                                                                    3-82
                                                                                               2-84
                                                                                                      (153)
  64 41fh_D 9C2 TCR delta chain; NK
                                                       0.0016
                                                                22.1
                                                                              75
                                                                                     4-82
                                                                                               3-85
                                                                                                      (236)
                                                                        6.5
  65 2vn6_A Cohesin, scaffolding pr
                                                       0.0002
                                                                                    19-39
                                                                                              24-52
                                        53.2
                                                                27.8
                                                                        1.7
                                                                              21
                                                                                                      (151)
  66 3sob_L Antibody light chain; b
                                        53.0
                                                   37
                                                      0.0011
                                                                23.2
                                                                        5.4
                                                                              59
                                                                                    18-82
                                                                                              38-102
                                                                                                      (237)
  67 3b83_A Ten-D3; beta sheet, com
                                        52.9
                                                   33 0.00095
                                                                20.6
                                                                        4.7
                                                                              47
                                                                                    34-84
                                                                                              32-78
                                                                                                      (100)
                                                      0.0015
                                                                                    12-92
                                                                                             567-637
  68 1e07 A Carcinoembryonic antige
                                        52.6
                                                   51
                                                                26.3
                                                                        6.8
                                                                              71
                                                                                                      (642)
  69 3q9a B Minimizer; antibody com
                                                       0.0015
                                                                21.7
                                                                              76
                                                                                     3-82
                                                                                               1-88
                                                                                                      (139)
                                        52.5
                                                                        6.1
  70 3qs7_E FL cytokine receptor; i
                                                       0.0017
                                                                24.8
                                                                              57
                                                                                    19-80
                                                                                             341-399
                                                                                                      (423)
                                                        0.001
  71 4hjj_L Anti-IL12 anti-IL18 DFA
                                                   36
                                                                24.1
                                                                              72
                                                                                     5-82
                                                                                               1-79
                                                                                                      (327)
  72 2znx A SCFV; fluorotryptohpan,
                                        52.2
                                                  36
                                                        0.001
                                                                23.7
                                                                        5.3
                                                                              58
                                                                                    19-82
                                                                                              16-79
                                                                                                      (242)
                                                   47
                                                      0.0013
                                                                                              14-87
  73 3zkx C XA4815; hydrolase; 2.37
                                        52.1
                                                                20.8
                                                                        7.2
                                                                              61
                                                                                    18-82
                                                                                                      (122)
  74 4bsj A Vascular endothelial gr
                                                      0.0018
                                                                                               3-76
                                        51.6
                                                   64
                                                                22.3
                                                                        6.9
                                                                              71
                                                                                    3-80
                                                                                                      (232)
  75 4c57_C Nanobody, cyclin-G-asso
                                                      0.0014
                                                                              74
                                                                                                      (141)
  76 2c4x A Endoglucanase, ctcel9D-
                                                   11 0.00031
                                                                28.9
                                                                        2.6
                                                                              29
                                                                                    68-98
                                                                                              65-93
                                                                                                      (260)
  77 1kxv_C Camelid VHH domain CAB1
                                        51.3
                                                   43 0.0012
                                                                20.2
                                                                        7.1
                                                                              61
                                                                                    18-82
                                                                                              14-86
                                                                                                      (121)
000000000
  78 4qci_A ANTI-PDGF-BB antibody -
                                        50.8
                                                  22 0.00063
                                                                23.8
                                                                        3.9
                                                                              72
                                                                                    5-82
                                                                                               1-78
                                                                                                      (209)
  79 3j69 7 Nanobody VHH PVSP6A; pi
                                        50.6
                                                   50
                                                      0.0014
                                                                20.7
                                                                        6.0
                                                                              63
                                                                                    18-82
                                                                                              14-87
                                                                                                      (126)
  80 2y23 A Myomesin; structural pr
                                        50.2
                                                   59
                                                       0.0017
                                                                22.9
                                                                        6.2
                                                                              72
                                                                                    19-94
                                                                                             236-311
                                                                                                      (312)
  81 2bk8_A Connectin, M1, titin he
                                                       0.0012
                                                                19.7
                                                                              71
                                                                                     5-80
                                                                                               1-79
                                                                                                      (97)
  82 4ms8_C 42F3 alpha; IG, TCR MHC
                                        49.9
                                                   58
                                                       0.0017
                                                                21.3
                                                                        5.9
                                                                              77
                                                                                    2-82
                                                                                               2-86
                                                                                                      (212)
                                                                                                      (268)
  83 1x9q_A SCFV, 4M5.3 anti-fluore
                                        49.4
                                                   42
                                                      0.0012
                                                                23.6
                                                                        5.4
                                                                              73
                                                                                     4-82
                                                                                              14-98
  84 2dj4 A Filamin-B; beta-sandwic
                                        49.3
                                                   47
                                                      0.0013
                                                                21.4
                                                                        5.2
                                                                              61
                                                                                    17-79
                                                                                              26-86
                                                                                                      (108)
  85 1moe A Anti-CEA MAB T84.66; an
                                                        0.001
                                                                                               1-83
                                        49.2
                                                   36
                                                                23.3
                                                                        4.9
                                                                              72
                                                                                    5-82
                                                                                                      (240)
  86 4ndm_B AB18.1 TCR delta chain;
                                                      0.0019
                                                                              77
                                                                                               9-93
                                        49.1
                                                   66
                                                                21.7
                                                                        7.4
                                                                                     2-82
                                                                                                      (235)
  87 4wem_B Anti-F4+ETEC bacteria V
                                                      0.0015
                                                                                               1-86
                                                                20.6
                                                                              76
                                                                                    5-82
                                                                                                      (127)
  88 3ul4 A Cellulosome-anchoring p
                                        49.0
                                                   9 0.00026
                                                                27.4
                                                                        1.7
                                                                              21
                                                                                    19-39
                                                                                              20-47
                                                                                                      (157)
                                                                                                      (108)
  89 3d33 A Domain of unknown funct
                                        48.7
                                                   65 0.0019
                                                                21.5
                                                                        9.1
                                                                              64
                                                                                    14-80
                                                                                              31-95
  90 2yz1 A Tyrosine-protein phosph
                                       48.7
                                                  26 0.00074
                                                                21.2
                                                                        3.7
                                                                              78
                                                                                    4-82
                                                                                               6-86
                                                                                                      (120)
  91 2p9r A Alpha-2-M, alpha-2-macr
                                        48.5
                                                   55
                                                     0.0016
                                                                20.6
                                                                        8.7
                                                                              60
                                                                                    19-78
                                                                                              16-82
                                                                                                      (102)
  92 laoh_A Cellulosome-integrating
                                                 9.7 0.00028
                                                                26.8
                                                                                              18-45
                                                                                                      (147)
  93 4nof A Polymeric immunoglobuli
                                        47.7
                                                  48
                                                      0.0014
                                                                19.9
                                                                              68
                                                                                    6-75
                                                                                               4-92
                                                                                                      (125)
  94 4r5o_A Quinonprotein alcohol d
                                        47.5
                                                   43
                                                       0.0012
                                                                26.6
                                                                        5.7
                                                                              49
                                                                                    18-79
                                                                                              32-80
                                                                                                      (427)
  95 2rik A Titin; I-SET IG fold, p
                                        47.5
                                                   67
                                                       0.0019
                                                                23.0
                                                                        6.3
                                                                              81
                                                                                    7-92
                                                                                               7-94
                                                                                                      (284)
                                        47.1
  96 3bae H WO2 IGG2A FAB fragment
                                                   62
                                                       0.0018
                                                                22.0
                                                                        5.8
                                                                              61
                                                                                    18-82
                                                                                              14-88
                                                                                                      (228)
  97 4i2x E Signal-regulatory prote
                                        46.9
                                                   57
                                                       0.0016
                                                                23.6
                                                                        5.9
                                                                              78
                                                                                    4-82
                                                                                               2-82
                                                                                                      (328)
  98 2y3u_A Collagenase, collagenas
                                                 4.8 0.00014
                                                                35.7
                                                                              81
                                                                                     1-98
                                                                                             700-783
                                                                                                      (785)
                                                                                               1-89
  99 3qyc_A VH domain of IGG molecu
                                                                                    3-82
                                        46.8
                                                   65
                                                      0.0019
                                                                21.0
                                                                        5.9
                                                                              76
                                                                                                      (146)
100 4jfh_E BETA17 TCR allele; immu
                                        46.8
                                                   44
                                                      0.0013
                                                                23.1
                                                                        5.1
                                                                              60
                                                                                    18-82
                                                                                              15-82
                                                                                                      (244)
                                       PDB
  No 1
                                                   NCBI
                                                               Pub Med
 Stu6t_A COLH protein, collagenase; calcium-binding protein, hydrolase; HET: P33; 1.76A {Clostridium histolyticum}
  PDB: 4u7k A
```

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Probab=95.80 E-value=0.0083 Score=38.50 Aligned_cols=78 Identities=15% Similarity=0.213 Sum_probs=0.0
                   CCCCgeEeeCCCcgeeccCCCeeeeEEEecCC------CcEEEEEEEECCCCgeEEEEECCcgcgeEEEeCCCccCce
Q ss pred
                 1 RVKPSASLKLHHDLKLCLGDHSSVPVALKGQG-----PFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGD
O Thu Apr 23 00:
                                                                                         73 (111)
 Q Consensus
                 73 (111)
                 T Consensus
                                                                                         61 (86)
T 4u6t A
                                                                                         61 (86)
                   CCCCBCCCC--CCEEEETTS----CEECCCTTCBCTTSCEEEEEEECSSSCE-----ECCSSCEECCSSC----EE
T ss dssp
                   CCCCEEEe--CCcccCCC----EEEEEEeccCCCCCEEEEEEEECCCC------E
T ss_pred
Q ss_pred
                   Q Thu_Apr_23_00:
                74 YILSLVSIKDSTGCVVGLSOPDAKIO
                                           99 (111)
                74 y~v~L~sV~D~~GC~~~L~~~~v~I~
Q Consensus
                                           99 (111)
                   Ī.|.|+ |+|..||..............
                 62 Y~v~Lt-Vtd~~G~~~t~~~-~I~V~
T Consensus
                                           85 (86)
T 4u6t A
                 62 YTVKLK-VTDDKGESSVSTT-TAEIK
                                           85 (86)
T ss_dssp
                   EEEEEE-EEETTSCEEEEEE-EEEEE
                   EEEEE-EECCCCEEEEE-EEEe
T ss pred
                                                       Pub Med
>4jqu A COLH protein, collagenase; IG-like fold, beta-sandwich, calcium binding protein,, metal protein; 1.42A
 {Clostridium histolyticum}
 Probab=95.65 E-value=0.024 Score=37.03 Aligned_cols=79 Identities=19% Similarity=0.246 Sum_probs=0.0
Q ss_pred
                   CCCCceEEeCCCccceeccCCCeeeeEEEeCCC------CcEEEEEECCCCCEEEEECCcccccEEEeCCCccCCce
Q Thu Apr 23 00:
                 1 RVKPSASLKLHHDLKLCLGDHSSVPVALKGOG-----PFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGD
                                                                                         73 (111)
O Consensus
                 73 (111)
                   +++|-|.|. .....|.|+
                                      .|.|.|..
                                               +.+.+|++-+..+
                                                                                    ١.
T Consensus
                                   ------V-f----S-D-dg----y-W-fgdG------s----h-y--
T 4jgu_A
                 9 NKLPVIYMH--VPKSGALNQ----KVVFYGKGTYDPDGSIAGYQWDFGDGSD-----FSSEQNPSHVYTKK----GE
                                                                                        70 (95)
T ss_dssp
                   CCCCBCCCB--CCSEEETTS----EEECBCTTCBCTTSCEEEEEEECSSSCC------CBCCSSCEEECCSC----EE
                   CCCCEEEe--CCCcCCCc----EEEEEeeccCCCCCEEEEEEEeCCCC------EE
T ss_pred
Q ss pred
                   EEEEEEEEcccCCcccCCCCeEEE
 Q Thu_Apr_23_00:
                74 YILSLVSIKDSTGCVVGLSQPDAKIQ
                                           99 (111)
                74 y~v~L~sV~D~~GC~~~L~~~~v~I~
Q Consensus
                                           99 (111)
                 71 Y~v~Lt-Vtd~~G~~~t~~~~ItV~
T Consensus
                                            94 (95)
                 71 YTVTLR-VMDSSGQMSEKTM-KIKIT
T 4jgu_A
T ss_dssp
                   EEEEEE-EEETTSCEEEEEE-EEEE
T ss_pred
                   EEEEE-EEeCCCCEEEEE-EEEE
                           SCOPe PODEN PROTEIN DATA BANK
                                                NCBI
->1b4r_A Protein (PKD1_human); PKD domain 1 from human polycystein-1, polycystin (precursor), membrane protein;
NMR {Homo sapiens} SCOP: b.1.3.1
Probab=94.67 E-value=0.23 Score=31.70 Aligned cols=69 Identities=17% Similarity=0.165 Sum probs=0.0
                   eEEeCCCcceeccCCCeeeeEEEecCCCcEEEEEEEcCccccEEEEEeCcccccEEEEEEcccc
Q ss pred
Q Thu_Apr_23_00:
                 85 (111)
                 Q Consensus
                                                                                         85 (111)
                   |.|.|.|+ |.|..
                                                                      ----Ġ~Ÿ~Ÿ~Lt-vt~
T Consensus
                                                                                         67 (80)
                 1 ATLVGPHG-PLASGQLAAFHIA-APLPVTATRWDF---GDGSAEVDAAG--PAASHRYVLP-----GRYHVTAV-LALGA
T 1b4r A
                                                                                         67 (80)
                   CEEECCCS-CCBSSEEEEEEE-SCSSCSEEEEEC---CSSCCEEEEET--TEEEEEEECSS-----EEEEEEEE-EECSS
T ss_dssp
T ss_pred
                   CeEcCCC-cccCCCEEEEEe-CCCCcEEEEEe---CCCCccccCC--CceEEEcCCC-----eEEEEEEE-EEcCC
Q ss_pred
                   CC
Q Thu_Apr_23_00:
                86 GC
                       87 (111)
                86 GC
                       87 (111)
Q Consensus
                   \Pi
T Consensus
                 68 g-
                       69 (80)
T 1b4r A
                 68 GS
                       69 (80)
 T ss_dssp
                   CE
T ss pred
                            PDB<sup>M</sup>
PROTEIN DATA BANK

NCBI
       + - 1
                                               Pub Med
              ቖ
->4aqo_A Collagenase, collagenase G; hydrolase, PKD-like domain, collagenolysis, recrui two- tiered beta barrel;
0.99A {Clostridium histolyticum} PDB: 3jqu_A 4jrw_A 2y72_A
Probab=94.23 E-value=0.11 Score=33.62 Aligned_cols=78 Identities=17% Similarity=0.271 Sum_probs=0.0
                   CCCCceEEeCCCcceeccCCCeeeeEEEecCC------CcEEEEEEEECCCCcEEEEEeCcccccEEEECCCccCCce
Q ss pred
Q Thu_Apr_23_00:
                 1 RVKPSASLKLHHDLKLCLGDHSSVPVALKGQG-----PFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGD
                                                                                         73 (111)
                 Q Consensus
                                                                                         73 (111)
                 T Consensus
                                                                                         67 (92)
                 7 NKAPIAKVT--GPSTGAVGR----NIEFSGKDSKDEDGKIVSYDWDFGDGAT------SRGKNSVHA----YKKAGT
T 4ago A
                                                                                         67 (92)
 T ss_dssp
                   CCCCBCCCB--SCSEEETTS----EEEEECTTCBCTTSCEEEEEEECSSSCE-----EESSEEEEE----CSSCEE
 T ss_pred
                   CCCCEEEEE--CCCccCCCC----EEEEEEecccCCCCEEEEEEEeCCCCc-------ccccceEEE-----CCCCeE
                   EEEEEEEEcccCCcccCCCCeEEE
0 ss pred
```

```
Q Thu_Apr_23_00:
                  74 YILSLVSIKDSTGCVVGLSQPDAKIQ
                                                 99 (111)
 O Consensus
                   74 y \sim v \sim L \sim s V \sim D \sim \sim G C \sim \sim L \sim \sim \sim v \sim I \sim
                                                 99 (111)
                      1.|.|+ |+|..||...-.. .|.|.
                   68 Y~v~Lt-Vtd~~G~~~t~~~~VtV~
 T Consensus
                                                 91 (92)
                   68 YNVTLK-VTDDKGATATESF-TIEIK
 T 4aqo_A
                     EEEEEE-EEETTSCEEEEEE-EEEEE
 T ss_dssp
                     EEEEEE-EEECCCCEEEEEE-EEEE
 T ss pred
                                 SCOPe PROTEIN DATA BANK
 No 5
                                                                       Pub Med
🗌 >2dlg_A Filamin-B; beta-sandwich, immunoglobulin-like fold, filamin domain, NPPSFA, national project on protein
 structural and functional analyses; NMR {Homo sapiens} SCOP: b.1.18.10
 Probab=91.06 E-value=0.75 Score=30.58 Aligned cols=63 Identities=11% Similarity=0.095 Sum probs=0.0
                      eeccCCCeeeeEEEecCCCcEEEEEEEeCCCCcEEEEEE
 Q Thu_Apr_23_00:
                  15 KLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV
                                                                                     79 (111)
 O Consensus
                   79 (111)
                     .++.|.++++.|..+...-|+-+|+..+.+..+..|.|..-+-.-|+|.|.+.
---vg----ftv-----g---1-v-V--P--G-----v-d--dGtY-v-ytP----G-y-v-V-
                                                                                      74 (102)
 T Consensus
 T 2dlg_A
                   12 VATVGSICDLNLKIPEINSSDMSAHVTSP-SGRVTEAEIVPMGKNSHCVRFVPQE-MGVHTVSVK
                                                                                      74 (102)
                      SBCSSSCBCCEEECTTSCGGGCEEEEECT-TSCEEECEEECSSSEEEEEBCCCT-TCEEEEEEE
 T ss_dssp
                      CCCCCEEEEEecCCCCCCEEEEEECC-CCCEeeeEEEECCCCEEEEEECCC-CEEEEEEE
 T ss pred
 No 6
                                 PDB"
                                                              Pub Med
🗌 >4kdw_A Antifreeze protein; bacterial IG-like domain, extender domain, Ca2+-dependent, immunoglobulin-like
 beta-sandwich, extender; 1.35A {Marinomonas primoryensis} PDB: 4kdv _A
 Probab=89.93 E-value=0.64 Score=32.23 Aligned_cols=55 Identities=18% Similarity=0.313 Sum probs=0.0
 Q ss_pred
                      eEEEecCCC-----cEEEEEEEeCCCCcEEEEEeCcccccEEEeCCC--ccCCceEEEEEEEcccC
 Q Thu_Apr_23_00:
                  25 PVALKGQGP-----FTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPV--FTTGGDYILSLVSIKDSTG
                                                                                           86 (111)
                   O Consensus
                                                                                           86 (111)
                   ++.|.|.+ =++..| +|+..+++..+-.|+.+|.|.|.|.|.|.+++|+|.

46 ~v-I-Gta-g-d-~-G-VtVt-----g-t-t-tvd----G-Wsv-1----l-a-Gp-titv-t-tD-AG 109 (123)

46 TVAVSGTATGGDIAEGDTVTLEI----NGETYTTTVD-ANGEWSVDVAGSDLAADTAFDAVV-TSSDAAG 109 (123)
 T Consensus
 T 4kdw A
                      EEEEEEEESTTCCTTCEEEEEE.---TTEEEEEECC--TTSEEEEEEEHHHHHHHCCEEEEEE-EEECTTC
 T ss_dssp
                     CCEEEEECCCCCCCCEEEEE----CCEEEEEEC--CCCCEEEEE-EEECCC
 T ss pred
 No 7
                                                              Pub Med
>419d_A Protease; PKD domain, cell adhesion; 1.10A {Vibrio cholerae}
 Probab=88.03 E-value=0.4 Score=30.77 Aligned_cols=29 Identities=28% Similarity=0.484 Sum_probs=0.0
                     ccCceEEEEEEEEcccCCcccCCCCeEE
 Q ss_pred
 Q Thu_Apr_23_00:
                   68 FTTGGDYILSLVSIKDSTGCVVGLSQPDAKI
                                                     98 (111)
 Q Consensus
                   68 ~~~GG~y~v~L~sV~D~~GC~~~L~~~v~I
                                                     98 (111)
                     +..-|.|.|+|+|+|..||............|.|
 T Consensus
                   56 y~~~G~Y~VtLt-Vtd~~G~~~t~t~-~I~V
                                                     84 (88)
                   56 YTKAGSYSVTLT-VTDDKGDSDTHQQ-TIKV
 T 419d A
                                                     84 (88)
 T ss_dssp
                     CSSCEEEEEE-EEETTSCEEEEE-EEE
 T ss_pred
                     CCCCeEEEEEE-EEeCCCCEEEEEE-EEEE
                               SCOPe PDB
 No 8
                                                                       Pub Med
                                                      S NCBI
□ >1fo0_B Protein (BM3.3 T cell receptor beta-chain); class I MHC, H-2KB, TCR-PMHC complex, immune system; 2.50A
 {Mus musculus} SCOP: b.1.1.1 PDB: inam B* 2013 B* 1kb5 B 1kj2 B*
Probab=85.65 E-value=3.2 Score=25.72 Aligned_cols=75 Identities=9% Similarity=0.067 Sum_probs=0.0
                     ceEEeCC-CcceeccCCCeeeeEEEecCCCcEEEEEEECCCCcEEEEEECCCccc
 Q ss pred
 Q Thu_Apr_23_00:
                   5 SASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKT-----NEYVIKTPVFTTGGD
                                                                                                    73 (111)
                   Q Consensus
                                                                                                    73 (111)
                     +|.+...+.+=.|+++.++=.+.|.++..|--....
                    1 g--v-q-p-----i----i-----i-----i
 T Consensus
                                                                               ~~~~r~~~~~~~~~~~~
                                                                                                    75 (112)
                    1 VTLLEONPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQD--LQKQLQWLFTLRSPGDKEVKSLPGADYLATRVT---DTE
 T 1fo0 B
                                                                                                    75 (112)
                     CCSEEEECSEEECCTTCCEEEEEEESCTTCCEEEEEEEC--TTCCEEEEEEECCSTTCEEEEEEETTEEEEEEEE---TTE
 T ss_dssp
 T ss_pred
                     EEEEEEEECC
 Q ss pred
 Q Thu_Apr_23_00:
                  74 YILSLVSIKDS
                                   84 (111)
                   74 y~v~L~sV~D~
 Q Consensus
                                   84 (111)
                      +.|.|.+|.|+
 T Consensus
                   76 ~~L~I~~v~Ds
                                   86 (112)
                   76 LRLOVANMSOG
 T 1fo0 B
                                  86 (112)
                     EEEEESCCSC
 T ss dssp
                      EEEEEccccC
 T ss pred
                                                      Pub Med
>2yrl A KIAA1837 protein; PKD domain, NPPSFA, national project on protein structural and functional analyses; NMR
 {Homo sapiens}
              E-value=4.4 Score=26.29 Aligned_cols=55 Identities=13% Similarity=0.292 Sum_probs=0.0
                     Q ss pred
 Q Thu Apr_23_00: 25 PVALKGQG-----PFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLVSIKDSTGC 87 (111)
```

