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2fo7_A
                                                                                                                                         4gyo_A
                                                                                                                                         2kat_A
                                                                                                                                      4r7s_A
                                                                                                                                      1w3b_A
                                                                                                                                         3ro3_A
                                                                                                                                         3vtx_A
                                                                                                                                         4i1a_A
                                                                                                                                      2h6f_A
                                                                                                                                      3cv0_A
                                                                                                                                      1µ3h A
                                                                                                                                      2vsy_A
                                                                                                                                  4gco_A
                                                                                                                                         1ihg_A
                                                                                                                                       1p5q_A
                                                                                                                                         3u3u_A
                                                                                                                                         4ga2_A
                                                                                                                                        4i17_A
                                                                                                                                        4xi0_A
                                                                                                                                      3ieg_A
                                                                                                                                        4_j8e_A
                                                                                                                                         3rkv_A
                                                                                                                                      3hyn_B
                                                                                                                                      2lni_A
                                                                                                                                         3ro3_A
                                                                                                                                      44vo_A
                                                                                                                                              4ui9_J
                                                                                                                                      4uvq_C
 Query Fri Mar 04 23:23:54 +0100 2016 (seq=MACLSRIDAN...TDLRDELRGL Len=1037 Neff=7.0 Nseqs=160)
 Parameters score SS:yes search:local realign with MAP:no
No Hit Prob

1 4xmm_E Nucleoporin NUP120; str 100.0
2 3f7f_A Nucleoporin NUP120; nuc 100.0
3 5a9q_1 Nucleoporin SEH1; trans 100.0
4 4fhn_B Nucleoporin SEH1; trans 100.0
5 4qq2_M Nucleoporin NUP120; pro 100.0
6 4ycz_C NUP120; structural prot 100.0
7 3as5_A MAMA; tetratricopeptide 93.3
8 1na0_A Designed protein CTPR3; 93.2
9 4cqv_A Spaghetti, RNA polymera 92.2
10 2dba_A Smooth muscle cell asso 92.2
11 2p12_A Hypothetical conserved 91.8
12 3as5_A MAMA; tetratricopeptide 91.6
13 3vtx_A MAMA; tetratricopeptide 91.6
13 13vtx_A MAMA; tetratricopeptide 91.5
14 1elu_A TPR1-domain of HOP; HOP 91.4
15 4cgw_A Spaghetti, RNA polymera 91.3
16 5a9q_A Nuclear pore complex pr 91.3
17 3q49_B STIP1 homology and U bo 91.1
18 1hxi_A PEX5, peroxisome target 91.0
     No Hit
                                                        Prob E-value P-value Score
                                                                                                      SS Cols Query HMM Template HMM
     1 4xmm_E Nucleoporin NUP120; str 100.0 4E-209 1E-213 1966.2 72.0 1036
                                                                                                                      2-1037
                                                                                                                                   10-1045(1045)
     2 3f7f_A Nucleoporin NUP120; nuc 100.0 9E-142
                                                                            2E-146 1305.7
                                                                                                  61.0
                                                                                                          729
                                                                                                                      1-729
                                                                                                                                    1-729 (729)
     3 5a9q 1 Nucleoporin SEH1; trans 100.0 7E-127
                                                                            2E-131 1249.5
                                                                                                  75.4
                                                                                                           921
                                                                                                                    16-1036
                                                                                                                                   52-1189(1436)
      4 4fhn_B Nucleoporin NUP120; pro 100.0 4E-125 1E-129 1202.4
                                                                                                           904
                                                                                                                    20-1036
                                                                                                                                   21-1118(1139)
                                                                                                                                   18-950 (950)
      5 4gq2_M Nucleoporin NUP120; bet 100.0 1.3E-94 3.6E-99
                                                                                        915.5
                                                                                                           781
                                                                                                                    19-889
      6 4ycz_C NUP120; structural prot 100.0 3.8E-34
                                                                              1E-38
                                                                                        311.9
                                                                                                    8.5
                                                                                                           150
                                                                                                                   873-1036
                                                                                                                                   22-274 (313)
                                                                     1.4 3.8E-05
                                                                                                                   715-894
                                                                                         44.3
                                                                                                  14.0
                                                                                                           124
                                                                                                                                   39-163 (186)
                                                                                                                   750-894
                                                                   0.68 1.9E-05
                                                                                          42.5
                                                                                                  10.7
                                                                                                             92
                                                                                                                                    5-96
                                                                                                                                             (125)
                                                                    3.1 8.5E-05
                                                                                          37.8
                                                                                                  13.8
                                                                                                           131
                                                                                                                   709-895
                                                                                                                                    2-136 (136)
                                                                     1.5 4.3E-05
                                                                                                                   750-894
                                                                                                                                   24-118 (148)
                                                                                          41.7
                                                                       3 8.3E-05
                                                                                          43.1
                                                                                                  14.6
                                                                                                           154
                                                                                                                   714-894
                                                                                                                                    1-170 (217)
                                                                     1.8 4.9E-05
                                                                                          43.6
                                                                                                  12.2
                                                                                                           108
                                                                                                                   731-894
                                                                                                                                   22-129 (186)
                                                                     1.7 4.8E-05
                                                                                          43.2
                                                                                                  11.9
                                                                                                           138
                                                                                                                   731-894
                                                                                                                                   19-160 (184)
                                                                     1.5 4.1E-05
                                                                                                                   752-894
                                                                                          39.4
                                                                                                  10.4
                                                                                                             90
                                                                                                                                    2-91 (118)
                                                                              4E-05
                                                                                                   10.2
                                                                                                                   750-894
                                                                                                                                   14-105 (117)
                                                                     2.4 6.7E-05
                                                                                          56.7
                                                                                                  16.0
                                                                                                           236
                                                                                                                   724-1006
                                                                                                                                  823-1125(1391)
                                                                     1.9 5.4E-05
                                                                                          39.5
                                                                                                  11.1
                                                                                                             93
                                                                                                                   749-894
                                                                                                                                    4-96 (137)
                                                                                                                                   21-104 (121)
                                                                     1.4
                                                                            4E-05
                                                                                         39.8
                                                                                                 10.0
                                                                                                             84
                                                                                                                  758-894
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19 2hr2_A Hypothetical protein; a
                                                                                             8-121 (159)
                                       90.9
                                                1.3 3.5E-05
                                                               42.8
                                                                    10.0
                                                                           101
                                                                                753-894
                                                                                                    (447)
  20 4d10 B COP9 signalosome comple
                                       90.8
                                                8.2 0.00023
                                                               44.1
                                                                     18.3
                                                                           193
                                                                                 754-1008
                                                                                            73-291
  21 2fo7 A Synthetic consensus TPR
                                       90.7
                                                2.8 7.6E-05
                                                               38.3
                                                                     11.8
                                                                           109
                                                                                 731-895
                                                                                            15-123
                                                                                                    (136)
                                                    5.3E-05
  22 2vvi A SGTA protein: chaperone
                                       90.7
                                                1.9
                                                               40.6
                                                                     10.8
                                                                             88
                                                                                 754-894
                                                                                            12-99
                                                                                                    (131)
  23 2q7f_A YRRB protein; TPR, prot
                                                                                            54-178
                                                3.9 0.00011
                                                               43.1
                                                                     14.3
                                                                                 715-894
                                                                                                   (243)
                                                                                             8-100
  24 4gco_A Protein STI-1; structur
                                       90.5
                                                1.7 4.8E-05
                                                               39.1
                                                                      9.9
                                                                             93
                                                                                 749-894
                                                                                                    (126)
  25 4yvq_C Protein fluorescent in
                                       90.2
                                                2.7 7.5E-05
                                                               40.5
                                                                     11.6
                                                                            100
                                                                                 754-894
                                                                                            46-145 (159)
  26 4yvo A Protein fluorescent in
                                       90.1
                                                2.9
                                                      8E-05
                                                               40.4
                                                                     11.8
                                                                            100
                                                                                 754-894
                                                                                            52-151 (165)
                                                4.2 0.00012
  27 4xi0 A Magnetosome protein MAM
                                       90.1
                                                               40.3
                                                                     13.3
                                                                            157
                                                                                 712-894
                                                                                             1-162 (202)
  28 4nrh_B Chaperone SYCD; cytosol
                                                                                 749-894
                                                                                            55-147
                                                                                                   (178)
000000000000000000000000000000000
                                                1.9 5.1E-05
                                                               42.2
                                                                             93
                                                                     10.3
                                                                                                   (142)
  29 2xcb_A PCRH, regulatory protei
                                                2.3 6.4E-05
                                                                     10.3
                                                                                 749-894
                                                                                            13-105
  30 2kck A TPR repeat; tetratricop
                                                1.3 3.5E-05
                                                               39.0
                                                                      8.0
                                                                             91
                                                                                 751-894
                                                                                             3-95
                                                                                                    (112)
  31 2vgx A Chaperone SYCD; alterna
                                       89.5
                                                2.5 6.9E-05
                                                               39.5
                                                                     10.5
                                                                             94
                                                                                 749-895
                                                                                            16-109
                                                                                                   (148)
                                                                                 758-894
  32 3uq3 A Heat shock protein STI1
                                       89.3
                                                1.9 5.3E-05
                                                               45.7
                                                                     10.6
                                                                            110
                                                                                            83-192 (258)
                                                3.4 9.3E-05
  33 3upv A Heat shock protein STI1
                                                               37.2
                                                                                 754-894
                                       89.1
                                                                     10.8
                                                                             88
                                                                                             4-91
                                                                                                    (126)
  34 1na3 A Designed protein CTPR2;
                                                3.2 8.9E-05
                                                               35.9
                                                                     10.0
                                                                                             5-91
                                                                                                    (91)
  35 4gcn A Protein STI-1; structur
                                                3.2 8.8E-05
                                                               37.2
                                                                     10.3
                                                                             89
                                                                                 753-894
                                                                                             7-102 (127)
  36 2lni_A Stress-induced-phosphop
                                                3.1 8.6E-05
                                       88.7
                                                               37.9
                                                                     10.3
                                                                             92
                                                                                 750-894
                                                                                            12-103
                                                                                                   (133)
                                                                                                    (164)
  37 3sz7_A HSC70 cochaperone (SGT)
                                       88.7
                                                2.8 7.8E-05
                                                               40.4
                                                                     10.5
                                                                             92
                                                                                 750-894
                                                                                             7-98
                                                                                           180-367
                                                9.7 0.00027
                                                                            179
                                                                                 754-992
  38 4qyo A Response regulator aspa
                                       88.6
                                                               42.5
                                                                     16.3
                                                                                                   (373)
  39 2vyi A SGTA protein; chaperone
                                                  5 0.00014
                                                               37.7
                                                                     11.7
                                                                            107
                                                                                 730-892
                                                                                            25-131 (131)
  40 lelr A TPR2A-domain of HOP; HO
                                                3.3 9.2E-05
                                                               37.8
                                                                     10.2
                                                                                 754-894
                                                                                                    (131)
                                                                                            50-194
                                                                            139
  41 2ho1_A Type 4 fimbrial biogene
                                       87.9
                                                4.6 0.00013
                                                               42.0
                                                                     12.2
                                                                                 730-894
                                                                                                   (252)
  42 2c21_A CHIP, carboxy terminus
                                       87.8
                                                2.4 6.5E-05
                                                               46.1
                                                                     10.2
                                                                             92
                                                                                 751-895
                                                                                             1-92
                                                                                                    (281)
  43 1xnf_A Lipoprotein NLPI; TPR,
                                       87.6
                                                3.3 9.1E-05
                                                               43.5
                                                                     11.0
                                                                             89
                                                                                 753-894
                                                                                            42-130
                                                                                                   (275)
  44 3ma5 A Tetratricopeptide repea
                                                4.5 0.00012
                                                                                 749-890
                                       87.6
                                                               34.9
                                                                     10.2
                                                                             91
                                                                                             2-92
                                                                                                    (100)
  45 1hh8 A P67PHOX, NCF-2, neutrop
                                                                                 753-894
                                                                                            36-140
                                                                                                   (213)
                                                3.7
                                                     0.0001
                                                               42.1
                                                                     10.9
                                                                             89
     3gyz A Chaperone protein IPGC;
                                                3.8 0.00011
                                                               38.1
                                                                     10.3
                                                                             92
                                                                                 750-894
                                                                                            32-123
                                       87.2
                                                                                            88-212 (243)
  47 2q7f_A YRRB protein; TPR, prot
                                                7.5 0.00021
                                                               40.9
                                                                     13.4
                                                                           124
                                                                                 715-894
  48 3zn3_A Anaphase-promoting comp
                                       87.0
                                                4.7 0.00013
                                                               43.0
                                                                     11.9
                                                                           119
                                                                                 750-894
                                                                                           152-272 (291)
  49 4ila A Response regulator aspa
                                       86.8
                                                 14 0.00038
                                                               41.9
                                                                     16.3
                                                                            171
                                                                                 754-986
                                                                                           184-366 (391)
  50 4apo A AH receptor-interacting
                                       86.8
                                                3.5 9.5E-05
                                                               39.9
                                                                      9.8
                                                                           100
                                                                                 760-894
                                                                                            20-119 (165)
  51 2fo7_A Synthetic consensus TPR
                                                4.3 0.00012
                                                               36.9
                                                                     10.0
                                                                                 754-894
                                                                                             1-88
                                                                                                    (136)
  52 2e2e_A Formate-dependent nitri
                                                  3 8.3E-05
                                                               41.6
                                                                      9.5
                                                                             92
                                                                                 750-894
                                                                                            40-134 (177)
                                                                                                   (373)
  53 4gyo_A Response regulator aspa
                                       86.7
                                                3.8 0.0001
                                                               45.9
                                                                     11.4
                                                                             96
                                                                                 758-894
                                                                                           103-199
  54 4r7s_A Tetratricopeptide repea
                                       86.6
                                                 13 0.00037
                                                               38.0
                                                                     14.8
                                                                           154
                                                                                 715-894
                                                                                            35-196 (257)
                                                3.1 8.6E-05
                                                                                 749-894
                                                                                           134-226 (258)
  55 3uq3 A Heat shock protein STI1
                                       86.3
                                                               44.0
                                                                      9.9
                                                                             93
  56 2vq2 A PILW, putative fimbrial
                                       86.3
                                                     0.0005
                                                               36.0
                                                                     15.3
                                                                            126
                                                                                 715-894
                                                                                            39-166
                                                                                                   (225)
                                                 18
  57 2fbn_A 70 kDa peptidylprolyl i
                                                6.5 0.00018
                                                               40.0
                                                                     12.0
                                                                                 754-894
                                                                                            38-141 (198)
                                                                             93
     4cgv_A Spaghetti, RNA polymera
                                       86.3
                                                4.2 0.00012
                                                               36.8
                                                                      9.6
                                                                                 749-894
                                                                                             9-101
                                                                                                   (136)
                                                5.7 0.00016
00000000000000000
  59 2kat_A Uncharacterized protein
                                       86.3
                                                               35.9
                                                                     10.5
                                                                             92
                                                                                 750-894
                                                                                            15-108 (115)
  60 4r7s_A Tetratricopeptide repea
                                       86.2
                                                 11 0.0003
                                                               38.7
                                                                     13.9
                                                                            158
                                                                                 715-894
                                                                                            72-230
                                                                                                   (257)
                                                6.7 0.00019
                                                                                            30-188
  61 1w3b A UDP-N-acetylglucosamine
                                                                                 715-894
                                       86.1
                                                               44.1
                                                                     13.1
                                                                            155
                                                                                                   (388)
  62 3ro3 A PINS homolog, G-protein
                                                6.8 0.00019
                                                               37.8
                                                                     11.5
                                                                            100
                                                                                            49-148
                                                                                                   (164)
  63 4ule I Eukaryotic translation
                                       85.9
                                                4.6 0.00013
                                                               45.1
                                                                     11.5
                                                                            75
                                                                                 164-257
                                                                                            15-90
                                                                                                    (347)
                                                                                             2-126 (184)
  64 3vtx_A MAMA; tetratricopeptide
                                                4.7 0.00013
                                                               39.9
                                                                     10.5
                                                                           121
                                                                                 751-894
                                       85.9
  65 1na0_A Designed protein CTPR3;
                                       85.4
                                                 10 0.00028
                                                               34.4
                                                                     11.8
                                                                           104
                                                                                 730-889
                                                                                            22-125 (125)
                                                                                 758-894
  66 4ila A Response regulator aspa
                                       85.2
                                                5.1 0.00014
                                                               45.5
                                                                     11.6
                                                                            97
                                                                                           107-203 (391)
  67 2vq2 A PILW, putative fimbrial
                                                                                            73-201 (225)
                                       85.2
                                                 16 0.00043
                                                               36.5
                                                                     14.1
                                                                           124
                                                                                 715-894
  68 1hh8 A P67PHOX, NCF-2, neutrop
                                                5.2 0.00014
                                                               40.9
                                                                     10.5
                                                                                 753-894
                                                                                             5-90
                                                                                                    (213)
  69 2pl2_A Hypothetical conserved
                                                  6 0.00017
                                                               40.8
                                                                                 753-894
                                                                                             4-103 (217)
                                       84.8
                                                                     11.0
                                                                             89
  70 2h6f_A Protein farnesyltransfe
                                       84.8
                                                7.2 0.0002
                                                               43.9
                                                                     12.5
                                                                            155
                                                                                 714-894
                                                                                            90-259 (382)
  71 3cv0 A Peroxisome targeting si
                                       84.7
                                                 16 0.00045
                                                               39.0
                                                                     14.9
                                                                            129
                                                                                 715-894
                                                                                           169-305 (327)
                                                  7 0.00019
                                                                                 165-258
                                                                                           218-295
  72 4j87 A Coatomer subunit alpha;
                                       84.7
                                                               42.6
                                                                     12.1
                                                                             77
                                                                                                   (327)
  73 2xpi A Anaphase-promoting comp
                                       84.6
                                                 67
                                                     0.0018
                                                               37.8
                                                                     21.4
                                                                           228
                                                                                 704-981
                                                                                           326-573
                                                                                                   (597)
  74 2dba_A Smooth muscle cell asso
                                                6.4 0.00018
                                                               37.3
                                                                     10.3
                                                                            89
                                                                                 730-855
                                                                                            41-132 (148)
  75 1w3b_A UDP-N-acetylglucosamine
                                                                            154
                                                 12 0.00033
                                                               42.0
                                                                     14.2
                                                                                 715-894
                                                                                           132-290
                                                                                                    (388)
  76 2vsy A XCC0866; transferase, q
                                       84.4
                                                 11
                                                     0.0003
                                                               45.3
                                                                     14.6
                                                                           124
                                                                                 715-894
                                                                                            20-144
                                                                                                   (568)
                                                 14 0.00039
                                                               32.9
                                                                                 709-855
  77 4gco A Protein STI-1: structur
                                       84.4
                                                                     12.1
                                                                           110
                                                                                             1-114 (126)
  78 1ihg A Cyclophilin 40; ppiase
                                                4.2 0.00012
                                                                                 754-894
                                                                                           223-326 (370)
                                       84.3
                                                               46.2
                                                                     10.3
                                                                           104
  79 1p5q A FKBP52, FK506-binding p
                                                6.5 0.00018
                                                               43.6
                                                                     11.7
                                                                            108
                                                                                 731-894
                                                                                           161-283
                                                                                                   (336)
  80 3i5p_A Nucleoporin NUP170; hel
                                       84.0
                                                6.3 0.00017
                                                               47.4
                                                                     12.0
                                                                           155
                                                                                 823-1006
                                                                                            68-266
                                                                                                   (525)
  81 4ui9_F Cell division cycle pro
83.9
                                                 38 0.0011
                                                               43.0
                                                                     19.8
                                                                           219
                                                                                 750-1016
                                                                                           495-722 (824)
  82 1elw A TPR1-domain of HOP; HOP
                                       83.9
                                                5.9 0.00016
                                                               35.3
                                                                      9.3
                                                                            89
                                                                                 730-855
                                                                                            17-105 (118)
  83 3u3w A Transcriptional activat
                                       83.7
                                                6.8 0.00019
                                                               42.3
                                                                     11.2
                                                                             97
                                                                                 758-894
                                                                                           159-255 (293)
  84 4jsn_D Target of rapamycin com
                                                    0.00025
                                                               41.8
                                                                     12.4
                                                                             83
                                                                                 164-257
                                                                                           225-308
                                                                                                   (326)
  85 4ga2_A E3 SUMO-protein ligase
                                                7.8 0.00022
                                                               35.8
                                                                     10.3
                                                                             85
                                                                                 758-895
                                                                                            35-120
                                                                                                   (150)
  86 2xev_A YBGF; tetratricopeptide
                                       83.6
                                                 15 0.00042
                                                               32.8
                                                                     12.1
                                                                             90
                                                                                 758-894
                                                                                             6-95
                                                                                                    (129)
                                                                                                   (448)
  87 5aio_A Transcription factor TA
                                       83.6
                                                 16 0.00043
                                                               41.3
                                                                     14.7
                                                                            124
                                                                                 715-894
                                                                                            41-165
  88 4i17_A Hypothetical protein; T
                                       83.3
                                                9.3 0.00026
                                                               38.3
                                                                     11.5
                                                                            129
                                                                                 750-894
                                                                                             3-136
                                                                                                   (228)
                                                6.5 0.00018
                                                                                 751-894
  89 4xi0_A Magnetosome protein MAM
                                       83.3
                                                               38.9
                                                                     10.2
                                                                           121
                                                                                             4-128 (202)
  90 3ieg_A DNAJ homolog subfamily
                                                 12 0.00032
                                                                                 715-894
                                                                                            34-207
                                       83.3
                                                               41.8
                                                                     13.3
                                                                            150
                                                                                                    (359)
  91 4j8e_A HSC70-interacting prote
                                                                                            45-129
                                       83.1
                                                7.9 0.00022
                                                               37.5
                                                                     10.5
                                                                            85
                                                                                 758-895
                                                                                                    (175)
  92 3rkv_A Putative peptidylprolyl
                                                                                            15-117 (162)
                                       83.1
                                                9.4 0.00026
                                                               36.3
                                                                     10.9
                                                                           103
                                                                                 758-895
  93 4ui9_F Cell division cycle pro
                                       83.0
                                              1E+02
                                                     0.0028
                                                               39.0
                                                                     23.2
                                                                           230
                                                                                 702-1016
                                                                                           552-790 (824)
  94 3hvm B Cell division cycle pro
                                       83.0
                                                 29
                                                     0.0008
                                                               37.0
                                                                     16.0
                                                                           167
                                                                                 715-894
                                                                                            87-255 (330)
  95 1p5q A FKBP52, FK506-binding p
                                       82.8
                                                6.4 0.00018
                                                               43.7
                                                                     10.9
                                                                            103
                                                                                 754-894
                                                                                           147-249
                                                                                                   (336)
  96 21ni_A Stress-induced-phosphop
                                                 17 0.00047
                                                               32.7
                                                                     12.2
                                                                            105
                                                                                 730-890
                                                                                                   (133)
  97 3ro3 A PINS homolog, G-protein
                                       82.8
                                                8.8 0.00024
                                                               37.0
                                                                     10.7
                                                                            100
                                                                                 754-894
                                                                                             9-108
                                                                                                   (164)
  98 4yvo_A Protein fluorescent in
                                                7.1 0.0002
                                                                                            92-165 (165)
                                       82.8
                                                               37.6
                                                                     10.0
                                                                            74
                                                                                 754-855
  99 4ui9 J Cell division cycle pro
                                       82.6
                                                 71
                                                      0.002
                                                               38.0
                                                                     20.7
                                                                           227
                                                                                 715-991
                                                                                           262-511 (620)
100 4yvq_C Protein fluorescent in
                                                4.4 0.00012
                                       82.4
                                                               38.9
                                                                      8.2
                                                                             74
                                                                                 754-855
                                                                                            86-159 (159)
                                      PDB"
PROTEIN DATA BANK
                                                 NCBI
                                                             Pub Med
->4xmm_B Nucleoporin NUP120; structural protein, immune system, transport protein-immune complex; 7.38A
  {Saccharomyces cerevisiae S288C} PDB: 4xmn _E
                                   Score=1966.19
  Probab=100.00 E-value=4.5e-209
                                                   Aligned cols=1036 Identities=100% Similarity=1.483 Sum probs=0.0
                         Q ss pred
  Q Fri Mar 04 23:
                      2 ACLSRIDANLLOYYEKPEPNNTVDLYVSNNSNNNGLKEGDKSISTPVPOPYGSEYSNCLLLSNSEYICYHFSSRSTLLTF
                                                                                                                81 (1037)
```

Q Consensus T Consensus T 4xmm E T ss_dssp T ss pred	2ysr-I-wRv-dL-l +       + +++++      ++++++++ +  +  ++++	81 (1037) 89 (1045) 89 (1045)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4xmm_E T ss_dssp T ss_pred	82 ~sld~~~~~lri-Fp~ilp~~~v-i-e~~~L-I~viT~~~l-rl~lp~~f~~~~~dw~~~~p~f~r	161 (1037) 161 (1037) 169 (1045) 169 (1045)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4xmm_E T ss_dssp T ss_pred	162 ~P~-l~a~~~vsl~DGgLL~l~~~~~~~~~~~~~~~~~~~vsl~DGgLL~l~~l~~l~~lf~~~~vs~~vs~~~~vsl~blfL~-D~~ +   ++++++++++++++++++++++++++++++++	241 (1037) 241 (1037) 249 (1045) 249 (1045)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4xmm_E T ss_dssp T ss_pred	242 ~LRiWsl-t-~-l~~dL~~~~~~l~~vylp~~g-F~~~l~~~~l~~ip- +    ++ +++  ++++++++++++ +++ +  ++++ +	321 (1037) 321 (1037) 329 (1045) 329 (1045)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4xmm_E T ss_dssp T ss_pred	322	401 (1037) 401 (1037) 409 (1045) 409 (1045)
Q ss_pred Q Fri Mar_04_23: Q Consensus T Consensus T 4xmm_E T ss_dssp T ss_pred	402 d~E~IF~lpgrfs~~l~AL~iy~~~~d~~~~~~~~~~~~~~~~~el~~~~elsL~~~d-i~vv~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	481 (1037) 481 (1037) 489 (1045) 489 (1045)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4xmm_E T ss_dssp T ss_pred	482 s~ir~s~lE~~~n~~~~d~~Ll~l~f~~ls~~~~l~~l~~l~~~s~s~~~~~i~~~l~~~l~~~l~	561 (1037) 561 (1037) 569 (1045) 569 (1045)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4xmm_E T ss_dssp T ss_pred	562	641 (1037) 641 (1037) 649 (1045) 649 (1045)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4xmm_E T ss_dssp T ss_pred	642 ~~~~~l~l-l-l-l~~~~~l~~y~~~~l~~elf~~~~f~~g~kl~s~~~l~~~i~~~~~l~~~~np~~~ ++++++++++++    +++++ +++ ++++ ++++	721 (1037) 721 (1037) 729 (1045) 729 (1045)
Q ss_pred Q Fri_Mar_04_23: Q Consensus		801 (1037) 801 (1037)