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Q Consensus
                 25 \text{ $^{V-1-G------PftL-yeiv---gk----v-i-v-v-i-tp----GG-y-v-L-sV-D---GC}$}
                                                                                   87 (111)
                 T Consensus
                                                                                   83 (102)
                 23 STTLDGSKSSDDQKIISYLWEKTQGPDG----VQLENANSSVATVTGL---QVGTYVFTLT-VKDERNL
 T 2vrl A
                                                                                   83 (102)
                    EEEEECCTTCSSSCBCCCCEEEEESCTT----CEEESTTSSEEEEESC---CSSEEEEEE-EEBTTCC
 T ss dssp
                    EEEEEeEEecCCCceEEEEEEccCCce----eEEccCCCceEEEeCC---CCEEEEEEEE-EEeCCCC
 T ss pred
                              SCOPe PROTEIN DATA RANK
 No 10
                                                                    Pub Med
>1i3g_L Antibody FV fragment; antibiotic; 2.44A {Mus musculus} SCOP: b.1.1.1 PDB: 3iy6_A
Probab=79.34 E-value=7.4 Score=23.37 Aligned_cols=73 Identities=11% Similarity=0.177 Sum_probs=0.0
                    CceEeCC-CcceeccCCCeeeeEEEecCCCcEEEEEEeCCCCcEEEEE
 Q ss pred
 Q Thu_Apr_23_00:
                  4 PSASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGDYIL
                                                                                             76 (111)
                  Q Consensus
                                                                                             76 (111)
                    T Consensus
                                                                                             76 (111)
                  3 KDIVLTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQK--PGQSPKLLIYWASTRHTGVPDRFTGS----GSGTDFTL
 T 1i3a L
                                                                                             76 (111)
                    -CCCEEESCSEEECCTTCCEEEEEEESSCCTTCEEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE---EETTEEEE
 T ss dssp
 T ss_pred
                    ccceeccCCEEEEecCCCceEEEEecc-CCCceEEEEEC--CCCCEEEEEEcccCCCCCCCEEEE----ccCCeEEE
 Q ss_pred
                    EFFER
 Q Thu Apr 23 00:
                 77 SLVSIK
                            82 (111)
                 77 ~L~sV~
 Q Consensus
                            82 (111)
                    .|.+|+
                 77 ~ i~~v~
                            82 (111)
 T Consensus
 T 1i3g L
                 77 TISNVO
                            82 (111)
                    EESSCC
 T ss dssp
 T ss pred
                    EECCCC
 No 11
                                                         Pub Med
>3sd2 A Putative member of DUF3244 protein family; immunoglobulin-like beta-sandwich, structural genomics, JOIN
 for structural genomics; HET: MSE; 1.40A {Bacteroides thetaiotaomicron}
                                                               Similarity=0.116 Sum_probs=0.0
 Probab=79.29 E-value=13 Score=24.87 Aligned_cols=60 Identities=10%
                    eccCCceeeeEEEecCCCcEEEEEEEeCCCCcEEEEEECcccccCEEEeCCCccCCcEEEEEEE
 Q ss_pred
 Q Thu_Apr_23_00:
                 16 LCLGDHSSVPVALKGOGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLVS
                                                                                80 (111)
                 16 \ \text{``C-g--}v-v-\text{V-l-G--}PftL-yeiv----gk-----v--i--tp----GG-y-v-L-s
 Q Consensus
                                                                                80 (111)
                 30 ATLSN--ILNVSFGRAKD-YATTTVTNKATGETVHSKT-YHNTSTVMTDMSSCE-KGEYTTHTIL
 T 3sd2 A
                                                                                89 (101)
                    EEETT--EEEEEESSCCS-CEEEEEEETTTCCEEEEEE-ESSCSEEEEECTTSC-SEEEEEEEE
 T ss dssp
                    EEEcC--EEEEEcCcCC-CEEEEEECCCCcEEEEEe-cCCCcEEEEEEcCCcc-CceEEEEEE
 T ss pred
                              SCOPe PROTEIN DATA BANK
 No 12
                                                   NCBI
                                                                    Pub Med
->1sq2_N Novel antigen receptor; immunoglobulin fold, protein-protein complex, hydrolase-IMMU complex; 1.45A
 {Ginglymostoma cirratum} SCOP: b.1.1.1 PDB: 1t6v _N
 Probab=78.80 E-value=5.7 Score=24.45 Aligned cols=71 Identities=13% Similarity=0.157 Sum probs=0.0
                    eEEeCC-CaceeacCCCeeeeEEEecC--CCGEEEEEEECCCCGEEEEEEeCacaaacEEEeCCCaaCCaeEEEEEEEEE
 Q ss_pred
 Q Thu Apr 23 00:
                  6 ASLKI,H-HDI,KI,CI,GDHSSVPVAI,KGO--GPFTI,TYDITETFSSKRKTFETKETKTNEYVTKTPVFTTGGDYTI,SI,VSTK
                                                                                             82 (111)
                  Q Consensus
                                                                                             82 (111)
                    T Consensus
                                                                                             74 (113)
 T 1sq2_N
                  1 ARVDOTPRSVTKETGESLTINCVLRDASYALGSTCWYRKK--SGEGNEESIS--KGGRYVETVN--SGSKSFSLRINDLT
                                                                                             74 (113)
 T ss dssp
                    -CEEEECSEEECTTCCEEEEEECSCSSCCCCEEEEEE-TTSCCCEECC-CBTTEEEEEE-TTTTEEEEEECSCC
                    CeEEeCCcCEEEeCCCcEEEEEecCCCCCeeEEEEEecC--CCCCceeeee--cCCccEEEEEC--CCCceEEEEECCCC
 T ss pred
No 13 Pub Med

>3shs_A HOC head outer capsid protein; immunoglobulin-like domain, phage capsid decorative protein, interaction
 with bacteria; 1.95A {Enterobacteria phage RB49}
 Probab=78.18 E-value=13 Score=27.57 Aligned cols=62 Identities=15% Similarity=0.248 Sum probs=0.0
                    CcceeccCCceeeEEEe-cCC---CcEEEEEEECCCCcEEEEEeCcccccEEEeCCCcc--CCceEEEEEEEEccc
 Q ss pred
                 12 HDLKLCLGDHSSVPVALK-GQG---PFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFT--TGGDYILSLVSIKDST
 Q Thu Apr 23 00:
                                                                                             85 (111)
                 12 -----C-g--v-v-V-1--G-----PftL-yeiv----gk-----v-i------I-tp------GG-y-v-L-sV-D--
 Q Consensus
                                                                                             85 (111)
                    +.....+.++... ..|.|.. .+++...
                                                                                             75 (304)
 T 3shs A
                 10 NKRCFLAGDGFTLTATVAGDEPLPSNLTYTWTK----DDOP------HENNTATLTVADATSENAGSYKV---TVODTD
                                                                                             75 (304)
                    SCSSBCTTCCEEEEEEEESSSCCCCEEEEEE.---TTEE-----CSCCSSEEEESSCCGGGCEEEEE---EEETT
 T ss dssp
                    CCGeECCCCCEEEEEEEecCCCCCCCeEEEEEE.---CCEE------CcCCeeEEEEECCCCccCCEEEEE---EEEECC
 T ss_pred
 Q ss pred
                    CC
 Q Thu_Apr_23_00:
                 86 GC
                        87 (111)
 O Consensus
                 86 GC
                        87 (111)
                    76 g~
                        77 (304)
 T Consensus
 T 3shs A
                 76 TM
                        77 (304)
 T ss_dssp
                    TC
 T ss_pred
                    Cc
```

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Pub Med
                                               PDB<sup>N</sup>
>4nkd_B Engineered SCFV light chain; antibody fragment, eympme binding, immune system, immune SYS chaperone
  complex; 3.30A {Mus musculus} PDB: 4nkm _B 4nko _A
 Probab=76.92 E-value=8.5 Score=24.46 Aligned_cols=74 Identities=14% Similarity=0.249 Sum_probs=0.0
                              CCceEEeCC-CcceeccCCCeeeeEEEecCC-----CcEEEEEEEeCCCccEEEEEeCccc-----cccEEEECCCccC
 Q ss pred
 Q Thu Apr 23 00:
                         3 KPSASLKLH-HDLKLCLGDHSSVPVALKGQG----PFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTT
                                                                                                                                            70 (111)
                           O Consensus
                                                                                                                                            70 (111)
                            +..+.|.-.. .++....+....
 T Consensus
                                                                     77 (138)
                           4 YKDIVMTQTPSSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQK--PGQSPKLLIYKVSNRFSGVPDRFSGS----GS
 T 4nkd B
                                                                                                                                            77 (138)
 T ss_dssp
                              --CCCEEESCSCCEECTTCCEEEEEEESSCCCCSSSCCCEEEEEC--TTSCCEEEEETTTEECTTCCTTEECC----CB
 T ss_pred
                              cccceEeeCCCceEecCCCCEEEEeccCccccCCCEEEEEEEC--CCCCcEEEEEECCcCCCCCCCEEEe----cC
 Q ss_pred
                             CCEEEEEEEE
 Q Thu Apr 23 00:
                         71 GGDYILSLVSIK
                                                 82 (111)
                          71 GG~v~v~L~sV~
                                                  82 (111)
 O Consensus
                          .+.+.|.|.+|+
78 ~~~~L~I~~v~
 T Consensus
                                                  89 (138)
 T 4nkd B
                          78 GTDFTLKTSRVE
                                                  89 (138)
 T ss_dssp
                              TTEEEEEESSCC
 T ss pred
                              CCEEEEECCCC
 No 15
                                              SCOPe POBN
                                                                            NCBI
>2jju A Signal regulatory protein beta-1; immunoglobulin domain, immunoglobulin superfamily, immune system,
 transmembrane, paired receptor; 1.19A {Homo sapiens} SCOP: b.1.1.0 PDB: 4cmm A* 2jjv A 2uv3 A* 2jjt A* 2jjs A*
 Probab=76.77 E-value=6.8 Score=24.62 Aligned_cols=79 Identities=9% Similarity=0.108 Sum_probs=0.0
                              CCceEEeCC-CcceeccCCCeeeeEEEecCC-CcEEEEEEECCCCcEEEEEEeCccccEEEECCCc-cCCceEEEEE
 Q ss pred
                            3 KPSASLKLH-HDLKLCLGDHSSVPVALKGQG-PFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVF-TTGGDYILSLV
 O Thu Apr 23 00:
                                                                                                                                            79 (111)
                           3 -asA-F----C-g--v-v-V-l-G---PftL-yeiv---gk-----v-i-----I-tp-----GG-y-v-L-
                                                                                                                                            79 (111)
 Q Consensus
                              T Consensus
                            79 (127)
                           1 EDELQVIQPEKSVSVAAGESATLRCAMTSLIPVGPIMW-FRGAGAGRELIYNQKEGHFPRVTTVSELTKRNNLDFSISIS
 T 2jju A
                                                                                                                                            79 (127)
                              --CCEECCCSEEEEETTSCEEECCESCCSCCEEE-EECSSTTCEEEEESSSSCCTTEEEC-----CCBCCEEC
 T ss_dssp
                              T ss_pred
 Q ss_pred
                             EEE
 Q Thu Apr 23 00:
                          80 SIK
                                      82 (111)
 O Consensus
                          80 sV~
                                      82 (111)
                              + | +
                          80 ~v~
 T Consensus
                                      82 (127)
                          80 NIT
                                      82 (127)
 T 2jju A
 T ss_dssp
                              SCC
 T ss pred
                              CCC
                                              SCOPe
                                                                             S NCBI
                                                                                                    Pub Med
>2ywz A NEW antigen receptor variable domain; IG VNAR, immune system; 2.21A {Orectolobus maculatus} SCOP: b.1.1.1
 PDB: 2ywy A
 Probab=76.02 E-value=12 Score=22.66 Aligned cols=71 Identities=13% Similarity=0.156 Sum probs=0.0
                              PEROCC-Consecucional de la consecución de la con
 Q ss_pred
 Q Thu Apr 23 00:
                           6 ASLKLH-HDLKLCLGDHSSVPVALKGO--GPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLVSIK
                                                                                                                                            82 (111)
                           6 A~F~~~~C~g~~v~v~l~G~~~~PftL~yeiv~~~gk~~~~v~i~~~~I~tp~~~GG~y~v~L~sv~
 O Consensus
                                                                                                                                            82 (111)
                           1 AWVDQTPRTITKETGESLTIKCVLKDHSCGLSSTTWYRTQ--LGSTNEKTIS--IGGRYDETVD--KGSKSFSLRISDLR
 T 2ywz A
                                                                                                                                            74 (111)
 T ss_dssp
                              CEEEEECSEEECTTCCEEEEEEEESCSSCCCEEEEEEE--TTCCCCEECC--SBTTEEEEEE--TTTEEEEEECSCC
                              CeeecCCccEEEcCCCcEEEEeeCCCCCccEEEEEeec--CCCCeeeeee--cCCceEEEec--CCCCEEEEEECCCC
 T ss pred
                                           SCOPe PROTEIN DATA BANK
                                  Pub Med
>ldlf_L Anti-dansyl immunoglobulin IGG2A(S); FV fragment; 1.45A {Mus musculus} SCOP: b.1.1.1 PDB: lwz1_L* 2dlf_L lmaj_A lmak_A lktr_L 2cju_L* 2uud_K* ldsf_L 3nn8_B ln4x_L lbfv_L* lcfv_L* 2bfv_L* lwt5_C 4lci_L Probab=74.70 E-value=12 Score=22.39 Aligned_cols=72 Identities=13% Similarity=0.253 Sum_probs=0.0
                              Q ss pred
 Q Thu Apr 23 00:
                           5 SASLKLH-HDLKLCLGDHSSVPVALKGQG----PFTLTYDIIETFSSKRKTFEIKEIK----TNEYVIKTPVFTTGG
                                                                                                                                            72 (111)
                           5 sA~F~~~~C~g~~v~v~V~l~G~~~----PftL~yeiv~~~gk~~~~v~i~-----I~tp~~~~GG
 O Consensus
                                                                                                                                            72 (111)
                              .+.|....+.+=.|++++++-.+.|.+ +..+.|--....++....+....
                            1 ---v--p-----G--v-L-C---
 T Consensus
                                                                                                                                            74 (113)
                           1 DVVMTQTPLSLPVSLGNQASISCRSSQSLVHSNGNTYLHWYLQK--PGQSPKLLIYKVSNRFSGVPDRFSGS----GSGT
 T 1dlf L
                                                                                                                                            74 (113)
 T ss_dssp
                              CCCEEECSEEECTTCCEEEEEEESSCCBCTTSCBCEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETT
                              CceeecCCceEEeecCCCCEEEEeecccccCCCcEEEEEEEC--CCCCEEEEEEEeCCcCCCCCEEEe----ecCC
 T ss_pred
 Q ss pred
                              eEEEEEEEE
 Q Thu_Apr_23_00:
                          73 DYILSLVSIK
                                               82 (111)
 Q Consensus
                          73 ~y~v~L~sV~
                                               82 (111)
                              .+.|.|.+|+
```

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T Consensus
                 75 ~~~L~I~~v~
                              84 (113)
                75 DETLKISRVE
 T 1dlf L
                              84 (113)
 T ss dssp
                   EEEEECSCC
 T ss pred
                   eEEEECCCC
                                       PDB
 No 18
                                                                Pub Med
                             SCOPe
>4hgm A Shark V-NAR; IG-fold, human albumin, V-NAR, immune system; 2.34A (Squalus acanthias) SCOP: b.1.1.1
 Probab=74.63 E-value=8.4 Score=23.91 Aligned_cols=71 Identities=11% Similarity=0.212 Sum_probs=0.0
                   Q Thu_Apr_23_00:
                 6 ASLKLH-HDLKLCLGDHSSVPVALKGOG--PFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLVSIK
                                                                                         82 (111)
                 6 A~F~~~~C~g~~v~v~l~G~~~PftL~yeiv~~~gk~~~~v~i~~~~I~tp~~~GG~y~v~L~sv~
 Q Consensus
                                                                                         82 (111)
                 T Consensus
                                                                                         74 (112)
 T 4hgm_A
                 1 TRVDQSPSSLSASVGDRVTITCVLTDTSYPLYSTYWYQQK--PGSSNKEQISIS--GRYSESVN--KGTKSFTLTISSLQ
                                                                                         74 (112)
 T ss_dssp
                   CERRECSERECTTCCEREERERSCSSCREERERERC--TTCSCCERCCSC--TTRERERE--TTTTRERERESSCC
                   CeeEeCCCcEEEEcCCCCEEEEEccCCCCccEEEEECC--CCCCceEEEEC--CccEEEECc--CCCCEEEEEECCCCC
 T ss_pred
                            SCOPe PROTEIN DATA BANK
                                                 NCBI
                                                          Pub Med
□ >3u6r_L Antibody 1:7 (light chain); IG-like domain, neutralizing single chain FV, immune system; 2.67A {Homo
 sapiens | SCOP: b.1.1.0
 Probab=74.12 E-value=10 Score=23.87 Aligned_cols=71 Identities=14% Similarity=0.214 Sum_probs=0.0
                   eEEeCC-CcceeccCCCeeeeEEEecCCCcEEEEEEeCccc-----ccccEEEeEeCcCccCceEEEEE
 Q ss pred
                 6 ASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEI-----KTNEYVIKTPVFTTGGDYILSL
6 A-F-----C-g--v-v-V-l-G--PftL-yeiv----gk-----v--i------I-tp----GG-y-v-L
 Q Thu_Apr_23_00:
                                                                                         78 (111)
 O Consensus
                                                                                         78 (111)
                   +.|....+.+-.|+++.+.-.+.|.++..+.|.--...|+....+...
                                                                  ...+|.+.
                                                                             ..++.+.|.|
                  1 P-i---p-----r---r----r-----r-----
 T Consensus
                                                                                         74 (143)
                 1 \ \texttt{AELTQSPATLSLSPGERATLSCRASQSVNKYLAWYQQK} - \texttt{PGQAPRLLIYDASNRATGIPARFSGS} - - - \texttt{GSGTDFTLTI}
 T 3u6r L
                                                                                         74 (143)
 T ss_dssp
                   CCEEECSEEECTTCCEEEEEESSCCTTCEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETTEEEEE
 T ss pred
                   CccCcCceeeeccCcceeeeeecccccceeeeee
                   EEEE
 Q ss_pred
 Q Thu_Apr_23_00:
                79 VSIK
                         82 (111)
 Q Consensus
                 79 ~sV~
                         82 (111)
                   .+|+
                 75 ~~v~
                         78 (143)
 T Consensus
 T 3u6r_L
                 75 SNLE
                         78 (143)
 T ss dssp
                   CSCC
 T ss_pred
                   CCCC
 No 20
                             SCOPe
                                                                 Pub Med
                                                 S NCBI
🗌 >2coq_A NEW antigen receptor variable domain; IG VNAR, natural TYPE2, immune system; 2.10A {Orectolobus
 maculatus | SCOP: b.1.1.1
 Probab=74.12 E-value=11 Score=22.50 Aligned cols=71 Identities=10% Similarity=0.076 Sum probs=0.0
 Q ss pred
                   eEEeCC-CcceeccCCCeeeeEEEecCC--CcEEEEEEECCCCcEEEEEECCCccCceEEEEEEE
 Q Thu_Apr_23_00:
                  82 (111)
                 Q Consensus
                                                                                         82 (111)
 T Consensus
                                                                                         74 (108)
                  1 ARVDQTPRIATKETGESLTINCVLRDTACALDSTNWYRTK--LGSTKEQTIS--IGGRYSETVD--EGSNSASLTIRDLR
                                                                                         74 (108)
 T 2coq A
                   T ss dssp
 T ss_pred
                             SCOPe PROTEIN DATA BANK
 No 21
                                                 NCBI
                                                          Pub Med
🗌 >3bik_B Programmed cell death protein 1; CO-stimulation, receptor-ligand complex, immunoglobulin-like sandwich, T
 cell, B cell, programmed death; 2.65A {Mus musculus} SCOP: b.1.1.1
 Probab=73.13 E-value=16 Score=22.69 Aligned_cols=77 Identities=13% Similarity=0.242 Sum_probs=0.0
 Q ss pred
                   CCCceEEeCC-CcceeccCCCeeeeEEEecCC-CcEEEEEEeCCCCcEEEEEe------CcccccEEEEeCCCccCCc
 Q Thu_Apr_23_00:
                 2\ \ V\texttt{KPSASLKLH-HDLKLCLGDHSSVPVALKGQG-PFTLTYDIIETFSSKRKTFEI------KEIKTNEYVIKTPVFTTGG}
                                                                                         72 (111)
 Q Consensus
                 72 (111)
                   T Consensus
                                                                                         81 (134)
 T 3bik B
                 6 NGPWRSLTFYPAWLTVSEGANATFTCSLSNWSEDLMLNWNRLS--PSNQTEKQAAFSNGLSQPVQDARFQIIQLP--NRH
                                                                                         81 (134)
                   ----CCEEEECSEEEETTSCEEEEEEESSCCTTCEEEEEEEC--TTCCEEEEEEEETTEEEESSCTTEEEEECT--TSS
 T ss dssp
 T ss_pred
                   CCccceEEECCccEEEECCCCCEEEEEEec--CCCCceEEEEEEccCCccccCcEEEEEec--CCC
                   eeeeeeee
 Q ss_pred
 Q Thu_Apr_23_00:
                 73 DYILSLVSIK
                              82 (111)
                 73 ~y~v~L~sV~
 Q Consensus
                              82 (111)
                   .+.|.|.+|+
                 82 ~~~L~I~~v~
 T Consensus
                              91 (134)
 T 3bik B
                 82 DFHMNILDTR
                              91 (134)
 T ss_dssp
                   EEEEECSCC
 T ss_pred
                   eeeeeeccc
```

```
PDB
                                                                                                                                    Pub Med
                                                           SCOPe
>2dia A Filamin-B; beta-sandwich, immunoglobulin-like fold, filamin domain, structural genomics, NPPSFA; NMR
  {Homo sapiens} SCOP: b.1.18.10
  Probab=72.65 E-value=20 Score=23.50 Aligned_cols=75 Identities=17% Similarity=0.212 Sum_probs=0.0
                                       CCGERECCCCGGEGCCCCGGERERECCCCGGEREREECCCCGGREERECCGGGCGGEREREE
  Q ss pred
  Q Thu Apr 23 00:
                                   3 KPSASLKLHHDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV
                                                                                                                                                                                79 (111)
                                   79 (111)
  O Consensus
                                      85 (113)
                                  11 \ \text{$\sim$k$} \sim \text{$\sim$G-GL} \sim \text{$\sim$vg} \sim \text{$\sim$F-V} \sim \text{$\sim$dG} \sim \text{$1$} \sim \text{$v$} \sim \text{$\sim$-g} \sim \text{$\sim$v$} \sim \text{$\sim$v$} \sim \text{$\sim$dGty} \sim \text{$v$} \sim \text{$\sim$-G-Y} \sim \text{$\sim$v$} \sim \text{$\sim$-g} \sim \text{$
  T Consensus
  T 2dia A
                                  11 PSKVVASGPGLEHGKVGEAGLLSVDCSEAGPGALGLEAVSD-SGTKAEVSIONNKDGTYAVTYVPLTA-GMYTLTMK
                                                                                                                                                                                85 (113)
                                       GGGEEESGGGTCEETTCCCCEEEEESSCCSCCEEEEEET-TTEECEEEEEECTTSEEEEEEECSSC-EEEEEEE
  T ss dssp
                                       ccceEEECCCCCcccCCcEEEEEECcCCCcEEEEEECC-CCCEEEEEEECCCCEEEEEEE
  T ss pred
  No 23
                                                                               PDB
                                                                                                                                  PubMed
                                                           SCOPe
>4aj0 A Germinal LINE lambda 3 3RCW variant; immune system, amyloidosis; 1.70A (Homo sapiens) SCOP: b.1.1.1 PDB:
    4aix _A 4aiz _A* 4aiz _B*
  Probab=70.91 E-value=12 Score=22.31 Aligned cols=72 Identities=11% Similarity=0.115 Sum probs=0.0
                                       Q ss_pred
  Q Thu_Apr_23_00:
                                   5 SASLKLHHDLKLCLGDHSSVPVALKGOGPFTLTYDIIETFSSKRKTFEIKEIK----TNEYVIKTPVFTTGGDYILSL
                                                                                                                                                                                     78 (111)
                                   5 \ \text{sA-F---------} \text{C-g--v-v-V-l-G--PftL-yeiv----gk------v--i------------} \text{I-tp-----GG-y-v-L} \\
  Q Consensus
                                                                                                                                                                                     78 (111)
                                        .+.|..+..+..=.|+++.++..+.|.++..+.|.--.
                                                                                                                                                              ..++.+.|.|
                                                                                                                                                                                     74 (107)
  T Consensus
                                       T 4aj0_A
                                    1 SYELTOPPSVSVSPGOTASITCSGDKLGDKYAYWYOOK--PGOSPVLVIYODSKRPSGIPERFSGS----NSGNTATLTI
                                                                                                                                                                                     74 (107)
                                       -CCBBCCSEEEECTTSCEEEEEECTTGGGSEEEEEEC-TTSCCEEEEBTTTBCCTTCCTTEEEE----EETTEEEEE
  T ss_dssp
                                       CCceEcCCeEeecCCCCCEEEEeCCCCCCceEEEEEC--CCCCCEEEEEECCccCCCCCCCEEEE----ecCCeEEEE
  T ss pred
                                       EEEE
  Q ss pred
  Q Thu_Apr_23_00:
                                 79 VSIK
                                                   82 (111)
  O Consensus
                                  79 ~sV~
                                                   82 (111)
                                       .+|+
                                  75 ~~v~
  T Consensus
  T 4aj0 A
                                  75 SGTQ
                                                   78 (107)
  T ss_dssp
                                       SSCC
  T ss_pred
                                       CCCC
                                                         SCOPe PDB<sup>N</sup>
                                                                                                   S NCBI
>2d7t_L Anti polyhydroxybutyrate antibody FV, light chain; plastic, immune system; 1.70A {Homo sapiens} SCOP:
  b.1.1.1
  Probab=70.55 E-value=14 Score=22.74 Aligned_cols=72 Identities=15% Similarity=0.222 Sum_probs=0.0
  Q ss pred
                                       ceEEeCC-CcceeccCCCeeeeEEEecCCCcEEEEEEeCCCccEEEEE
  Q Thu_Apr_23_00:
                                   5 SASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGDYILS
                                                                                                                                                                                     77 (111)
  O Consensus
                                   77 (111)
                                       .+.|.....+.+=.|+++.++-.+.|.++..+.|.-...
                                                                                                                                       ..+|.+.
                                                ---p----v--Ġ--v-L-C---
                                                                                       ~~~~v~₩~k~~__~~
  T Consensus
                                                                                                                                                                                     74 (116)
  T 2d7t L
                                    1 \  \  \mathsf{DIVMTQSPSSLSASVGDRVTITCRASQNINNYLHWYQHE--PGKAPKLLIYAASNLQGGVTSRFSGS----GSGTDFTLT}
                                                                                                                                                                                     74 (116)
  T ss_dssp
                                       CCCEEECSEEECTTCCEEEEEESSCCTTCEEEEEC--TTSCCEEEEETTTECCTTSCTTEEEE----EETTEEEEE
  T ss_pred
                                       CCceEecCCeEEEeCCCCceEEEEECC--CCCceEEEEEEC-----eCCCEEEE
  Q ss pred
                                       EEEEE
  Q Thu_Apr_23_00:
                                 78 LVSIK
                                                     82 (111)
  O Consensus
                                  78 L~sV~
                                                     82 (111)
                                       1.+|+
  T Consensus
                                  75 I~~v~
                                                     79 (116)
                                  75 ISTLQ
  T 2d7t L
                                                    79 (116)
  T ss dssp
                                       ESSCC
  T ss pred
                                       ECCCC
                                                           PDB<sup>IN</sup>
PROTEIN DATA BANK
  No 25
                                                                              NCBI Pub Med
>3moq_A NEW antigen receptor variable domain, P3(40) PEPT amyloid beta A4 protein; AB-ignar, AB-12Y-2,
                                                                                                                                                                                    lver _A
  glycoprotein, membran protease inhibitor; 2.05A {Orectolobus maculatus} PDB: 228w _C 228v _C 1ves _A
  Probab=69.56 E-value=21 Score=22.57 Aligned cols=71 Identities=10% Similarity=.087 Sum probs=0.0
                                       eEEeCC-CcceeccCCCeeeeEEEecC--CCcEEEEEEEECCCCcCEEEEEEE
  Q ss pred
  Q Thu Apr 23 00:
                                   6 ASLKLH-HDLKLCLGDHSSVPVALKGQ--GPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLVSIK
6 A-F----C-g--v-v-V-l-G---PftL-yeiv---gk----v-i-----I-tp----GG-y-v-L-sV-
                                                                                                                                                                                     82 (111)
  Q Consensus
                                                                                                                                                                                     82 (111)
                                    T Consensus
                                                                                                                                                                                     74 (126)
                                   1 AWVDQTPRTATKETGESLTINCVLRDASFELKDTGWYRTK--LGSTNEQSIS--IGGRYVETV--NKGSKSFSLRISDLR
  T 3moq A
                                                                                                                                                                                     74 (126)
                                       CEEEECSEEEEETTCCEEEEEEEESCSSCCCEEEEEEEE--TTCCCCEECC--CBTTEEEEE--ETTTTEEEEEECSCC
  T ss dssp
                                       CEEECCCCEEEEcCCCCEEEEeecCCCCCCCEEEEEEC--CCCCEEEEe--cCCCCEEEEECCCC
  T ss pred
                                                          PDB NCBI Pub Med
  No 26
🗌 >4unu_A MCG, IG lambda chain V-II region MGC; immune system, bence-jones, light chains, immunoglobulin; HET: 15P;
  0.95A {Homo sapiens} PDB: 4unv A 4unt A 4y5y B* 2a9m L 2a9n L*
Probab=69.29 E-value=17 Score=21.61 Aligned cols=73 Identities=11% Similarity=0.145 Sum probs=0.0
```

```
Q ss pred
                                    CceEEeCCCcceeccCCCeeeeEEEecCCC---cEEEEEEEeCCCCcEEEEEeCccc------cccEEEeCCCccCCceE
 Q Thu_Apr_23_00:
                                 4 PSASLKLHHDLKLCLGDHSSVPVALKGOGP---FTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGDY
                                                                                                                                                                       74 (111)
                                 O Consensus
                                                                                                                                                                       74 (111)
                                 74 (111)
                                 1 \  \, \texttt{GQSALTQPPSASGSLGQSVTISCTGTSSDVGGYNYVSWYQQH--AGKAPKVIIYEVNKRPSGVPDRFSGSK----SGNTA} \\
 T 4unu A
                                                                                                                                                                       74 (111)
 T ss_dssp
                                    --CCBBCCSEEEECTTSCEEEEEECCTTTTTTCSCEEEEEEC--TTSCCEEEEBTTTBCCTTCCTTEEEEE---ETTEE
                                    CCcceeccCeEeeeCCCccEEEEEECccccCcceEEEEEC--CCCCcEEEEEEecccCCCCCccEEEEe----CCCEE
 T ss_pred
 Q ss_pred
                                    EEEEEEE
                                                     82 (111)
  Q Thu_Apr_23_00:
                               75 ILSLVSIK
 O Consensus
                               75 ~v~L~sV~
                                                     82 (111)
                                    . | . | . + | +
                               75 ~L~I~~v~
 T Consensus
                                                     82 (111)
 T 4unu A
                               75 SLTVSGLO
                                                     82 (111)
 T ss dssp
                                    EEEECSCC
 T ss_pred
                                    EEEECCCC
                                                       SCOPe PROTEIN DATA BANK
 No 27
                                                                                           NCBI
                                                                                                                         Pub Med
3bp6_A Programmed cell death protein 1; PD-1, PD-L2, complex, costimulation, glycoprotein, immunoglo domain,
 membrane, transmembrane, receptor; 1.60A {Mus musculus} SCOP: b.1.1.1 PDB: 3rnk_A 3sbw_A 3bp5_A 1npu_A 3rnq_A Probab=69.27 E-value=18 Score=21.70 Aligned cols=72 Identities=13% Similarity=0.257 Sum probs=0.0
                                    EEECC-CcceeccCCCeeeeEEEecCC-CcEEEEEEECCCCcEEEEEE
 Q ss pred
 Q Thu Apr 23 00:
                                 7 SLKLH-HDLKLCLGDHSSVPVALKGQG-PFTLTYDIIETFSSKRKTFEI-----KEIKTNEYVIKTPVFTTGGDYILS
                                                                                                                                                                       77 (111)
 O Consensus
                                 7 \  \  \, \text{``F`} - - - - - - \text{`C'} - \text{`g'} - \text{`V'} - \text{V'} - \text{`G'} - \text{`PftL'} y \\ \text{eiv} - - - \text{`gk'} - - - - \text{`i} - - - - \text{`i} - - - - \text{`I} \\ \text{`tp} - - - \text{`GG'} y - \text{`V'} - \text{`J'} - \text{`gk'} - \text{`J'} - \text{
                                                                                                                                                                       77 (111)
                                 T Consensus
                                                                                                                                                                       76 (117)
 T 3bp6_A
                                 1 \ \mathtt{SLTFYPAWLTVSEGANATFTCSLSNWSEDLMLNWNRLS-PSNQTEKQAAFSNGLSQPVQDARFQIIQLP--NRHDFHMN}
                                                                                                                                                                       76 (117)
 T ss_dssp
                                    \tt CEEEECSEEEECTTCCEEEEEEEESSCCTTCEEEEEEEC--TTCCEEEEEEEETTEEEESSCTTEEEEECT--TSSEEEEE
 T ss pred
                                    CGEECCCGEECCCCCEEEEEecCCCCCCGEEEEEEeC--CCCCCEEEEEEeCCCGCGGGGCGCEEEEECC--CCCEEEEE
 Q ss pred
                                    EFFE
 Q Thu_Apr_23_00:
                              78 LVSIK
                                                 82 (111)
 Q Consensus
                               78 L~sV~
                                                 82 (111)
                                    |.+|+
 T Consensus
                                77 I~~v~
                                                 81 (117)
 T 3bp6 A
                               77 ILDTR
                                                 81 (117)
 T ss dssp
                                    ESSCC
  T ss_pred
 No 28
                                                       SCOPe PROTEIN DATA BANK
                                                                                                                          Pub Med
                           ≡≡
□ >3rgh_A Filamin-A; cell adhesion, cytoskeleton-complex, disease mutation, immun like, cytoskeleton,
  actin-binding, cell junction, shape; HET: CME; 2.44A {Homo sapiens} SCOP: b.1.18.0
 Probab=68.99 E-value=22 Score=22.58 Aligned_cols=75 Identities=13% Similarity=0.120 Sum_probs=0.0
                                    \texttt{CCceEEeCCCcceeccCCCeeeeEEEecCCCcEEEEEEeCCCCcEEEEEE}
 Q ss pred
 Q Thu_Apr_23_00:
                                 {\tt 3~KPSASLKLHHDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV}
                                                                                                                                                                   79 (111)
                                 Q Consensus
                                                                                                                                                                   79 (111)
                                 ++....++....+.|+++.+.|...+.=|+-+|..+.|.+..+.+..|.+.-...|.|.|.|.+.
8 ~k~~~G-G1~~~g~~~F-V~~daG~~l~v-i~~~g~~~v-d~dGty~v-Y-p~~G-y-i~V~
 T Consensus
                                                                                                                                                                   82 (100)
                                 8 ASKVKCSGPGLERATAGEVGOFOVDCSSAGSAELTIEICSE-AGLPAEVYIODHGDGTHTITYIPLCPG-AYTVTIK
                                                                                                                                                                   82 (100)
 T 3rgh A
                                    GGGCEESGGGTEETTSCEEEEEECTTSCSCCEEEEEECT-TSCBCEEEEEECSSSEEEEEECCSSE-EEEEEE
 T ss_dssp
 T ss_pred
                                    SCOPe POB PROTEIN DATA BANK
 No. 29
                                                                                           NCBI
                                                                                                                       Pub Med
->1jhl_L IGG1-kappa D11.15 FV (light chain); complex(antibody-antigen); 2.40A (Mus musculus) SCOP: b.1.1.1
  Probab=68.60 E-value=18 Score=21.38 Aligned_cols=72 Identities=14% Similarity=0.152 Sum_probs=0.0
                                    ceEecC-CcceeccCCceeeeEEecCCCcEEEEEEeCcCccEEEEEecCcc------cccEEEecCCccCceEEEE
 Q ss pred
 Q Thu Apr 23 00:
                                 5 SASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEI-----KTNEYVIKTPVFTTGGDYILS
                                                                                                                                                                       77 (111)
                                 5 sA~F~~~~C~g~~v~V~l~G~~PftL~yeiv~~~~gk~~~~v~i-----I~tp~~~~GG~y~v~
 Q Consensus
                                                                                                                                                                       77 (111)
                                 74 (108)
 T Consensus
                                 1 DIELTOSPSYLVASPGETITINCRASKSISKSLAWYOEK--PGKTNNLLIYSGSTLOSGIPSRFSGS----GSGTDFTLT
 T 1jhl L
                                                                                                                                                                       74 (108)
                                    CCCEEECSEEECTTSCEEEEEEESSCCTTCEEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE---ESSEEEEE
 T ss dssp
                                    CCEEEecCCeEEEecCCCCeEEEeecCCCcceEEEEEEC--CCCCcEEEEEECCccCcccCcEEEE----cCCCEEEEE
 T ss pred
 Q ss_pred
                                    EFFER
                               78 LVSIK
 Q Thu Apr 23 00:
                                                 82 (111)
 O Consensus
                               78 L~sV~
                                                 82 (111)
                                    1.+|+
 T Consensus
                               75 ISSLE
 T 1jhl L
                                                 79 (108)
 T ss_dssp
                                    ECSCC
 T ss_pred
                                    ECCCC
                                                    SCOPe PDB<sup>N</sup>
PROTEIN DATA BANK
                                                                                           NCBI (1)
                                                                                                                       Pub Med
>1i8k A Epidermal growth factor receptor antibody MRISCFV light chain; antibody-peptide complex, immunoglobulin
```

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fold, type II' beta turn., immune system; 1.80A {Mus musculus} SCOP: b.1.1.1 PDB: 1i8i _A
Probab=67.56 E-value=17 Score=21.45 Aligned cols=72 Identities=13% Similarity=0.198 Sum probs=0.0
                 ceEecC-CcceeccCCCeeeeEEEecCCCcEEEEEEeCcc-----cccEEEecCCCccEEEE
0 ss pred
 Q Thu Apr 23 00:
                5 SASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEI-----KTNEYVIKTPVFTTGGDYILS
                                                                                 77 (111)
                Q Consensus
                                                                                 77 (111)
                T Consensus
                                                                                 74 (107)
                1 DIELTQSPASLSVATGEKVTIRCMTSTDIDDDMNWYQQK--PGEPPKFLISEGNTLRPGVPSRFSSS----GTGTDFVFT
T 1i8k A
                                                                                 74 (107)
                 CCCEEECSEECCTTCCEEEEEEESSCCTTCEEEEEEC--TTSCCEEEEETTTEECTTSCTTEEEE----EETTEEEEE
T ss dssp
                 CceeEccCCcEEEEeccCCCCceEEEEec---CCCCCEEEEEECCccCCCCCEEEE----cCCCEEEEE
T ss_pred
                 EEEEE
Q ss pred
Q Thu Apr 23 00: 78 LVSIK
                       82 (111)
               78 L~sV~
                       82 (111)
O Consensus
                 |.+|+
T Consensus
               75 I~~v~
                        79 (107)
T 1i8k A
               75 IENTL
                       79 (107)
T ss_dssp
                 ESSCC
T ss pred
                 ECCCC
                          SCOPe PDB"
No 31
>1qfw M FV, antibody (anti beta subunit) (light chain); glycoprotein hormone; HET: NAG; 3.50A {Mus musculus}
 SCOP: b.1.1.1
 Probab=67.50 E-value=18 Score=21.37 Aligned_cols=59 Identities=8% Similarity=0.179 Sum probs=0.0
                 0 ss pred
Q Thu Apr 23 00:
              18 LGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGDYILSLVSIK
                                                                          82 (111)
O Consensus
               18 ~g~~v~v~V~l~G~~PftL~yeiv~~~~gk~~~~~v~~i~~~~~~I~tp~~~~GG~y~v~L~sV~
                                                                          82 (111)
                 .|+++.+-.+.|.++..+.|.--...|+.....
T Consensus
               15 -G--v-L-C-----v-W-----
                                        79 (108)
               15 VGERVTLSCKASETVDSFVSWYOOK--PEOSPKLLIFGASNRFSGVPDRFTGS----GSATDFTLTISSVO
T 1qfw_M
                                                                          79 (108)
                 TTCCEEEEEESSCCCSCEEEEEC--TTSCCEEEECSSSCBCTTCCTTEECC----BCSSEEEEEESSCC
T ss_dssp
T ss pred
                 CCCCEEEEEeCCCCCccEEEEEEC--CCCCcEEEEEecCccCCCCCCEEEE----ecCCEEEEEECCCC
                          SCOPe PDB
No 32
                                                           Pub Med
□ >3r8b_ G5-8, enterotoxin type B; immunoglobulin-like, OB-fold, toxin-immune system complex; 2.95A {Rattus
norvegicus} SCOP: b.1.1.1
 Probab=67.05 E-value=21 Score=21.77 Aligned_cols=74 Identities=8% Similarity=0.078 Sum_probs=0.0
                 Q ss pred
O Thu Apr 23 00:
              4 PSASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGD
                                                                                 73 (111)
                Q Consensus
                                                                                 73 (111)
                 +.+.|....+..=.|+++.++-.+.|.++..+.|.-..
T Consensus
                78 (125)
                4 LEAAVTQSPRNKVAVTGEKVTLSCKQTNSYFNNMYWYRQD-TGHELRLIFMSHGIRNVEKGDIPDGYKASRP---SQEN
T 3r8b B
                                                                                 78 (125)
                 -CCEEEEECSEEEEETTCCEEEEEEEECCCSEEEEEEEC--TTSCEEEEEEESSTTCCEECSSCTTCEEEEE---ETTE
T ss dssp
                 T ss_pred
Q ss_pred
                 EEEEEEEE
Q Thu_Apr_23_00:
               74 YILSLVSIK
                          82 (111)
Q Consensus
               74 y~v~L~sV~
                          82 (111)
                 +.|.|.+|+
               79 ~~L~İ~~v
T Consensus
                           87 (125)
               79 FSLILELAT
T 3r8b B
                          87 (125)
T ss_dssp
                 EEEEETTCC
T ss_pred
                 EEEEEccCC
                          SCOPe PROTEIN DATA BANK
                                            S NCBI
>2e27_L Anti-ciguatoxin antibody, light chain; immunoglobulin fold, immune system; HET: ABO; 1.70A {Mus musculus}
Probab=66.30 E-value=19 Score=22.24 Aligned_cols=74 Identities=12% Similarity=0.177 Sum_probs=0.0
                 {\tt 3~KPSASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEI-----KTNEYVIKTPVFTTGGDYI}\\
Q Thu_Apr_23_00:
                                                                                 75 (111)
                O Consensus
                                                                                 75 (111)
                                                                                 74 (119)
T 2e27 L
                1 MADIQMTQSPSSLSASLGGKVTITCKANQDIKKKIAWYQHK--PGKGPRLLIYYTSTLKSGISSRFSGS----GSGRDYS
                                                                                 74 (119)
T ss dssp
                 ---CCEEECSEEEEETTCCEEEEEEESSCCTTCEEEEEC--TTSCCEEEETTTEECTTSCTTEEE----EETTEEE
                 T ss pred
                 EEEEEEE
Q ss_pred
 Q Thu_Apr_23_00:
               76 LSLVSIK
                         82 (111)
 Q Consensus
               76 v~L~sV~
                         82 (111)
                 |.|.+|+
               75 L~I~~v~
                         81 (119)
T Consensus
T 2e27_L
               75 FSISNLE
                         81 (119)
T ss dssp
                 EEECSCC
                 EEECCCC
T ss pred
```