```
T Consensus
                                    730 ~-l~~vi~-q~~~~fl~i~-j~~~~~fl~g~~-l~~~A~~F~a~~~~~lp~-l~~l~~~~
                                                                                                                                                                                                       809 (1045)
                                    730 TFFRSYIIENTSHKNIRFFLENVECPFYLRHNEVOEFMFAMTLFSCGNFDOSYEIFOLHDYPEAINDKLPTFLEDLKSEN
 T 4xmm E
                                                                                                                                                                                                       809 (1045)
 T ss dssp
                                           НННС-----CTTHHHHHHHSTTC------CHHHHHHHHHHC----CHHHHHHHHHC-----
                                            T ss pred
 Q ss_pred
                                           ссссссссьный десссссьный дессссссьный десссссссьный десссссссой десссссссой дессссссой дессссссой дессссссой дессссссой десссссой десссссой дессссои десссссой десссои дессои дессои дессои десссои десссои дессои дессои дессои дессои дессои дессои дессои дессои дес
                                    802 \ \ Y \\ HGDSIWKDLLCTFTVPY \\ RHSAFYY \\ QLSLLFD \\ RNNSQEFALK \\ CISKSAEY \\ SLKEIQIEEL \\ QDFKEK \\ QHIHYLNLLIHFR \\ MINGRAF \\ MINGR \\ MINGRAF \\ MINGRAF \\ MINGRAF \\ MINGRAF \\ MINGRAF \\ MINGRAF \\ MI
 Q Fri Mar 04 23:
                                                                                                                                                                                                       881 (1037)
 Q Consensus
                                    802
                                                 ----l----l-----e---e---
                                                                                                                                                                              ---1---i-
                                                                                                                                                                                                       881 (1037)
                                           T Consensus
                                    810
                                                                                                                                                                                                        889 (1045)
                                    810 YHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRM
 T 4xmm E
                                                                                                                                                                                                       889 (1045)
 T ss dssp
                                            ссссссссный объекты в получения в получения
 T ss_pred
                                           НИНИН
 Q ss_pred
 Q Fri_Mar_04_23:
                                    882 FEEVLDVLRLGHECLSDTVRTNFLOLLLOEDIYSRDFFSTLLRLCNAHSDNGELYLRTVDIKIVDSILSONLRSGDWECF
                                                                                                                                                                                                       961 (1037)
 O Consensus
                                    882 F---L-1----ayL----r--1-11-------lv--L------11------vd-iL---ar---
                                                                                                                                                                                                       961 (1037)
                                            T Consensus
                                                                                                                                                                                                       969 (1045)
 T 4xmm E
                                                                                                                                                                                                        969 (1045)
                                            T ss_dssp
                                            T ss pred
                                           Q ss pred
                                    962 KKLYCFRMLNKSERAAAEVLYQYILMQADLDVIRKRKCYLMVINVLSSFDSAYDQWILNGSKVVTLTDLRDELRGL 1037 (1037)
  Q Fri Mar 04 23:
                                    962 ~~LYs~ri~~~~R~AA~~mYe~~~rl~~~~~~k~yL~~iN~L~~~~~d~WI~~~~vvtL~dl~~Ey~~~ 1037 (1037)
 O Consensus
                                          T Consensus
 T 4xmm E
                                            T ss dssp
                                            T ss_pred
                                                                    PDB
 No 2
                                                                                                                             Pub Med
🗌 >3f7f_A Nucleoporin NUP120; nuclear pore complex, macromolecular assembly, membrane coat, nucleocytoplasmic
  transport, beta-propeller; 2.60A {Saccharomyces cerevisiae} PDB: 3h7n _A 3hxr _A
 Probab=100.00 E-value=9e-142 Score=1305.70 Aligned_cols=729 Identities=100% Similarity=1.465 Sum_probs=0.0
                                           Q ss pred
  Q Fri_Mar_04_23:
                                        1 \ \ \texttt{MACLSRIDANLLQYYEKPEPNNTVDLYVSNNSNNNGLKEGDKS} \\ \texttt{ISTPVPQPYGSEYSNCLLLSNSEYICYH} \\ \texttt{FSSRSTLLT} \\ \texttt{TSTRUMERATION STATE STAT
                                                                                                                                                                                                         80 (1037)
                                                                                                                                                --ys----r-I-wRv--d---I.-
 O Consensus
                                       1 ~~
                                                                                     ----1---
                                                                                                                                                                                                         80 (1037)
                                            T Consensus
                                                                                         ~1-
                                                                                                                                                            ----r~I~WRv~~d~~~Le
                                                                                                                                                                                                         80 (729)
                                                                                                                                                 ~~vs~
                                       1 MACLSRIDANLLQYYEKPEPNNTVDLYVSNNSNNNGLKEGDKSISTPVPQPYGSEYSNCLLLSNSEYICYHFSSRSTLLT
 T 3f7f A
                                                                                                                                                                                                         80 (729)
                                           T ss dssp
 T ss_pred
                                            EEEcccccCCCeEEEEcCcccCCCCeEEEEecCCceEEEEEcCCCcEEEEEECHHHccCccccccccceeeccCcCCC
 Q ss pred
 Q Fri Mar 04 23:
                                      \textbf{81} \ \textbf{FYPLSDAYHGKTINIHLPNASMNQRYTLTIQEVEQQLLVNVILKDGSFLTLQLPLSFLFSSANTLNGEWFHLQNPYDFTV}
                                                                                                                                                                                                       160 (1037)
                                      81 l~sld~~~~~lri~Fp~~ilp~~~~v~i~e~~~L~I~viT~~~~l~rl~lp~~~f~~~~~~dw~~~
                                                                                                                                                                                                       160 (1037)
  Q Consensus
                                      T Consensus
                                                                                                                                                                                                       160 (729)
 T 3f7f A
                                                                                                                                                                                                       160 (729)
                                            EEEGGGTTTSCEEEEECSSCBTTGGGGEEEEECSSEEEEEEEBSSSCEEEEEEHHHHHSCCSCCCSCCCCCCCCCTTT
 T ss dssp
 T ss_pred
                                            EEEccccCCCeEEEEcCcccCCCCeEEEEecCCEEEEEEcCCCcEEEEEEChhhccccccCcccceeecccCC
                                           Q ss_pred
 Q Fri Mar 04 23:
                                    161 RVPHFLFYVSPOFSVVFLEDGGLLGLKKVDGVHYEPLLFNDNSYLKSLTRFFSRSSKSDYDSVISCKLFHERYLIVLTON
                                                                                                                                                                                                       240 (1037)
                                    240 (1037)
 O Consensus
                                            161 r-P--l-a-s---lvVsl-DGgLL-l----e--f---s----L--lf-
                                                                                                                                                   ----vs----
 T Consensus
                                                                                                                                                                                              ~~D
                                                                                                                                                                                                       240 (729)
 T 3f7f A
                                           RVPHFLFYVSPOFSVVFLEDGGLI.GLKKVDGVHYEPLLFNDNSYLKCLTRFFSRSKSDYDSVTSCKLFHERYLTVT.TON
                                                                                                                                                                                                       240 (729)
                                            SCEEEEEECSSSBEEEEETTSCEECCEESSSSCEECCCCCCGGGGGGGSTTCCTTCSSCCCCEEEEEETTTEEEEEETT
 T ss_dssp
                                           CCceEEEecCCCEEEEEecCCCCcceeeeccccHHhhHHHHhCCCCCCcccEEEEEcCCcEEEEEcC
 T ss pred
                                           CeEEEEECCCceEEeeccccccccCccChhHHHHHHhhheEEEEEecCCceEEEeecccC
 Q ss pred
 Q Fri Mar 04 23: 241 CHLKIWDLTSFTLIQDYDMVSQSDSDPSHFRKVEAVGEYLSLYNNTLVTLLPLENGLFQMGTLLVDSSGILTYTFQNNIP
                                                                                                                                                                                                       320 (1037)
                                    241 ~~LRiWsl~t~~l~~dL~~~~~~l~~~l~vvlp~~~q~F~~~l~~~~l~~~~lp
 O Consensus
                                                                                                                                                                                                       320 (1037)
                                            ~~LRiWsl~t~~~l~~~dL~~~~~~l~~~~l~~~~
 T Consensus
                                    241 CHLKIWDLTSFTLIQDYDMVSQSDSDPSHFRKVEAVGEYLSLYNNTLVTLLPLENGLFQMGTLLVDSSGILTYTFQNNIP
 T 3f7f A
                                                                                                                                                                                                       320 (729)
 T ss_dssp
                                            T ss_pred
                                            CeEEEEcCCCceEEeeccccccccccccccchhHHHHHhhhhEEEEEEcCCCcEEEEEEEccCCcEEeeecccC
                                           Q ss_pred
  Q Fri Mar 04 23:
                                    321 TNLSASAIWSIVDLVLTRPLELNVEASYLNLIVLWKSGTASKLQILNVNDESFKNYEWIESVNKSLVDLQSEHDLDIVTK
                                                                                                                                                                                                       400 (1037)
  O Consensus
                                    400 (1037)
                                           T Consensus
                                                                                                                                                                                                       400 (729)
 T 3f7f A
                                    321 TNLSASAIWSIVDLVLTRPLELNVEASYLNLIVLWKSGTASKLQILNVNDESFKNYEWIESVNKSLVDLQSEHDLDIVTK
                                                                                                                                                                                                       400 (729)
  T ss dssp
                                            T ss pred
```

```
Q ss_pred
                       Q Fri Mar 04 23: 401 TGDVERGFCNLKSRYGTQIFERAQQILSENKIIMAHNEDEEYLANLETILRDVKTAFNEASSITLYGDEIILVNCFQPYN
                                                                                                           480 (1037)
                   O Consensus
                                                                                                           480 (1037)
                    401 -d--E--IF-lpGrFs---L--AL-iy---g--d---e----W--F--lc-el-----eplsL----d-i-vv----
 T Consensus
                                                                                                           480 (729)
                   401 TGDVERGFCNLKSRYGTOIFERAQOILSENKIIMAHNEDEEYLANLETILRDVKTAFNEASSITLYGDEIILVNCFOPYN
 T 3f7f A
                                                                                                           480 (729)
 T ss_dssp
                       T ss pred
                       Q ss_pred
 Q Fri Mar 04 23: 481 HSLYKLNTTVENWFYNMHSETDGSELFKYLRTLNGFASTLSNDVLRSISKKFLDIITGELPDSMTTVEKFTDIFKNCLEN
                                                                                                           560 (1037)
 O Consensus
                   481 -s-ir--s-lE----n-----d---Ll--l--f---ls------l---l--l----s-s----
                                                                                                           560 (1037)
                       --s-s--d----if---l--
 T Consensus
                                                                                                           560 (729)
                   481\ {\tt HSLYKLNTTVENWFYNMHSETDGSELFKYLRTLNGFASTLSNDVL}_{RSISKKFLDIITGELPDSMTTVEKFTDIFKNCLEN
 T 3f7f A
                                                                                                           560 (729)
 T ss_dssp
                       T ss_pred
                       Q ss_pred
                                                                                                           640 (1037)
                   561 \ \ QFEITNLKILFDELNSFDIPVVLNDLINNQMKPGIFWKKDFISAIKFDGFTSIISLESLHQLLSIHYRITLQVLLTFVLF
 Q Fri Mar 04 23:
                   640 (1037)
 Q Consensus
                       561 ~i~~~i~l~eL~si~v~l~Li~~~~~~~~~~s-f~~l~l~~l~llll-~
                                                                                                           640 (729)
 T Consensus
                   561 QFEITNLKILFDELNSFDIPVVLNDLINNQMKPGIFWKKDFISAIKFDGFTSIISLESLHQLLSIHYRITLQVLLTFVLF
 T 3f7f A
                                                                                                           640 (729)
                        T ss dssp
                       T ss pred
                       Q ss pred
 Q Fri_Mar_04_23:
                   \mathbf{641} \  \  \mathbf{DLDTEIFGQHISTLLDLHYKQFLLLNLYRQDKCLLAEVLLKDSSEFSFGVKFFNYGQLIAYIDSLNSNVYNASITENSFF}
                                                                                                           720 (1037)
                       641
                         T Consensus
                                                                                                           720 (729)
                   641 DLDTEIFGQHISTLLDLHYKQFLLLNLYRQDKCLLAEVLLKDSSEFSFGVKFFNYGQLIAYIDSLNSNVYNASITENSFF
 T 3f7f A
                                                                                                           720 (729)
 T ss dssp
                       T ss pred
                       нинининн
 Q ss_pred
 Q Fri_Mar_04_23: 721 MTFFRSYII
                                  729 (1037)
                                  729 (1037)
 O Consensus
                        .+|+..||+
 T Consensus
                   721 ~~
                                  729 (729)
 T 3f7f A
                   721 MTFFRSYTT
                                  729 (729)
 T ss dssp
                       НННННННС
 T ss pred
                                    PDB'
                                                                   Pub Med
>5a9q 1 Nucleoporin SEH1; transport protein; 23.00A {Homo sapiens}
 Probab=100.00 E-value=6.6e-127
                                  Score=1249.51 Aligned_cols=921 Identities=15% Similarity=0.183 Sum_probs=0.0
                       cccCCcceEEEEecCCCcccccc--cccccccccccc-ccceeEec---CCCCEEEEEEECCceEEEEEEccccc
 Q ss pred
                    16 EKPEPNNTVDLYVSNNSNNNGLKEG--DKSISTPVPQPYG-SEYSNCLLL---SNSEYICYHFSSRSTLLTFYPLSDAYH
 Q Fri Mar 04 23:
                                                                                                            89 (1037)
                    16 ~~~
                                                           -----ys-----r-I-wRv--d---L-l-sld----
 Q Consensus
                              ~~~~1~~
                                                                                                            89 (1037)
                                                               + -. | +++..+ ++ | | | | | +++ | +++ | ++.++ | .+..
                                                               -Gg~~y~~~~t~~R~i~Wr~~~d~leL~e~sld~nl~
 T 5a9q 1
                    52 ERERPRHFREFTVCSIGTANAVAGAVKYSESA-----GGFYYVESGKLFSVTRNRFIHWKTSGDTLELMEESLDINLL
                                                                                                           124 (1436)
 T ss dssp
                       CCCCSSCCEEECCCCSCCCCCCSHHHHCCSC-----EEEEECCC----CSCCEEEEEECC---CEEEEEECSSS
                       CCCCcccEEEEecCCCcccCCCcc-----ceeeecCCccccCCCCEEEEEEEcCCEEEEEEeecCCCCC
 T ss_pred
                       CCeEEEECC-cccCCCCeEEEEecCCeEEEEEECCCceEEEEEEC-HH-HccC------cccccc-----cccee
 Q ss_pred
 Q Fri_Mar_04_23:
                    90 GKTINIHLP-NASMNQRYTLTIQEVEQQLLVNVILKDGSFLTLQLP-LS-FLFS-----SANTLNG----EWFHL
                                                                                                           152 (1037)
                    90 ~~~lri-Fp-~~ilp~~~v-i-e~~~L~I~viT~~~l~rl~lp~~~~f~~~~dw~~~
 O Consensus
                                                                                                           152 (1037)
                       +++||+|| .||+| ||+|+++.||+|+| +++||+|| +|++| .|++ ..|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|+...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++
                                                                                                           201 (1436)
 T Consensus
                                                                                                    -dw
                   125 NNAIRLKFQNCSVLP--GGVYVSETQNRVIILMLT-NQTVHRLLLPHPSRMYRSELVVDSQMQSIFTDIGKVDFTDPCNY
 T 5a9q_1
                                                                                                           201 (1436)
                        CCCEEEECCC-CCCT--TCCEEC-CTTCEEEEEES-SSCEEEEEC-CHHHHCCC------CCCCSCSEEE
 T ss dssp
 T ss pred
                       CceEEEEcCCCccc--CceEEEEcCCeEEEEEe-CCeEEEEEecCchHhhacccccccchhhacccchhacccc
                       e-ccCccCC-CCEEEEe--cC--CCEEEEEeCCCCEEEEEecC---CCCeeEEEecCcgHHHH-HHHHhcC---CCCCC
 Q ss pred
                   153 \ \ Q-NPYDFTVR-VPHFLFY-VS--PQFSVVFLEDGGLLGLKKVD---GVHYEPLLFNDNSYLKS-LTRFFSR---SSKSD
 Q Fri Mar 04 23:
                                                                                                           219 (1037)
 O Consensus
                   153 ~--p~-f~-r--P~-l~a------vsl~DGgLL-l~--------s-l~-L~-lf~--------
                                                                                                           219 (1037)
                   T Consensus
                                                                                                           281 (1436)
                   202 QLIPAVPGISPNSTASTAWLSSDGEALFALPCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLTGWMPTAIRGDQSP
 T 5a9q 1
                                                                                                           281 (1436)
                       T ss dssp
                        eccCccccccceeEEeeecCCCceEEEEEeCCCCEEEEEccCccCCCceeeeccccchhhhhhhccCccccCCcC
 T ss pred
                       CCCCeEEEE---CCCEEEEEECCCeEEEEECCCceEEeecc-cccccccCCccChhHHHHHHhhh-----eEEEE
 Q ss pred
 Q Fri Mar 04 23: 220 YDSVISCKLF---HERYLIVLTQNCHLKIWDLTSFTLIQDYDM-VSQSDSDPSHFRKVEAVGEYLSLYNN-----TLVTL
                                                                                                           290 (1037)
                       ----vs-----lftL--D--LRiWsl-t---dL-----
                                                                                    ----1--vy
                                                                                                           290 (1037)
 Q Consensus
                       .++|+|++++ +++|||||+||+||+||+|++++|| +....+.+..+.| +++++|+++..
                   T Consensus
                                                                                                    ~1~v~
                                                                                                           359 (1436)
```

T 5a9q_1 T ss_dssp T ss_pred	282 SDRPLSLAVHCVEHDAFIFALCQDHKLRMWSYKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLYLGIY TTCEEEEEEECCCCEEEEEETTSEEEEEETTTTEEEEEEEECCCCCCCCCCCCCEEECSSCSCEEEEE CCcceeEEEEecCCceeEeeeeccCceEEEEechhccCCCccccCCCCCcEEEEE	359	(1436)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	Eec-CCceEEEEEEecCCCcEEEeeccccCCCCCCCceeEeeeEEecccccccCCccEEEEEEecCC-ceEEEEEEE 291 LPL-ENGLFQMGTLLVDSSGILTYTFQNNIPTNLSASAIWSIVDLVLTRPLELNVEASYLNLIVLWKSGT-ASKLQILNV 291 lpg-Flipsw-L-DF-lpl-Lw-LWksvl ++. ++ + + ++++++++++++++++++++++++++++		(1037) (1037)
T Consensus T 5a9q_1 T ss_dssp T ss_pred	360G-Fk1i-lw-L-DF-lt		(1436) (1436)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	ccccCCCCCeeecccCCCCCccccccCCCCCchheeeecCCCCCHHHHHHHHHHHHHCC		(1037) (1037)
T Consensus T 5a9q_1 T ss_dssp T ss_pred	425		(1436) (1436)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	CCCCCCHHHHHHHHHHHHHHHHHHHHHHH		(1037) (1037)
T Consensus T 5a9q_1 T ss_dssp T ss_pred	498 iiivvS-iRs 498 VTLAVENELQGSVTEYEFSQEEFRNLQQEFWCKFYACCLQYQEALSHPLALHLNPHTNMVCLLKKGYLSFLIPSSLV НИНИНИНССВСВСЯЗЯВСИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИН		(1436) (1436)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	######################################		(1037) (1037)
T Consensus T 5a9q_1 T ss_dssp T ss_pred	575 E-11		(1436) (1436)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	hcccCCHHHHHHHHHHhCCC-HHHHHHHHHHhCCCccccccc		(1037) (1037)
T Consensus T 5a9q_1 T ss_dssp T ss_pred	647 is-ds-fliiiiiii647 ITIDVENV-MEDICSKLQEIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLTQLYGSNTAGYIVCRGVHKIAS CCHTCCTT-HHHHHHHHHHSSSHHHHHHHHHHHHHHHCCCCCCBCCSCCCHHHHHHHHHH		(1436) (1436)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	######################################		(1037) (1037)
T Consensus T 5a9q_1 T ss_dssp T ss_pred	726 ~i-dLLiLl-lllllyl-wltesls 726 TRFLICRDLLILQQLLMRLGDAVIWGTGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATDVPLDTLESNLQHLS НИНИНИНИНИНИНИНИНИТСССИНИНИТСССИНИНИНИНИНИН		(1436) (1436)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	hhccCcceeeccchHH683 SSEFSFGVKFFNYGQLIAYIDSLNSNYYNASITENSFFM-T 683 ~-fg-klsl		(1037) (1037)
T Consensus T 5a9q_1 T ss_dssp T ss_pred	+.+.+.+. ++ +++++++		(1436) (1436)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	#######hecch###########################		(1037) (1037)
T Consensus T 5a9q_1 T ss_dssp T ss_pred	881 -L		(1436) (1436)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	cccccccchhhhccCccHHHHHHHHHHHHHCCCHHHHHHHH		(1037) (1037)
T Consensus T 5a9q_1 T ss_dssp	948		