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PDB"
                                SCOPe
                                                                     Pub Med
>2yc1 B Single chain antibody fragment 9004G; immune system-toxin complex, scorpion toxin; 1.90A {Homo sapiens}
 SCOP: b.1.1.0 PDB: 2ybr B 4kv5 I 3lh2 L 3h3p L 3lhp L 4llv B
 Probab=66.25 E-value=18 Score=23.65 Aligned_cols=75 Identities=11% Similarity=0.175 Sum_probs=0.0
                     CCCceEEeCC-CcceeecCCCCeeeeEEEecCCCcEEEEEEECCCCcEEEEEECCcc-----cccEEEeCCCccCCeE
 Q ss pred
 Q Thu Apr 23 00:
                   2 VKPSASLKLH-HDLKLCLGDHSSVPVALKGOGPFTLTYDIIETFSSKRKTFEIKEIK----TNEYVIKTPVFTTGGDY
                                                                                                 74 (111)
                   2 --asA-F-----C-g--v-v-V-l-G--PftL-yeiv---gk-----v-i------I-tp----GG-y
 Q Consensus
                                                                                                 74 (111)
                     86 (146)
 T Consensus
                  T 2yc1 B
                                                                                                 86 (146)
                     --CCCCEEECSEEECTTSCEEEEEEESSCCTTCEEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETTEE
 T ss dssp
                     T ss pred
 Q ss_pred
                    EEEEEEE
 Q Thu_Apr_23_00:
                  75 TLSLVSTK
                               82 (111)
 O Consensus
                  75 ~v~L~sV~
                               82 (111)
                     .|.|.+|+
 T Consensus
                  87 ~L~İ~~v
                               94 (146)
                  87 TLTISSLE
 T 2yc1 B
                               94 (146)
 T ss_dssp
                     EFFESSCC
 T ss_pred
                     EEEECCCC
                               SCOPe
                                                                      Pub Med
                                                     S NCBI
>1mgk L Antibody 7E2 FV fragment, light chain; membrane protein, cytochrome C oxidase, high-resolution
structure, immune system; 1.28A {Mus musculus} SCOP: b.1.1.1 PDB: lar1 _D 3ehb _D* 3hb3 _D* lqle _L* 1f61 _L 3iy2 _A ldvf _A lkir _A 1g7i _A 1g7j _A la2y _A lkip _A lkiq _A lvfb _A 1g7h _A la7o _L 1g7l _A 1g7m _A la7n _L ... Probab=66.25 E-value=20 Score=21.90 Aligned_cols=72 Identities=14% Similarity=0.176 Sum_probs=0.0
 Q ss_pred
                     CERECC-CoceeccCCCeeeeRERecCCCCEEEEEEECCCCCEEEEEE
                   5 SASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIK----TNEYVIKTPVFTTGGDYILS
 Q Thu Apr 23 00:
                                                                                                 77 (111)
                   5 sA-F----C-q--v-v-V-l-G--PftL-yeiv----qk-----v--i------I-tp----GG-y-v-
 O Consensus
                                                                                                 77 (111)
                   T Consensus
                                                                                                 74 (120)
                   1 DIELTQTPVSLSASVGETVTITCRASENIYSYLAWYQQK-QGKSPQFLVYNAKTLGEGVPSRFSGS---GSGTOFSLK
 T 1mqk_L
                                                                                                 74 (120)
                     CCCEEECSEEECTTCCEEEEEEESSCCTTCEEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETTEEEEE
 T ss_dssp
                     CcceEecCcEEEEcCCCCEEEEEecCCCCcceEEEEEEC--CCCCCEEEEEECCccCCCcccEEEe----cCCCEEEEE
 T ss pred
 Q ss_pred
                     EFFE
 Q Thu_Apr_23_00:
                  78 LVSIK
                            82 (111)
 O Consensus
                  78 L~sV~
                            82 (111)
                     |.+|+
                  75 I~~v~
                            79 (120)
 T Consensus
                  75 INSLL
 T 1mqk_L
                            79 (120)
 T ss_dssp
                     ESSCC
 T ss_pred
                     ECCCC
                                          PDB"
 No 36
                                SCOPe
                                                                      Pub Med
🗌 >2dmc_A Filamin-B; beta-sandwich, immunoglobulin-like fold, filamin domain, structural genomics, NPPSFA; NMR
 {Homo sapiens} SCOP: b.1.18.10
 Probab=64.37 E-value=4.6 Score=27.04 Aligned cols=62 Identities=18% Similarity=0.199 Sum probs=0.0
                     eeccCCCeeeeEEEecCCCcEEEEEEeCcCccEEEEE
 Q ss pred
 Q Thu_Apr_23_00:
                 15 KLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSL
                                                                                  78 (111)
                  15 ~~C-g~v-v-V-l-G~~PftL-yeiv~~~gk~~~-v~i~~~~~I-tp~~~GG~y-v~L .+..|.++++.|...+..+.=.|+-+|...+|+|+....+.+..+..|.|.--+-.-|+|.|+
 O Consensus
                                                                                  78 (111)
                  26 ---vG----f-v-----g---l-v-v--p--g-----v-d--dGty-v-ytP----G---v-V
 T Consensus
                                                                                  87 (116)
                  26 QVKLGSAADFLLDISETDLSSLTASIKAP-SGRDEPCLLKRLPNNHIGISFIPRE-VGEHLVSI
 T 2dmc A
                     \tt CCCTTSCEEEECCCSCCCSTTBCCEEECT-TSCBCCEEEEEETTTEEEEEECCCS-CEEEEEEC
 T ss dssp
 T ss_pred
                     CCCCCCEEEEEecCCCCCCEEEEEECC-CCCEEEEEECCCCEEEEEEECC-ceeEEEEE
                                          PDB"
 No 37
                                SCOPe
                                                                      Pub Med
🔝 >4kjy_B High-affinity sirpa variant FD6; immunoglobulin fold, immune regulation, N-linked glycosylati plasma
 membrane, immune system; HET: NAG; 1.93A {Homo sapiens} SCOP: b.1.1.0
Probab=64.01 E-value=21 Score=22.51 Aligned_cols=79 Identities=5% Similarity=0.078 Sum_probs=0.0
                     \texttt{CCceEEeCC-CcceeccCCCeeeeEEEecC-CCcEEEEEEeCCCCcEEEEEeCcccccEEEeCCCc-cCCceEEEEEE}
 Q ss_pred
 Q Thu_Apr_23_00:
                   3 KPSASLKLH-HDLKLCLGDHSSVPVALKGQ-GPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVF-TTGGDYILSLV
                                                                                                 79 (111)
                   O Consensus
                                                                                                 79 (111)
                     83 (133)
 T Consensus
                   5 EEEVQIIQPDKSVSVAAGESAILHCTITSLFPVGPIQW-FRGAGPARVLIYNQRQGPFPRVTTISETTRRENMDFSISIS
 T 4kjy_B
                                                                                                 83 (133)
                     \tt CCCCEECCCSEEEECTTSCEEECCEESCCSSCCEEE-EESSSTTCEEEECSSSCCCTTEEESSCTTSTTCCBCCEEEC
 T ss dssp
                     ccceEEEcCCceEEEecCCCCEEEEEECCCCCCEEEE-EECCCCCceEEEEECCCCcccccceeeeccccCCCeEEEEEC
 T ss_pred
 Q ss pred
 Q Thu_Apr_23_00:
                  80 SIK
                          82 (111)
                  80 sV~
 Q Consensus
                          82 (111)
                     + | +
                  84 ~v~
                          86 (133)
 T Consensus
```

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T 4kjy_B
                                                         84 NIT
                                                                                  86 (133)
   T ss_dssp
                                                                 SCC
   T ss pred
                                                                 CCC
   No 38
                                                                                                                                    PDB"
                                                                                                                                                                     NCBI
                                                                                                                                                                                                                            Pub Med
                                                                                                   SCOPe
>2d7p A Filamin-C; beta-sandwich, immunoglobulin-like fold, filamin domain, structural genomics, NPPSFA; NMR
    {Homo sapiens} SCOP: b.1.18.10 PDB: 2eeb A
    Probab=63.62 E-value=32 Score=22.58 Aligned_cols=74 Identities=12% Similarity=0.131 Sum_probs=0.0
                                                                 CCCEEECCCCcceeeccCCCceeeeEEEecCCCcEEEEEEECCCCcEEEEEECCccccEEEECCCccCceEEEEEE
   Q Thu Apr 23 00:
                                                           3 KPSASLKLHHDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV
                                                                                                                                                                                                                                                                                                     79 (111)
                                                           3 ~asA-F---------C-q--v-v-V-l-G--PftL-yeiv----qk-----v--i------I-tp----GG-y-v-L-
                                                                                                                                                                                                                                                                                                     79 (111)
   Q Consensus
                                                                84 (112)
   T 2d7p_A
                                                         11 ARRLTVTSLOETGLKVNOPASFAVOLNGA-RGVIDARVHTP-SGAVEECYVSELDSDKHTIRFIPHEN-GVHSIDVK
                                                                                                                                                                                                                                                                                                     84 (112)
   T ss_dssp
                                                                 GGGCEECSSCSBCCCTTCCEEEEEECTTC-CSCEEEEEECS-SSCBCCCEECSCBTTEEEEEECCSSC-EEEEEEE
   T ss_pred
                                                                 SCOPe POB®
   No 39
                                                                                                                                                                     NCBI
                                                                                                                                                                                                     Pub Med
>4hbc L Antigen binding fragment, immunoglobulin IGG - LI; FAB, rabbit, conformation-specific, amyloid, immune
   system; 1.54A (Oryotolagus cuniculus) SCOP: b.1.1.0 b.1.1.0 PDB: 4jo4 L* 4jo3 L* 4jo1 L 4jo2 L Probab=63.34 E-value=21 Score=23.96 Aligned_cols=72 Identities=11% Similarity=0.150 Sum_probs=0.0
                                                                  ceEEeCC-CcceeccCCCeeeeEEEecCCCcEEEEEEeCc-----ccccEEEeeCCCccCEEEEE
   Q ss pred
                                                           Q Thu_Apr_23_00:
                                                                                                                                                                                                                                                                                                             77 (111)
   O Consensus
                                                                                                                                                                                                                                                                                                              77 (111)
                                                                 .+.|....+.+=.|+++.+.-.+.|.|+..+.|---...|+....+..
                                                                 q {\scriptstyle \sim} {\scriptstyle V {\scriptstyle \sim} \sim} p {\scriptstyle \sim} {\scriptstyle \sim} {\scriptstyle V {\scriptstyle \sim} G} {\scriptstyle \sim} {\scriptstyle V {\scriptstyle \sim} L {\scriptstyle \sim} C} {\scriptstyle \sim}   T Consensus
                                                                                                                                                                                                                                                                                                             74 (213)
   T 4hbc L
                                                            1 \  \, \text{DVVMTQTPASVSEPVGGTVTI} \\ \text{KCQASQSISSYLAWYQQK} - \text{PGQRPRLLIYETSTLASGVPSRFKGS} --- - \text{GSGTDFTLT} \\ \text{The properties of the pro
                                                                                                                                                                                                                                                                                                             74 (213)
   T ss_dssp
                                                                 CCCEEECSEEEETTCCEEEEEESSCCTTCEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETTEEEEE
   T ss pred
                                                                 EEEEE
   Q ss_pred
   Q Thu_Apr_23_00:
                                                        78 LVSIK
                                                                                        82 (111)
   Q Consensus
                                                         78 L~sV~
                                                                                        82 (111)
                                                                 |.+|+
                                                          75 T~~v~
                                                                                        79 (213)
   T Consensus
   T 4hbc_L
                                                         75 ISDLE
                                                                                        79 (213)
   T ss_dssp
                                                                 ECSCC
   T ss_pred
                                                                 ECCCC
   No 40
                                                                                                   SCOPe
                                                                                                                                   PDB'
                                                                                                                                                                     NCBI
                                                                                                                                                                                                                            Pub Med
->194b_ Antibody variable light chain; FV antibody, antigen peptide binder, SCFV, picomolar binder, immune
   system; 2.35A {Mus musculus} SCOP: b.1.1.1 PDB: 1p4i _L
   Probab=63.18 E-value=29 Score=21.94 Aligned cols=74 Identities=9% Similarity=0.021 Sum probs=0.0
   Q ss pred
                                                                 CCceEEeCCCcceeccCCCeeeeEEEecCCC---cEEEEEEEECCCCcEEEEEEeCccc-----ccEEEeCCCccCCce
   Q Thu_Apr_23_00:
                                                           {\tt 3~KPSASLKLHHDLKLCLGDHSSVPVALKGQGP---FTLTYDIIETFSSKRKTFEIKEIKT-----NEYVIKTPVFTTGGD}\\
                                                                                                                                                                                                                                                                                                             73 (111)
                                                            Q Consensus
                                                                                                                                                                                                                                                                                                             73 (111)
                                                            .+|.+..
   T Consensus
                                                                                                                                                                                                                                                                                                              77 (135)
                                                                                                                                                                                                                                                           ~r~
                                                            4 YADAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYASWVQEK--PDHLFTGLIGGTNNRAPGVPARFSGSL----IGDK
   T 1p4b L
                                                                                                                                                                                                                                                                                                             77 (135)
                                                                  -CCCCEECCSEEEECTTCEEEEEEEETTSSCCGGGCCEEEEE---GGGEEEEEETTTEECTTCCTTEEEEE----ETTE
   T ss dssp
                                                                 ccceeECCCcEEecCCCeEEEEEEcCCccCCCCEEEEEEEC--CCCCcEEEEEEecccCCCCccEEEEE----CCCc
   T ss_pred
                                                                 EEEEEEEE
   Q ss pred
                                                         74 YILSLVSIK
   Q Thu_Apr_23_00:
                                                                                                    82 (111)
   Q Consensus
                                                         74 \ y^{\sim}v^{\sim}L^{\sim}sV^{\sim}
                                                                                                    82 (111)
                                                                  +.|.|.+|+
                                                         78 ~sL~I~~v~
   T Consensus
                                                                                                    86 (135)
                                                         78 AALTITGAQ
   T 1p4b L
                                                                                                   86 (135)
   T ss_dssp
                                                                 EEEEEESCC
   T ss_pred
                                                                 EEEEECCCC
                                                                                                   SCOPe PROTEIN DATA BANK
   No 41
                                                                                                                                                                    NCBI
                                                                                                                                                                                                                        Pub Med
🗌 >1j05_L T84.66 antibody, anti-CEA MAB T84.66, light chain; immunoglobulin, immune system; 1.50A {Mus musculus}
  SCOP: b.1.1.1 PDB: 1qfw L* 1qnz L 3iy3 A 3iy4 A
Probab=63.09 E-value=24 Score=20.90 Aligned cols=59 Identities=10% Similarity=0.086 Sum probs=0.0
                                                                 Q ss pred
   Q Thu_Apr_23_00:
                                                         18 LGDHSSVPVALKGQG----PFTLTYDIIETFSSKRKTFEIKEI-----KTNEYVIKTPVFTTGGDYILSLVSIK
                                                                                                                                                                                                                                                                                                82 (111)
                                                         Q Consensus
                                                                                                                                                                                                                                                                                                82 (111)
                                                                  ..++.+.|.|.+|+
   T Consensus
                                                         15 ~G~~v~L~C~~~
                                                                                                                                                               83 (111)
                                                         15 LGQRATMSCRAGESVDIFGVGFLHWYQQK--PGQPPKLLIYRASNLESGIPVRFSGT----GSRTDFTLIIDPVE
   T 1j05 L
                                                                                                                                                                                                                                                                                                83 (111)
   T ss_dssp
                                                                 TTSCEEEEEESSCCEETTEECEEEEEC--TTSCEEEEEETTTEECTTSCTTEEEE----EETTEEEEEESSCC
   T ss_pred
                                                                 CCCCEEEEEeccccCCCccEEEEEec---CCCCCEEEEEECCcCCCcccEEEe----ccCCeEEEEECCCC
```

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SCOPe PROTEIN DATA BANK
  No 42
                                                                                                                                      Pub Med
>4ffy L DENV1-E111 single chain variable fragment (light; viral envelope proteins, structural genomics, antibody
  epito flavivirus, niaid; 2.50A (Mus musculus) SCOP: b.1.1.1
  Probab=62.89 E-value=18 Score=22.18 Aligned_cols=72 Identities=11% Similarity=0.145 Sum_probs=0.0
                                        Q ss pred
  Q Thu Apr 23 00:
                                    5 SASLKLH-HDLKLCLGDHSSVPVALKGOG----PFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGD
                                                                                                                                                                                          73 (111)
                                    5 sA-F-----C-g--v-v-V-l-G------PftL-yeiv---gk-----v-i------I-tp----GG-
  Q Consensus
                                                                                                                                                                                           73 (111)
                                        74 (126)
  T Consensus
                                     1 \ \texttt{NIVLTQSPASLAVSLGQRATISCRASESVDHYGNSFIYWYQQK--PGQPPKLLIYLASNLESGVPARFSGS----GSETD}
  T 4ffy L
                                                                                                                                                                                          74 (126)
                                        CCCEEECSEEEETTSCEEEEEEESSCCETTEECEEEEEC--TTSCCEEEEETTTEECTTSCTTEEEE----EETTE
  T ss dssp
                                        CCccEecCCEEEEcCCCCEEEEEECCccccCCCccEEEEEEC--CCCCCEEEEEecccCCCCCCCEEEe----cCCCE
  T ss pred
  Q ss_pred
                                       EEEEEEEE
  Q Thu_Apr_23_00:
                                  74 YILSLVSIK
                                                             82 (111)
  O Consensus
                                   74 y~v~L~sV~
                                                             82 (111)
                                        +.|.|.+|+
                                   75 ~~L~I~~v
  T Consensus
                                                             83 (126)
                                   75 FTLTIDSVE
  T 4ffy L
                                                             83 (126)
  T ss_dssp
                                        EEEEESSCC
  T ss_pred
                                        EEEEECCCC
                                                             SCOPe PROTEIN DATA BANK
                                                                                                      NCBI Pub Med
>3r06_A Anti-mouse CD3epsilon antibody 2C11 FAB light CHA; anti-CD3epsilon, T-cell receptor, signalling, IMMU; 2.50A {Cricetulus migratorius} SCOP: b.1.1.0 b.1.1.0 PDB: 3r08_L 3ld8_B 3ldb_B*
  Probab=62.77 E-value=21 Score=24.02 Aligned_cols=59 Identities=15% Similarity=0.171 Sum_probs=0.0
                                        ccceeeeeeeecccceeeeeeecccc
  Q Thu_Apr_23_00:
                                  18 LGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEI-----KTNEYVIKTPVFTTGGDYILSLVSIK
                                                                                                                                                                           82 (111)
                                   18 \ \text{``g} \sim v \sim v \sim V \sim 1 \sim G \sim PftL \sim yeiv \sim \cdots \circ gk \sim \cdots \sim v \sim i - \cdots \sim r \cdot I \sim tp \sim \cdots \sim GG \sim y \sim v - L \sim sV \sim r \cdot I \sim tp \sim r \cdot GG \sim y \sim v \sim L \sim sV \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim tp \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot GG \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim r \cdot I \sim 
  O Consensus
                                                                                                                                                                          82 (111)
                                   T Consensus
                                   15 LGDRVTINCQASQDISNYLNWYQQK--PGKAPKLLIYYTNKLADGVPSRFSGS----GSGRDSSFTISSLE
  T 3r06 A
                                                                                                                                                                           79 (213)
  T ss_dssp
                                        TTCCEEEEEESSCCTTCEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETTEEEEEESSCC
                                        CCCCEEEEEEcCCCccEEEEEEC--CCCCCEEEEEEcCCCCCccCCeEEEE----ccCCEEEEEEccCC
  T ss_pred
                                                          SCOPe PROTEIN DATA BANK NCBI
                                                                                                                                        Pub Med
🗌 >2d7n_A Filamin-C; beta-sandwich, immunoglobulin-like fold, filamin domain, structural genomics, NPPSFA; NMR
  {Homo sapiens} SCOP: b.1.18.10
  Probab=62.33 E-value=28 Score=22.39 Aligned_cols=60 Identities=13% Similarity=0.025 Sum_probs=0.0
  Q ss pred
                                        ccCCCeeeeEEEecCCCcEEEEEEEcCcccccEEEEEE
  Q Thu_Apr_23_00:
                                  17 CLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV
                                                                                                                                                            79 (111)
  O Consensus
                                   17 C~g~~v~v~l~G~~PftL~yeiv~~~~qk~~~~v~~i~~~~~I~tp~~~~GG~y~v~L~
                                                                                                                                                             79 (111)
                                        T Consensus
                                                                                                                                                             65 (93)
  T 2d7n A
                                     6 SGLRPFNLVIPFA-VQKGELTGEVRMP-SGKTARPNITDNKDGTITVRYAP-TEKGLHQMGIK
                                                                                                                                                             65 (93)
  T ss_dssp
                                        CCBCCEEEECCC-CSSSCEEEEECT-TSCEECCEEECSSSCEEEEECC-SSCEEEEEE
  T ss_pred
                                        PDB"
                                                                                                      Pub Med
                                                                                 NCBI
>4wnq A TCR variable delta 1 chain and TCR constant alpha; immunity, immune system; 1.80A {Homo sapiens} PDB:
4wo4 C* 4mnh B 2ak4 D 3kxf D 4jrx D 4g9f D 4g8g D 3ffc D 4onh A*
Probab=61.86 E-value=35 Score=22.38 Aligned_cols=76 Identities=8% Similarity=0.135 Sum_probs=0.0
                                        CCceEEeCC-CcceeccCCCeeeeEEEecC-CCcEEEEEEeCCCCcEEEEEEeCccc-----cccEEEeCCCccCceE
  Q ss pred
  Q Thu_Apr_23_00:
                                    3 KPSASLKLH-HDLKLCLGDHSSVPVALKGQ-GPFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGDY
                                                                                                                                                                                          74 (111)
                                    O Consensus
                                                                                                                                                                                          74 (111)
  T Consensus
  T 4wnq_A
                                    1 HMAQKVTQAQSSVSMPVRKAVTLNCLYETSWWSYYIFWYKQL--PSKEMIFLIRQGSDEQNAKSGRYSVNFK--KAAKSV
                                                                                                                                                                                           76 (207)
  T ss_dssp
                                         ---CEEECCCSEEEEETTSCEEECCEECCCSSCEEEEEEC--TTCCEEEEEEEETTSSCCEETTEEEEEE--TTTTEE
                                        CCccceecCCceEEEccCCeEEEEeeecCCCCceeEEEEEEC--CCCCcEEEEEec--CCCCCEE
  T ss_pred
                                       EEEEEEE
  Q ss pred
  Q Thu_Apr_23_00:
                                  75 ILSLVSIK
                                                            82 (111)
  Q Consensus
                                   75 ~v~L~sV~
                                                            82 (111)
                                        .|.|.+|+
                                   77 ~L~I~~v~
  T Consensus
                                                            84 (207)
  T 4wnq_A
                                   77 ALTISALQ
                                                            84 (207)
  T ss dssp
                                        EEEECSCC
  T ss pred
                                        EEEECCCC
                                                                                 PDB'
  No 46
                                                             SCOPe
                                                                                                                                     Pub Med
                                                                                                      S NCBI
->4hgk_C Shark V-NAR antibody; IG-fold, human albumin, immune system; 3.04A {Squalus acanthias} SCOP: b.1.1.1
  Probab=61.51 E-value=22 Score=22.21 Aligned_cols=73 Identities=10% Similarity=0.127 Sum_probs=0.0
                                        Q ss pred
```