```
T ss_pred
              ННННhhcchhHHH--hCh----НhHHHHHHHhhhccccнHHHHHHHHhcCCccccCccccChh-hHHHHHHHHH
0 ss pred
Q Fri_Mar_04_23: 883 EEVLDVLRLGHEC--LSD----TVRTNFLQLLLQEDIYSRDFFSTLLRLCNAHSDNGELYLRTV-DIKIVDSILSQNLRS
                                                                   955 (1037)
           T Consensus
T 5a9q 1
              T ss_dssp
T ss_pred
              Q ss pred
Q Fri Mar 04 23: 956 GD---WECFKKLYCFRMLNKSERAAAEVLYQYILMQADLD-----VIRKRKCYLMVINVLSSFDSAYDQWILNGS---- 1022 (1037)
           O Consensus
T Consensus
T 5a9q_1
              T ss_dssp
T ss pred
              Q ss_pred
              -----евевининин
Q Fri_Mar_04_23: 1023 ------KVVTLTDLRDELRG 1036 (1037)
           1023 -----vvtL~dl~~Ey~~ 1036 (1037)
Q Consensus
                            +||||+|||+||+||+.
           1152 ----kr----r---IvtL-dlr-Ey-l 1189 (1436)
T Consensus
T 5a9q_1
           1152 DRPGASPKRNHDGECTAAPTNRQIEILELEDLEKECSL 1189 (1436)
T ss dssp
              -----ССИНИНИНИНИ
              T ss_pred
                                          Pub Med
>4fhn_B Nucleoporin NUP120; protein complex,structural protein,nuclear pore complex,mRNA transport,protein
 transport, WD repeat; 6.99A {Schizosaccharomyces pombe 972h-}
Probab=100.00 E-value=3.9e-125 Score=1202.45 Aligned_cols=904 Identities=15% Similarity=0.163 Sum_probs=0.0
Q ss pred
              20 PNNTVDLYVSNNSNNNGLKE----GDKSISTPVPQPYGSEYSNCLLL---SNSEYICYHFSSRSTLLTFYPL-----SDA
Q Fri_Mar_04_23:
                                                                    87 (1037)
Q Consensus
            87 (1037)
            99 (1139)
T 4fhn B
            21 LEGTLALWVPALENDSEDDSEAIETADDNEKLFKKECVAYDAGVYTSNKSKGSQTLRWSIFQNRTL-TIFDVSLNSKKEP
                                                                    99 (1139)
T ss dssp
              SCEEEECC-----CHHHHHTTCCCSSEEEEECSSSCEEEEEETTEE-EEECCCCCSSSS
T ss_pred
              CCceEEEECCCCCcccccccCCCCCchHHHhhhccccccceEeccCCCCCCeEEEEEECCCcE-EEeeccccccc
              Q ss_pred
Q Fri_Mar_04_23:
            88\ \mathtt{YHGKTINIHLPNASMNQRYTLTIQE} - \mathtt{VEQQLLVNVILKDGSFLTLQLPLSFLFSSANTLNGEWFHLQNPYDFTVRVPHF}
                                                                   165 (1037)
            88 -----lri-Fp--ilp----v-i-e-----L-I-viT----l-rl-lp---f-------dw-----p--f--r-P--
Q Consensus
                                                                   165 (1037)
              T Consensus
                                                                   177 (1139)
            100 LSKFNVKIHFPSNVMK--DGVAFSFSEHSDTTIIYAITHARVLYYIRLSKTWFQLPDARLDDDWCLCYRPISFLNQKPDL
                                                                   177 (1139)
T 4fhn B
              T ss_dssp
              cCCceEEEEccccCC--CeEEEEEcCCCceEEEEEEcCCCeEEEEEECHHHhhccccccccccccccccCCeE
T ss pred
              EEecCCCEEEEEeCCCCEEEEEecCC-CCeeEEEecCccHHHHHHHHh--cCCCC--CCccceEEEEe-cCcEEEEEE
Q ss pred
            166 \ {\tt LFYVSPQFSVVFLEDGGLLGLKKVDG-VHYEPLLFNDNSYLKSLTRFF--SRSK--SDYDSVISCKLF-HERYLIVLTQ}
Q Fri Mar 04 23:
                                                                   239 (1037)
O Consensus
            166 l-a----vsl-DGqLL-l------lftL--
                                                                   239 (1037)
            T Consensus
                                                                   257 (1139)
            178 MAAISTSEICVSFFNGGLTKIILNPKDASHYEQHIDDSSYLFSLKKYLSLQAFKADYRSPNTIISMIFLSTYNVLVMLSL
T 4fhn B
                                                                   257 (1139)
              EEECCSSEEEEETTSCEEEEEETTEEEEEEEC-------CCCCTTCBSCCEEETTTTEEEEEBT
T ss dssp
              EEEECCCcEEEEEccCccceeEEeccCccHHHhhhhhhccccCCCCCccceEEEEEeCCcCEEEEEEC
T ss pred
              CCeEEEEcCCCceEeeec-ccccccc---ccCCccChhHHHHHhhhheEEEEEec-CCceEEEEEEEcCC-CcEE-
Q ss pred
Q Fri Mar 04 23: 240 NCHLKIWDLTSFTLIQDYDM-VSQSDSDPS--HFRKVEAVGEYLSLYNNTLVTLLPL-ENGLFQMGTLLVDSS-GILT- 312 (1037)
Q Consensus
            240 D--LRiWsl-t---l---dL----------l------l--vylp----g-F----l------l--
            T Consensus
                                                                   328 (1139)
            258 DYKLKVLDLSTNOCVETIELSOTILPLOSFPYLTSDH--TTNSF-----IALYYPDNSHGSFSIYKLNANAHSFKLNV
T 4fhn B
                                                                   328 (1139)
              TCEEEEEETTTTEEEEEEECCCSSSTTSCCSSCCSEE--ESSSS-----EEECCCCGGGCCCCCEEEEECSSSEEE
T ss dssp
              CCeEEeeCCCCCeEeeecccccCCcccccccCC--ccce-----EEEEecCCCCceEEEEEEEecCCCcceeE
T ss pred
Q ss_pred
              -EeecccCCCCCCC--ceeEeeeEEecccccCCCccEEEEEEecCCceEEEEEEccccCC-----CCCeee--
Q Fri Mar 04 23: 313 -YTFQNNIPTNLSASA--IWSIVDLVLTRPLELNVEASYLNLIVLWKSGTASKLQILNVNDESFKN-----YEWIES-
                                                                   381 (1037)
            381 (1037)
Q Consensus
            T Consensus
T 4fhn B
            329 VIEK-GIIPPSLPDDEFIPWMLSDFQLISSEG---SQSKFLLIIAWKSNLNTVIQKCNLSLDQDESFSCVWSHSLDSFSL
                                                                   404 (1139)
              T ss_dssp
              T ss pred
              cccCCCCCccccccCCCCchhee---eecCCCCCHHHHHHHHHHHhCC------
Q ss pred
Q Fri Mar 04 23: 382 VNKSLVDLQSEHDLDIVTKTGDVERG---FCNLKSRYGTQIFERAQQILSEN------ 430 (1037)
```

Q Consensus	382 ~~~l~~~e~~~~d~E~~IF-lpgrfs~~l~AL-iy~~	430 (1037)
T Consensus T 4fhn_B T ss_dssp T ss_pred	405LIFPGT-sLetAL-iylL-e-i-s-i 405 IEKTFFDVPTNMSSGDISEIWLQHIFA-HNT-SIESIQVALLSFQNSSSQVSKNKLDKFGALTISELKNAVLSSI СТТТТТSССССGGGCSSHHHHHHHHHHCC-ССНИННННННННSSSSCCSТТИНИНННННССНИННННННН сссссссссссссСССҺННННННННН-С-ССС-СНННННННННН	477 (1139) 477 (1139)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4fhn_B T ss_dssp		486 (1037) 486 (1037) 554 (1139) 554 (1139)
T ss_pred  Q ss_pred  Q Fri_Mar_04_23: Q Consensus  T Consensus  T 4fhn_B  T ss_dssp  T ss_pred	hhhheecccccCCCHHHHHHHHHHHHHHHHHHHHHHHHHH	558 (1037) 558 (1037) 626 (1139) 626 (1139)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4fhn_B T ss_dssp T ss_pred	cccCCHHHHHHHHHHHHCCc-HHHHHHHHHhccCCcccccccccc	631 (1037) 631 (1037) 696 (1139) 696 (1139)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4fhn_B T ss_dssp T ss_pred	НИНИНИННИНИНИНИНИНИНИНИНИНИНИНИНИНИНИН	696 (1037) 696 (1037) 760 (1139) 760 (1139)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4fhn_B T ss_dssp T ss_pred		742 (1037) 742 (1037) 836 (1139) 836 (1139)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4fhn_B T ss_dssp T ss_pred	hcCCccccCCchнинининининининининининининининининини	820 (1037) 820 (1037) 896 (1139) 896 (1139)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4fhn_B T ss_dssp T ss_pred	-ННИННИНН-ИННИННИННИННИННИННИННИННИННИНН	896 (1037) 896 (1037) 961 (1139) 961 (1139)
Q ss_pred Q Fri_Mar_04_23: Q Consensus T Consensus T 4fhn_B T ss_dssp T ss_pred	ChНЫННИННИНЫНЫННОССССССССССССССССНЬ-ВИНИНИНИННИННО-ССССС-ВИНИНИ           897         SDTVRTNFLQLLLQEDIYSRDFFSTLLRLCNAHSDNGELYLRTV-DIKIVDSILSQNLRS-GDWEC-FKKLYC           897	
Q ss_pred Q Fri_Mar_04_23: Q Consensus	#hhcCCChHHHHHHHHHHHHhhhhh	

```
T Consensus
                      1029 ~-i-r-dyR-AA--mYe---Rl-------l------yl--iNaL-lv----aWi-------iv 1107 (1139)
                      1029 WRYKHONYRDAAATTYEKI,SRYISTTELIGKKERTFIIEHYLIVLNTLELLPK-EDTWILVTDMSVDKEPDPNFLPOKLL 1107 (1139)
 T 4fhn B
 T ss dssp
                            T ss pred
 Q ss_pred
                            ЕННИННИННЫМ
 Q Fri_Mar_04_23: 1026 TLTDLRDELRG 1036 (1037)
 Q Consensus
                      1026 tL~dl~~Ey~~ 1036 (1037)
                            ||+|||+||+.
 T Consensus
                      1108 tL~dl~kEY~l 1118 (1139)
                      1108 TLDAIVAEYHL 1118 (1139)
 T 4fhn B
 T ss dssp
                            нинининини
                            ЕННИННИННИ
 T ss_pred
 No 5
                                                         NCBI
>4gq2_M Nucleoporin NUP120; beta propeller alpha helical, component of nuclear pore COMP transport protein; 2.40A
 {Schizosaccharomyces pombe} PDB: 4fhm B
 Probab=100.00 E-value=1.3e-94 Score=915.47 Aligned_cols=781 Identities=13% Similarity=0.123 Sum_probs=0.0
                            Q ss pred
                        19 EPNNTVDLYVSNNSNNNGLKE----GDKSISTPVPQPYGSEYSNCLLLSNS---EYICYHFSSRSTLLTFYPLSDAY---
 Q Fri Mar 04 23:
                                                                                                                                   88 (1037)
 Q Consensus
                        19 -----l-wkv-d---L-l-sld-----
                                                                                                                                  88 (1037)
                            ..+.+|++.+-...+ |||+|||++|+++ +++|.+.
 T Consensus
                            ----v---p-----p-----e--f----lA--g------r-i-WRv--d-------dl---
                                                                                                                                   94 (950)
                         18 CLEGTLALWVPALENDSEDDSEAIETADDNEKLFKKECVAYDAGVYTSNKSKGSQTLRWSIFQNRTL---TIFDVSLNSK
 T 4gq2_M
                                                                                                                                   94 (950)
 T ss dssp
                            TCCEREEEECCCCTTCCCCH-----HHHHHHHHHCCSEEEEEECTTSSSCCEEEEEEETTTEE--EEEECCCSCC
                            CCCceEEEECCCCCCCcccccCCCCCchhhhhhhhccccceeEeecCCCCCCeEEEEEECCceE---EEEeccccc
 T ss pred
 Q ss_pred
                            ---cCCeEEEEcCcccCCCCeEEEEecCCe-EEEEEEcCCceEEEEECHHHccCccccccccceeeccCccCCC
 Q Fri_Mar_04_23:
                         89 \hspace{0.1in} ---- \hspace{0.1in} + \hspace{0.1in} -\hspace{0.1in} + \hspace{0.1in} -\hspace{0.1in} + \hspace{0.1in} + \hspace{0.1
                                                                                                                                 162 (1037)
                        162 (1037)
 O Consensus
                                 172 (950)
 T Consensus
                         95 KEPLSKFNVKIHFPSNVMK--DGVAFSFSEHSDTTIIYAITHARVLYYIRLSKTWFQLPDARLDDDWCLCYRPISFLNQK
 T 4gq2_M
                                                                                                                                 172 (950)
 T ss_dssp
                            T ss pred
                            CEEEEecCCCEEEEEecCC-CCeeEEEecCccHHHHHHHHh--cCCCC--CCccceEEEEe-cCcEEEE
 Q ss pred
                       163~P_{\tt HFLFYVSPQFSVVFLEDGGLLGLKKVDG-VHYEPLLFNDNSYLKSLTRFF--SRSSK--SDYDSVISCKLF-HERYLIV}
 Q Fri Mar 04 23:
                                                                                                                                 236 (1037)
 O Consensus
                       163 P--l-a----vsl-DGqLL-l-----s-l--L--lf-----vS------lft 236 (1037)
                       T Consensus
                                                                                                                                 252 (950)
                       173 PDLMAAISTSEICVSFFNGGLTKIILNPKDASHYEQHIDDSSYLFSLKKYLSLQAFKADYRSPNTIISMIFLSTYNVLVM
 T 4gg2 M
                                                                                                                                 252 (950)
                            EEEEEECSSSEEEEETTSCEEEEEEETTTTEEEEEEECCCCCCBCC------CCSSCCCTTCEEEEEEETTTTEEEE
 T ss dssp
 T ss_pred
                            CeEEEEeCCCceEEEEecCCcceeEEEecCccHHHHHhhhccccCCCCccceEEEEEeCCccEEEE
                            EECCCeEEEEECCCCceEEeecc-ccccccc---ccCCccChhHHHHHHhhhheEEEEEec-CCceEEEEEEEcCC-Cc
 Q ss pred
 Q Fri Mar 04 23:
                       237 LTQNCHLKIWDLTSFTLIQDYDM-VSQSDSDPS---HFRKVEAVGEYLSLYNNTLVTLLPL-ENGLFQMGTLLVDSS-GI
                                                                                                                                 310 (1037)
                       237 L--D--LRiWsl-t---l---dL--------------------l--vylp----g-F-----l------
                                                                                                                                 310 (1037)
 Q Consensus
                             ||+||+||||++||+|+++|| +....+...
                                                                        .++| ++
                                                                                          +.||++|+|+ ++|+||+|++..++. +.
                       253 L--D--LRiWsl-t---l---dl------------ll-vy-p----g-F------
 T Consensus
                                                                                                                                 323 (950)
                       253 I.SI.DYKI.KVI.DI.STNOCVETTEI.SOTTI.PI.OSFPYI.TSDH--TT-----NSFTAI.YYPDNSHGSFSTYKI.NANAHSFK
                                                                                                                                 323 (950)
 T 4gq2_M
                            T ss dssp
 T ss_pred
                            Q ss_pred
                            EE--Eeeccc-cCCCCCCC-ceeEeeeEEeccccccCCccEEEEEEeccCcceEEEEEEcccccCC------CCCee
 Q Fri Mar 04 23: 311 LT--YTFQNN-IPTNLSASA-IWSIVDLVLTRPLELNVEASYLNLIVLWKSGTASKLQILNVNDESFKN-----YEWIE
                                                                                                                                 380 (1037)
                       O Consensus
                                                                                                                                 380 (1037)
                             T Consensus
                                                                                                                                 399 (950)
 T 4gq2_M
                       324 INVVIEK-GIIPPSI,PDDEFIPWMI,SDFOLISSEG---SOSKFIJ,IIAWKSNI,NTVIOKCNI,SI,DODESFSCVWSHSI,DS
                                                                                                                                 399 (950)
                            EEEEESC-SCCCCCCCCCTTSCCEEEEEEECSS---CSSEEEEEEEEETTEEEEEEEECCC---CEEEEEECCCC
 T ss_dssp
                            T ss pred
                               -ccccCCCCccccccCCCCc<mark>hhee---eec</mark>CCCCC<del>HHHHHHHHHHh</del>cC------
 Q ss pred
 Q Fri Mar_04_23: 381 S-VNKSLVDLQSEHDLDIVTKTGDVERG--FCNLKSRYGTQIFERAQQILSEN-----
                                                                                                                                 430 (1037)
                       O Consensus
                                                                                                                                 430 (1037)
                                                    +.|++|+| ||+ ||| +.++|+|||+||+|
----d-e-yl--IF--PGr-s---l--AL-iy----
                             + ...+.+++++..
 T Consensus
                       400 FSLIEKTFFDVPTNMS----SGDISEIWLQHIFA-HNT-SIESIQVALLSFQNSSSQVSKNKLDKFGALTISELKNAVL
 T 4gq2_M
 T ss_dssp
                            T ss_pred
                            cccccccCCcccC----CcChнининннhhc-CCC-Снининнннннhhhccccccccccccccchнининнн
                              -----CCcccHH---HHHHHHHHHHHHHHHhCCceEEEe--cCCeEEEEEcCCccEEEEEe----
 Q ss_pred
 Q Fri Mar 04 23:
                       431 -----KIIMAHNE---DEEYLANLETILRDVKTAFNEASSITL--YGDEIILVNCFQPYNHSLYKL----
                                                                                                                                 486 (1037)
                       431 -----d~i~vv~~~~s~ir~---
 O Consensus
                                                                                                                                 486 (1037)
                       T Consensus
                                                                                                                                 549 (950)
                       473 SSIVSTIQIEPNSDLTGYDYYEYKRLLYNEWERFAKLVAYLDHFGDEILSINFDPSNAVTYINYAN---KVAFIRDPYLI
 T 4gg2 M
                                                                                                                                 549 (950)
 T ss_dssp
                            T ss pred
```