```
Q Thu_Apr_23_00:
                   4 PSASLKLH-HDLKLCLGDHSSVPVALKGQ--GPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLVS
                                                                                                     80 (111)
                   O Consensus
                                                                                                     80 (111)
 T Consensus
                                                                                                     91 (128)
                   18 HSTRVDQTPRTATRETGESLTINCVLTDTSYPLYSTYWYRKN-PGSSNKEQIS-ISGRYVESVN-KGTKSFSLRIKD
 T 4hgk_C
                                                                                                     91 (128)
                      -- \texttt{CEEEEECSEEEEETTCCEEEEEEEESCSSCEEEEEEEC--TTCSCCEECC--CCTTEEEEEE--TTTTEEEEEESS
 T ss_dssp
                      T ss pred
 Q ss pred
                      EE
                          82 (111)
 Q Thu_Apr_23_00:
                   81 IK
                   81 V~
                           82 (111)
                      1+
                   92 v~
                          93 (128)
 T Consensus
                   92 LT
 T 4hgk C
                          93 (128)
                      CC
 T ss dssp
 T ss_pred
 No 47
                                            PDB"
                                 SCOPe
                                                                        Pub Med
🗌 >loaq_L Light chain; immune system, allergy, IGE, conformational diversity, multispecificity; 1.50A {Mus
 musculus} SCOP: b.1.1.1 PDB: locw_L 2bjm_L* loau_L* loar_L* loaz_L lmfa_L* la6v_L* loax_L* loay_L* loay_L* 1a6w
 Probab=61.05 E-value=28 Score=20.99 Aligned cols=72 Identities=10% Similarity=0.034 Sum probs=0.0
                      ceEEeCCCcceeccCCCeeeeEEEecCC---CcEEEEEEECCCCcEEEEEECCcc------cccEEEeCCCccCCceEE
 Q ss pred
 Q Thu Apr 23 00:
                    5 SASLKLHHDLKLCLGDHSSVPVALKGQG---PFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGDYI
                                                                                                     75 (111)
 O Consensus
                    5 sA~F~~~~~C~g~~v~V~l~G~~---PftL~yeiv~~~gk~~~~v~i~-----I~tp~~~GG~y~
                                                                                                     75 (111)
                     T Consensus
                                                                                                     74 (120)
 T loaq L
                    1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEK--PDHLFTGLIGGTNNRAPGVPARFSGSL----IGNKAA
                                                                                                     74 (120)
 T ss dssp
                      {\tt CCCEECSEEEECTTCEEEEEEEETTBCCCGGGCCEEEEEE--TTTEEEEEEETTTEECTTSCTTEEEEE----ETTEEE
 T ss_pred
                      CcceEcCCcEEeecCCccEEEEEecccccCCccEEEEEEEC--CCCcEEEEEeecCccCCCCceEEEEe----cCCeEE
 Q ss pred
                     EEEEEEE
 Q Thu_Apr_23_00:
                  76 LSLVSIK
                               82 (111)
 Q Consensus
                   76 v~L~sV~
                               82 (111)
                      |.|.+|+
 T Consensus
                   75 L~T~~v~
                               81 (120)
 T loag L
                   75 LTITGAQ
                               81 (120)
 T ss_dssp
                      EEEESCC
 T ss_pred
                      EEECCCC
 No 48
                                 SCOPe
                                                                         Pub Med
□ >3hqx_A UPF0345 protein aciad0356; DUF1255,PF06865,PSI2,MCSG, structural genomics, protein STRU initiative,
 midwest center for structural genomics; 1.66A {Acinetobacter SP} SCOP: b.82.1.0
 Probab=60.97 E-value=24 Score=24.31 Aligned_cols=64 Identities=19% Similarity=0.281 Sum_probs=0.0
                      CCceEEeCC-CcceeccCC--CeeeeEEEecCCCcEEEEEEECCCCcEEEEEECCccccEEEeCCC------ccCCce
 Q ss pred
                    3 KPSASLKLH-HDLKLCLGD--HSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPV-----FTTGGD
 Q Thu_Apr_23_00:
                                                                                                     73 (111)
                    3 ~asA~F~~~~~~C~g~--~v~v~V~l~G~~PftL~yeiv~~~gk~~~~v~i~~~~~I~tp~----~~~GG~
 Q Consensus
                                                                                                     73 (111)
                   +++,+|.+..+..+|..++-|.+-|+-|+|+|. +...+-..+++|. +...+|...+..|

17 kaNvYFdGkv-S-----dG--kTlGVm-PGe--Y-F------T--E-Mei---vsG-1-V-lpg--eW----aGes

17 KSNVYFGGLCISHTVQFEDGTKKTLGVILPTEQPLTFE------THVPERMEI---ISGECRVKIADSTESELFRAGQS
 T Consensus
                                                                                                     86 (111)
 T 3hqx A
                                                                                                     86 (111)
                      SCEEETTTEEEEEEECTTSCEEEEEECCCSSCEEEE-----CSSCEEEEE---ESEEEEEETTCSSCEEEETTCE
 T ss dssp
 T ss_pred
                      EeeEEeCCceEEEEEeccCcceEEc-----CCccEEEEE---EEeEEEEccCcccEEECCCC
 Q ss_pred
                     EEE
 O Thu Apr 23 00:
                   74 YIL
                           76 (111)
                           76 (111)
 Q Consensus
                   74 y~v
                      1.1
 T Consensus
                   87 F~V
                           89 (111)
 T 3hqx A
                   87 FYV
                           89 (111)
 T ss_dssp
                      EEE
                      EEE
 T ss pred
 No 49
                                            S NCBI
                                                             Pub Med
🗌 >2kzw_A Uncharacterized protein; structural genomics, northeast structural genomics consortiu PSI-2, protein
 structure initiative; NMR {Methanosarcina mazei}
 Probab=60.92 E-value=6.3 Score=27.56 Aligned_cols=19 Identities=32% Similarity=0.754 Sum_probs=0.0
 Q ss pred
                      CCCCCEEEEEEEEECCCCC
 Q Thu_Apr_23_00:
                  68 FTTGGDYILSLVSIKDSTGC
                                            87 (111)
                   68 ~~~GG~y~v~L~sV~D~~GC
                                            87 (111)
 Q Consensus
                      +..-|.|+|+|+|+|..||
                  110 y~~~G~YtV~Lt-vt~~~G
                                           128 (145)
 T Consensus
                  110 FFNEGEYIVSLI-VSNENDS 128 (145)
 T 2kzw A
                      CSSCEEEEEEE-EECSSCE
 T ss dssp
                      cccceeeeeeeeecccc
 T ss pred
                                 SCOPe
                                             PDB"
```

```
🗌 >leeq_A Kappa-4 immunoglobulin (light chain); protein stability, hydrogen bonds, immune system; 1.50A {Homo
 sapiens) SCOP: b.1.1.1 PDB: leeu A 11ve A 21ve A 31ve A 51ve A 41ve A 1efq A 1qac A 1ek3 A 2imm A 1mvu lap2 A 4oga D* 3w12 D* 3w13 D* 3w11 D* 3bd3 A* 3bd4 A* 3bd5 A* ...

Probab=60.77 E-value=22 Score=21.21 Aligned_cols=72 Identities=14% Similarity=0.213 Sum_probs=0.0
                    ceEEeCC-CcceeccCCCeeeeEEEecCC-----CcEEEEEEEECCCCcEEEEEEeCccc-----cccEEEeCCCccCC
                 5 SASLKLH-HDLKLCLGDHSSVPVALKGQG-----PFTLTYDIIETFSSKRKTFEIKEIK----TNEYVIKTPVFTTG
 Q Thu_Apr_23_00:
                                                                                          71 (111)
                  \texttt{5} \ \texttt{sA-F-----C-g--v-v-v-l-G------PftL-yeiv---gk-----v-i------l-tp----G} \\
 Q Consensus
                                                                                          71 (111)
                   ...|....+..+=.|+++++-.+.|.+ +..+.|.--...|+....+|
                                                                           ..+|.+.. .+
                   ~~~v~~~p~~~~~Ġ~~v~L~C~~~~
                                                                                          74 (114)
 T Consensus
 T leeq_A
                 1 DIVLTQSPDSLAVSLGERATINCKSSQSVLDSSNSKNYLAWYQQK--PGQPPKLLIYWASTRESGVPDRFSGSG----SG
                                                                                          74 (114)
                    T ss_dssp
 T ss_pred
                   CCceEecCCeEEEecCcccCCCcceEEEEEc---CCCceEEEEEEccccCCCCcCEEEEc----CC
 Q ss_pred
                   ceeeeeeee
 Q Thu_Apr_23_00:
                72 GDYILSLVSIK
                               82 (111)
 O Consensus
                 72 G~y~v~L~sV~
                               82 (111)
                 +.+.|.|.+|+
75 ~~~~L~I~~v~
 T Consensus
                               85 (114)
 T leeq A
                 75 TDFTLTISSLQ
                               85 (114)
 T ss dssp
                   TEEEEEESSCC
                   CeEEEECCCC
 T ss pred
 No 51
                              SCOPe
                                                                  Pub Med
🔲 >2dia A Filamin-B; beta-sandwich, immunoglobulin-like fold, filamin domain, structural genomics, NPPSFA; NMR
 {Homo sapiens} SCOP: b.1.18.10
 Probab=60.58 E-value=36 Score=22.16 Aligned cols=67 Identities=4% Similarity=-0.018 Sum probs=0.0
 Q ss_pred
                   eeeEEEecCCCcEEEEEEeCCCCcEEEEEeCcccccEEEeCC---CccCCceEEEEEEECcCCCcc
 Q Thu_Apr_23_00: 23 SVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTP---VFTTGGDYILSLVSIKDSTGCVVG
                 O Consensus
                                                                                   90 (111)
 T Consensus
                                                                                  112 (113)
                 43 ALGLEAVSDSGTKAEVSIQNNKDG-TYAVTYVPLTAGMYTLTMKYGGELVPHFPARVKVEPAVDTSSGPSS 112 (113)
 T 2dia A
                    CEEEEEETTTEECEEEEECTTS-EEEEEEECSSCEEEEEEEETTEECTTCSEEEEEEECCCCSSCCCCC
 T ss_dssp
 T ss_pred
                    SCOPe PROTEIN DATA BANK
 No 52
                                                 S NCBI
                                                                  Pub Med
>2j3s_A Filamin-A; cytoskeleton, phosphorylation, structural protein; 2.5A (Homo sapiens) SCOP: b.1.18.10
 b.1.18.10 PDB: 2e9i A
 Probab=58.72 E-value=14 Score=28.20 Aligned cols=62 Identities=19% Similarity=0.216 Sum probs=0.0
                   eccCCeeeeEEEecCCCcEEEEEEeCcCccEEEEEeCcccccEEEeCCcccCceEEEEE
 Q ss_pred
 Q Thu_Apr_23_00:
                16 LCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV
                 O Consensus
                                                                             79 (111)
                T Consensus
                                                                           174 (288)
                113 ANVGSHCDLSLKIPEISIQDMTAQVTSP-SGKTHEAEIVEGENHTYCIRFVPAE-MGTHTVSVK 174 (288)
 T 2j3s A
 T ss_dssp
                   CSCCSSCCC-----CCCEEEEECT-TCCEEEEBC-----CCCBCCCCS-CEEEEEEEE
                    eecCcceEEEEEcccCCCCceEEEEECC-CCCeeeeEEEECCCCEEEEEEEccc-cEeEEEEE
 T ss pred
       PDB NCBI Pub Med
 No 53
->4uyp_A SCAC, cellulosomal scaffoldin anchoring protein C; cell adhesion-protein binding complex, cellulosome,
 type 1 C dockerin intereactions; HET: EPE; 1.49A {Acetivibrio cellulolyticus} PDB: 4uyq _A
 Probab=58.72 E-value=5.1 Score=28.76 Aligned_cols=21 Identities=29% Similarity=0.581 Sum_probs=0.0
                   CCCeeeeEEEecCC-----CcEEEEE
 Q ss pred
 Q Thu_Apr_23_00:
                19 GDHSSVPVALKGQG-----PFTLTYD
                 19 g~~v~v~V~l~G~~----PftL~ye
 Q Consensus
                                              39 (111)
                 T Consensus
                                              41 (151)
                 14 GSVVSVPITFTNVPKSGIYALSFRTNFD
 T 4uyp A
                                              41 (151)
 T ss_dssp
                   TCEEEEEEESCCTTCBCEEEEEECC
 T ss_pred
                   CCEEEEEEEcCccCCceeEEEEEEC
              SCOPe PROTEIN DATA BANK
 No 54
                                                 NCBI
                                                                 Pub Med
>2xt1_B Camelid VHH 9; viral protein-immune system complex; 1.32A {Vicugna pacos} SCOP: b.1.1.1 PDB: 2xv6_B
 2xxc B 2xxm B
 Probab=58.67 E-value=34 Score=21.18 Aligned cols=78 Identities=10% Similarity=0.026 Sum probs=0.0
                   CCceEEeCCCcceeccCCCeeeeEEEecC--CCcEEEEEEeCCCCcEEEEEEeCccc------ccEEEeCCCccCC
 Q ss pred
 Q Thu_Apr_23_00:
                  3 KPSASLKLHHDLKLCLGDHSSVPVALKGQ--GPFTLTYDIIETFSSKRKTFEIKEIKT-----NEYVIKTPVFTTG
                                                                                          71 (111)
                  Q Consensus
                                                                                          71 (111)
                  .+..+..+..+=.|+++.+=.+.|. ++..+.|--...+.....1
 T Consensus
                                                                          ~~~~R~~~~~~~~~~
                                                                                          78 (121)
                  1\ \texttt{MAQVQLVESGGGLVQAGGSLRLSCAASGSFFMSNVMAWYRQAPGKARELIAAIRGGDMSTVYDDSVKGRFTITRDD--DK}
 T 2xt1 B
                                                                                          78 (121)
 T ss_dssp
                    T ss_pred
                   CEEEEEEEE
 Q ss pred
```

```
Q Thu_Apr_23_00:
                           72 GDYILSLVSIK
                                                     82 (111)
 O Consensus
                            72 G~y~v~L~sV~
                                                     82 (111)
                             +.+.|.|.+|+
79 ~~~sL~I~~v~
                                                     89 (121)
 T Consensus
                            79 NILYLOMNDLK
 T 2xt1 B
                                                     89 (121)
                                 TEEEEECSCC
 T ss_dssp
 T ss_pred
                                 CEEEEEECCCC
 No 55
                                                                  PDB<sup>™</sup>
PROTEIN DATA BANK
                                                                                                 Pub Med
                                                  SCOPe
                                                                                   NCBI
>2k7q A Filamin-A; IG-like, ABP-280, actin binding protein, acetylation, actin-binding, cytoplasm, cytoskeleton,
 disease mutation, phosphoprotein; NMR {Homo sapiens} SCOP: b.1.18.0 b.1.18.0 Probab=57.02 E-value=13 Score=26.60 Aligned cols=66 Identities=14% Similarity=0.224 Sum probs=0.0
                                 CcceccCCCeeeeEEEecCCCcEEEEEEEeCCCCcEEEEEEE
 Q Thu_Apr_23_00:
                           12 HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV
                                                                                                                                       79 (111)
 O Consensus
                            79 (111)
                              T Consensus
                                                                                                                                       74 (191)
 T 2k7q A
                                                                                                                                       74 (191)
                                 EEEEEEEECCCEECSCSSCCSSSEEEEEECT-TSCCEECEEECCTTSCEEEECCCSS-SEEEEEEE
 T ss_dssp
                                 CCCCCCCCceEEEEecCCCCceEEEEEECC-CCCEeeeEEEECCC-cEeEEEEE
 T ss pred
 No 56
                                                   PDB<sup>W</sup> NCBI
                                                                                   Pub Med
->4xtl_C Nanobody 7; GPCR, chemokine, membrane protein, complex, viral protein-SI protein complex; HET: CLR OLC
 UNL; 2.89A {Vicugna pacos} PDB: 3k81 _A
Probab=56.78 E-value=40 Score=21.49 Aligned cols=79 Identities=11% Similarity=0.074 Sum probs=0.0
 Q ss pred
                                 CCCceEEeCCCcceeccCCCeeeeEEEecC--CCcEEEEEEEeCCCccEEEEE
 Q Thu_Apr_23_00:
                             2 VKPSASLKLHHDLKLCLGDHSSVPVALKGQ--GPFTLTYDIIETFSSKRKTFEI-----KEIKTNEYVIKTPVFTTG
                                                                                                                                                        71 (111)
                             O Consensus
                                                                                                                                                        71 (111)
 T Consensus
                                                                                                                                                         79 (134)
                               2 \  \  PGSQVQLVESGGGLVRPGGSLRLSCAASGSIFTIYAMGWYRQAPGKQRELVARITFGGDTNYADSVKGRFTISRDN--AK \\
                                                                                                                                                         79 (134)
 T 4xt1_C
                                 ---CCCEEECCTTCEEEEEEEESSCCSCEEEEEEEECTTSCEEEEEETTSCEEECTTBTTEEEEET--TT
 T ss_dssp
                                 CcccEEEEccCCeEeCCCCEEEEEEeCCCccceEEEEEEcCCCccEEEEEEcCCCceEeCcccCeEEEEEeC--CC
 T ss pred
                                ceeeeeeee
 Q ss pred
                            72 GDYILSLVSIK
 Q Thu_Apr_23_00:
                                                     82 (111)
                             72 G~y~v~L~sV~
                                                     82 (111)
                            +.+.|.|.+|+
80 ~~~sL~I~~v~
                                                     90 (134)
 T Consensus
 T 4xt1 C
                            80 NAVYLOMNSLK
                                                     90 (134)
                                 TEEEEEESCC
 T ss dssp
 T ss_pred
                                 CEEEEECCCC
 No 57
                                                  SCOPe PROTEIN DATA BANK
                                                                                                             Pub Med
                                                                                   S NCBI
>2e9j_A Filamin-B; beta-sandwich, immunoglobulin-like fold, structural genomics, NPPSFA, national project on
 protein structural and functional analyses; NMR {Homo sapiens} SCOP: b.1.18.10
 Probab=56.73 E-value=21 Score=23.50 Aligned cols=61 Identities=16% Similarity=0.208 Sum probs=0.0
                                 ccCCceeeeEEEecCCCcEEEEEEEeCcccccEEEEEEE
 Q ss pred
                             17 CLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV
 Q Thu Apr 23 00:
                                                                                                                                 79 (111)
                             17 C~g~~v~v~V~l~G~~PftL~yeiv~~~~gk~~~~v~i~~~~I~tp~~~~GG~y~v~L~
                            | . | +++++ | .... + = . | +- | ... + | + | +... + ... + ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ...
 T Consensus
                                                                                                                                97 (119)
 T 2e9j_A
                                                                                                                                97 (119)
                                 ETTSCEEEEEESSCCCCCEECCEECT-TCCCCCEEEEECCSSEEEEEECCCSC-SEEEECCE
 T ss dssp
                                 T ss pred
                                                SCOPe POB™
                                                                                  NCBI Pub Med
 No 58
>2ccl_A Cellulosomal scaffolding protein A; cell adhesion, cohesin/dockerin complex, cellulosome, cohesi
 dockerin, scaffolding, cellulose degradation; 2.03A {Clostridium thermocellum} SCOP: b.2.2.2 PDB: 1ohz _A
 Probab=55.88 E-value=4.4 Score=29.24 Aligned_cols=37 Identities=22% Similarity=0.432 Sum_probs=0.0
                                 CCceEEeCC-CcceeccCCCeeeeEEEecC-----CCcEEEEE
 Q ss pred
 Q Thu Apr 23 00:
                              3 KPSASLKLH-HDLKLCLGDHSSVPVALKGQ-----GPFTLTYD
                                                                                                      39 (111)
                             3 ~asA~F~~~~C~g~~v~v~V~l~G~-----PftL~ye
                                                                                                      39 (111)
                                .|+..+-. ...+.=.|+++++||.|.+- .+|.|.|+
                              1 ~as~~vqi~vq~~~~~G~tf~V~V~~~nvP~~qi~s~~f~l~yD
 T Consensus
                                                                                                      45 (158)
 T 2ccl A
                             1 MASDGVVVEIGKVTGSVGTTVEIPVYFRGVPSKGIANCDFVFRYD
                                                                                                      45 (158)
                                 ----CEEEEECECCCTTCEEEEEEEECCTTCBSEEEEEECC
 T ss dssp
 T ss_pred
                                 CCCCCEEEECceeecCCCEEEEEEEccCccCCcEEEeEEECC
 No 59
                                                 SCOPe PROTEIN DATA BANK
                                                                                   NCBI
                                                                                                             Pub Med
->4nzu_L 13PL heavy chain; antibody FAB, multiple myeloma, primary antibody, immune SYS; HET: GOL; 1.20A (Homo
 sapiens) SCOP: b.1.1.2 b.1.1.0 PDB: 2xra L 4hg4 K* 4jha L 4jhw L 1b6d A 4fn1 L 4fp8 L* 4fqr b* 4p59 L* 3
3idy L* 1cel L 4cni L* 3eo9 L 3eoa L 3eob L 1bey L 3wd5 L 2fjh L 3bn9 C ...
Probab=55.83 E-value=32 Score=23.07 Aligned_cols=59 Identities=14% Similarity=0.200 Sum_probs=0.0
```