```
Q ss_pred
                      -----Соринния Ссессссинний инфиниции и при ссесссиний и при ссесссии и при ссессии и при ссесии и при сс
 Q Fri Mar 04 23: 487 -----NTTVENWFYNMHSETDGSELFKYLRTLNGFASTLSNDVLRSISKKFLDIITGELPDSMTTVEKFTDIFK
                                                                                                    555 (1037)
                  487 -----s-lE----n----d---Ll--l--f---ls------l---l---l-----s-s------i--
 O Consensus
                                                                                                    555 (1037)
                  T Consensus
                                                                                                    621 (950)
                  550 ESFDEEPLTKLISSLETD--DPS----LIEGYOILDLGRSLHSCMSFSTLSEIRYSLRELVODL--PSYSLFDTLWVFYD
                                                                                                    621 (950)
 T 4gq2 M
                      T ss_dssp
                      T ss pred
                      ННhcccCCнининининин
 Q ss_pred
 Q Fri_Mar_04_23: 556 NCLENQFEITNLKILFDELNSFD-IPVVLNDLINNQMKPGIFWKKDFISAIKFDG--FTSII--SLESLHQLLSIHYRIT
                                                                                                    630 (1037)
                  O Consensus
                                                                                                    630 (1037)
                     T Consensus
                                                                                                    694 (950)
                  622 KHIYPNVDPDYISTLIDTLVSLENPMRDIDSLIQRLRSFDIYNHSA-QSPSLFLCASVARVLDSILKKFQVSIE-----
 T 4gq2_M
                                                                                                    694 (950)
 T ss_dssp
                      ННИНЬcCCнининининнь
 T ss_pred
                      Q ss_pred
                  631 LQVLLTFVLFDLDTEIFGQHISTLLDLHYKQFLLLNLYRQDKCLLAEVLLKDSSEFSFGVKFFN------
 Q Fri Mar 04 23:
                                                                                                    694 (1037)
                  631 ~~lLll~~~~~~~l~~ll~ll~l~~~~~l~~l-~ll~~l~~y~~~~~l~~elf~~~~~f~~g~kl~s-------
 Q Consensus
                                                                                                    694 (1037)
                  T Consensus
                                                                                                    766 (950)
                  695 GFIFLLSLITSQQDYELQSKFAGC-DKLF--LSLLEDWR-----LVSFLLENSALLLEKFEEEDVDSTNCNLNTMEALAS
 T 4gq2 M
                                                                                                    766 (950)
                      T ss dssp
                      HHHHHHHHhcccccccccc-HHHH--HHHHHHHH-----HHHHHHhcCccccCCcchhccccCCccccccCc
 T ss pred
                      -----cchннинининннын-cccchhни--ннининннынноссья
 Q ss pred
 Q Fri_Mar_04_23:
                  695 -----YGQLIAYIDSLNSNVYNA-SITENSFFM-TFFRSYIIENTSHKNIRFFLENVECPFYL
                                                                                                    750 (1037)
                  695 ------np-----l---vi--q-----fl--i--p
                  ...|.++..++.+.....||++|.+....++|+....++|+...|
767 --t-le----l-----q--la--ell-----
 T Consensus
                                                                                                    837 (950)
                  767 VNTALQFFSALNYSECFSESQISPLHATVISSLSAIFIRDDTENDLVTELVEKLFL--FKQYNACM-QLI----GWLN
 T 4gq2 M
                                                                                                    837 (950)
                      T ss dssp
 T ss_pred
                      Q ss_pred
 Q Fri Mar_04_23: 751 RHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTF-TV-PYR-HSAFYYQ
                                                                                                    827 (1037)
                  827 (1037)
 O Consensus
 T Consensus
                                                                                                    902 (950)
                  838 SDPIAV-YLKALIYI.KSKEAVKAVRCFKTTSI.VI.YSH-----TSO--F-AV-I.REFOETAEKYHHONI.I.SCYYI.H
 T 4gq2_M
                                                                                                    902 (950)
                      SSHHH-HHHHHHHHTCHHHHHHHHTCCCTTCSS-----C-GG-GHHHHHHHHHTTCSHHHHHHH
 T ss dssp
 T ss pred
                      Q ss_pred
                      НН-НННННСССНИНННННННННННННННН
 Q Fri_Mar_04_23:
                  828 LS-LLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVL
                                                                                   889 (1037)
                  828 l~-~Lfe~~~~al~~a~~Ai~~~~e~~~~e~~~~l~~i~~~F~~~L~l~
 Q Consensus
                                                                                    889 (1037)
                                                                 |+|+|+++|++|
                      |+ +||| +++++|++||++||+++++++ ...| .++
 T Consensus
                      v---LFE----vi-fA-1A1-----
                                                           ---l----srlF-a-l--
                  903 LSKKLFE-ESAYIDALEFSLLADASKETDD-----EDLS-IAI------THETLKTACAAG
 T 4gq2 M
                                                                                    950 (950)
 T ss dssp
                      НННННН-ссснинннннннннннннннннннссСС----сссh-hнн------ннннннннн
 T ss pred
                                  PDB<sup>®</sup>
PROTEIN DATA BANK
                                            NCBI
                                                       Pub Med
>4ycz C NUP120; structural protein complex, nuclear pore complex, macromolec assemblies, structural protein;
 4.10A {Thielavia heterothallica}
 Probab=100.00 E-value=3.8e-34 Score=311.89 Aligned_cols=150 Identities=19% Similarity=0.303 Sum_probs=0.0
                      Q ss pred
 945 (1037)
                                                                                                    945 (1037)
                   22 l~~~Lws~lFk~aL~l~~ydeAY~AL~~npd~~~rk~cLr---
                                                                 ----LV~~Lce~g~l---~Ll~lpf~gl~~~V
 T Consensus
                                                                                                     88 (313)
                   22 LRTEMLSRLFTAATSISHFEEAHSALLSMDDEAMQKSYLR------RLVEKMCETGQS---SELITLPFSGLQTKV
 T 4ycz C
                                                                                                    88 (313)
 T ss dssp
                      ----CHHHHHHHHCCSSCSSHHHHHHHC----CCCTTHH------HHHHHHHHSSCS---HHHHCCSCHHHHHHH
                      T ss_pred
                      ННИННИНЬсс----CCcc-hhHHhhhhhhcCCChннинниннниннннhhhhhh-----------
 Q ss_pred
 Q Fri_Mar_04_23: 946 DSILSQNLRSG---DWEC-FKKLYCFRMLNKSERAAAEVLYQYILMQADLDV------IRKRKCYLMVI 1004 (1037)
 O Consensus
                  T Consensus
                   89 DDILVEKCRATROVLNGVPYHQILYAWRINHNDYRGGAAILLDRLQKLRRAGEGDKVIANEHGNEDALDTQVTRQYLLLI
 T 4ycz_C
                                                                                                   168 (313)
                      НИНИНТТТТСС----СССТИНИНИНИНИНИНИНИНИНИНИНИТС--------СИНИНИНИНИНИНИ
 T ss_dssp
 T ss_pred
                      HHHhhCCchhcCeecCC-----
 Q ss pred
 Q Fri_Mar_04_23: 1005 NVLSSFDSAYDQWILNG------ 1021 (1037)
 Q Consensus
                 |||+||+| ++|||+.+
```

```
T Consensus
                                       169 NaLslvd~-~daWIl~~~~~
                                                                                                                                                                                                                          247 (313)
                                       169 NALSCVPP-OEAYILEDVLPGDGRGGDDADGDRNGGKAGDDLEADIDELEKKLDVEGGADAAKGDEMAAEEDAALIEKMK 247 (313)
  T 4ycz C
  T ss dssp
                                                T ss pred
                                                Q ss_pred ------Ceeeehhhhhhhhhhhhhh Q Fri_Mar_04_23: 1022 ------SKVVTLTDLRDeLRG 1036 (1037)
                                     1022 -----vvtL~dl~~Ey~~ 1036 (1037)
  Q Consensus
                                                       +.||||+|||||
                                       248 ~~~~r~ivtl~dlRkeyq~
  T Consensus
                                                                                                          274 (313)
                                        248 RFSTRNGQNLPARRLLMLADLRKQYQQ
  T 4ycz C
  T ss dssp
                                                нининсс----ссссссинининин
                                                ссссссссеЕЕееНННННННН
  T ss_pred
🗌 >3as5_A MAMA; tetratricopeptide repeats (TPR) containing protein, TPR PROT protein-protein interactions, protein
  binding; 2.00A {Magnetospirillum magnetotacticum} PDB: 3as4 A 3as6 A 3asg A 3ash A 3as8 A 3asf A Probab=93.30 E-value=1.4 Score=44.35 Aligned_cols=124 Identities=7% Similarity=0.008 Sum_probs=0.0
                                                Q Fri_Mar_04_23: 715 TENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTF
                                                                                                                                                                                                                         793 (1037)
                                        715 \ \ {\sim} np {\sim} {\sim} {\sim} 1 {\sim} vi {\sim} {\sim} q {\sim} {\sim} {\sim} f1 {\sim} i {\sim} p {\sim} {\sim} {\sim} f1 {\sim} g {\sim} {\sim} 1 {\sim} {\sim} {\sim} A {\sim} {\sim} F {\sim} a {\sim} {\sim} {\sim} {\sim} 1 {p} {\sim} 1 {\sim} {\sim} 1 {p} {\sim} 1 {\sim} 1 {p} {p
  Q Consensus
                                                                                                                                                                                                                         793 (1037)
                                                |.++....+.|.+++|.++|+++
  T Consensus
                                               p----A---
                                                                                                        --al----p-----lg-----g----A----a-
                                                                                                                                                                                                                          102 (186)
                                          39 AFDVDVALHLGIAYVKTGAVDRGTELLERSLA--DAPDNVKVATVLGLTYVQVQKYDLAVPLLIKV-----
  T 3as5 A
  T ss dssp
                                                T ss_pred
  Q ss_pred
                                                HhhhhheecceeccehhhheeCceннинниннинниннинниннинниннинниннинн
  Q Fri_Mar_04_23:
                                       794 LEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYOLSLLFDRNNSOEFALKCISKSAEYSLKEIOIEELODFKEKOHIHYL
                                                                                                                                                                                                                         873 (1037)
  O Consensus
                                        ....+.....++..+....|.++..|++...++|++...+.+.
                                                                              -----l~~p~~~~~lg~~~~~g~~~~Å~~~~~al~~~p~~~--
  T Consensus
                                                                                                                                                                                                                         146 (186)
                                                -----AEANPINFNVRFRLGVALDNLGRFDEAIDSFKIALGLRPNEG------KV---- 146 (186)
  T 3as5_A
  T ss_dssp
                                                T ss pred
                                                hhhнннннннннньсеннн
  Q ss pred
                                       874 NLLIHFRMFEEVLDVLRLGHE
  Q Fri Mar 04 23:
                                                                                             894 (1037)
                                       874 ~~~i~~~F~~~L~l~~~~a 894 (1037)
  O Consensus
                                                        |.++=....|+++.|
  T Consensus
                                                         ~~~1~~~~~q~~~~A 163 (186)
                                        147 ----HRAIAFSYEQMGRHEEA 163 (186)
  T 3as5_A
                                                ----НИНИНИННИТТСИНИН
  T ss dssp
  T ss_pred
                                                ----НННННННННСССИННН
                                                                                                 PDB"
  No 8
                                                                        SCOPe
                                                                                                                                                                 Pub Med
>1na0_A Designed protein CTPR3; de novo protein; HET: IPT; 1.60A (Unidentified) SCOP: k.38.1.1 PDB: 2wqh _A 3kd7 _A
      Probab=93.21 E-value=0.68 Score=42.49 Aligned_cols=92 Identities=10% Similarity=0.194 Sum_probs=0.0
                                                Q ss pred
  Q Fri Mar 04 23: 750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLS
                                                                                                                                                                                                                          829 (1037)
                                                ~~~~~fl-g-~l~~~~A-~F~a-~~~lp~l~l~~~~~l~~~~l~~~~l~~~~Yy~l~
                                        750
                                                                                                                                                                                                                          829 (1037)
                                                +.+.+..+.|.+++|.++|+++
  T Consensus
                                            5 ~~~~~A~~~~A~~~~a~-
                                                                                                                                                                                     _~~~~p~~~~~1a
                                                                                                                                                                                                                            50 (125)
                                           5 PGNSAEAWYNLGNAYYKOGDYDEATEYYOKA------LELDPNNAEAWYNLG
  T 1na0 A
                                                                                                                                                                                                                            50 (125)
  T ss_dssp
                                                ссссинининининин
  T ss pred
                                                Q ss_pred
  Q Fri_Mar_04_23: 830 LLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                                                                                                                                                                                          894 (1037)
  Q Consensus
                                        830 ~Lfe~~~~al~~a~~Ai~~~~~e~~~~
                                                                                                                             -----l---i----F----L-l-----a
                                                                                                                                                                                          894 (1037)
                                                .++...|.++.|++..+.|++..+..
                                                                ----A-----a---p---------------
                                                                                                                                                      --1----A
  T Consensus
                                                                                                                                                                                             96 (125)
  T 1na0_A
                                         51 NAYYKQGDYDEAIEYYQKALELDPNNA-----EA-----WYNLGNAYYKQGDYDEA
                                                                                                                                                                                            96 (125)
                                                T ss_dssp
                                                T ss pred
                                                                                                                                         Pub Med
                                                                                                                        >4cgv A Spaghetti, RNA polymerase II-associated protein 3: chaperone, R2TP, TAH1, PIH1: 2.54A (Homo sapiens)
  Probab=92.24 E-value=3.1 Score=37.78 Aligned_cols=131 Identities=11% Similarity=-0.033 Sum_probs=0.0
                                                ННюсССССhhнининин----сcchнинининныноССсссСchнининининининининининин
  Q Fri Mar_04_23: 709 VYNASITENSFFMTFFRSYII---ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPE
Q Consensus 709 1------q------fl--i--p-------fl-g---1------A---F--a---
                                                                                                                                                                                                                         784 (1037)
                                                                                                                                                                                                                          784 (1037)
                                                .+...+...|-+.+|......|+++|..+.+|.++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..++|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|
                                                                       .....a...a....A....A....
  T Consensus
                                                                                                                                                                                                                            74 (136)
  T 4cqv A
                                            2 SEEDGIHVDSQKALVLKEKGNKYFKQGKYDEAIDCYTKGMD---ADPYNPVLPTNRASAYFRLKKFAVAESDCNLA----
                                                                                                                                                                                                                            74 (136)
  T ss_dssp
                                                -----СССИНИНИНИНИНИНИТСИНИНИНИНИНИН---ИСТТСТИНИНИНИНИТСИНИНИНИНИН----
  T ss_pred
                                                сырыр сестем сестем объем сесте
```

```
Q ss_pred
                                 сссссьниный рисссссссссьный расссссссьный рассссссссс
 O Fri Mar 04 23: 785 AINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYOLSLLFDRNNSOEFALKCISKSAEYSLKEIOIEELODF
                                                                                                                                                      864 (1037)
                           O Consensus
                                                                                                                                                      864 (1037)
                                                                      _____la~~~~
                                                                                                            ----A-----p-----
                             75 ------VALNRSYTKAYSRRGAARFALQKLEEAKKDYERVLELEPNNF------ 116 (136)
 T 4cgv_A
                                 T ss_dssp
                                 ------нһсССССНИНИНИНИНННННННННННННННННННННН
 T ss pred
                                 hнинныныннинниннин
 Q ss_pred
 Q Fri Mar 04 23: 865 KEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC
                                                                                895 (1037)
                           865 ----av
 O Consensus
                                                                                895 (1037)
                                                +..+-....++++.|+
                                             -----\hat{\lambda}
 T Consensus
                           117 ---EA-----TNELRKISQALASKENSY 136 (136)
 T 4cgv_A
 T ss_dssp
                                 ---НН------ННННННННННННСС----
 T ss_pred
                                 ---нн-----ннининининин
                                                PDB"
PROTEIN DATA BANK
 No 10
                                                                  NCBI
                                                                                              Pub Med
🗌 >2dba_A Smooth muscle cell associated protein-1, isoform 2; tetratricopeptide repeat, structural genomics,
 NPPSFA; NMR {Homo sapiens}
 Probab=92.24 E-value=1.5 Score=41.72 Aligned cols=92 Identities=13% Similarity=0.105 Sum probs=0.0
                                 cCCchнининининенсСсининининин
 Q Fri_Mar_04_23: 750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYR---HSAFYY
                                                                                                                                                      826 (1037)
                           O Consensus
                                                                                                                                                       826 (1037)
 T Consensus
                             24 -----g
                                                                          ~~a-----1~~~p~~~
                                                                                                                                                        69 (148)
 T 2dba A
                             24 GASSVEQLRKEGNELFKCGDYGGALAAYTQA-----LGLDATPQDQAVLHR
                                                                                                                                                        69 (148)
 T ss_dssp
                                 TCCCHHHHHHHHHHTTCHHHHHHHHHH
 T ss_pred
                                 ррининининининини
 Q ss_pred
                                 ннинниньсссинининниннинн
 Q Fri Mar 04 23:
                           827 QLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                                                                                                                                     894 (1037)
 O Consensus
                           827 ~l~~Lfe~~~~~al~~a~~Ai~~~~~e~~~~~l~~~i~~~F~~~L~l~~~~a
                             T Consensus
                             70 NRAACHLKLEDYDKAETEASKAIEKDGGDV-----KA-----LYRRSQALEKLGRLDQA
 T 2dba A
                                                                                                                                     118 (148)
                                 T ss_dssp
 T ss pred
                                 No 11
                                                                                   Pub Med
              Hypothetical conserved protein TTC0263; TPR, protein binding; 2.50A {Thermus thermophilus}
Probab=91.83 E-value=3 Score=43.12 Aligned_cols=154 Identities=11% Similarity=-0.010 Sum_probs=0.0
                                 CCCChhнинниннh-ccchниннинннhecccccCchнинниннннннннннннннннннннн
 Q ss pred
 Q Fri_Mar_04_23: 714 ITENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAIND----
                                                                                                                                                      788 (1037)
                           788 (1037)
 T Consensus
                                                                                                                                                        77 (217)
                              1 MOTAEONPLRLGVOLYALGRYDAALTLFERALK---ENPODPEALYWLARTOLKLGLVNPALENGKTLVARTPRYLGGYM
 T 2pl2 A
                                                                                                                                                        77 (217)
                                 ---ССНИНИНИНИНИТТСИИНИНИНИНИТ---TSSSCHИНИНИНИНИТСИИНИНИНИНИНИНИНИНИНИНИ
 T ss_dssp
                                 T ss_pred
                                 Q ss pred
 Q Fri Mar 04 23: 789 KLPTFLEDL-----KSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQ
                                                                                                                                                       857 (1037)
                           Q Consensus
                                                                                                                                                       857 (1037)
                                 .+..+..+..+..+..+..+..+..+...
                             T Consensus
                                                                                                                                                       151 (217)
                             T 2pl2 A
                                                                                                                                                       151 (217)
 T ss dssp
                                 НИНИНИННЫН НА НА НЕВ В НЕВ В
 T ss pred
 Q ss_pred
                                 сссссснинныныныннинниннын
 Q Fri_Mar_04_23:
                           858 IEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                           O Consensus
                                              .. |.++-....|+++.|
 T Consensus
                                                               ---lg-----A
                           152 -----EI------RSALAELYLSMGRLDEA 170 (217)
 T 2pl2 A
 T ss_dssp
                                 T ss_pred
                                 -----НН------НН-ННННННННСССНННН
                                                PDB<sup>N</sup>
PROTEIN DATA BANK