```
Q ss pred
                           cccceeeeEEeccccceEEEEEeccccceEEEEEecc-----cccceEEEecccccceEEEEEEE
 Q Thu_Apr_23_00:
                        18 LGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKE-----IKTNEYVIKTPVFTTGGDYILSLVSIK
                                                                                                                    82 (111)
 O Consensus
                        82 (111)
                        ..++.+.|.|.+|+
 T Consensus
                                                                                                                    79 (211)
                        15 TGDKVTITCQASQDIAKFLDWYQQR--PGKTPKLLIYDASNLAIGVPSRFTGS----GSGTDFTFTISSLQ
 T 4nzu L
                                                                                                                    79 (211)
 T ss_dssp
                           TTCCEEEEEESSCCTTCEEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETTEEEEEESSCC
                           CCCCEEEEEeCCCCccEEEEEEC.--CCCCCEEEEEeCCCCCCCCCCEEEe.----ecCCEEEEEECCCC
 T ss_pred
                                         SCOPe PROTEIN DATA BANK
                                                                     NCBI
                                                                                   Pub Med
>11k3_L 9D7 light chain; antigen-antibody complex, immune system; 1.91A {Rattus norvegicus} SCOP: b.1.1.1 b.1.1.2
 PDB: 1fn4 A 3u9p L 1c5d L 1bfo A 3b9k L*
 Probab=55.68 E-value=32 Score=23.00 Aligned_cols=59 Identities=8% Similarity=0.180 Sum_probs=0.0
                           82 (111)
 Q Thu_Apr_23_00:
                       18 LGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEI-----KTNEYVIKTPVFTTGGDYILSLVSIK
 O Consensus
                        82 (111)
                        T Consensus
                                                                                                                    78 (210)
                        14 PGEKLTISCKASESVTSRMHWYQQK--PGQQPKLLIYKASNLASGVPARFSGS----GSGTDFTLTIDPVE
 T 11k3_L
                                                                                                                    78 (210)
 T ss_dssp
                           TTSCEEEEEESSCCTTCEEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETTEEEEEESSCC
 T ss_pred
                           SCOPe PDB<sup>N</sup>
                                                                      NCBI
                                                                                             Pub Med
>4idl_A Single domain antibody VHH A9; V-type immunoglobin fold, cholera toxin, immune SY single domain antibody;
 2.09A {Lama glama} SCOP: b.1.1.1
 Probab=54.92 E-value=43 Score=21.27 Aligned_cols=76 Identities=11% Similarity=0.122 Sum_probs=0.0
                          CCceEecCCCceeccCCCeeeeEEEecC--CCcEEEEEEeCCCCcEEEEEe------CcccccEEEEeCCCccC
 Q Thu_Apr_23_00:
                        3 KPSASLKLHHDLKLCLGDHSSVPVALKGQ--GPFTLTYDIIETFSSKRKTFEI-----KEIKTNEYVIKTPVFTT
                                                                                                                               70 (111)
                         O Consensus
                                                                                                                               70 (111)
                         T Consensus
                         1 MAKVQLQQSGGAVQTGGSLKLTCLASGNTASIRAMGWYRRA--PGKQREWVASLTTTGTADYGDFVKGRFTISRDN--A
 T 4idl A
                                                                                                                               76 (136)
 T ss_dssp
                            --CEERRECCERETTCCERERERESGGGEERREREC--TTSCCRERERETTCCERECTTTTTCRERERET--T
 T ss_pred
                           CCCEEEEeCCCCEEEEeeCCCCcCceEEEEEeC--CCCCcEEEEEECCCCCeeeChhhCCEEEEEEC--C
 Q ss_pred
                           CceEEEEEEE
                       71 GGDYILSLVSIK
 Q Thu_Apr_23_00:
                                             82 (111)
 O Consensus
                        71 GG~y~v~L~sV~
                                             82 (111)
                        .+.+.|.|.+|+
77 ~~~sL~I~~v~
 T Consensus
                                             88 (136)
 T 4idl_A
                        77 NNAATLOMDSLK
                                             88 (136)
 T ss_dssp
                           TTEEEEECSCC
                           CCERERECCCC
 T ss pred
                                           PDB<sup>™</sup>
PROTEIN DATA BANK
                                                        NCBI
 No 62
                                                                     Pub Med
🗌 >2cdp_A Beta-agarase 1; carbohydrate-binding module, hydrolase; HET: GAL AAL; 1.59A {Saccharophagus degradans}
 PDB: 2cdo A*
 Probab=54.84 E-value=40 Score=23.56 Aligned cols=73 Identities=18% Similarity=0.281 Sum probs=0.0
 Q ss pred
                           Q Thu_Apr_23_00:
                        19 GDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEI-----KTNEY----VIKT-PVFTTGGDYILSLVSIK
                                                                                                                               82 (111)
 O Consensus
                        82 (111)
                        | +-+...|.|...+++|++.+-...++.....+++.....+++.....+++...|...++...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...++|...|...|...++|...|...++|...|...++|...|...|...++|...|...|...++|...|...|...++|...|...|...++|...|...|...++|...|...|...++|...|...|...++|...|...|...|...++|...|...|...|...++|...|...|...|...++|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...
 T Consensus
                                                                                                                              144 (160)
                        66 GDYADYTIAVAQAGNYTISYQAGSGVTGGSIEFLVNENGSWASKTVTAVPNQGWDNFQPLNGGSVYLSAGTHQVRLH-GA
 T 2cdp A
                                                                                                                              144 (160)
 T ss dssp
                            CCEEEEEECCCCCeEEEEEEccCCCceeeEEEEccCccceeEEEEecccccceeEEEeeccccceeEEEEecccceeEEEEe
 T ss pred
                           cccCCccccC
 Q ss pred
 Q Thu_Apr_23_00:
                        83 DSTGCVVGLS
                                           92 (111)
                        83 D~~GC~~~L~
                                           92 (111)
                           ..++|...|+
 T Consensus
                       145 g~~~~nlD 154 (160)
                       145 GSNNWQWNLD 154 (160)
 T 2cdp A
                           SSSSBCCEEE
 T ss_dssp
 T ss_pred
                            CCCCCEEeE
                                                                     Pub Med
 No 63
->4ut7_L Broadly neutralizing human antibody EDE2 All; immune system, broadly neutralizing antibody , immune
 system protein complex, viral protein; 1.70A (Homo sapiens) PDB: 4ut9 _L*
 Probab=54.76 E-value=45 Score=21.49 Aligned_cols=74 Identities=9% Similarity=0.094 Sum probs=0.0
                           CCceEEeCCCcceeccCCCeeeeEEEecCCC---cEEEEEEECCCCcEEEEEECCc------cccEEEeCCCccCCce
 Q ss pred
 Q Thu Apr 23 00:
                         3 KPSASLKLHHDLKLCLGDHSSVPVALKGQGP---FTLTYDIIETFSSKRKTFEIKEI-----KTNEYVIKTPVFTTGGD
                                                                                                                               73 (111)
                         3 ~asA~F~~~~~C~g~~v~v~V~l~G~~P---ftL~yeiv~~~~gk~~~~v~i-----~~~~~I~tp~~~~GG~
                                                                                                                               73 (111)
                         T Consensus
                                                                                                                               75 (153)
                         2 \  \  ASQSVLTQPVSVSGSPGQSITISCTGTSSNADTYNLVSWYQQR--PGKAPKLMIYEGTKRPSGVSNRFSASK----SATA
 T 4ut7 L
                                                                                                                               75 (153)
```

```
T ss_dssp
                    CCCCEECCSEEECTTCCEEEEEEESCCHHHHHTCEEEEEC--TTSCCEEEEBTTTBCCTTSCTTEEEEE----CSSE
 T ss_pred
                    CCCEEEECCCCEEEECCCCCCCCCCCCCCCCEEEEEEC---CCCCCEEEEEecccCCCCCCCCEEEEc----CCCE
                    EEEEEEEE
 Q ss_pred
 Q Thu_Apr_23_00:
                 74 YILSLVSIK
                              82 (111)
                 74 y\sim v\sim L\sim sv\sim
                              82 (111)
 O Consensus
                    +.|.|.+|+
                 76 ~sL~I~~v~
 T Consensus
                              84 (153)
                 76 ASLTISGLQ
 T 4ut7 L
                              84 (153)
 T ss_dssp
                    EEEEECSCC
 T ss_pred
                    EEEEECCCC
 No 64
                              SCOPe PDB PROTEIN DATA BANK
                                                  NCBI (1)
9C2 TCR delta chain; NKT cells, gammadelta TCR, CD1D, lipid recognition, PBS-44, system; HET: NAG; 2.30A
 {Homo sapiens} SCOP: b.1.1.0 b.1.1.0 PDB: 41hu _D*
 Probab=53.24 E-value=56 Score=22.12 Aligned cols=75 Identities=8% Similarity=0.130 Sum probs=0.0
                    CceEECC-CcceeccCCCeeeeEEEecC-CCcEEEEEEECCCCcEEEEEECCcc-----cccEEEECCCccCCceEE
 Q ss pred
 Q Thu Apr 23 00:
                  75 (111)
                  O Consensus
                                                                                            75 (111)
                                                                     ----r---
 T Consensus
                                                                                            78 (236)
 T 41fh D
                  3 GAQKVTQAQSSVSMPVRKAVTLNCLYETSWWSYYIFWYKQL--PSKEMIFLIRQGSDEQNAKSGRYSVNFKK--AAKSVA
                                                                                            78 (236)
 T ss_dssp
                    --CEEECCCSEEEEETTSCEEECCEEECCCSSCEEEEEEC--TTCCEEEEEEEETTSCCCEETTEEEEEET--TTTEEE
                    T ss_pred
 Q ss pred
                   EEEEEEE
 Q Thu_Apr_23_00:
                 76 LSLVSIK
                            82 (111)
                 76 v~L~sV~
                             82 (111)
                   |.|.+|+
 T Consensus
                 79 T.~T~~v~
                             85 (236)
 T 41fh D
                 79 LTISALO
                            85 (236)
 T ss dssp
                    EEECSCC
 T ss_pred
 No 65
                              SCOPe PROTEIN DATA BANK
                                                  NCBI
                                                          Pub Med
>2vn6_A Cohesin, scaffolding protein; cell adhesion, carbohydrate metabolism, polysaccharide degradation,
 hydrolase, glycosidase, cellulose degradation; 1.49A {Clostridium cellulolyticum} SCOP: b.2.2.2 PDB: 2vn5 A 1g1k A Probab=53.19 E-value=7 Score=27.85 Aligned_cols=21 Identities=43% Similarity=0.743 Sum_probs=0.0
                    CCCeeeeEEEecCC-----CcEEEEE
 0 ss pred
 Q Thu_Apr_23_00:
                 19 GDHSSVPVALKGQG-----PFTLTYD
                                                39 (111)
                 19 g~~v~v~l~G~~----PftL~ye
                    |+++++||.|.+-|
                                      +|.|.|+
                 24 G~tf~V~V~~~vp~~gi~~~f~l~yD
24 GDTVTVPVTFADVAKMKNVGTCNFYLGYD
                                                52 (151)
 T Consensus
 T 2vn6 A
                                                52 (151)
                    TCEEEEEEESTTTTTCBCEEEEEECC
 T ss dssp
 T ss_pred
                    CCEEEEEEECCCCCCCEEEEEEEEC
 No 66
                             SCOPe PROTEIN DATA BANK
                                                  NCBI
                                                                  PubMed
                                                           3sob L Antibody light chain; beta propeller, protein binding-immune system complex; 1.90A {Homo sapiens} SCOP:
b.1.1.0 b.1.1.0 PDB: 4iof D 4mlc D 1pkq A 3uls L* 1y01 L* 1y18 L* 3cfj L 3cfk L* 4k07 Probab=53.03 E-value=37 Score=23.16 Aligned_cols=59 Identities=14% Similarity=0.229 Sum_probs=0.0
                    0 ss pred
 Q Thu_Apr_23_00:
                 18 LGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKE----IKTNEYVIKTPVFTTGGDYILSLVSIK
                                                                                    82 (111)
                 ...++.+-.+.|.++.+.|---...|+.....+..
 T Consensus
                 102 (237)
                 38 VGDRVTITCRASODVSTAVAWYOOK--PGKAPKLLIYSASFLYSGVPSRFSGS----GSGTDFTLTISSLQ 102 (237)
 T 3sob L
                    TTCCEEEEEESSCCTTCEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETTEEEEEESSCC
 T ss dssp
                    CCCcEEEEeEccCCCcceEEEEEc--CCCCcEEEEEecccCCCCCccEEEE----cCCCEEEEEEcCCC
 T ss_pred
 No 67
                              SCOPe PROTEIN DATA BANK
                                                                  PubMed
>3b83 A Ten-D3; beta sheet, computational redesigned protein, cell adhesion, domain, extracellular matrix,
 glycoprotein, phosphorylation secreted; 2.40A {Homo sapiens} SCOP: b.1.2.0
 Probab=52.92 E-value=33 Score=20.56 Aligned_cols=47 Identities=9% Similarity=0.101 Sum_probs=0.0
                    CEEEEEEeCCCCCEEEEEeCcccccEEEeCCCccCCceEEEEEEE
 0 ss pred
 Q Thu_Apr_23_00:
                 34 FTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLVSIKDS
                                                                   84 (111)
                 84 (111)
                 T Consensus
                                                                   78 (100)
 T 3b83 A
                 32 ILVTFGRKN--DPSDETTVDLTSSITSLTLT--NLEPNTTYEIRIVARNGO
                                                                   78 (100)
                    EEEEEESS--CTTTCEEEEECTTEEEEEC--SCCTTCEEEEEEEETT
 T ss dssp
                    EEEEEEEcc--CCCceEEEEecCCccEEEEe--CCCCCCEEEEEEECCC
 T ss pred
                               PDB"
                                                          Pub Med
```