POBLE

POBL
                                                                                              Pub Med
>3as5_A MAMA; tetratricopeptide repeats (TPR) containing protein, TPR PROT protein-protein interactions, protein binding; 2.00A {Magnetospirillum magnetotacticum} PDB: 3as4_A 3asd_A 3asg_A 3ash_A 3as8_A 3asf_A Probab=91.59 E-value=1.8 Score=43.56 Aligned_cols=108 Identities=11% Similarity=0.122 Sum_probs=0.0
                                 Q Fri_Mar_04_23: 731 NTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKD 810 (1037)
                           731 ~q~~~~fl~~i~p~~~~~fl~q~~fl~q~~l~~~F~~a~~~~lp~~l~~l~~~~l~~~ 810 (1037)
 O Consensus
```

```
+++.....|-+.+.
             22 g----A-----al-----p------l------g-----A-----a----
T Consensus
                                                                    68 (186)
             22 GRYSQAVMLLEQVYD---ADAFDVDVALHLGIAYVKTGAVDRGTELLERS------
T 3as5 A
                                                                    68 (186)
              T ss dssp
T ss_pred
              Q ss pred
Q Fri_Mar_04_23:
            811 LLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLR
                                                                   890 (1037)
            811 ~l~~~~~Yy~~l~~Lfe~~~~~al~~a~~Ai~~~~e~~~~e~~~~~l~~~i~~~F~~~L~l~~
                                                                   890 (1037)
Q Consensus
                 ....+....+...+...|.++..|++...+.
             69 ----l---p------lg------g-----A-----al---p------------
T Consensus
                                                          ~~~lg~~~~~g~
             69 ----TADAPDNVKVATVI.GI.TYVOVOKYDI.AVPI.I.TKVAFANPINF-----NV------RFRI.GVAI.DNI.GR
T 3as5 A
                                                                   125 (186)
              T ss dssp
               T ss pred
Q ss_pred
              hhHH
            891 LGHE 894 (1037)
Q Fri_Mar_04_23:
Q Consensus
            891 ~~~a 894 (1037)
            126 ~~~Å 129 (186)
T Consensus
            126 FDEA
                  129 (186)
T 3as5 A
T ss_dssp
              нннн
T ss_pred
              нннн
                       PDB<sup>IM</sup>
PROTEIN DATA BANK
                            NCBI Pub Med
>3vtx_A MAMA; tetratricopeptide repeats (TPR) containing protein, peptide protein, protein binding; 1.75A
{Candidatus magnetobacterium bavaricum} PDB: 3vty _A
Probab=91.49 E-value=1.7 Score=43.19 Aligned_cols=138 Identities=12% Similarity=0.037 Sum_probs=0.0
              Q Fri_Mar_04_23: 731 NTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAIND----KLPTFLEDLKSENYHGDS
                                                                   806 (1037)
            Q Consensus
                                                                   806 (1037)
              +.+....+ | -+.+. ...++++...+ | .+| ... | ++++ | .++ | +++-...... .+=..+....+
             T Consensus
                                                                    92 (184)
T 3vtx A
             19 GDFDGAIRAYKKVLK---ADPNNVETLLKLGKTYMDIGLPNDAIESLKKFVVLDTTSAEAYYILGSANFMIDE---KQAA
                                                                    92 (184)
T ss_dssp
               T ss_pred
               Q ss_pred
O Fri Mar 04 23:
            807 IWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVL
                                                                   886 (1037)
O Consensus
            886 (1037)
             T Consensus
             93 -IDALQRAIALNTVYADAYYKLGLVYDSMGEHDKAIEAYEKTISIKPGFI------RA-------YQSIGLAYE 152 (184)
T 3vtx A
               -ининининсттсинининининттсинининининин
T ss_dssp
T ss_pred
               -нинининоссеснинининининин
Q ss pred
              hhcchhHH
Q Fri_Mar_04_23: 887 DVLRLGHE 894 (1037)
            887 ~1~~~~a
Q Consensus
                     894 (1037)
            ..|+++.|
153 ~~q~~~A
T Consensus
                    160 (184)
            153 GKGLRDEA
T 3vtx A
                    160 (184)
T ss dssp
T ss_pred
              НСССИНИН
                              PDB<sup>®</sup>
No 14
                      SCOPe
                                     NCBI
                                           Pub Med
>1elw_A TPR1-domain of HOP; HOP, TPR-domain, peptide-complex, helical repeat, HSP70, protein binding, chaperone;
1.60A {Homo sapiens} SCOP: a.118.8.1
Probab=91.41 E-value=1.5 Score=39.43 Aligned cols=90 Identities=11% Similarity=0.042 Sum probs=0.0
              Сенининининнессенинининн
Q ss pred
Q Fri_Mar_04_23: 752 HNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLL
                                                                   831 (1037)
            831 (1037)
              ..+...+|.+++..|++++|.++|.++
T Consensus
             2 ----A----
                               ~~a-----
                                                   _____]a~~
                                                                    47 (118)
T lelw A
             2 EQVNELKEKGNKALSVGNIDDALQCYSEA-----IKLDPHNHVLYSNRSAA
                                                                    47 (118)
T ss_dssp
              СНИНИНИНИНИТСИВИНИНИНИН
T ss_pred
               сhннннннннннссСннннннннн-----
              Q ss pred
O Fri Mar 04 23: 832 FDRNNSOEFALKCISKSAEYSLKEIOIEELODFKEKOHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
            832 fe------al--a--Ai------e-----------l----i----F----L-l-----a
                                                        894 (1037)
Q Consensus
               +...|.++.|++....|++..+...
T Consensus
                  ....A....a...p....p....1.....1.....1
                                                         91 (118)
             48 YAKKGDYQKAYEDGCKTVDLKPDWG-----KG----YSRKAAALEFLNRFEEA
T lelw A
                                                         91 (118)
              T ss dssp
               T ss pred
                       PDB"
```

```
>4cgw_A Spaghetti, RNA polymerase II-associated protein 3; chaperone, R2TP, TAH1, PIH1; 3.00A {Homo sapiens}
 Probab=91.34 E-value=1.5 Score=39.02 Aligned cols=92 Identities=10% Similarity=0.011 Sum probs=0.0
                          cCCchнининининеCCнининининин
 Q ss pred
 Q Fri Mar 04 23:
                      750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLS
                                                                                                                        829 (1037)
                      750 \quad \text{$^{750}$ } \\ -\text{$^{750}$ } \\ -\text{$^{7
 Q Consensus
                                                                                                                        829 (1037)
                          ..+.+...+...|++++|.++|.++
                       14 -----A-----A------
 T Consensus
                                                                                                                          59 (117)
                       14 NKQQAISEKDRGNGFFKEGKYERAIECYTRG----IAADGANALLPANRA
 T 4cqw A
                                                                                                                         59 (117)
                          T ss dssp
 T ss_pred
                          hhнинининининининининининининин
                          нинньссининининнынныесссссссиннынынынынныннынын
 Q ss pred
 Q Fri Mar 04 23: 830 LLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                      830 ~Lfe~~~~al~~a~~Ai~~~~e~~~~e~~~~l~~~i~~~F~~~L~l~~~~a 894 (1037)
 O Consensus
                          .++...|.++.|++..+.|++..+...
                                                                               |.++-....|+++.|
                                                                                               .
----À 105 (117)
 T Consensus
                       60 MAYLKIQKYEEAEKDCTQAILLDGSYS------KA-----FARRGTARTFLGKLNEA 105 (117)
 T 4cgw_A
                          T ss_dssp
 T ss pred
                          No 16
                                                                           Pub Med
>5a9q A Nuclear pore complex protein NUP155; transport protein; 23.00A {Homo sapiens}
 Probab=91.31 E-value=2.4 Score=56.66 Aligned_cols=236 Identities=11% Similarity=0.097 Sum_probs=0.0
                          нининьсесьничнинины сСссссССсьнинининин ССни-----нининины в досссссьни
 Q ss_pred
 Q Fri_Mar_04_23: 724 FRSYIIENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFD------QSYEIFQLHDY--PEAINDKLPT
                                                                                                                        792 (1037)
 O Consensus
                      792 (1037)
                           823 F-dL----g--la--Li-alIn--i---sv-d-is--Lr--Cpsf-s-dDv---kA-E-L--Ak-------------L-e
 T 5a9q A
                      823 FKDLVIR--DKELTGALIASLINCYIRDNAAV-DGISLHLQDICPLLYSTDDAICSKANELLQRSRQVQNKTEKERMLRE
                                                                                                                        899 (1391)
 T ss_dssp
                          нинньс--синининининининин
 T ss_pred
 Q ss pred
                          HHhhhhhccccccccchhhhccCccннининнниннннннннн
 Q Fri_Mar_04_23: 793 FLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISK-----SAEYSLKEIQIEELQ
                                                                                                                        862 (1037)
 Q Consensus
                      793 ~l~~l~~~~~~l~~~l~~~~~Yy~~l~~Lfe~~~~al~~a~~~----Ai~~~~~e~~
                                                                                                                        862 (1037)
                                                        ...+...|.+.+.|+.|++++... |+.+..+.+.+.+.-
------L--ic-----l--y-GaVeL-L--A---Dp---Al-----g----D--
                          .++-..+
                                                                                                     |+.+...+.+.+.
                      900 al~Lf~~---va~~l-
 T Consensus
                                                                                                                        960 (1391)
                      900 SLKEYQK---ISNQV------DLSNVCAQYRQVRFYEGVVELSLTAAEKKDPQGLGLHFYKHGEPEEDIV
 T 5a9q A
                                                                                                                        960 (1391)
 T ss_dssp
                          T ss_pred
                          Q ss pred
                      863 DFKEKQHIHYLNLLIHFRMFEEVLDVLRL-----GHEC--LSDTV
 Q Fri Mar 04 23:
                                                                                                                        900 (1037)
                      863 ~~~~~l~~i~~~F~~~L~l~~~~ay--L~~~
 O Consensus
                                                                                                                        900 (1037)
                      +++| +..+-
 T Consensus
                                                                                                                ~1~s~D 1032 (1391)
                      961 GLQAFQE-----RLNSYKCITDTLQELVNQSKAAPQSPSVPKKPGPPVLSSDPNMLSNEEAGHHFEQMLKLSQRSKD 1032 (1391)
 T 5a9q A
 T ss_dssp
                          T ss_pred
                          Q ss pred
                      901 RTNFLQLLLQEDIYSRDFFSTLLRLCNAHSDNGELYLRTVDIKIVDSILSQNLRSG--DWECFKKLYCFRMLNKSERAAA 978 (1037)
 Q Fri_Mar_04_23:
                    Q Consensus
 T Consensus
                    1033 ELFSIA------LYNWLIQVDLA--DKLLQVA--SPFLEPHLVRMAKVDQNRVRYMDLLWRYYEKNRSFSNAA 1095 (1391)
 T 5a9g A
 T ss_dssp
                          -СНИН-------СНИНИНИНТТН---НИНИНСС--СТТИНИНИННТС-----СНИНИНИННННССЯНИНИ
                          ННННН-------HHHHHHhCCCc---ceeccCC---СссНННННННhhccCcchhhHHHHHHHHhhccHHHHH
 T ss pred
                          нининининировория ---
 Q ss_pred
 Q Fri_Mar_04_23: 979 EVLYQYILMQADLDVIRKRKCYL--MVINV 1006 (1037)
                     979 ~~mYe~~~rl~~~~~~k~yL--~~iN~ 1006 (1037)
 Q Consensus
                    +++|.-+.+-....++|-.|| ++.||
1096 ~vL~LA~s~~~i~L~~RieyLsrA~~~a
                                                           a 1125 (1391)
 T Consensus
                    1096 RVLSRLADMHSTEISLQQRLEYIARAILSA 1125 (1391)
 T 5a9q_A
                          нинининсс-ссссинининининитс
 T ss dssp
                          ннининносссссснининнинниннин
 T ss pred
 No 17
                                                                           Pub Med
->3q49_B STIP1 homology and U box-containing protein 1; E3 ubiquitin ligase, ligase-chaperone complex; 1.54A {Mus
 musculus} PDB: 3q47 B 3q4a B* 4kbq A
Probab=91.12 E-value=1.9 Score=39.51 Aligned_cols=93 Identities=13% Similarity=0.104 Sum_probs=0.0
 Q ss pred
                          ссСсьнинининнесСсинининнинны
 Q Fri Mar 04 23: 749 YLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQL
                                                                                                                        828 (1037)
                          ~~~~fl~g~~l~~r~~A~~F~~a~~~~~lp~~l~~l~~~~~l~~~l~~~~~Yy~~l
 Q Consensus
                      749
                                                                                                                        828 (1037)
                          ....+...+...
                        4 MKSPSAOELKEOGNRI, FVGRKYPEAAACYGRA------TRNPI, VAVYYTNR
 T 3q49 B
                                                                                                                         49 (137)
 T ss dssp
```

```
T ss_pred
                         ССссЬНИНИНИНИНИСССИИНИНИНИНИ
                         0 ss pred
 Q Fri_Mar_04_23: 829 SLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                     829 ~~Lfe~~~~al~~a~~Ai~~~~e~~~e~~~l~~i~~~F~~~L~l~~~~a
                                                                                                    894 (1037)
                         ..++...|.++.|++..+.|...
                                                                          |.++-....++++.|
                      50 a----a----a-----1-----1-----1
 T Consensus
                                                                                                     96 (137)
                      50 ALCYLKMQQPEQALADCRRALELDGQSV-----KA-----HFFLGQCQLEMESYDEA
 T 3q49 B
                                                                                                     96 (137)
                         T ss dssp
 T ss_pred
                         PDB"
 No 18
                                                               NCBI
                                      SCOPe
                                                                         Pub Med
🗌 >1hxi_A PEX5, peroxisome targeting signal 1 receptor PEX5; alpha helical, transport protein; 1.60A {Trypanosoma
 brucei} SCOP: a.118.8.1
 Probab=91.04 E-value=1.4 Score=39.79 Aligned cols=84 Identities=11% Similarity=0.110 Sum probs=0.0
                         нинининессининининин
 0 ss pred
                    758 FMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNS
 Q Fri_Mar_04_23:
                     Q Consensus
                                                                                                                   837 (1037)
                         |.+|.+++.|+++|.++
                                                                                       ....+....+..+..+...|.
 T Consensus
                          ____a~~~a
                                                                                                                    66 (121)
                      21 MEEGLSMLKLANLAEAALAFEAV------------------CQKEPEREEAWRSLGLTQAENEK
 T 1hxi A
                                                                                                                    66 (121)
 T ss_dssp
                         нинининттснининининининин
 T ss_pred
                         Q ss pred
 Q Fri Mar 04 23: 838 QEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
 O Consensus
                     838 ---al--a--Ai-----e----e-----l---i---F---L-l-----a
                                                                                         894 (1037)
                         ++.|++..+.|++..+...
 T Consensus
                      67 ---- A----- a----p------la------
                      67 DGLAIIALNHARMLDPKDI-----AV-----HAALAVSHTNEHNANAA 104 (121)
 T 1hxi A
                         T ss_dssp
 T ss pred
                         SCOPe PROTEIN DATA BANK
 No 19
>2hr2_A Hypothetical protein; alpha-alpha superhelix fold, structural genomics, joint CENT structural genomics,
 JCSG, protein structure initiative; 2.54A {Chlorobium tepidum} SCOP: a.118.8.8
 Probab=90.91 E-value=1.3 Score=42.79 Aligned cols=101 Identities=10% Similarity=-0.078 Sum probs=0.0
                         сhнинининин--сссинининининининин
 Q ss pred
 Q Fri Mar 04 23: 753 NEVQEFMFAMTLFS--CGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSL
                                                                                                                   830 (1037)
                     753 \quad \text{$^{-753}$ } \\ -\text{$^{-1}$} \\ -\text{$^{
                                                                                                                   830 (1037)
 O Consensus
                       T Consensus
                                                                                                            ~~lg~
                                                                                                                    65 (159)
                       8 VVGAYLALSDAQRQLVAGEYDEAAANCRRAMEISHTM------PPE----EAFDHAGFDAFCHAGLAE
 T 2hr2 A
                                                                                                                    65 (159)
                         T ss dssp
                         T ss_pred
 Q ss_pred
                         Q Fri_Mar_04_23: 831 LFDRNNSQEFALKCISKSAE------YSLKEIQIEELQDFKEKQHIHYLNLLIH----FRMFEEVLDVLRLGHE 894 (1037)
Q Consensus 831 Lfe------al--a--Ai-------e------e------l--i-------a 894 (1037)
                      ..+... | .++=.....|+|+.|
                                                                                      ----lg-----
 T Consensus
                                                                                                            121 (159)
 T 2hr2 A
                      66 ALAGLRSFDEALHSADKALHYFNRRGELNQDEG-----KL-----WISAVYSRALALDGLGRGAEA 121 (159)
 T ss_dssp
                         НИНИСССИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИСССИНИН
 T ss_pred
 No 20
                                                  NCBI
                                                                        Pub Med
>4d10 B COP9 signalosome complex subunit 2; signaling protein; 3.80A (Homo sapiens) PDB: 4d18 B
 Probab=90.78 E-value=8.2 Score=44.11 Aligned cols=193 Identities=8% Similarity=-0.068 Sum probs=0.0
 Q ss pred
                         Q Fri_Mar_04_23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD 833 (1037)
 Q Consensus
                     754 ~~~fl~g~~l~~~~A~~F~a~~~~lp~l~~l~~~l~~~l~~~l~~~2y~~l~Lfe
                                                                                                                   833 (1037)
                         +...+.+|..+|...|++++|.++|+++-.....
                                                                                        ...+.-+..+..++.
                             ---lg----g----A----al-------
                                                                                          ----lq~
 T Consensus
                      73 FKALKQMIKINFKLTNFPEMMNRYKQLLTYIRSA-----VTR----NYSEKSINSILDYIS
 T 4d10 B
 T ss_dssp
                         T ss_pred
                         Q ss_pred
                     834 RNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC--LSDTVRT-----
 Q Fri Mar 04 23:
                     834 ~~~~~al~~a~Ai~~~~e~~~e~~~~e~~~~l~~i~~~f~~L~l~~~ay-L~~~r~~-----
 Q Consensus
                                                                                                                   902 (1037)
                         125 ~~
 T Consensus
                                                                                                                ~ 191 (447)
                     125 TSKQMDLLQEFYETTLEALKDAKNDR----LWFKT-----NTKLGKLYLEREEYGKLQKILRQLHQSCQTDDGEDD 191 (447)
 T 4d10 B
 T ss_dssp
                         T ss_pred
                         0 ss pred
```

```
Q Fri_Mar_04_23: 903 ------NFLQLLLQEDIYSRDFFSTLLRLCNAHSDNGELYLRTV-DIKIVDSILSQNLRSGDWEC----FKKLYCFRM 969 (1037)
O Consensus
             ..+=-.+.
             192 ~~~~~
T Consensus
                                                                 ~1a~-
                                                                       250 (447)
             192 LKKGTQLLEIYA-----LEIQMYTAQKNN-----KKLKALYEQSLHIKSAIPHPLIMGVIRECGGKMHL
T 4d10 B
               ----СИНИНИН------НИНИНИНИТСН-------НИНИНИНИНИТТ СССС СВИНИНИНИНИН
T ss_dssp
               hhachнинин------нинининдассн------нинининининдасссссининининин
T ss pred
               сСССНИНИНИНИНИНИННЫННЫНННЫН--НИНИННЫ
Q ss pred
Q Fri_Mar_04_23:
             970 LNKSERAAAEVLYQYILMQADLDVIRKRKC--YLMVINVLS 1008 (1037)
             T Consensus
             251 REGEFEKAHTDFFEAFKNYDESGSPRRTTCLKYLVLANMLM 291 (447)
T 4d10 B
               ннтснининининининин
T ss_dssp
               hccCннинниннинннынhhhhhccCннинниннинннин
T ss_pred
                       SCOPe PODEN PROTEIN DATA BANK
No 21
                                                    Pub Med
      Synthetic consensus TPR protein; tetratricopeptide repeat, consensus protein, superhelix, de novo
protein; 2.30A {Synthetic} SCOP: k.38.1.1 PDB: 2hyz _A
Probab=90.75 E-value=2.8 Score=38.30 Aligned_cols=109 Identities=11% Similarity=0.225 Sum_probs=0.0
               сснинининнин
Q ss pred
Q Fri_Mar_04_23: 731 NTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKD
                                                                       810 (1037)
             810 (1037)
             T Consensus
                                                                       61 (136)
T 2fo7 A
             15 GDYDEAIEYYQKALE--LDPRSAEAWYNLGNAYYKQGDYDEAIEYYQKA-----
                                                                       61 (136)
T ss_dssp
               ТСНИНИНИНИН --- НСТТСИНИНИНИНИН СИНИНИНИНИН ------
T ss_pred
               сhhhhccCccннинниннниннниннниннниннниннниннн
Q ss pred
                                                                       890 (1037)
Q Fri Mar 04 23:
             811 LLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLR
             811 ~l~~~~~Yy~~l~~Lfe~~~~~al~~a~~Ai~~~~~e~~~~~~l~~~i~~~F~~~L~l~~
Q Consensus
                                                                       890 (1037)
                  ....+...+...+....|.++.|++...+.++...+.+.
T Consensus
             62 -----1-----1-----1
                                                                       118 (136)
T 2fo7 A
             62 ----LELDPRSAEAWYNLGNAYYKOGDYDEATEYYOKALELDPRSA------EA------WYNLGNAYYKOGD
                                                                       118 (136)
               T ss dssp
               ----несссенининининининининининин
T ss_pred
Q ss_pred
               hhHHH
Q Fri_Mar_04_23: 891 LGHEC 895 (1037)
            891 ~~~ay 895 (1037)
O Consensus
               ++.|.
             119 ~~~Å~
T 2fo7 A
            119 YDEAI
                    123 (136)
T ss_dssp
               ннннн
T ss pred
               ннннн
                       SCOPe PODEN PROTEIN DATA BANK
No 22
                                       NCBI
                                                    Pub Med
🗌 >2vyi_A SGTA protein; chaperone, TPR repeat, phosphoprotein, tetratricopeptide repeat protein, HOST-virus
interaction; 2.4A {Homo sapiens} SCOP: a.118.8.1
Probab=90.74 E-value=1.9 Score=40.61 Aligned_cols=88 Identities=6% Similarity=-0.017 Sum_probs=0.0
               Q ss pred
Q Fri Mar 04 23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
                                                                       833 (1037)
             O Consensus
                                                                       833 (1037)
               +...+.|..++..|++++|.++|.++
                                                         ....+..+.|..+..++.
T Consensus
                                                       --1~~~p~~~~
                                                                       57 (131)
             12 AERLKTEGNEOMKVENFEAAVHFYGKA------IELNPANAVYFCNRAAAYS
T 2vyi A
                                                                       57 (131)
T ss_dssp
               НИНИНИНИНИТТСИНИНИНИНИ
               ННИНИНИННИНСССИНИНИНИНИН
T ss pred
               Q ss pred
Q Fri_Mar_04_23:
             834 RNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                                                          894 (1037)
Q Consensus
             834 -----al--a--Ai-----e-----e----l---i----F---L-l-----a
                                                          894 (1037)
               ..|.++.|++...+||+.-+...
                  ----À-----al----p------
                                     ---~-lg~~~~A
T Consensus
T 2vyi_A
             58 KLGNYAGAVQDCERAICIDPAYS-----KA-----YGRMGLALSSLNKHVEA
                                                           99 (131)
T ss_dssp
               T ss_pred
                       SCOPe PODE PROTEIN DATA BANK
                                       S NCBI
                                                    Pub Med
>2q7f_A YRRB protein; TPR, protein binding; 2.49A {Bacillus subtilis} SCOP: a.118.8.1
Probab=90.69 E-value=3.9 Score=43.15 Aligned_cols=124 Identities=10% Similarity=0.188 Sum_probs=0.0
               Q ss pred
Q Fri_Mar_04_23: 715 TENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTF 793 (1037)
             Q Consensus
T Consensus
```

```
54 KEDAIPYINFANLLSSVNELERALAFYDKALE---LDSSAATAYYGAGNVYVVKEMYKEAKDMFEKA------ 117 (243)
T 2q7f_A
T ss_dssp
              T ss_pred
              ссенинининининессининининини-----------
              HhhhhhccccccccchhhhccCcснинининнинниннинниннинниннинниннинн
Q ss pred
Q Fri_Mar_04_23: 794 LEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYL 873 (1037)
Q Consensus
            ...+....|..+...|..+...|++...+|++..+...+...+....+.....+....
T Consensus
            118 -----EAGMENGDLFYMLGTVLVKLEQPKLALPYLQRAVELNENDT----EA--- 161 (243)
T 2q7f_A
T ss_dssp
              T ss_pred
              ------
Q ss_pred
              hhhhhhhhhhhhhhhhhhhh
Q Fri_Mar_04_23: 874 NLLIHFRMFEEVLDVLRLGHE 894 (1037)
O Consensus
            874 ~~~i~~~F~~~L~l~~~~a
                            894 (1037)
               +.++=....|+++.|
            162 -----à 178 (243)
T Consensus
            162 ----RFQFGMCLANEGMLDEA 178 (243)
T 2q7f A
             ---ннинниннинтссини
T ss_dssp
              ----ННИННИННННСССИННИ
T ss pred
                            PDB"
No 24
                     SCOPe
                                                Pub Med
                                    S NCBI
->4gco_A Protein STI-1; structural genomics, PSI-biology, midwest center for structu genomics, MCSG,
tetratricopeptide repeat domain; 1.60A {Caenorhabditis elegans} SCOP: a.118.8.0
Probab=90.47 E-value=1.7 Score=39.09 Aligned cols=93 Identities=10% Similarity=0.025 Sum probs=0.0
Q ss pred
              ссСсьнинининининессинининин
Q Fri_Mar_04_23: 749 YLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQL
                                                                  828 (1037)
O Consensus
            828 (1037)
              ...+++...+|.+++..|++++|.++|+++
             8 ~~~~~
                    ----à-----À---
T Consensus
                                                                  53 (126)
                                                               ~1
T 4qco A
             8 INPELAQEEKNKGNEYFKKGDYPTAMRHYNEA------VKRDPENAILYSNR
                                                                  53 (126)
              ССИНИНИНИНИНИНТТСИНИНИНИНИ
T ss_dssp
T ss_pred
              Q ss pred
Q Fri_Mar_04_23: 829 SLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
            829 ~—If=~~~~al~a~Ai~~~~e~~~~l~~i~~F~~L-l~~~a 894 (1037) ..++..|.++..|++...|++...
            54 -----A----A 100 (126)
T Consensus
            54 AACLTKLMEFQRALDDCDTCIRLDSKFI-----KG-----YIRKAACLVAMREWSKA 100 (126)
T 4gco A
T ss_dssp
              T ss_pred
              PROTEIN DATA BANK

PROTEIN DATA BANK

Pub Med
No 25
>4yvq C Protein fluorescent in blue light, chloroplastic, glutamyl-tRNA reductase 1, chloroplastic; TPR,
protein-protein interaction; 2.40A {Arabidopsis thaliana}
Probab=90.17 E-value=2.7 Score=40.46 Aligned_cols=100 Identities=14% Similarity=0.068 Sum_probs=0.0
              Q ss pred
Q Fri_Mar_04_23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
                                                                  833 (1037)
              833 (1037)
            46 -----a--
                                                           ---lq----
T Consensus
                                     .___]~~~~~____~~~
                                                                  97 (159)
            46 LISKLKTGKTFLRNQEPEKAYTEFKIA------LELAQS--LKDP-----TEEKKAARGLGASLQ
T 4yvq C
                                                                  97 (159)
T ss_dssp
              T ss pred
              Q ss_pred
Q Fri_Mar_04_23: 834 RNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
Q Consensus
                ----al--a--Ai-----e----e----l---i----F---L-l-----a
                                                      894 (1037)
              ..|.++.|++..++|++....... +.++=..+...|+|+.|
            98 --g----A-----al-------A
T Consensus
            98 RQGKYREAIQYHSMVLAISKRESEDS----GITEA-----YGAIADCYTELGDLEKA 145 (159)
T 4yvq C
              ННТСНИНИНИНИНИНИНИНИТССТ----ТИНИН------НИНИНИНИНИТСНИНИ
T ss_dssp
T ss pred
              PDB<sup>®</sup>
PROTEIN DATA BANK

NCBI
No 26
                                    S
                                         Pub Med
          ቖ
>4yvo A Protein fluorescent in blue light, chloroplastic; TPR, fluorescent protein; 1.45A {Arabidopsis thaliana}
 Probab=90.14 E-value=2.9 Score=40.44 Aligned_cols=100 Identities=14% Similarity=0.068 Sum_probs=0.0
              T 4yvo A
            52 LISKLKTGKTFLRNQEPEKAYTEFKIA-----LELAQS---LKDP-----TEEKKAARGLGASLQ
                                                                 103 (165)
              T ss_dssp
T ss_pred
```

```
Q ss_pred
                                  Q Fri Mar 04 23: 834 RNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                                                                                                                              894 (1037)
                                                                                                                       ~~~a
                                                                                                                               894 (1037)
 O Consensus
                            834 ~~
                                         ---al--a--Ai------e-----el----l---i----F---L-l--
                                  ..|.++.|++..++|++.....
                            104 ~~g~~~A~~~~al~~~~~A
 T Consensus
                            104 RQGKYREAIQYHSMVLAISKRESEDS----GITEA------YGAIADCYTELGDLEKA 151 (165)
 T 4yvo_A
                                  НТТСИНИНИНИНИНИНИНИТССТ----ТИНИН------НИНИНИНИНИТТСИНИН
 T ss_dssp
                                  T ss pred
 No 27
                                                                                                 Pub Med
>4xi0 A Magnetosome protein MAMA; magnetosome associated protein, protein-protein interaction, motif, protein
  binding; 2.88A {Desulfovibrio magneticus rs-1}
  Probab=90.06 E-value=4.2 Score=40.28 Aligned cols=157 Identities=11% Similarity=0.148 Sum probs=0.0
                                  Q ss_pred
 Q Fri Mar 04 23: 712 ASITENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAIND-- 788 (1037)
                            O Consensus
                                                                                                                                                           788 (1037)
                               ~~~~À~~~
                                                                                                                                                             77 (202)
 T Consensus
 T 4xi0 A
                               1 MAMGDKAKLYRNISQRCLRRGSPEEALRYLKEWAR---HEKNDPEPLYQMGIALANLGDYQRAVTVFDKVLKLRPNHFMA
                                                                                                                                                            77 (202)
                                  T ss_dssp
                                  T ss pred
                                 Q ss_pred
 2 55_5254

9 Fri Mar_04_23: 789 --KLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQBFALKCISKSABYSLKEIQIEELQDFKE
                                                                                                                                                           866 (1037)
                            O Consensus
                                                                                                                                                           866 (1037)
                                   .+-..+...+
                                                      ...+ ...+-....+...+...+...|.++..|++...+...
                             78 ---la-----A-----A-----la-----
 T Consensus
                                                                                                                                                           143 (202)
 T 4xi0 A
                             78 SYRKGAVLLKIKQ---YKLA-LPVLEAVVAAAPADARAYYLLGLAYDGDEQLEKGIEAMQKAVDLDPEEI------
 T ss_dssp
                                  T ss_pred
                                  НИНИНИНИННЫ СС---НИН-НИНИНИННЫ ССССИНИНИНИННЫ ССССИНИНИННЫ В НИКОССИТОРИИ СССИТИТЕЛЬНИЕ В НИКОССИТИТЕЛЬНИЕ В НИКОСИТИТЕЛЬНИЕ В НИКОСИТИТЕЛЬНИЕ В НИКОСИТИТЕЛЬНИЕ В НИКОСИТИТЕЛЬНИЕ В НИСИТИТЕЛЬНИЕ В НИКОСИТИТЕЛЬНИЕ В НИКОСИТИТЕЛЬНИЕ В НИКОСИТ
 Q ss_pred
                                  НННhhhhhhhHННННННННН
  Q Fri Mar 04 23:
                            867 KQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
 O Consensus
                            867 -----l---i----F---L-l-----a
                                                                              894 (1037)
                            T Consensus
                            144 -KY-----HQHLGFMNVRKDDHKTA 162 (202)
 T 4xi0 A
                                  -нн-----нннннннннттсннн
 T ss_dssp
 T ss pred
                                  -НН-----НННННННННННН
                                                    PDB
 No 28
                                                                                                 Pub Med
              Chaperone SYCD; cytosol, chaperone-protein binding complex; 2.20A {Chlamydia pneumoniae}
->4nrh B
 Probab=89.94 E-value=1.9 Score=42.20 Aligned_cols=93 Identities=11% Similarity=0.066 Sum_probs=0.0
                                  сеССсhнннннннннннеССннннннннннhhhheccccchннhhhhhheccccccchhhhecCссннннннн
 Q ss pred
                            749 YLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQL
 Q Fri_Mar_04_23:
                                                                                                                                                           828 (1037)
                            828 (1037)
                                  ..++++...+|.++...|++++|.++|.++
 T Consensus
                              55 ~~p~~~~~la~~~~~A~~~~a---
                                                                                                                        _____]
                                                                                                                                                           100 (178)
                             55 ISSEDLEKVYKEGYHAYLDKDYAKSITVFRWL-----VFFNPFVSKFWFSL
 T 4nrh B
                                                                                                                                                           100 (178)
                                  ССНИНИНИНИНИНИТСИНИНИНИНИН
  T ss_dssp
  T ss_pred
                                  сСссснинининининининининининини
                                  НИНИННЬССИНИНИНИНИНННЫННЬ
Насессссссенийн
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Насенийн
Насенийн
Насессссенийн
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Н
 Q ss pred
 O Fri Mar 04 23: 829 SLLFDRNNSOEFALKCISKSAEYSLKEIOIEELODFKEKOHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                            829 ~Lfe~~~~al~a~Ai~~~e~~~e~~~~l~~~i~~~f~~Ll~~~a 894 (1037)
 O Consensus
                                  ..++...|.++.|++..+.|++..+.
 T Consensus
                            101 ~~~~~
                                              ~~~~À~~~~~à~~~~p~~~----
                                                                                                     ----A
                                                                                                                                     147 (178)
                            101 GASLHMSEQYSQALHAYGVTAVLRDKDP-----YP-----HYYAYICYTLTNEHEEA 147 (178)
 T 4nrh B
 T ss dssp
                                  ННИНИТТСИНИНИНИНИНИСТТСS------НН------ННИНИНИНИТТСИНИН
                                  T ss pred
 No 29
                                                                                               Pub Med
>2xcb_A PCRH, regulatory protein PCRH; protein transport, bacterial toxin, type III secretion, protein binding;
  1.85A {Pseudomonas aeruginosa} PDB: 2xcc A 4j10 A
                                                                                 3wxx _A*
 Probab=89.61 E-value=2.3 Score=39.44 Aligned_cols=93 Identities=18% Similarity=0.201 Sum_probs=0.0
                                  ссССсhнининниннесСнининнинннинн
 Q ss pred
 Q Fri Mar 04 23: 749 YLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQL
                                                                                                                                                           828 (1037)
                                        ----fl-g---l----A---F--a--
                                                                                      ~~~~~lp~~l~~l~~
 Q Consensus
                            749 ~~
                                                                                                                                            ~~~~Yy~~1
                                                                                                                                                           828 (1037)
 T Consensus
                                                                                                                                  -~~~p~~~~~1
                             13 LSEDTLEOLYALGFNOYOAGKWDDAOKIFOAL-----CMLDHYDARYFLGL
 T 2xcb A
                                                                                                                                                            58 (142)
                                  ССНИНИНИНИНИНИТСИИНИНИНИНИН
 T ss dssp
                                  ССсррнинининининин
 T ss_pred
                                  нниннессининининин
  Q ss pred
  Q Fri_Mar_04_23: 829 SLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                                              ----al--a--Ai-----e----e------l---i----F---L-l----a 894 (1037)
                            829 ~~Lfe~~
  O Consensus
```

```
T Consensus
                      59 a~~~~~
                                  ----A----a---p-----A 105 (142)
                      59 GACROSLGLYEOALOSYSYGALMDINEP------RF------PFHAAECHLOLGDLDGA 105 (142)
 T 2xcb A
                         T ss dssp
                         T ss_pred
 No 30
                                       PDB"
PROTEIN DATA BANK
                                                   NCBI
                                                               Pub Med
>2kck_A TPR repeat; tetratricopeptide repeat, structural genomics, unknown function, PSI-2, protein structure
 initiative; NMR {Methanococcus maripaludis}
 Probab=89.57 E-value=1.3 Score=38.96 Aligned_cols=91 Identities=11% Similarity=0.135 Sum_probs=0.0
                         Q ss pred
 Q Fri_Mar_04_23: 751 RHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSL
                                                                                                                    830 (1037)
                     830 (1037)
                         .+++...+|.+++..|++++|.++|.++
                       3 p-----a-----A----a-----a-----
 T Consensus
                                                                                           ._____la~
                                                                                                                     48 (112)
                       3 DONPEEYYLEGVLOYDAGNYTESIDLFEKA-----IOLDPEESKYWLMKGK
 T 2kck A
                                                                                                                     48 (112)
                         СSSTTGGGGHHHHHHSSCCHHHHHHHHHH
 T ss dssp
 T ss_pred
                         ниньсСсинининининны--рессссссссьнинный принцининный принцининнинный принцининный принцининный принцининный принцининный принцининный пр
 Q ss pred
 Q Fri Mar 04 23: 831 LFDRNNSQEFALKCISKSAEY--SLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                                                                                                    894 (1037)
                     831 Lfe-----al--a--Ai----e---e-----l---i---F---L-l-----a
 Q Consensus
                                                                                                     894 (1037)
                         ______A
 T Consensus
 T 2kck A
                      49 ALYNLERYEEAVDCYNYVINVIEDEYNK-----DV-----WAAKADALRYIEGKEVE
                                                                                                      95 (112)
                         HHHHTTCHHHHHHHHHHHHTSCCTTCH-----HH------HHHHHHHHTTCSSCSHH
 T ss dssp
 T ss pred
                         НННННЫННННННННННННННННННН
                                      SCOPe PROTEIN DATA BANK
 No 31
                                                                                    Pub Med
>2vgx_A Chaperone SYCD; alternative dimer assembly, tetratricopeptide repeat, type III secretion; HET: MLY; 1.95A {Yersinia enterocolitica} SCOP: a.118.8.1 PDB: 4am9 A 2vgx_B* 2vgy_A*
 {Yersinia enterocolitica} SCOP: a.118.8.1 PDB: 4am9 A 2vgx B* 2vgy A*
Probab=89.46 E-value=2.5 Score=39.55 Aligned_cols=94 Identities=17% Similarity=0.227 Sum_probs=0.0
                         ссССсьнинининннеССнинининнныннын
 Q ss_pred
 Q Fri Mar 04 23: 749 YLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQL
                                                                                                                    828 (1037)
                     Q Consensus
                                                                                                                    828 (1037)
 T Consensus
 T 2vgx_A
                      16 ISSDTLEOLYSLAFNOYOSGXYEDAHXVFOAL------CVLDHYDSRFFLGI
                                                                                                                     61 (148)
                         ССИНИНИНИНИНИНИТСИНИНИНИНИН
 T ss dssp
                         T ss pred
                         нининессинининининин
 Q ss pred
 Q Fri Mar 04 23:
                     829 SLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC
                                                                                                      895 (1037)
                     829 ~Lfe~~~~al~a~Ai~~~e~~~e~~~~l~~i~~~F~~L~l~~~ay
 Q Consensus
                                                                                                      895 (1037)
                          ..++...|.++.|++....|++..+.
                                                                              |..+-....++++.|.
 T Consensus
                                    ~~~À~~~~~
                                                                                 ---a-----
                      62 GACRQAMGQYDLAIHSYSYGAVMDIXEP------RF-----PFHAAECLLQXGELAEAE
 T 2vqx A
                                                                                                      109 (148)
                         T ss_dssp
                         нининньеснинининный Сссси-----ининининный Сссинини
 T ss_pred
                                      PDB™
PROTEIN DATA BANK
                                                 NCBI 🖁
                                                                        Pub Med
>3uq3 A Heat shock protein STI1; HSP90, peptide binding, chaperone; 2.60A {Saccharomyces cerevisiae}
Probab=89.27 E-value=1.9 Score=45.67 Aligned_cols=110 Identities=8% Similarity=0.014 Sum_probs=0.0
 Q ss_pred
                         нинининессининининин
 Q Fri_Mar_04_23: 758 FMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNS
                                                                                                                    837 (1037)
 O Consensus
                     837 (1037)
                         154 (258)
 T Consensus
 T 3uq3_A
                      83 ARIGNAYHKLGDLKKTIEYYQKSLTEHRTA----DILTKLRN---AEKE-LKKAEAEAYVNPEKAEEARLEGKEYFTKSD
                                                                                                                    154 (258)
 T ss dssp
                         T ss pred
                         ннинниннинниннинн
 Q ss pred
                     838 QEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
 Q Fri Mar 04 23:
                     838 ---al--a--Ai-----e----e-----l---i----F---L-l-----a 894 (1037)
 O Consensus
                         ++.|++..+.||+..+.+.
                                                                    |.++-....+++|+.|
                     155 ~~A~~~~al~~p~~~~~al~~p~~~~~lg~~~~~A 192 (258)
 T Consensus
                     155 WPNAVKAYTEMIKRAPEDA------RG-----YSNRAAALAKLMSFPEA 192 (258)
 T 3uq3_A
                         T ss dssp
                         НННННННННННННССcch-------НН---------НННННННННСССНННН
 T ss pred
 No 33
                                     PDB"
PROTEIN DATA BANK
                                                 NCBI Pub Med
🔝 >3upv_A Heat shock protein STI1; TPR-fold, adaptor protein for HSP70 and HSP90, C-terminal PA HSP70, peptide
 binding protein; 1.60A {Saccharomyces cerevisiae}
 Probab=89.14 E-value=3.4 Score=37.19 Aligned_cols=88 Identities=9% Similarity=0.024 Sum_probs=0.0
```