```
>1e07_A Carcinoembryonic antigen; glycoprotein, CEA, tumour marker, immunoglobulin-fold; NMR {Homo sapiens} PDB:
   2dks _A
 Probab=52.62 E-value=51 Score=26.34 Aligned cols=71 Identities=11% Similarity=0.097 Sum probs=0.0
                                     Q ss_pred
  Q Thu_Apr_23_00:
                               12 HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLVSIKDSTGCVVGL
                                                                                                                                                                           91 (111)
                                12 \quad \text{$\sim\sim\sim\sim\text{$C-g$}$} \\ \text{$\sim\text{$V-V$}$} \\ \text{$1$} \\ \text{$\sim\text{$W-D$}$} \\ \text{$W-D$} \\ \text{$\sim\text{$W-D$}$} \\ \text{$W-D$}   O Consensus
                                                                                                                                                                           91 (111)
                                     .....|+++++....|.||-+++|....+|+|+....+...|.--...|.|...+-.-.+...|
~~~~V~~g~~~1~C~~~g~~v~W~~----g~~1~------Li~~~~~d~G~Y~C~a~N~~G~~~s~1
 T Consensus
                                                                                                                                                                         636 (642)
 T 1e07 A
                               567 PDSSYLSGANLNLSCHSASNPSPQYSWRI---NGIPQQ-----HTQVLFIAKITPNNNGTYACFVSNLATGRNNSIVK
                                                                                                                                                                         636 (642)
 T ss_pred
                                     CCCEEECCCcEEEEEeCCCCCCceEEEE----CCEEcc-----cCceEEEecCcccCceEEEEEecccCccceEEE
 Q ss pred
                               92 S
 Q Thu Apr 23 00:
                                           92 (111)
 O Consensus
                                92 ~
                                           92 (111)
                              637 ~ 637 (642)
 T Consensus
 T 1e07 A
                               637 S 637 (642)
 T ss_pred
                                                                          PDB"
                                                        SCOPe
                                                                                                                          PubMed
>3q9a B Minimizer; antibody complex, chromophore, luminescence, photoprotein, fluorescent protein-immune system
 complex, nanobody; HET: GYS; 1.61A {Camelus dromedarius} SCOP: b.1.1.1
 Probab=52.53 E-value=54 Score=21.66 Aligned_cols=76 Identities=12% Similarity=0.146 Sum_probs=0.0
 Q ss_pred
                                     Q Thu Apr 23 00:
                                 3 KPSASLKLHHDLKLCLGDHSSVPVALKGO--GPFTLTYDIIETFSSKRKTFEI------KEIKTNEYVIKTPVFTT
                                                                                                                                                                           70 (111)
                                 3 ~asA~F~~~~~C~g~~v~v~V~l~G~~~PftL~yeiv~~~qk~~~~v~~~~i~~~~I~tp~~~~
 O Consensus
                                                                                                                                                                           70 (111)
                                  76 (139)
 T 3q9a B
                                  1 MADVOLOESGGGSVOAGGSLRLSCAASGDTFSSYSMAWFROA--PGKECELVSNILRDGTTTYAGSVKGRFTISRDD--A
                                                                                                                                                                           76 (139)
 T ss dssp
                                      ---CCEREESCERECTTCCEREEERECSSCGGGSEREEREC--TTSCEREERECTTCCERECTTTTTTTEERERET--T
                                     T ss pred
 Q ss pred
                                     CceEEEEEEE
  Q Thu_Apr_23_00:
                                71 GGDYILSLVSIK
                                                             82 (111)
 Q Consensus
                                71 GG~y~v~L~sV~
                                                             82 (111)
                                     .+.+.|.|.+|+
                                77 ~~~sL~I~~v~
 T Consensus
                                                             88 (139)
                                77 KNTVYLOMVNLK
 T 3q9a B
                                                             88 (139)
 T ss_dssp
                                     TTEEEEEECSCC
 T ss_pred
                                     CCEEEEECCCC
                                                          PDB'
                                                                           NCBI
                                                                                                        Pub Med
S3qs7_E FL cytokine receptor; immunoglobulin-like domain, four-helical bundle cytokine, CY receptor complex,
 extracellular complex; HET: NAG; 4.30A {Homo sapiens}
 Probab=52.46 E-value=59 Score=24.83 Aligned cols=57 Identities=23% Similarity=0.203 Sum probs=0.0
                                     CCCeeeeEEEecCCCcEEEEEEeCccccEEEE--eCCCccCCceEEEEEE
 Q ss pred
 Q Thu_Apr_23_00:
                                19 GDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVI--KTPVFTTGGDYILSLVS
                                                                                                                                                 80 (111)
 Q Consensus
                                19 g~~v~V~l~G~~PftL~yeiv~~~gk~~~~v~i~~~~I--~tp~~~~GG~y~v~L~s
                                                                                                                                                 80 (111)
                               | +++++...+.|.||-++.|...+||++...-...+.|.| ...-...|.|+...+

341 G---1-C---g-P-p-i-W-k----g-1-------D-G-Y-C-A-N 399 (423)
 T Consensus
                               341 YEEFCFSVRFKAYPQIRCTWTF----SRKSFPCEQKG-LDNGYSISKFCNHKHQPGEYIFHAEN
 T 3qs7_E
                                                                                                                                               399 (423)
 T ss_dssp
                                     TCCCCEEEEEECCCTTCCSCEEEEE
                                     CCGEEREEECCCCEEREEE.---CCCCCCCC-ccceEREEEccCCCCCeeREEEEC
 T ss_pred
 No 71
                                                        SCOPe
                                                                                                                             Pub Med
                                                                                              NCBI
- >4hjj_L Anti-IL12 anti-IL18 DFAB light chain; DFAB complex, dual variable domain immunoglobulin, IM system; 2.10A
  {Homo sapiens} SCOP: b.1.1.0 b.1.1.0 b.1.1.0
 Probab=52.25 E-value=36 Score=24.14 Aligned cols=72 Identities=11% Similarity=0.221 Sum probs=0.0
 Q ss pred
                                     ceEEeCC-CcceeccCCCeeeeEEEecCCCcEEEEEEEcCcc-----cccEEEeCCCccCceEEEE
  Q Thu_Apr_23_00:
                                  5 \ \ SASL \verb|KLH-HDLKLCLGDH| SSVPVAL \verb|KGQGPFTLTYDIIETFSSKRKTFEIKEIK| ----- TNEYVIKTPVFTTGGDYILS
                                                                                                                                                                           77 (111)
 Q Consensus
                                  77 (111)
                                     .+.|... +|+=.|+++.+.-.+.|.|+-.+.|--.. +|+....+...
                                                                                                                                 ..+|.+.
                                                                                                                              -----r
                                     ~~~V~~~p~~~~V~~G~~V~L~C~~~~p~~~V~W~k~~~~~g~~~~
 T Consensus
                                                                                                                                                                           74 (327)
                                  1 DIVMTQSPDSLAVSLGERATINCKASQSVSNDVAWYQQK-PGQPPKLLIYYASNRYTGVPDRFSGS----GSGTDFTLT
 T 4hjj_L
                                                                                                                                                                           74 (327)
 T ss_dssp
                                     CCCEEECSEEECTTSCEEEEEESSCCTTCEEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETTEEEEE
 T ss_pred
                                     CcceecCCCceEEEcccCCceEEEEEec---cCCceEEEEE
 Q ss_pred
                                     EEEEE
 Q Thu_Apr_23_00:
                               78 LVSIK
                                                  82 (111)
 Q Consensus
                                78 L~sV~
                                                  82 (111)
                                      |.+|+
 T Consensus
                                75 i~~v~
                                                  79 (327)
                                75 ISSLE
 T 4hjj L
                                                  79 (327)
  T ss_dssp
                                     ESSCC
 T ss_pred
                                     EccCC
```

```
PDB
No 72
                            SCOPe
                                                              Pub Med
>2znx A SCFV; fluorotryptohpan, 5-fluorotryptophan, 19F, single chain FV, allergen, antimicrobial, bacteriolytic
 enzyme, glycosidase, hydrolase; HET: FTR 1PG; 2.30A (Mus musculus) SCOP: b.1.1.0 b.1.1.0 PDB: 2znw A*
 Probab=52.22 E-value=36 Score=23.65 Aligned_cols=58 Identities=19% Similarity=0.197 Sum_probs=0.0
                  CCCeeeeEEEecCCCcEEEEEEEcCCCcEEEEEEcccc-----cccEEEecCcccCceEEEEEEEE
Q ss pred
Q Thu Apr 23 00:
                19 GDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIK----TNEYVIKTPVFTTGGDYILSLVSIK
                                                                             82 (111)
                19 g~~v~v~l~G~~PftL~yeiv~~~~gk~~~~v~i~-----I~tp~~~~GG~y~v~L~sV~
O Consensus
                                                                             82 (111)
                   |+++.+.-.+.|.|+-.+.|---...|+....
                                                      ..+|.+. ..++.+.|.|.+|+
                                                                             79 (242)
                T Consensus
T 2znx_A
                16 GNSVSLSCRASOSIGNNLHXYOOK--SHESPRLLIKYASOSISGIPSRFSGS----GSGTDFTLSINSVE
                                                                             79 (242)
                  TCCEEEEEESSCCTTCEEEEEC--TTSCCEEEEETTTEECTTSCTTEEE----EETTEEEEEESSCC
T ss dssp
T ss pred
                  CCeEEEEeEcCCCcceEEEEEec--CCCCceEEEEEcccCCCccCceEe----cCCCeEEEEcccCC
                            SCOPe
                                                              Pub Med
>3zkx C XA4815; hydrolase; 2.37A {Lama glama} SCOP: b.1.1.1
Probab=52.08 E-value=47 Score=20.84 Aligned_cols=61 Identities=8% Similarity=0.164 Sum_probs=0.0
                  CCCCeeeeeeecc--CCceeeeeeeeccCCcceeeeee
Q Thu Apr 23 00:
                18 LGDHSSVPVALKGQ--GPFTLTYDIIETFSSKRKTFEI-----KEIKTNEYVIKTPVFTTGGDYILSLVSIK
                                                                                    82 (111)
                Q Consensus
                                                                                    82 (111)
T Consensus
                                                                                    87 (122)
                14 AGGSLRLSCAASGFTFSRAAMRWVRRA--PERGLEWVANINAGDGSASYADFVKGRFTASRDK--AGNRLYLQMDNLR
T 3zkx C
                                                                                    87 (122)
T ss_dssp
                  TTCCEEEEECCSSEETTCCEEEEEE--TTTEEEEEEEECSSSCCEECTTTTTCEEEEECS--SSSEEEEECSCC
                  CCCcEEEEEcCCCcccceEEEEEEC--CCCCCEEEEEEecCCCcEecCccccceEEEEcC--CCCEEEEEEcCCC
T ss_pred
No 74
                                              Pub Med
>4bsj_A Vascular endothelial growth factor receptor 3; transferase, lymphangiogenesis, angiogenesis, IG D
glycoprotein, receptor tyrosine kinase; HET: NAG; 2.50A {Homo sapiens}
Probab=51.59 E-value=64 Score=22.29 Aligned_cols=71 Identities=23% Similarity=0.268 Sum_probs=0.0
                  Q ss pred
                  \textbf{3} \quad \textbf{KPSASLKLH--HDLKLCLGDH-SSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV} \\ 
Q Thu Apr 23 00:
                                                                                     79 (111)
                 3 ~asA~F~~~~~C~g~~v~v~V~l~G~~PftL~yeiv~~~gk~~~~v~i~~~~I~tp~~~GG~y~v~L~
                                                                                     79 (111)
Q Consensus
                  75 (232)
T Consensus
                 3 NPFISVEWLKGPILEATAGDELVKLPVKLAAYPPPEFQWYK----DGKALSGR---HSPHALVLKEVTEASTGTYTLALW
T 4bsj A
                                                                                     75 (232)
T ss_dssp
                  CCEEEEESSCSEEEEETTCEEEEEEEEEEEEEEEEEEE.---TTEECCSC---CCSSEEEEEECCGGGCEEEEEEE
T ss_pred
                  CcceEeccCCCcEEEeccCEEEEEEeeeCCCEEEEEc----CCeccCC---CCcceEEEccCChhhCeEEEEEE
Q ss_pred
Q Thu_Apr_23_00:
                80 S
                     80 (111)
O Consensus
                80 s
                     80 (111)
                76 n
                     76 (232)
T Consensus
T 4bsj_A
                76 N
                      76 (232)
T ss dssp
T ss pred
No 75
                             PDB"
                                              Pub Med
>4c57_C Nanobody, cyclin-G-associated kinase; transferase, conformational plasticity, activation; HET: FEF; 2.55A
 {Lama glama}
           E-value=49 Score=20.98 Aligned cols=74 Identities=11% Similarity=0.081 Sum probs=0.0
Probab=51.59
                  Q ss pred
                 5 SASLKLHHDLKLCLGDHSSVPVALKGQ--GPFTLTYDIIETFSSKRKTFEI-----KEIKTNEYVIKTPVFTTG
                                                                                     71 (111)
Q Thu Apr 23 00:
O Consensus
                 71 (111)
                 ..-..+|.+....
                                                                     ~~~~R~~~~
T Consensus
                                                                                     76 (141)
                1 QVQLQESGGGLVQPGGSLRLSCSASGFKFNDSYMSWVRRV--PGKGLEWVAGIWEDSSAAHYRDSVKGRFTISRDN--AK
T 4c57_C
                                                                                     76 (141)
 T ss dssp
                  T ss_pred
                  ceeeeeeee
Q ss pred
Q Thu Apr 23 00:
                72 GDYILSLVSIK
                             82 (111)
 Q Consensus
                72 G~y~v~L~sV~
                              82 (111)
                  +.+.|.|.+|+
                77 ~~~sL~I~~v~
T Consensus
                             87 (141)
T 4c57 C
                77 NMLYLOMSSLK
                             87 (141)
                  TEEEEECSCC
T ss dssp
T ss_pred
                  CEEEEEccCC
No 76
                             PDB
                                                    Pub Med
>2c4x A Endoglucanase, ctcel9D-CEL44A; cellulase ctcel9D-CEL44A, PKD domain, CBM44, carbohydrate BI module,
beta-sandwich proteins, cellulosome; 2.0A {Clostridium thermocellum} PDB: 2c26 _A
Probab=51.51 E-value=11 Score=28.89 Aligned_cols=29 Identities=21% Similarity=0.558 Sum_probs=0.0
                  ccCceEEEEEEEcccCccccCCCceEE
Q ss pred
```

```
Q Thu_Apr_23_00:
                68 FTTGGDYILSLVSIKDSTGCVVGLSQPDAKI
                                               98 (111)
O Consensus
                \texttt{68} \quad \text{---} \texttt{GG-} \texttt{y-} \texttt{v-} \texttt{L-} \texttt{sV-} \texttt{D---} \texttt{GC----} \texttt{L-----} \texttt{v-} \texttt{I}
                                               98 (111)
                  +..-|.|.|+ |+|..||........
                65 y~~~G~YtVtLt-Vtd~~G~s~t~t~-~ItV
T Consensus
                                               93 (260)
                65 YKNPGTYKVKLI-VTDNQGASSSFTA-TIKV
T 2c4x A
                                               93 (260)
                   CSSCEEEEEE-EEETTSCEEEEE-EEE
T ss_dssp
                   eccceeeeee=eecccceeeee=eee
T ss pred
No 77
                            SCOPe PROTEIN DATA BANK
                                                                Pub Med
->1kxv_C Camelid VHH domain CAB10; beta 8 alpha 8, beta barrel, hydrolase, immune system; 1.60A {Camelus
dromedarius | SCOP: b.1.1.1
Probab=51.28 E-value=43 Score=20.24 Aligned cols=61 Identities=15% Similarity=0.196 Sum probs=0.0
                   Q ss pred
Q Thu_Apr_23_00:
                18 LGDHSSVPVALKGQ--GPFTLTYDIIETFSSKRKTFEIKEIKT----NEYVIKTPVFTTGGDYILSLVSIK
                                                                                     82 (111)
                82 (111)
O Consensus
                   .++.+.... ..+.+.|.|.+|+
                14 ~G~~v~L~C~~~
                                                                          ~~~sL~I~~v~
                                                                                     86 (121)
T Consensus
                                                               ~r~~
T 1kxv_C
                14 AGGSLRLSCAASGNTLCTYDMSWYRRA--PGKGRDFVSGIDNDGTTTYVDSVAGRFTISQGN--AKNTAYLQMDSLK
                                                                                     86 (121)
                   T ss_dssp
                   T ss pred
                             PDB<sup>N</sup>
PROTEIN DATA BANK
NCBI
No 78
                                               Pub Med
->4qci_A ANTI-PDGF-BB antibody - light chain; growth factor cytokine fold, growth factor hormone, PDGFR-BE
receptor, extracellular; 2.30A {Homo sapiens}
Probab=50.81 E-value=22 Score=23.76 Aligned cols=72 Identities=10% Similarity=0.171 Sum probs=0.0
Q ss pred
                   ceEEeCCCcceeccCCCeeeeEEEecCCCcEEEEEEeCccc-----ccccEEEeEeCCCccCceEEEEE
Q Thu_Apr_23_00:
                 5 SASLKLHHDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEI-----KTNEYVIKTPVFTTGGDYILSL
                                                                                       78 (111)
                 O Consensus
                                                                                       78 (111)
T Consensus
                                                                                       74 (209)
                 1 SYELTQPPSVSVAPGQTARISCSGDSLGSYFVHWYQQK--PGQAPVLVIYDDSNRPSGIPERFSGSN----SGNTATLTI
T 4qci_A
                                                                                       74 (209)
                   -\texttt{CCCBCCSEEEECTTSCEEEEECTTGGGBCCEEEEC--TTSCCEEEEBTTTBCCTTCCTTEEEEE----ETTEEEEEE
T ss_dssp
                   CCCEEeCCeEEEeCcCcceEEEEEEc--CCCcEEEEEEc---cCCccEEEEE
T ss pred
                   ERRE
Q ss pred
Q Thu_Apr_23_00:
                79 VSIK
                         82 (111)
                79 ~sV~
                         82 (111)
                  .+|+
                75 ~~v~
                         78 (209)
T Consensus
T 4qci_A
                75 SGTO
                        78 (209)
T ss_dssp
                   SSCC
T ss_pred
                                      NCBI Pub Med
        Nanobody VHH PVSP6A; picornavirus, antibody, poliovirus, mechanism neutralization, virus-immune system
 complex; HET: MYR PLM; 4.80A {Camelus dromedarius}
Probab=50.57 E-value=50 Score=20.71 Aligned_cols=63 Identities=10% Similarity=0.056 Sum_probs=0.0
                   Q ss pred
                18 LGDHSSVPVALKGQG--PFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGDYILSLVSIK
Q Thu Apr 23 00:
                                                                                    82 (111)
                82 (111)
                T Consensus
                                                                                    87 (126)
                14 TGGSLRLSCAASGFTFSHGYMAWFRQAPEKEREWVACVRTSGVSAYYADSVLGRFTISQDN--AKSTLYLQMNNLK
T 3i69 7
                                                                                    87 (126)
                   TTCCEEEEEECSCCCCSSEEEEEECCSSSSCEEEEEEESSCCCEEECTTTTTTEEEEEEG--GGTEEEEEECSCC
T ss dssp
T ss pred
                   CCCcEEEEEecCCcccceEEEEEEcCCCCCEEEEEEEcCCcceeEEEEEcC--CCCEEEEEECCCC
                             PDB"
                                               Pub Med
No 80
                                      NCBI
        Myomesin; structural protein, sarcomere, M-BAND, immunoglobulin- like; 2.50A {Homo sapiens} PDB: 4v10 _A
 Probab=50.15 E-value=59 Score=22.90 Aligned_cols=72 Identities=8% Similarity=0.108 Sum_probs=0.0
                   CCCeeeeEEEec-CCCcEEEEEEECCCCcEEEEE-eCcccccEEEeCCCc--CCceEEEEEEEECccCCcccCCC
Q ss pred
Q Thu_Apr_23_00:
                19 GDHSSVPVALKG-QGPFTLTYDIIETFSSKRKTFE-IKEIKTNEYVIKTPVFT--TGGDYILSLVSIKDSTGCVVGLSQP
                                                                                       94 (111)
Q Consensus
                94 (111)
               T Consensus
                                                                                      311 (312)
               236 ECNVLLKCKVANIKKETHIVWYK----DEREISVDEKHDFKDGICTLLITEFSKKDAGIYEVILKDDRGKDKSRLKLVDE
T 2y23 A
                                                                                      311 (312)
                   TTEEEEEEEECCSCEEEEE----TTEEEEEECCC----CEEEEEECSCSGGGCEEEEEEESTTCCEEEEEECSC
T ss dssp
                   CCEEEEEEEeCCCCCcEEEEE----CCEECCCCcEEEECCEEEEECcCcccCEEEEEEecCCCEEEEEEeee
T ss pred
No 81
                             PDB<sup>N</sup>
                                      NCBI
                                                Pub Med
>2bk8 A Connectin, M1, titin heart isoform N2-B; IG domain, M-BAND, structural protein, muscle, antibo; 1.69A
 {Homo sapiens}
            E-value=42 Score=19.74 Aligned_cols=71 Identities=14% Similarity=0.169 Sum_probs=0.0
                   GEEECC-CCCeeccCCCCeeeeEEEEc-CCCCEEEEEEEECCCCCEE----EEECCCCCCEEEECCCCC--CCGEEEE
Q ss pred
Q Thu_Apr_23_00:
                 5 SASLKLH-HDLKLCLGDHSSVPVALKG-QGPFTLTYDIIETFSSKRK----TFEIKEIKTNEYVIKTPVFT--TGGDYIL
                                                                                       76 (111)
```

```
Q Consensus
                               5 sA-F----C-g--v-v-V-l-G---PftL-yeiv---gk-----v-v-i-----I-tp-----GG-y-v
                                                                                                                                                              76 (111)
                               T Consensus
                                                                                                                                                               75 (97)
                               1 GAMVSGQIMHAVGEEGGHVKYVCKIENYDQSTQVTWYF----GVRQLENSEKYEIT-YEDGVAILYVKDITKLDDGTYRC
 T 2bk8 A
                                                                                                                                                               75 (97)
                                   CCCEECCCCEEECTTCCEEEEEEESCCTTCEEEEEE.---TTEECCSSSSEEEE-EETTEEEEEECSCCGGGCEEEEE
 T ss dssp
                                  CCCEECCCEEEEEEECCCCCCEEEEEEE.----CCEECCCCCEEEE-ECCCEEEEEECCCCHHHCEEEEE
 T ss pred
 Q ss pred
                                  EEEE
 Q Thu_Apr_23_00:
                             77 SLVS
                                             80 (111)
 Q Consensus
                             77 ~L~s
                                             80 (111)
                              76 ~a~n
 T Consensus
                                             79 (97)
 T 2bk8 A
                              76 KVVN
                                            79 (97)
 T ss_dssp
                                  EEEC
 T ss_pred
             Pub Med

C 42F3 alpha; IG, TCR MHC, immune system; 1.92A {Mus musculus} PDB: 3tfk _C 3tpu _A 3tjh _C 3vxm _D 1j8h _D*

Apdk C* 1mwa A* 1g6r _A* 1tcr _A* 2ckb _A 1zgl _M 3c5z _A 1i9e _A* 20i9 _B 2e71
 No 82
   1fyt D* 4gkz A* 3rev A 4p4k C* 1mwa A* 1g6r A* 1tcr A* 2ckb A 1zg1 M 3c5z A 1i9e A* 2ci9 B 2e71 A
 Probab=49.95 E-value=58 Score=21.34 Aligned_cols=77 Identities=9% Similarity=0.062 Sum_probs=0.0
                                  Q ss pred
 Q Thu_Apr_23_00:
                                2 VKPSASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKT----NEYVIKTPVFTTGGD
                                                                                                                                                               73 (111)
                               T Consensus
                                                                                                                                                               77 (212)
 T 4ms8 C
                               2 SHMAQSVTQPDARVTVSEGASLQLRCKYSYSATPYLFWYVQY--PRQGLQMLLKYYSGDPVVQGVNGFEAEFS--KSDSS
                                                                                                                                                               77 (212)
 T ss dssp
                                   ----CEECSCSEEEEETTSCEEECCECCSSCCEEEEEEC--TTSCEEEEEECSSCSEEECGGEEEEE--TTTTE
 T ss_pred
                                  cccceEEEecCCeEEEecCcceEEEEec--CCCCceEEEEEc--CCCCc
                                  EEEEEEEE
 Q ss pred
 Q Thu Apr 23 00:
                              74 YILSLVSIK
                                                    82 (111)
 Q Consensus
                              74 y\sim v\sim L\sim sV\sim
                                                    82 (111)
                                   +.|.|.+|+
 T Consensus
                              78 ~~L~i~~v~
                                                    86 (212)
 T 4ms8 C
                              78 FHLRKASVH
                                                    86 (212)
 T ss dssp
                                  EEEEESSCC
 T ss_pred
                                  EEEEEccCC
 No 83
                                                                      PDB"
                                                    SCOPe
                                                                                                                    Pub Med
>1x9q_A SCFV, 4M5.3 anti-fluorescein single chain antibody fragment; VERY high affinity, antibody binding,
  electrostatics, directed evolution; HET: FLU; 1.50A (Homo sapiens) SCOP: b.1.1.0 b.1.1.0
 Probab=49.39 E-value=42 Score=23.63 Aligned_cols=73 Identities=14% Similarity=0.249 Sum_probs=0.0
                                  CceEecC-CcceeccCCCeeeeEEEecCC-----CcEEEEEEEECCCCcEEEEEECCCccCC
 Q ss pred
 Q Thu Apr 23 00:
                                4 PSASLKLH-HDLKLCLGDHSSVPVALKGQG-----PFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTG
                                                                                                                                                               71 (111)
                                4 \ \text{asA-F----} \text{C-g--v-v-v-l-G------} \text{PftL-yeiv----gk-----v-i-t------} \text{I-tp----G------} \text{I-tp------} \text{Section } \text{S
 Q Consensus
                                                                                                                                                               71 (111)
                                  +.+.|....|+++.+.-.+.|.+
                                                                                      +..+.|---. .|+....+....
 T Consensus
                              87 (268)
                              14 \  \   SDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLRWYLQK--PGQSPKVLIYKVSNRVSGVPDRFSGS----GSG
 T 1x9q A
                                                                                                                                                               87 (268)
                                  CCCCEEECSEECCTTCCEEEEEEESSCCBCTTSCBCEEEEEEC--TTSCCEEEEETTTEECTTSCTTEEEE----EET
 T ss_dssp
                                  T ss_pred
 Q ss_pred
                                  CERRERERER
 Q Thu Apr 23 00:
                             72 GDYILSLVSIK
                                                       82 (111)
                              72 G~v~v~L~sV~
 O Consensus
                                                       82 (111)
                                  +.+.|.|.+|+
 T Consensus
                              88 ~~~~L~I~~v~
                                                       98 (268)
                              88 TDFTLKINRVE
 T 1x9q A
                                                       98 (268)
 T ss_dssp
                                  TEEEEEESSCC
 T ss pred
                                  CEEEEECCCC
                                                    SCOPe
                                                                                                                  Pub Med
                                                                                      S NCBI
>2dj4 A Filamin-B; beta-sandwich, immunoglobulin-like fold, filamin domain, NPPSFA, national project on protein
 structural and functional analyses; NMR {Homo sapiens} SCOP: b.1.18.10
Probab=49.31 E-value=47 Score=21.43 Aligned_cols=61 Identities=11% Similarity=0.077 Sum_probs=0.0
                                  Q ss_pred
 Q Thu Apr 23 00:
                             17 CLGDHSSVPVALKGOGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV
                                                                                                                                     79 (111)
                              17 C~g~~v~v~l~G~~PftL~yeiv~~~~gk~~~~v~i~~~~~I~tp~~~~GG~y~v~L~
 O Consensus
                                                                                                                                     79 (111)
                                  +. | .++.+. | .....+.=. | +-. | ..+. | +....+.+-.+.. | ++.--... | . | . | .+.
                              26 ~~g~~~F~V~~~~aG~~~l~v~i~~p~~g~~~~v~d~~dGty~v~Y~p~~~G~~y~i~V~
                                                                                                                                     86 (108)
                              26 RARVLQSFTVDSSKAGLAPLEVRVLGPR-GLVEPVNVVDNGDGTHTVTYTPSQEG-PYMVSVK
 T 2dj4 A
                                                                                                                                     86 (108)
                                  BTTSCEEEEECTTTCSCCEEEEECSS-SCEECCCCEECSSSEEEEECCSSCE-EEEEEE
 T ss_dssp
 T ss_pred
                                  ecCceEEEEEEccCCCCCEEEEEECCC-CCEeeEEEEECCCCEEEEEEE
                                                 SCOPe PDB SNCBI Pub Med
> > 1moe_A Anti-CEA MAB T84.66; anti carcinoembryonic antigen, diabody, dimer, SCFV, variable domain, immune system;
```

```
2.60A {Mus musculus} SCOP: b.1.1.1 b.1.1.1
 Probab=49.19 E-value=36 Score=23.32 Aligned cols=72 Identities=11% Similarity=0.110 Sum probs=0.0
                   ceEEeCC-CcceeccCCCeeeeEEEecCC----CcEEEEEEEECCCCcEEEEEEeCccc------ccEEEeCCCccCCce
 0 ss pred
 Q Thu Apr 23 00:
                  5 SASLKLH-HDLKLCLGDHSSVPVALKGQG----PFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGD
                                                                                           73 (111)
                  Q Consensus
                                                                                           73 (111)
                  ..+|.+. ..++.
 T Consensus
                                                                          ---r-----
                                                                                           74 (240)
                  1 DIVLTQSPASLAVSLGQRATMSCRAGESVDIFGVGFLHWYQQK--PGQPPKLLIYRASNLESGIPVRFSGT----GSRTD
 T 1moe A
                                                                                           74 (240)
                   CCCEEECSEEECTTSCEEEEEEESSCCEETTEECEEEEEC--TTSCCEEEEETTTEECTTCCTTEEEE----EETTE
 T ss dssp
                   CCceEeCCCEEEEecCCCCEEEEeecCcccCCCceEEEEEEC--CCCCcEEEEEECCccCCCCCCEEEe----cCCCE
 T ss_pred
                   EEEEEEEE
 Q ss pred
                              82 (111)
 Q Thu Apr 23 00:
                 74 YILSLVSIK
 O Consensus
                 74 y~v~L~sV~
                              82 (111)