```
Q ss pred
                            Q Fri Mar 04 23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
                                                                                                                                 833 (1037)
 O Consensus
                       833 (1037)
                            +...+.|.+++..|++++|.++|.++
                                                                                                      ....+....+..+..+.
                                                                                                                                   49 (126)
                          4 AEEARLEGKEYFTKSDWPNAVKAYTEM------IKRAPEDARGYSNRAAALA
 T 3upv A
                                                                                                                                   49 (126)
                            T ss_dssp
                            T ss_pred
                            Q ss_pred
                                                                                                          894 (1037)
 Q Fri_Mar_04_23: 834 RNNSQEFALKCISKSAEYSLKETQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                       O Consensus
                                                                                                          894 (1037)
 T Consensus
                        50 KLMSFPEAIADCNKAIEKDPNFV------RA-----YIRKATAQIAVKEYASA
 T 3upv_A
                                                                                                           91 (126)
                            T ss_dssp
 T ss pred
                            SCOPe PROTEIN DATA BANK
                                                                       NCBI
 No 34
                                                                                              Pub Med
->1ma3_A Designed protein CTPR2; de novo protein; HET: IPT; 1.55A {Unidentified} SCOP: k.38.1.1 PDB: 2avp_A
 Probab=88.84 E-value=3.2 Score=35.91 Aligned_cols=87 Identities=10% Similarity=0.172 Sum_probs=0.0
                            cCCchниннинниннеCCниннинниннhhhhcccccchнинhhhhhcccccccchhhhccCcсниннинн
 Q ss pred
 Q Fri_Mar_04_23: 750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLS
                       829 (1037)
                            +.+.+..+|.++...|++++|.++|+++
                         T Consensus
                                                                                                                                  50 (91)
 T 1na3_A
                         5 PGNSAEAWYNLGNAYYKQGDYDEAIEYYQKA------LELDPNNAEAWYNLG
                                                                                                                                  50 (91)
 T ss_dssp
                            T ss_pred
                            ССССИНИНИНИНИНННЕССИИНИНИНИНН
                            нннннссснинининининин
 Q ss pred
 Q Fri Mar 04_23: 830 LLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVL 889 (1037)
                       Q Consensus
                        T Consensus
                        51 NAYYKOGDYDEATEYYOKALELDPNNA-----EA-----KONLGNAKOKOG
 T 1na3 A
                                                                                                          91 (91)
                            T ss dssp
                            ннинессининининининин
 T ss pred
 No 35
                                         PDB<sup>N</sup>
PROTEIN DATA BANK
                                                      Pub Med
>4gcn_A Protein STI-1; structural genomics, PSI-biology, midwest center for structu genomics, MCSG,
 tetratricopeptide repeat domain; HET: PGE; 1.85A {Caenorhabditis elegans}
 Probab=88.71 E-value=3.2 Score=37.15 Aligned_cols=89 Identities=9% Similarity=0.084 Sum_probs=0.0
                            Q ss pred
 Q Fri Mar 04 23: 753 NEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLF
                                                                                                                                 832 (1037)
                       753 \quad \text{$\sim\sim\sim$} \\ \text{$f1$-$g$-$\sim$} \\ \text{$\sim\sim\sim\text{$A$-$\sim$}} \\ \text{$\sim\sim\text{$A$-$\sim$}} \\ \text{$\sim\sim\sim\text{$A$-$\sim$}} \\ \text{$\sim\sim\text{$A$-$\sim$}} \\ \text{$A$-$\sim$}} \\ \text{$\sim\sim\text{$A$-$\sim$}} \\ \text{$A$-$\sim$} \\ \text{$A$-$\sim$}} \\ \text{$A$-$\sim$} \\ \text{$A$-$\sim$}} \\ \text{$A$-$\sim$} \\ \text{$A$-$\sim$}} \\ \text{$A$-$\sim$}} \\ \text{$A$-$\sim$} \\ \text{$A$-$\sim$}} \\ \text{
                                                                                                                                 832 (1037)
                            .+...+.|.+++|.++|.++
 T Consensus
                          7 ~~~~~A~~~~a_____la~~~la~~~
                                                                                                                                  52 (127)
                         7 AAIAEKDLGNAAYKOKDFEKAHVHYDKA------IELDPSNITFYNNKAAVY
 T 4gcn A
                                                                                                                                  52 (127)
                            T ss_dssp
                            T ss_pred
 Q ss_pred
                            ньсСенининининининины
 Q Fri_Mar_04_23: 833 DRNNSQEFALKCISKSAEYSLKE-----IQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                       833 e------al--a--Ai---------e----e-----l---i----F---L-l-----a 894 (1037)
 O Consensus
                        T Consensus
                        53 FEEKKFAECVQFCEKAVEVGRETRADYKLIA------KA-----KA-----KA-ONAFQKQNDLSLA 102 (127)
 T 4gcn A
                            T ss_dssp
                            НННСснининининининин
 T ss pred
                               SCOPe PROTEIN DATA BANK
                                                                      NCBI
                                                                                             Pub Med
>21ni A Stress-induced-phosphoprotein 1; structural genomics, northeast structural genomics consortiu PSI-biology, protein structure initiative, chaperone; NMR {Homo sapiens} SCOP: a.118.8.0 Probab=88.69 E-value=3.1 Score=37.86 Aligned_cols=92 Identities=10% Similarity=0.034 Sum_probs=0.0
                            cCCchнининининсСсинининининhhhhcccccchнинhhhhhcccccccchhhhccCcсинининини
 Q ss_pred
 Q Fri Mar 04 23: 750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLS
                                                                                                                                 829 (1037)
                       O Consensus
                                                                                                                                 829 (1037)
                        12 NPDLALMVKNKGNECFQKGDYPQAMKHYTEA-----IKRNPKDAKLYSNRA
 T 2lni A
                                                                                                                                  57 (133)
 T ss_dssp
                            сһһһнининининссининининин
 T ss pred
 Q ss pred
                            Q Fri_Mar_04_23: 830 LLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                       Q Consensus
```

```
~~~~~A 103 (133)
T Consensus
              58 ACYTKLLEFOLALKDCEECIQLEPTFI-----KG------YTRKAAALEAMKDYTKA 103 (133)
T 2lni A
                T ss dssp
                T ss pred
No 37
                          PDB'
                                               Pub Med
>3sz7 A HSC70 cochaperone (SGT); TPR domain, GET4, GET5, GET3, MDY2, SSA1, SSE1, chaperone regulator; 1.72A
 {Aspergillus fumigatus}
 Probab=88.67 E-value=2.8 Score=40.41 Aligned cols=92 Identities=5% Similarity=0.009 Sum probs=0.0
                сССсhнининининсССнинининининhhhhcccccchнинhhhhhcccccccchhhhccCcснининини
0 ss pred
Q Fri Mar 04 23: 750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLS
                                                                           829 (1037)
O Consensus
             750 -----fl-g---l-----A---F--a------lp--l--l-----
                                                      -----1---1-----yv--1-
                                                                           829 (1037)
T Consensus
                              ----A----a--
                                                              --~~~p~~~~~~la
                                                                            52 (164)
               7 PTPESDKLKSEGNAAMARKEYSKAIDLYTOA-----LSIAPANPIYLSNRA
T 3sz7 A
                                                                            52 (164)
                ССИНИНИНИНИНИТСИИНИНИНИНИ
T ss dssp
                сһһһнинининининнин
T ss pred
Q ss_pred
                ниннрессининининниннин
Q Fri_Mar_04_23: 830 LLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                                                                894 (1037)
Q Consensus
             830 ~Lfe~~~~al~a~~Ai~~~~e~~~~e~~~l~~i~~~f~~L~l~~~a
                                                                894 (1037)
                .++...+.++.|++..+.|++...+
                                                  |.++-....++|+.|
T Consensus
                ~~~~a~~~p~~~-
                                                   ---la-----
              53 AAYSASGQHEKAAEDAELATVVDPKYS-----KA-----WSRLGLARFDMADYKGA
T 3sz7 A
T ss dssp
                T ss pred
No 38
                         PDB"
                                 NCBI
                                         Pub Med
🗌 >4gyo_A Response regulator aspartate phosphatase J; tetratricopeptide repeat, hydrolase; 2.16A {Bacillus subtilis
subspl
Probab=88.59 E-value=9.7 Score=42.54 Aligned_cols=179 Identities=10% Similarity=-0.025 Sum_probs=0.0
                hнининининиессининининины hhaccccch нин hhabaccccccccch hhacccccch hhacccc
Q ss pred
Q Fri_Mar_04_23:
             754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD 833 (1037)
             754 ~~~fl~q~~l~~~A~~F~a~~~~lp~~l~~l~~l~~l~~l~~~l~~~ly~~l~~Lfe 833 (1037)
Q Consensus
                +.+.+.+|.+|...|++++|.++|.++-.....
T Consensus
             180 ~~~~lg~~
                                                                     ~1g~~y~
                                                                           231 (373)
             180 VQCEFIIAGNLTDVYHHEKALTHLCSALEHARQL----EEA----YMIAAAYYNVGHCKY
T 4gyo_A
                                                                           231 (373)
T ss dssp
                НИНИНИНИНИТТСИНИНИНИНИНИНИНИНИ
T ss_pred
                НИНИНИНИНИЕССИНИНИНИНИНИНИНИС------CCh------НИНИНИНИНИНИНИНИ
                Q ss_pred
Q Fri_Mar_04_23:
             834 RNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC--LSD---TVRTNFLQLL
                                                                           908 (1037)
             908 (1037)
O Consensus
                   ..|.++.|++..++|++......
                                                                           295 (373)
T Consensus
             232 SLGDYKEAEGYFKTAAAIFEEHNFQQ-----A-VQA------VFSLTHIYCKEGKYDKAVEAYDRGIKSAAEWEDD--
T 4gyo_A
                                                                           295 (373)
                ННТСИНИНИНИНИНИНИТТСТИ----И-ИНИ------НИНИНИНИНИТСИНИНИНИНИНИНИНИНИТТСИ-
T ss_dssp
                T ss_pred
                Q ss pred
             909 LQEDIYSRDFFSTLLRLCNAHSDNGELYLRTVDIKIVDSILSQNLRSGDWEC----FKKLYCFRMLNKSERAAAEVLYQY
Q Fri Mar 04 23:
                                                                           984 (1037)
O Consensus
             909 l~~~~~lv~~L~~~~~~R~AA~~mye~
                                                                           984 (1037)
                                  +.....+.++..+...++. +..|-..+..|++.+|.+..|+.
             296 -----la--y-----al------ala--y---q----A----
                                                                           359 (373)
T Consensus
T 4qvo A
             296 -----MYLTKFRLIHEL-----YLGSGDLNVLTECFDLLESRQLLADAEDLLHDTAERFNQLEHYESAAF-FYRR
                                                                           359 (373)
                T ss dssp
T ss_pred
                HHHHhhhh
Q ss_pred
Q Fri Mar 04 23:
             985 ILMQADLD 992 (1037)
                ~~rl~~~~
                       992 (1037)
Q Consensus
             985
T Consensus
             360 al~~~~i 367 (373)
             360 LMNIKKKL 367 (373)
T 4gyo_A
T ss dssp
                нининин
T ss pred
                                 PDB
No 39
                         SCOPe
                                                       Pub Med
>2vyi_A SGTA protein; chaperone, TPR repeat, phosphoprotein, tetratricopeptide repeat protein, HOST-virus
 interaction; 2.4A {Homo sapiens} SCOP: a.118.8.1
Probab=88.40 E-value=5 Score=37.68 Aligned_cols=107 Identities=14% Similarity=0.063 Sum_probs=0.0
                ссснинининненнесссссснининининниннининнинниннинн
Q ss pred
Q Fri Mar 04 23: 730 ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWK
                                                                           809 (1037)
             730 --q------fl--i--p-------fl-g---l----------A---F--a---
                                                         ----lp--l--l----l-
                                                                           809 (1037)
Q Consensus
                                            -~~~À~~~
              25 ----al----p----a----a
T Consensus
                                                   ~~a--
                                                                            72 (131)
              25 VENFEAAVHFYGKAIE---LNPANAVYFCNRAAAYSKLGNYAGAVODCERA-----
T 2vyi_A
                                                                            72 (131)
```

T ss\_dssp

```
T ss_pred
                       0 ss pred
 Q Fri_Mar_04_23: 810 DLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVL
                                                                                                           889 (1037)
                   810 ~-l~~~~~Yy~-l~-Lfe~~~~al~a~Ai~~~~e~~~e~~~~l~~i~~i~~~F~~L-l~
                                                                                                           889 (1037)
                    T Consensus
                                                                                                           128 (131)
 T 2vyi A
                                                                                                           128 (131)
                     T ss dssp
                        T ss_pred
 Q ss pred
                      chh
 Q Fri Mar 04 23: 890 RLG 892 (1037)
 O Consensus
                   890 ~~~
                            892 (1037)
                   129 ~~~
 T Consensus
                            131 (131)
 T 2vyi_A
                   129 EAP 131 (131)
 T ss_dssp
                       TCC
 T ss_pred
                       cCC
 No 40
                                  SCOPe POB®
                                                           NCBI
                                                                             Pub Med
>1elr A TPR2A-domain of HOP; HOP, TPR-domain, peptide-complex, helical repeat, protein binding, chaperone; 1.90A
 {Homo sapiens} SCOP: a.118.8.1 PDB: 3esk A 3fwv A
 Probab=88.19 E-value=3.3 Score=37.80 Aligned_col=88 Identities=7% Similarity=0.064 Sum_probs=0.0
                       0 ss pred
 Q Fri Mar 04 23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
                                                                                                           833 (1037)
 O Consensus
                   833 (1037)
                       +....+|.+++..|++++|.++|.++
 T Consensus
                     4 a----a---a---a---
                                                                                  ----l~~~~~~~la~~~
                                                                                                            49 (131)
                     4 ALKEKELGNDAYKKKDFDTALKHYDKA-----KELDPTNMTYITNQAAVYF
 T lelr A
                                                                                                            49 (131)
 T ss_dssp
                       T ss_pred
                       ННИНИНИНИНИНДЬ В СТАТИТИ В СТАТИТИТИ В СТАТИТИ В СТАТИТИ В СТАТИТИ В СТАТИТИ В СТАТИТИ В СТАТИТИ В СТАТИТИТИ В СТАТИТИТИТИ В СТАТИТИТИ В СТАТИТИ В СТАТИТИТИ В СТАТИТИТИТИТИ В СТАТИТИТИ В СТАТИТИТИ В СТАТИТИ В СТАТИТИ В СТАТИТ
 Q ss_pred
                       Q Fri_Mar_04_23: 834 RNNSQEFALKCISKSAEYSLKE------IQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
 Q Consensus
                   834 -----al--a--Ai----a 894 (1037)
                    T Consensus
                                                                                                98 (131)
 T lelr_A
                    50 EKGDYNKCRELCEKAIEVGRENREDYROIA-----KA-----YARIGNSYFKEEKYKDA
                                                                                                98 (131)
 T ss dssp
                       T ss pred
                       PDB NCBI Pub Med
>2hol_A Type 4 fimbrial biogenesis protein PILF; type IV pilus biogenesis, TPR, superhelix, protein binding; HET:
 MSE; 2.00A {Pseudomonas aeruginosa} PDB: 2fi7 A
 Probab=87.91 E-value=4.6 Score=41.96 Aligned_cols=139 Identities=12% Similarity=0.034 Sum_probs=0.0
                       ссернинининнесСссссСсернининининнесСнининининны
 123 (252)
                    50 RONTEQAKVPLRKALE---IDPSSADAHAALAVVFQTEMEPKLADEEYRKALASDSRNARVLNNYGGFLYEQKR---YEE 123 (252)
 T 2ho1 A
 T ss dssp
                       ТТСТСБСБИНИНИНН --- НСТТСИНИНИНИНИН НИТСИНИНИНИНИН НИТСИТСИИ НИНИНИНИНИНИН НИТС--- НИ
                       сССИНИНИНИНИН---hСссинининининин
 T ss_pred
                       Q ss_pred
 Q Fri_Mar_04_23:
                   806 SIWKDLLCTFT--VPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFE 883 (1037)
 O Consensus
                   883 (1037)
                   T Consensus
                                                                                                           183 (252)
 T 2ho1_A
                   124 A-YQRLLEASQDTLYPERSRVFENLGLVSLQMKKPAQAKEYFEKSLRLNRNQP-----SV-----ALEMAD 183 (252)
                       T ss_dssp
                       T ss_pred
 Q ss_pred
                       HHHhhcchhHH
 Q Fri_Mar_04_23: 884 EVLDVLRLGHE 894 (1037)
 O Consensus
                   884 ~~L~l~~~~a 894 (1037)
                   ....|+++.|
184 ~~~~q~~~A 194 (252)
 T Consensus
 T 2ho1 A
                   184 LLYKEREYVPA 194 (252)
 T ss dssp
                       ниниттенни
 T ss_pred
                       ННННhcCHHHH
 No 42
                                  SCOPe PROTEIN DATA BANK
                                                                    Pub Med
>2c21_A CHIP, carboxy terminus of HSP70-interacting protein; chaperone, E3 ligase, ubiquitinylation, TPR,
 heat-shock protein complex; 3.3A {Mus musculus} SCOP: a.118.8.1 g.44.1.2
 Probab=87.85 E-value=2.4 Score=46.07 Aligned_cols=92 Identities=13% Similarity=0.109 Sum_probs=0.0
```

```
Q ss pred
               ССснинининининессининининин
Q Fri_Mar_04_23: 751 RHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSL
                                                                     830 (1037)
O Consensus
            830 (1037)
               ..++-..+.|..++..|++++|.++|.++
             1 ---a----g----g----A----a--
                                                        --1~~~p~~~~
                                                                      46 (281)
T 2c21_A
             1 SPSAQELKEQGNRLFVGRKYPEAAACYGRA-----ITRNPLVAVYYTNRAL
                                                                      46 (281)
               T ss_dssp
T ss_pred
               Сссинининининининининининини
                                                   -----нннссссьниннинн
               ннинессинининининининин
Q ss_pred
                                                           895 (1037)
Q Fri_Mar_04_23: 831 LFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC
            O Consensus
                                                           895 (1037)
T Consensus
                                                            92 (281)
             47 CYLKMQQPEQALADCRRALELDGQSV-----KA-----HFFLGQCQLEMESYDEAI
T 2c21 A
                                                            92 (281)
               T ss dssp
T ss pred
               SCOPe POB<sup>M</sup> PROTEIN DATA BANK
                                      NCBI
No 43
->1xmf_A Lipoprotein NLPI; TPR, tetratricopeptide, structural genomi unknown function; 1.98A {Escherichia coli}
SCOP: a.118.8.1
Probab=87.57 E-value=3.3 Score=43.48 Aligned cols=89 Identities=9% Similarity=-0.042 Sum probs=0.0
               снинининининессинининининин
Q ss pred
Q Fri_Mar_04_23: 753 NEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLF
                                                                     832 (1037)
            O Consensus
                                                                     832 (1037)
              .+...+|.++...|++++|.++|.++
                                                      ---1~~~p~~
T Consensus
               ----a---a----a----
                                                                ~1g~~
                                                                      87 (275)
T 1xnf A
             42 RAQLLYERGVLYDSLGLRALARNDFSQA-----LAIRPDMPEVFNYLGIYL
                                                                      87 (275)
T ss dssp
               T ss pred
               Q ss pred
               Q Fri_Mar_04_23:
            833 DRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
Q Consensus
            833 e-----al--a--Ai-----e----e----l---i---F---L-l-----a
                                                         894 (1037)
             T Consensus
             88 TQAGNFDAAYEAFDSVLELDPTYN-----YA------HLNRGIALYYGGRDKLA 130 (275)
T 1xnf A
               T ss_dssp
T ss_pred
               ННСССИНИНИНИНИННИННСССссс------hH--------ННИНИНИНННЕССИНИЕ
                       PDB NCBI Pub Med
No 44
□ >3ma5_A Tetratricopeptide repeat domain protein; NESG, structural genomics, PSI-2, protein structure initiative;
2.80A {Salinibacter ruber} PDB: 2kcl _A 2kcv _A
Probab=87.56 E-value=4.5 Score=34.94 Aligned_cols=91 Identities=13% Similarity=0.172 Sum_probs=0.0
               сеССсhнннннннннннеССннннннннннhhhheccccchннhhhhhheccccccchhhhecCссннннннн
Q ss pred
Q Fri_Mar_04_23: 749 YLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQL
                                                                     828 (1037)
            828 (1037)
             2 ~~p~~~~a~~~~A~~~~a------
T Consensus
                                                      _____1
                                                                      47 (100)
             2 EDPEDPFTRYALAQEHLKHDNASRALALFEEL-------VETDPDYVGTYYHL
T 3ma5 A
                                                                      47 (100)
               T ss_dssp
T ss_pred
               нниннессинининининин
Q ss pred
O Fri Mar 04 23: 829 SLLFDRNNSOEFALKCISKSAEYSLKEIOIEELODFKEKOHIHYLNLLIHFRMFEEVLDVLR 890 (1037)
            829 ~~Lfe~~~~~al~~a~~Ai~~~~~e~~~~e~~~~l~~~i~~~F~~~L~l~~ 890 (1037)
O Consensus
               ..++...|.++.|++..+.|++...+...+
                    ----A-----al----p------l------l------
T Consensus
                                                          92 (100)
             48 GKLYERLDRTDDAIDTYAQGIEVAREEG--T----QKD-----LSELQDAKLKAEG
T 3ma5 A
                                                          92 (100)
T ss dssp
               НННННТТСНИНИНИНИНИНИНННЯ -- C------НИН--------НИНИНИНИНИН
T ss_pred
               ННИНННСССИНИНИНИНИНИНИНИНИНОСССИ--Н------НИН--------НИНИНИНИНИНССС
                       SCOPe PROTEIN DATA BANK
No 45
                                                  Pub Med
>1hh8_A P67PHOX, NCF-2, neutrophil cytosol factor 2; cell cycle, phagocyte oxidase factor, SH3 domain, repeat,
 TPR repeat cell cycle; HET: FLC; 1.8A {Homo sapiens} SCOP: a.118.8.1 PDB: 1wm5 A 1e96 B
Probab=87.43 E-value=3.7 Score=42.07 Aligned_cols=89 Identities=9% Similarity=0.072 Sum_probs=0.0
               сhнининининесссининининининининин
Q ss pred
Q Fri Mar 04 23: 753 NEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLF
                                                                     832 (1037)
            ~~~Yv~~l~~Lf
                                                                     832 (1037)
Q Consensus
             36 ~~~~~1g~~~~~g~~~~A~~~~~a------
T Consensus
                                                               ~~lg~~~
                                                                      81 (213)
             36 HSRICFNIGCMYTILKNMTEAEKAFTRS------INRDKHLAVAYFORGMLY
T 1hh8 A
                                                                      81 (213)
T ss dssp
               СНИНИНИНИНИТТСИНИНИНИНИН------
                                                    -----НННСТТСНИНННННННН
               Сининининининессинининини
T ss pred
               НьсССнинининининининины
Q ss pred
Q Fri_Mar_04_23: 833 DRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEK------QHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                  833 e~~~
O Consensus
```

```
T Consensus
                    82 YQTEKYDLAIKDLKEALIQLRGN-----QLIDYKILGLQFKLFACEV-----LYNIAFMYAKKEEWKKA 140 (213)
 T 1hh8 A
                       HHTTCHHHHHHHHHHHTTTC-----SEEECGGTBCCEEEHHHH------HHHHHHHHHHTTCHHHH
 T ss dssp
 T ss_pred
                        PDB NCBI Pub Med
 No 46
□ >3gyz_A Chaperone protein IPGC; asymmetric homodimer, tetratricopeptide repeat, TPR, chapero virulence; 2.15A
 {Shigella flexneri} PDB: 3gz1 _A 3gz2 _A 3ks2 _A
 Probab=87.41 E-value=3.8 Score=38.10 Aligned_cols=92 Identities=8% Similarity=0.099 Sum_probs=0.0
                       cCCchнининининеCCнининининин
 Q ss pred
 Q Fri_Mar_04_23: 750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLS
                                                                                                            829 (1037)
                   ....+...+.+|.+++..|++++|.++|.++
                    T Consensus
                                                                                                            77 (151)
                    32 PDDMMDDIYSYAYDFYNKGRIEEAEVFFRFL----CIYDFYNVDYIMGLA
 T 3gyz_A
                                                                                                            77 (151)
                       СНИНИНИНИНИНИТСИНИНИНИНИН
 T ss dssp
 T ss_pred
                        Сһһһнинининининисссинининини
                       нниньессинининининины
 Q ss pred
 Q Fri Mar 04 23:
                   830 LLFDRNNSQEFALKCISKSAEYSLKEIQIEELODFKEKOHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                   Q Consensus
                                                                                            894 (1037)
                    78 ~~~~~A~~~~A~~~~~A~~~~~A
 T Consensus
                    78 AIYQIKEQFQQAADLYAVAFALGKNDY-----TP-----VFHTGQCQLRLKAPLKA 123 (151)
 T 3gyz_A
                       T ss dssp
 T ss pred
                        SCOPe POB®
 No 47
                                                           NCBI
>2q7f_A YRRB protein; TPR, protein binding; 2.49A {Bacillus subtilis} SCOP: a.118.8.1
              E-value=7.5 Score=40.94 Aligned_cols=124 Identities=7% Similarity=-0.021 Sum_probs=0.0
                       СССЬЬНИНИНИННЫ—сесьнининининны сСсессСсьнининининне ССнинининин в в сесссесьни
 Q Fri_Mar_04_23: 715 TENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTF 793 (1037)
Q Consensus 715 ~np-~~1-~vi-~q~~~~fl~i~p~~~~~fl-g~~l~~~~A~~F~~a~~~~~lp-~ 793 (1037)
                    T Consensus
 T 2q7f A
 T ss dssp
                       ссенининининине
 T ss_pred
                       Q ss_pred
 Q Fri_Mar_04_23: 794 LEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYL 873 (1037)
                   O Consensus
 T Consensus
                       T 2q7f_A
                       T ss_dssp
                        T ss pred
                       hhhHHHHHHHHHhhcchhHH
 Q ss pred
 Q Fri_Mar_04_23: 874 NLLIHFRMFEEVLDVLRLGHE
                                              894 (1037)
               874 ~~~i~~~F~~~L~l~~~~a 894 (1037)
 O Consensus
                   |.++=.....++++.|
196 ----~alg~~~ag~~A 212 (243)
 T Consensus
 T 2g7f A
                   196 ----FYNAGVTYAYKENREKA 212 (243)
                    ----НИННИННИННТТСТТИН
 T ss dssp
 T ss_pred
                       ----НИННИНННННСССИННИ
                                    PDB<sup>™</sup>
PROTEIN DATA BANK
 No 48
                                                           Pub Med
□ >3zn3_A Anaphase-promoting complex subunit 8; cell cycle, TPR; 1.90A {Schizosaccharomyces pombe}
 Probab=87.03 E-value=4.7 Score=43.02 Aligned_cols=119 Identities=4% Similarity=-0.131 Sum_probs=0.0
                       сССсьнининининеССнининининный в соссесственный в соссесст
 Q ss pred
                   750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPY-RHSAFYYQL 828 (1037)
 Q Fri_Mar_04_23:
                   T Consensus
                                                                                                           224 (291)
                   152 GNKDPYLLYLSGVVYRKRKQDSKAIDFLKSCVLKAPFF---WSAWLELSL---SIDSLETLTTVVSQLPSTHIMTKIFY
 T 3zn3 A
                                                                                                           224 (291)
                       T ss dssp
                        СССсећинининининесССнинининининеСССс---инининини----инссинининин
 T ss pred
                       нининьесси-ининининины
 Q ss pred
 Q Fri Mar_04_23: 829 SLLFDRNNSQ_EFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLLLGHE 894 (1037)
Q Consensus 829 ~Lfe~~~~~al~~a~Ai~~~~e~~~~~l~~i~~~f~~L-l~~~a 894 (1037)
                   T Consensus
                                                                                              272 (291)
                   225 VYASHELHQVNSSAYEKLAEAEIIFPNSR-----YL-----KTQRALLTYDSRDFDEA 272 (291)
 T 3zn3 A
                       T ss_dssp
                        T ss_pred
```