                   +.|.|.+|+
 T Consensus
                 75 ~~L~I~~v~
                              83 (240)
 T 1moe A
                 75 FTLIIDPVE
                              83 (240)
 T ss_dssp
                   EEEEESSCC
 T ss pred
                   EEEEECCCC
 No 86
                              SCOPe
                                                                 Pub Med
>4ndm_B AB18.1 TCR delta chain; immunoglobulin, histocompatibility antigens, T cell receptor immunological,
 lymphocytes, T cell recognition, activation; 3.01A {Homo sapiens} SCOP: b.1.1.2 b.1.1.0
 Probab=49.11 E-value=66 Score=21.68 Aligned_cols=77 Identities=9% Similarity=0.168 Sum_probs=0.0
                   CCCceEEeCC-CcceeccCCCeeeeEEEecC-CCcEEEEEEEeCcCccEEEEEeCccc------cccEEEeCCCccCCce
 0 ss pred
 Q Thu Apr 23 00:
                  2 VKPSASLKLH-HDLKLCLGDHSSVPVALKGQ-GPFTLTYDIIETFSSKRKTFEIKEIK-----TNEYVIKTPVFTTGGD
                                                                                           73 (111)
                  2 --asA-F-----I-tp----GG-
 O Consensus
                                                                                           73 (111)
                  T Consensus
                                                                                           84 (235)
                  9 EDPAQKVTQAQSSVSMPVRKAVTLNCLYETSWWSYYIFWYKQL--PSKEMIFLIRQGSDEQNAKSGRYSVNFK--KAAKS
 T 4ndm B
                                                                                           84 (235)
                    ---CCEEECCCCEEEETTSCEEEEEEEECCCSSCEEEEEEC-TTCCEEEEEEEESSSCCCEETTEEEEEE-TTTTE
 T ss_dssp
 T ss pred
                   Q ss_pred
                   EFFFFFFFF
 Q Thu_Apr_23_00:
                 74 YTLSTVSTK
                              82 (111)
 Q Consensus
                 74 y~v~L~sV~
                              82 (111)
                   +.|.|.+|+
 T Consensus
                              93 (235)
                 85 VALTISALO
 T 4ndm B
                              93 (235)
 T ss dssp
                   EFFESSCO
 T ss pred
                   EEEEEccCC
 No 87
                               PDB"
                                                 Pub Med
                                        NCBI
>4wem B Anti-F4+ETEC bacteria VHH variable region; complex, llama single domain antibody, adhesin, nanobody, ST
 protein; 1.55A {Lama glama}
 Probab=49.07 E-value=54 Score=20.65 Aligned_cols=76 Identities=9% Similarity=0.027 Sum_probs=0.0
                   GERECCCCGeecaCCCCeeeeREEcc--CCGEEEEEEECCCCGEEEEEE-------CGGGGGGEEEECCCGGCCGEE
 Q ss pred
                  5 SASLKLHHDLKLCLGDHSSVPVALKGQ--GPFTLTYDIIETFSSKRKTFEI-----KEIKTNEYVIKTPVFTTGGDY
 Q Thu_Apr_23_00:
                                                                                           74 (111)
                  5 sA-F-----C-g--v-v-V-l-G----PftL-yeiv----gk-----v-i-----i-----I-tp----GG-y
 Q Consensus
                                                                                           74 (111)
                   T Consensus
                                                                                           78 (127)
                  1 \  \, \text{QVQLQESGGGLVQAGGSLRLSCEASGNVDRIDAMGWFRQAPGKQREFVGYISEGGILNYGDFVKGRFTISRDN--AKNTV}
 T 4wem B
                                                                                           78 (127)
 T ss dssp
                   CEEEEECCEEEETTCCEEEEEEESGGGCCCEEEEECTTSCCEEEEECTTCCEEECTTCCTTEEEEEEG--GGTEE
 T ss_pred
                   EEEEEEE
 Q ss_pred
 Q Thu_Apr_23_00:
                 75 ILSLVSIK
                             82 (111)
 O Consensus
                 75 ~v~L~sV~
                             82 (111)
                   .|.|.+|+
 T Consensus
                 79 sL~I~~v~
                             86 (127)
 T 4wem_B
                 79 YLOMSNLK
                             86 (127)
                   EEEECSCC
 T ss_dssp
                   EEEECCCC
 T ss pred
 No 88
                              SCOPe
                                        PDB"
                                                                 Pub Med
🔝 >3u14_A Cellulosome-anchoring protein; cohesin, type I cohesin-dockerin COMP protein-protein interaction, cell
 adhesion; HET: PEG; 1.95A {Clostridium thermocellum} SCOP: b.2.2.0
 Probab=49.02 E-value=9 Score=27.40 Aligned_cols=21 Identities=48% Similarity=0.822 Sum_probs=0.0
 Q ss_pred
                   CCCeeeeEEEecCC-----CcEEEEE
 Q Thu_Apr_23_00:
                 19 GDHSSVPVALKGQG-----PFTLTYD
                                              39 (111)
 Q Consensus
                 19 g~~v~v~V~l~G~~----PftL~ye
                                              39 (111)
                 |+++++|.|.+-| +|.|.|+
20 G-tf-V-V---nvp--gi-s--f-1-YD
                                              47 (157)
 T Consensus
                 20 GDRIEVPVSLKNVPDKGIVSSDFVIEYD
 T 3u14_A
                                              47 (157)
 T ss dssp
                   TCEEEEEEESCCTTCEEEEEEECC
                   CCEEEEEEEcCccCCeeeEEEEEEC
 T ss pred
```

```
PDB"
 No 89
                                                                                                      Pub Med
>3d33 A Domain of unknown function with AN immunoglobulin beta-sandwich fold; structural genomics, joint center
  for structural genomics; HET: MSE; 1.70A {Bacteroides vulgatus atcc 8482}
  Probab=48.72 E-value=65 Score=21.49 Aligned_cols=64 Identities=9% Similarity=0.013 Sum_probs=0.0
                                    ceeccCCCeeeeEEEecCCCcEEEEEEEeCCCCcEEEEEeCccc-ccEEEEeCCCccCceEEEEEE
 Q ss pred
 Q Thu Apr 23 00:
                               14 LKLCLGDHSSVPVALKGOGPFTLTYDIIETFSSKRKTFEIKEIKT-NEYVIKTPVFTTGGDYILSLVS
                                                                                                                                                     80 (111)
                                14 ----C-g---v-v-V-l-G---PftL-yeiv----gk-----v--i------I-tp-----GG-y-v-L-s
 Q Consensus
                                                                                                                                                     80 (111)
                                +.+++.+. .+.|.| -.+==.++-.|.+-.+|+..-... .+.|.+..+...|+|.|-|.+
31 i-a-id---L-I-F------vtItV--d-tG-iVY------I-L-----G-Y-lei--
                                                                                                                                                     95 (108)
 T Consensus
                                31 ITVFTDGY-LLTLKN-ASPDRDMTIRITDMAKGGVVYENDIPEVQSAYITISIANF-PAEEYKLEITG
EEEEEETT-EEEEEE-SSCCSEEEEEEEETTTCCEEEEEEECGGGTTEEEECTTS-CSEEEEEEEE
 T 3d33 A
                                                                                                                                                     95 (108)
 T ss dssp
                                    T ss pred
 No 90
                                                                         PDB
                                                                                                                        PubMed
                                                       SCOPe
>2yz1_A Tyrosine-protein phosphatase non-receptor type substrate 1; beta-sandwich, structural genomics, NPPSFA;
 1.40A {Mus musculus} SCOP: b.1.1.0
 Probab=48.69 E-value=26 Score=21.22 Aligned cols=78 Identities=6% Similarity=0.066 Sum probs=0.0
                                    CGERECC-CGGeeggCCCeeeeEEEEgC-CCGEEEEEEECCGCGEEEEEECCGGGGGGEEEECCCG-CCCGEEEEEEE
 Q ss_pred
 Q Thu_Apr_23_00:
                                 4 PSASLKLH-HDLKLCLGDHSSVPVALKGQ-GPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVF-TTGGDYILSLVS
                                                                                                                                                                        80 (111)
                                 4 asA-F----I-tp----GG-y-v-L-s
 Q Consensus
                                                                                                                                                                        80 (111)
                                 T Consensus
                                                                                                                                                                        84 (120)
 T 2yz1_A
                                 {\small \textbf{6} \ \ \textbf{KELKVTQPEK}SVSVAAGDSTVLNCTLTSLLPVGPIKW-YRGVGQSRLLIYSFTGEHFPRVTNVSDATKRNNMDFSIRISN} \\
                                                                                                                                                                        84 (120)
                                     -CCCEECCSSEEECTTCCEEECCESCCCSCCCEEE-EESSSTTCEEEEEECECTTTCCSEEECCBSSTTBCCEEECS
 T ss dssp
 T ss pred
                                    Q ss_pred
                                    EE
 Q Thu_Apr_23_00:
                               81 IK
                                            82 (111)
 O Consensus
                               81 V~
                                            82 (111)
                                     +
                                85 v~
 T Consensus
                                            86 (120)
                                85 VT
 T 2yz1 A
                                            86 (120)
 T ss_dssp
                                    CC
 T ss_pred
                                    CC
                                                    SCOPe PROTEIN DATA BANK
                                                                                           NCBI (1)
                                                                                                                           Pub Med
🗌 >2p9r_A Alpha-2-M, alpha-2-macroglobulin; human alpha2-macroglobulin, Mg2 domain, X-RAY, signaling protein; 2.30A
  {Homo sapiens} SCOP: b.1.29.3
  Probab=48.50 E-value=55 Score=20.60 Aligned_cols=60 Identities=8% Similarity=0.100 Sum_probs=0.0
 Q ss pred
                                    CCCeeeeEEEecC----CCcEEEE-EEEeCCCCcEEEEEeCcccc--cEEEeCCCccCCceEEEEE
 Q Thu_Apr_23_00:
                               19 GDHSSVPVALKGQ----GPFTLTY-DIIETFSSKRKTFEIKEIKTN--EYVIKTPVFTTGGDYILSL
                                                                                                                                                   78 (111)
 O Consensus
                                \  \  \, \text{19}\  \, \text{g} \sim \sim v \sim v \sim 1 \sim G \sim --- \sim P \\ \text{ftL} \sim y - \\ \text{ei}v \sim -- \sim g \\ \text{k} \sim --- \sim v \sim \\ \text{i} \sim --- \sim I \sim \\ \text{tp} \sim -- G \\ \text{G} \sim y \sim v \sim \\ \text{L} \sim --- \\ \text{ftL} \sim --- \\ \text{ftL} \sim --- \\ \text{ftL} \sim y - \\ \text{ei}v \sim --- \\ \text{gk} \sim --- \\ \text{ftL} \sim y - \\ \text{ei}v \sim --- \\ \text{ftL} \sim --- \\ \text{ftL} \sim y - \\ \text
                                                                                                                                                   78 (111)
                                T Consensus
                                                                                                                                                    82 (102)
 T 2p9r A
                                16 GQTVKFRVVSMDENFHPLNELIPLVYIQDPKGNRIAQWQSFQLEGGLKQFSFPLSSEPFQGSYKVVV
                                                                                                                                                   82 (102)
 T ss_dssp
                                    TCEEEEEEECGGGCBCCCEEEEEEECTTSCEEEEEEECBTTEEEEEECCSSCCCEEEEEE
 T ss_pred
                                    SCOPe PDB
                                                                                           NCBI
                                                                                                                          Pub Med
□ >laoh A Cellulosome-integrating protein CIPA; cellulosome subunit, B-barrel, cellulose degradation; 1.70A {Clostridium thermocellum} SCOP: b.2.2.2 PDB: lanu A
  Probab=47.95 E-value=9.7 Score=26.83 Aligned_cols=21 Identities=38% Similarity=0.774 Sum_probs=0.0
                                    CCCeeeeEEEecCC-----CcEEEEE
 Q ss pred
 Q Thu_Apr_23_00:
                              19 GDHSSVPVALKGQG-----PFTLTYD
                                                                                     39 (111)
 O Consensus
                               19 g~~v~v~V~l~G~~----PftL~ye
                                                                                     39 (111)
                                |+++++||.|.+-| +|.|.|+

18 G-tf-V-V---nvp--gi-----f-l-yD
 T Consensus
                                                                                     45 (147)
 T laoh A
                                18 GDTVRIPVRFSGIPSKGIANCDFVYSYD
                                                                                     45 (147)
 T ss_dssp
                                    TCEEEEEEEECCTTCBSEEEEEECC
 T ss_pred
                                    CCEEEEEEEecCccCCceeEEEEEEC
 No 93
                                                         PDB
                                                                         NCBI
                                                                                                        Pub Med
>4nof A Polymeric immunoglobulin receptor; immune system, ortholog, structural genomics, PSI-biology, N structural genomics research consortium, nysqrc; HET: NAG; 1.65A {Mus musculus}
 Probab=47.72 E-value=48 Score=19.86 Aligned_cols=68 Identities=16% Similarity=0.232 Sum_probs=0.0
                                     Q ss pred
 Q Thu_Apr_23_00:
                                 6 ASLKLH-HDLKLCLGDHSSVPVALKGQG-PFTLTYDIIETFSS-----KRKTFEIKEIKTNEYVIKTP
                                                                                                                                                                        66 (111)
 O Consensus
                                 66 (111)
                                    T Consensus
                                                                                                                                                                        81 (125)
                                 4 GGLPSDTHVYTKDIGRNVTIECPFKRENAPSKKSLCKKT--NQSCELVIDSTEKVNPSYIGRAKLFMKGTDLTVFYVNIS
 T 4nof A
                                                                                                                                                                        81 (125)
 T ss_dssp
                                    {\tt CCCCTTCEEEEEETTCCEEEEEECCGGGTTSCEEEEEC--SSCEEEEEETTSCBCTTTTTTEEEECCTTCTTEEEEEEC}
 T ss_pred
```

```
Q ss pred
                     Ccc--CCceEE
                  67 VFT--TGGDYT
 Q Thu_Apr_23_00:
                                  75 (111)
 O Consensus
                  67 ~~~--~GG~v~
                                  75 (111)
                     .+. ..|.|.
                   82 ~v~~~D~G~Y
                                  92 (125)
                  82 HLTHNDAGLYI
 T 4nof A
                                  92 (125)
 T ss_dssp
                     SCCGGGCEEEE
 T ss_pred
                     CCChhhCEEEE
                                 PDB'
                                           NCBI
                                                             Pub Med
🗌 >4r5o_A Quinonprotein alcohol dehydrogenase-like protein; two domain protein, immunoglobulin-like beta-sandwich
 fold, family; HET: 7PE; 2.64A {Bacteroides thetaiotaomicron vpi-5482}
 Probab=47.53 E-value=43 Score=26.64 Aligned_cols=49 Identities=16% Similarity=0.148 Sum_probs=0.0
                     CCCCeeeeEEecCCCcEEEEEEeCCCCcEEEEEeCcccccEEEeCCCccCCceEEEEE
 Q Thu_Apr_23_00:
                  18 LGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILSLV
                                                                                  79 (111)
 O Consensus
                  18 ~g~~v~V~l~G~~PftL~yeiv~~~gk~~~~v~i~~~~I~tp~~~~GG~y~v~L~
                                                                                  79 (111)
                   ....+++.. ..-|.|.|+
 T Consensus
                                                                                  80 (427)
                  32 LGETLEITPELLNPEGATYSWLV----NGKEY-----STEPTFSYKI---DNPCRADLSCI
 T 4r5o A
                                                                                  80 (427)
 T ss_dssp
                     TTCEEEECCCBSSCTTCEEEEEE----TTEEE-----ECSSSEEEEC---CSSCEEEEEE
                     CCCEEEEeEeecCCCcEEEEEE.---CCEEe----ccCCceEeee---cCCceEEEEE
 T ss_pred
                                SCOPe POB<sup>N</sup>
PROTEIN DATA BANK
                                                      NCBI
                                                                        Pub Med
>2rik_A Titin; I-SET IG fold, poly-IG linear array, structural protein; 1.60A {Oryctolagus cuniculus} SCOP:
 b.1.1.0 b.1.1.0 b.1.1.0 PDB: 2rjm A
 Probab=47.46 E-value=67 Score=23.01 Aligned_cols=81 Identities=16% Similarity=0.378 Sum_probs=0.0
                     EEECC-CcceeccCCCeeeeEEEecCCCcEEEEEEEcCCCcEE----EEEeCcccccEEeCCCcc--CCceEEEEEE
 Q Thu_Apr_23_00:
                  7 SLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTYDIIETFSSKRK----TFEIKEIKTNEYVIKTPVFT--TGGDYILSLV
                                                                                                   79 (111)
 O Consensus
                   7 ~F~~~~~~C~g~~v~v~l~G~~PftL~yeiv~~~qk~~---~~v~~i~~~~~I~tp~~~-~GG~y~v~L~
                                                                                                   79 (111)
                     T Consensus
                   7 FFDLKPVSVDLALGESGTFKCHVTGTAPIKITWAK----DNREIRPGGNYKMT-LVENTATLTVLKVTKGDAGQYTCYAS
 T 2rik A
                                                                                                   81 (284)
                     EEEECCCCEEEETTCCEEEEEEEESSSCCEEEEEE.---TTEECCSSSEEEE-EETTEEEEEEESSCCGGGCEEEEEEE
 T ss_dssp
                     T ss_pred
 Q ss_pred
                     EEEcccCCcccC
 Q Thu_Apr_23_00:
                  80 SIKDSTGCVVGLS
                                    92 (111)
 O Consensus
                  80 sV~D~~GC~~~L~
                                    92 (111)
                     +.....
 T Consensus
                  82 N~~q~~~
                                    94 (284)
 T 2rik_A
                  82 NVAGKDSCSAOLG
                                    94 (284)
 T ss_dssp
                     ETTEEEEEEEEE
 T ss_pred
                     eccererere
                                SCOPe PROTEIN DATA BANK
 No 96
                                                      S NCBI
                                                                        Pub Med
🗌 >3bae_H WO2 IGG2A FAB fragment heavy chain; abeta, FAB, WO2, alzheimer'S disease, immunotherapies, APP, immune
 system; 1.59A {Mus musculus} SCOP: b.1.1.2 PDB: 3bkc H 3bkj H 3bkm H 4f37 F 3mck H 2r0w H* 2iqa H 2iq9 H 1
3u9u A 1ggb H 1ggc H 3eys H* 2ipt H 2ipu H 3eyu H* 2r0z H* 3rkd H 1r0a H* 1n5y H* ...
Probab=47.07 E-value=62 Score=22.04 Aligned_cols=61 Identities=10% Similarity=0.090 Sum_probs=0.0
                     Q ss pred
 Q Thu_Apr_23_00:
                  18 LGDHSSVPVALKGQGP----FTLTYDIIETFSSKRKTFEIK-----EIKTNEYVIKTPVFTTGGDYILSLVSIK
                                                                                                  82 (111)
 O Consensus
                  18 -q--v-v-V-l-G--P----ftL-yeiv----qk-----v-----i-----i-ttp----GG-y-v-L-sV-
                                                                                                  82 (111)
                     .|+++.+=.+.|.++ ..+.|---. .|+....+. .-...+|.+.... .++.+.|.|.+|+
                                  ----v-W-k----g-----
 T Consensus
                  14 ~G~~v~L~C~~
                                                                  ----r---r
                                                                                                  88 (228)
                  14 PSQTLSLTCSFSGFSIRTSKVGVSWIRQP--SGKGLEWLAHIYWDDDKRYNPSLESRLTISKDT--SRDMVFMKITSVD
 T 3bae H
                                                                                                  88 (228)
                     TTCCEEEEEEESSCHHHHCCEEEEEEEE-TTCCCEEEEEECTTSCEEECTTTGGGEEEEEET-TTTEEEEEECSCC
 T ss dssp
 T ss_pred
                     CCCcEEEEEecCcceEecCccEEEEEEC--CCCCCEEEEEEecCCccCCccCcceEEEEecC--CCCEEEEEECCCC
 No 97
                                                             Pub Med
>4i2x_E Signal-regulatory protein gamma; protein-FAB complex, structural genomics, oxford protein Pro facility, OPPF, CD47, cell surfa immune system; HET: NAG; 2.48A {Homo sapiens} PDB: 2wng _A* 2d9c _A
Probab=46.89 E-value=57 Score=23.56 Aligned_cols=78 Identities=9% Similarity=0.075 Sum_probs=0.0
                     \texttt{CceEEeCC-CcceeccCCCeeeeEEEec-CCCcEEEEEEeCccccEEEEEeCcccccEEEeeCCcc-CCceEEEEEEE}
 Q ss_pred
 Q Thu_Apr_23_00:
                    {\tt 4~PSASLKLH-HDLKLCLGDHSSVPVALKG-QGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFT-TGGDYILSLVS}\\
                                                                                                   80 (111)
                   O Consensus
                                                                                                   80 (111)
                                                                                                   80 (328)
 T Consensus
                   2 EELQMIQPEKLLLVTVGKTATLHCTVTSLLPVGPVLW-FRGVGPGRELIYNQKEGHFPRVTTVSDLTKRNNMDFSIRISS
 T 4i2x E
                                                                                                   80 (328)
                     T ss dssp
                     T ss_pred
 Q ss pred
 Q Thu_Apr_23_00:
                  81 IK
                          82 (111)
                  81 V~
                          82 (111)
                     +
                  81 v~
                          82 (328)
 T Consensus
```

```
T 4i2x E
                                      81 IT
                                                    82 (328)
   T ss dssp
                                           CC
   T ss_pred
                                           CC
   No 98
                                                                                       S NCBI
                                                                                                           8
                                                                                                                         Pub Med
 >2y3u_A Collagenase, collagenase G; hydrolase, gluzincin, metalloprotease; HET: P6G FLC; 2.55A {Clostridium
   histolyticum PDB: 2y50 A* 2y6i A*
   Probab-46.88 E-value=4.8 Score=35.71 Aligned_cols=81 Identities=17% Similarity=0.162 Sum_probs=0.0
                                           CCCCceEEeCCCcceeccCCCeeeeEEEe---cCCCcEEEEEEEeCCCccEEEEEEeCcccccEEEE
   Q ss pred
                                       1 RVKPSASLKLHHDLKLCLGDHSSVPVALK---GOGPFTLTYDIIETFSSKRKTFEIKEIKTNEYVIKTPVFTTGGDYILS
   Q Thu_Apr_23_00:
                                                                                                                                                                                                   77 (111)
                                       1 ---asA-F-----I--p--PftL-yeiv---qk----v-i----I-tp----GG-y-v-
   Q Consensus
                                                                                                                                                                                                   77 (111)
                                            +++|-|.|..+.. .|.+.+|.++-.-+
                                                                                                     .-. | -+.. | ++-+..+.
                                                                                                                                                   ....++...
                                                                                                                                                                                  |.|+|+
                                    700 N~~PvA~f~~~~~V~F~~~S~D~dG~i~sy~WdFGDG~ts-
   T Consensus
                                                                                                                                                   -t~~np~htY~~
                                                                                                                                                                                                 764 (785)
   T 2y3u_A
                                    700 NKAPIAKVTGPST--GAVGRNIEFSGKDSKDEDGKIVSYDWDFGDGATS-----RGKNSVHAYKKA----GTYNVT
                                                                                                                                                                                                 764 (785)
   T ss_dssp
   T ss_pred
                                           CCCCEEEECCCc--CCCCcEEEeccccCCCCCeEEEEEEeCCCCcc-----CCCCceEEecCC----eEEEEE
                                           EEEEEcccCCcccCCCCeEE
   Q ss pred
   Q Thu_Apr_23_00:
                                      78 LVSIKDSTGCVVGLSOPDAKI
                                                                                       98 (111)
                                      78 L~sV~D~~GC~~~L~~~~v~I
   Q Consensus
                                                                                       98 (111)
                                               .|+|..||...-+. .|.|
   T Consensus
                                    765 L-TVtD~~G~s~t~t~-~ItV
                                                                                    783 (785)
   T 2y3u_A
                                    765 L-KVTDDKGATATESF-TIEI
                                                                                     783 (785)
   T ss dssp
   T ss_pred
                                           E-EEE-CCCCEEEEE-EEEE
                                                                   PDB
   No 99
                                                                                       NCBI
                                                                                                                         Pub Med
 ->3qyc_A VH domain of IGG molecule; immunoglobulin V domain fold, antibody, immune system; 1.60A {Homo sapiens}
   PDB: 1ieh A 2uzi H* 4kfz C
   Probab=46.82 E-value=65 Score=20.97 Aliqned cols=76 Identities=11% Similarity=0.131 Sum probs=0.0
                                           Q ss pred
   Q Thu_Apr_23_00:
                                       3 KPSASLKLHHDLKLCLGDHSSVPVALKGQ--GPFTLTYDIIETFSSKRKTFE-----IKEIKTNEYVIKTPVFT
                                                                                                                                                                                                   69 (111)
                                       3 ~asA~F~~~~~C~g~~v~vV~l~G~--~PftL-yeiv~~~gk~~~~------v~~i~~~~~I-tp~~~
   Q Consensus
                                                                                                                                                                                                   69 (111)
                                           ...-..++.+...
                                                                                                                                    ---1--
   T Consensus
                                                                                                                                                                       ~~~R~~
                                                                                                                                                                                                   76 (146)
                                        T 3qyc_A
                                                                                                                                                                                                   76 (146)
   T ss dssp
                                            ---CEEEEECCEEECTTCCEEEEEEESSCGGCCEEEEEC--TTSCEEEEEECTTTSSCEEECTTTTTTEEEEEEG--
                                           CCceEEEecCCEEEcCCCCEEEEEEeCCCCccCcEEEEEEC--CCCCCEEEEEEecCCCccCcCcEEEEECC--
   T ss_pred
   Q ss_pred
                                           CCCEEEEEEEE
   Q Thu_Apr_23_00:
                                     70 TGGDYILSLVSIK
                                                                         82 (111)
                                      70 ~GG~y~v~L~sV~
   O Consensus
                                                                         82 (111)
                                           ..|.+.|.|.+|+
   T Consensus
                                                                         89 (146)
                                                 ~~~sL~I~~v~
                                      77 SKNTVYLOMNSLR
   T 3qyc A
                                                                         89 (146)
   T ss_dssp
                                           GGTEEEEECSCC
                                            CCCEEEEECCCC
   T ss_pred
   No 100
                                                                                      PDB"
                                                                                                                                            Pub Med
                                                                 SCOPe
                                                                                                            S NCBI
 - >4jfh_B BETA17 TCR allele; immunoglobulin, HLA, melanoma, immune system, high AFFI; 2.40A (Homo sapiens) SCOP:
   b.1:1.2 b.1:1.0 PDB: 4jff E* 4jfe E 4jfd E* 3hg1 E
Probab=46.81 E-value=44 Score=23.07 Aligned_cols=60 Identities=13% Similarity=0.149 Sum_probs=0.0
                                           cccceeeeeeeeccccceeeeeeeccccceeeeeee
   Q ss pred
   Q Thu_Apr_23_00:
                                     18 LGDHSSVPVALKGQGPFTLTYDIIETFSSKRKTFEIKE-----IKTNEYVIKTPVFTTGGDYILSLVSIK
                                                                                                                                                                                      82 (111)
                                      18 \ \text{``g`} \sim \text{$v$} \sim \text{$v$} \sim \text{$V$} \sim \text{$l$} \sim \text{$g$} \sim \text{$v$} \sim \text{$v$} \sim \text{$l$} \sim \text{$t$} \sim \text{$t
   Q Consensus
                                                                                                                                                                                      82 (111)
                                      . | +....+..
                                                                                                                                                        .+|.+.|.|.+|+
   T Consensus
                                                                                                                              ~~~~R~~~~~~L~I~~V~
                                                                                                                                                                                      82 (244)
                                      15 VGSPLSLECTVEGTSNPNLYWYRQA--AGRGPQLLFYWGPFGQISSEVPQNLSASRP---QDRQFILSSKKLL
   T 4jfh E
                                                                                                                                                                                      82 (244)
                                           TTCCEEEEEEESCSSCEEEEEEC--TTSCCEEEEEEETTEEEECSSCCSCEEEE---ETTEEEEEESSCC
   T ss_dssp
   T ss_pred
                                            Done!
Please cite as appropriate:
HHpred: Söding, J. (2005) Protein homology detection by HMM-HMM comparison. Bioinformatics 21: 951-960.
PSIPRED: Jones, D.T. (1999) Protein secondary structure prediction based on position-specific scoring matrices. JMB 292: 195-202.
PDB: Bourne, PE, et al. (2004) The distribution and query systems of the RCSB Protein Data Bank, NAR 32: D223.
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