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PDB"
No 49
                              NCBI
                                      Pub Med
🗌 >4ila_A Response regulator aspartate phosphatase I; tetratricopeptide repeat, SPOOF, hydrolase; 2.44A {Bacillus
 subtilis subsp}
Probab=86.82 E-value=14 Score=41.89 Aligned cols=171 Identities=10% Similarity=-0.003 Sum probs=0.0
               Q ss pred
            754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
Q Fri_Mar_04_23:
                                                                    833 (1037)
            754 ~~~fl~g~~l~~~~A~~F~a~~~~~lp~l~~l~~~~~~l~~~l~~~~~~Yy~~l~~Lfe
                                                                    833 (1037)
               +.+.+|.+|.+|.++|.++|.++
                                                         ...+..|..+..++.
T Consensus
            184 -----lg--y-----A-----al------al-----
                                                    -----nlg~~y~
                                                                    235 (391)
T 4ila_A
            184 VRCQFIVAGNLIDSLEYERALEQFLKSLEISKES-----NIE-----HLIAMSHMNIGICYD
                                                                    235 (391)
T ss_dssp
               T ss_pred
               Q ss pred
O Fri Mar 04 23:
            834 RNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC-----LSDTVRTNFL
                                                                    905 (1037)
               905 (1037)
Q Consensus
               ..|.++.|++..++|++....+.
                                           +.++=.....|+++.|.
T Consensus
            236 ~~
                 ~~~A~~~~al~~~~~al~~~~al~~~~al~~~~al~~~~
                                                                    301 (391)
            236 ELKEYKKASOHITLALETFEKSKHSF----I.-TKT-----I.FTLTYVEAKOONYNVALTYFRKGRFTADKSDDKEY
T 4ila A
                                                                    301 (391)
               НТТСНИНИНИНИНИНИНИТСТИ----И-ИНИ-------НИНИНИНИТТСИНИНИНИНИНИНИНИТСКИН
T ss dssp
T ss_pred
               Q ss_pred
               Q Fri Mar 04 23:
            906 OLLLOEDIYSRDFFSTLLRLCNAHSDNGELYLRTVDIKIVDSILSONLRSGDWEC----FKKLYCFRMLNKSERAAAEVL
                                                                    981 (1037)
O Consensus
            906 ~-11~~~~~lv~~L~~~~~~ll~~~~~vd~iL~~~ar~~~~y~~Lys~ri~~~~R~AA~~m
                                                                    981 (1037)
                      ..+..
                                ..++..-..+.+...+...+...+...
                                                    ...-.+...|++.+|.+..
                            -----ly~~~~~al~~~~~~
                                                      ---la--y---g----A----
T 4ila_A
            302 S-----AKFKIL-----EGLFFSDGETQLIKNAFSYLASRKMFADVENFSIEVADYFHEQGNLMLSNEYY
                                                                    361 (391)
T ss_dssp
               T ss_pred
Q ss pred
               ннннн
Q Fri_Mar_04_23:
            982 YOYIL
                   986 (1037)
Q Consensus
            982 Ye~~~
                   986 (1037)
               -+...
               ~~a~~
T Consensus
            362
                   366 (391)
T 4ila A
            362 RMSIE
                   366 (391)
T ss_dssp
               нинин
T ss_pred
               нинин
                       PDB"
                              NCBI
                                          Pub Med
->4apo_A AH receptor-interacting protein; signaling protein-peptide complex, ARYL hydrocarbon receptor; HET: 12P;
1.90A (Homo sapiens) PDB: 4aif A
Probab=86.79 E-value=3.5 Score=39.88 Aligned cols=100 Identities=9% Similarity=-0.014 Sum probs=0.0
               ниннинессинининнинны
Q ss pred
Q Fri_Mar_04_23: 760 FAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQE
                                                                    839 (1037)
Q Consensus
            839 (1037)
               .|..++..|++++|.++|.++-
-g----g----A-----al---
                               T Consensus
                                                           ~la~~
                                                                     83 (165)
             20 EGNRLYREGHVKEAAAKYYDAI------ACLKNLQMKEQPGSP----EWIQLDQQITPLLLNYCQCKLVVEEYY
T 4apo_A
                                                                     83 (165)
T ss_dssp
               T ss_pred
               ннинниннинниннинн
Q ss_pred
Q Fri_Mar_04_23:
            840 FALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
            840 ~al~~a~~Ai~~~~~e~~~~e~~~~l~~~i~~~F~~~L~l~~~~a
O Consensus
                                                    894 (1037)
             .. | .++=....+|+|+.|
T Consensus
                                                    119 (165)
             84 EVLDHCSSILNKYDDNV------KA-----YFKRGKAHAAVWNAQEA 119 (165)
T 4apo A
T ss_dssp
               НННННННННННТТСН------НН------НННННННН
               НННННННННННННННННННННННННННННННННННН
T ss pred
                      SCOPe PROTEIN DATA BANK
No 51
     NCBI
                                                  Pub Med
           >2fo7_A Synthetic consensus TPR protein; tetratricopeptide repeat, consensus protein, superhelix, de novo
protein; 2.30A {Synthetic} SCOP: k.38.1.1 PDB: 2hyz _A
Probab=86.74 E-value=4.3 Score=36.93 Aligned cols=88 Identities=11% Similarity=0.223 Sum probs=0.0
               Q ss pred
Q Fri Mar 04 23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
                                                                    833 (1037)
            Q Consensus
                                                                    833 (1037)
               +...+.+|.+++..|++++|.++|.++
                                                       ....+....+..+..+..+..
                    ~~~~~A~~~
T Consensus
              1 a~~~~l~
                                                             ~~~la~~~
                                                                     46 (136)
             1 AEAWYNLGNAYYKQGDYDEAIEYYQKA-----LELDPRSAEAWYNLGNAYY
T 2fo7 A
                                                                     46 (136)
T ss_dssp
               СИНИНИНИНИНТСИИНИНИНИНИ
T ss_pred
               СНИНИНИНИНИНССИИНИНИНИНИН
               0 ss pred
```

```
Q Fri_Mar_04_23: 834 RNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                    O Consensus
                   834 -----al--a--Ai-----e-----e-----l---i----F---L-l-----a
                                                                   |.++-....++++.|
 T Consensus
                                                                     ---1----
                                                                                        88 (136)
                    47 KQGDYDEAIEYYQKALELDPRSA-----EA-----WYNLGNAYYKQGDYDEA
 T 2fo7 A
                       ННТСНИНИНИНИНИНИТСТТСН------НН------НННИНИНИНТТТСНИНИ
 T ss_dssp
 T ss_pred
                       No 52
                                                          Pub Med
>2e2e_A Formate-dependent nitrite reductase complex NRFG; TPR, cytochrome C biogenesis, 0157:H7 EDL933, formate-
 nitrite reductase complex, lyase; 2.05A {Escherichia coli}
Probab=86.67 E-value=3 Score=41.58 Aligned_cols=92 Identities=10% Similarity=0.113 Sum_probs=0.0
                       cCCchниннинниннеCCниннинниннhhhhccccccchнинhhhhhcccccccchhhhccCcснинниннин
 Q ss_pred
                                                                                                          829 (1037)
 Q Fri_Mar_04_23: 750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLS
                                                                                                          829 (1037)
 O Consensus
                   .++++...+|.+|...|++++|.++|.++
                       T Consensus
                                                                                                            85 (177)
 T 2e2e A
                    40 NPQNSEQWALLGEYYLWQNDYSNSLLAYRQA-----LQLRGENAELYAALA
                                                                                                            85 (177)
                       T ss_dssp
                       ССССИНИНИНИНИНИСССИИНИНИНИНИНИ
 T ss pred
                       Q ss pred
 Q Fri_Mar_04_23:
                   {\tt 830\ LL-FDRNNSQE--FALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE}
                   830 ~L-fe-----al--a--Ai-----e----e------l---i----F----L-l-----a
                    T Consensus
                                                                                             134 (177)
 T 2e2e_A
                    86 TVLYYQASQHMTAQTRAMIDKALALDSNEI-----TA-----TALLASDAFMQANYAQA 134 (177)
 T ss dssp
                       T ss_pred
                       PDB<sup>™</sup>
PROTEIN DATA BANK
 No 53
                                               NCBI Pub Med
🗎 >4gyo_A Response regulator aspartate phosphatase J; tetratricopeptide repeat, hydrolase; 2.16A {Bacillus subtilis
 subsp}
 Probab=86.66 E-value=3.8 Score=45.91 Aligned_cols=96 Identities=14% Similarity=0.178 Sum_probs=0.0
                       нинининессининининин
 Q ss pred
 Q Fri_Mar_04_23:
                   758 FMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNS
                                                                                                          837 (1037)
                   |.+|..++..|++++|.++|++|.....
                                                                                     ...+..|..+..++...|.
                   154 (373)
 T Consensus
 T 4gyo_A
                   103 YFRGMYEFKQKNFILAIDHYKHAEEKLEYV-----EDE-----IEKAEFLFKVAEVYYHIKQ
                                                                                                          154 (373)
                       НИНИНИНТТСИИНИНИНИНИТТGGGC-------CCH------НИНИНИНИНИНИНИТТС
 T ss dssp
 T ss_pred
                       Q ss pred
 Q Fri Mar 04 23:
                   838 QEFALKCISKSAEYSLKEIQ-IEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                       \hbox{\tt ----al--a--Ai------e-----e-----l---i-----F----L-l-------a}
                                                 +.++=....|+|+.|
                   T Consensus
                   155 TYFSMNYASQALDIYTKYELYGR-----RRVQC------EFIIAGNLTDVYHHEKA 199 (373)
 T 4gyo_A
                       ННИНИНИНИНИНИНИТТССSH-----НИНИН-------НИНИНИНИТТСИНИН
 T ss_dssp
                       hнинининининининининисссен----hнини------нинининининисссинин
 T ss_pred
 No 54
                                                           Pub Med
>4r7s_A Tetratricopeptide repeat protein; TPR family protein, structural genomics, joint center for ST genomics,
 JCSG; HET: MSE; 2.39A {Parabacteroides merdae atcc 43184}
 Probab=86.56 E-value=13 Score=37.99 Aligned_cols=154 Identities=6% Similarity=-0.095 Sum_probs=0.0
                       СССhh---нининин-ссchинининин-ссcсссссссссссснинининин-сссиинининин-
 Q ss pred
 Q Fri Mar 04_23: 715 TENSF---FMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAIND--
                                                                                                          788 (1037)
                   788 (1037)
 Q Consensus
                    111 (257)
 T Consensus
 T 4r7s A
                    35 PANPLNYALLTNLGTIORROGKLOEALISYTSALS---GHTKNITILENRASLYTELGETEKALNDYNTLLIENPEHOEA
                                                                                                          111 (257)
                       T ss dssp
                       T ss pred
 Q ss_pred
                       --ссриннруру в соссесственный в соссесст
 Q Fri Mar 04 23: 789 --KLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELODFKE
                                                                                                          866 (1037)
                   O Consensus
                                                                                                          866 (1037)
                         ·----A------1--------
                   112 LYCRGLLYIQLQN---YMWA-EQDFDKILEVNEKSVRARLGHAILEKMRGNYDESERIFNYLISEMPRDW------
 T 4r7s A
                                                                                                          177 (257)
 T ss_dssp
                       T ss pred
                       Q ss pred
                       нннынннннннннн
 Q Fri_Mar_04_23: 867 KQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
 Q Consensus
                   867 -----l---i----F---L-l-----a
                                                     894 (1037)
                                  |.++=....|+++.|
```

```
T Consensus
            178 -~~--- 1~~~~~A 196 (257)
           178 -TI-----YEGRADLYFMMGKNARA 196 (257)
T 4r7s A
T ss dssp
              -НН------ННННННННННТТСННН
              -нн-----нннннннннессинн
T ss pred
                      PDB"
No 55
                                          Pub Med
□ >3uq3_A Heat shock protein STI1; HSP90, peptide binding, chaperone; 2.60A {Saccharomyces cerevisiae}
 Probab=86.32 E-value=3.1 Score=44.02 Aligned_cols=93 Identities=9% Similarity=0.009 Sum_probs=0.0
              ссССсhннннннннннссСнннннннннннhhhheccccchнннhhhhh
Q Fri_Mar_04_23: 749 YLRHNEVQBFMFAMTLFSCGNFDQSYB1FQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQL
Q Consensus 749 ------Yy-1
                                                                   828 (1037)
                                                                   828 (1037)
              ..+..+..+|.+++|.++|+++
            T 3uq3 A
            134 VNPEKAEEARLEGKEYFTKSDWPNAVKAYTEM-----IKRAPEDARGYSNR
                                                                  179 (258)
              ССИНИНИНИНИНИНИТТСИИНИНИНИНИН
T ss_dssp
              сСсининининининисский инфиниции
T ss_pred
              Q ss pred
Q Fri_Mar_04_23:
            829 SLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
            829 ~Lfe~~~al~~a~Ai~~~e~~~l-~i~~F~~Ll~~a 894 (1037)
..++..|.++..|+..+..|+..+... ... |.++=....++|+..|
180 g~~~~A~~~~al~~p~~~~a-~~~a-~~~l~~~~A 226 (258)
Q Consensus
T Consensus
T 3uq3_A
            180 AAALAKLMSFPEAIADCNKAIEKDPNFV-----RA-----YIRKATAQIAVKEYASA 226 (258)
              T ss dssp
T ss_pred
              No 56
                            NCBI
                                         Pub Med
>2vq2_A PILW, putative fimbrial biogenesis and twitching motility protein; secretin, TPR repeat, type IV pilus,
bacterail virulence; 1.54A {Neisseria meningitidis}
Probab=86.28 E-value=18 Score=36.05 Aligned_cols=126 Identities=8% Similarity=-0.071 Sum probs=0.0
              СССһһниннинн-сссһниннинннннь-сссссссснинниннннн-сс-снинниннннн-
Q Fri_Mar_04_23: 715 TENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCG-NFDQSYEIFQLHDYPEAINDKLPT 792 (1037)
            Q Consensus
T Consensus
T 2vq2_A
            39 PKNELAWLVRAEIYQYLKVNDKAQESFRQALS--IKPDSAEINNNYGWFLCGRLNRPAESMAYFDKALA--D----- 106 (225)
T ss dssp
              ТТСНИНИНИНИННИТТСИНИНИНИНИН---НСТТСИНИНИНИНИНТТССИНИНИНИНИТ--S-----
              T ss_pred
Q ss_pred
              HHhhhhheeceeceechhhheeCeeннининнинниннинниннинниннинн
Q Fri_Mar_04_23: 793 FLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHY 872 (1037)
            O Consensus
                                                                   872 (1037)
            T Consensus
            107 -----PTY------PTYIANLNKGICSAKQGQFGLAEAYLKRSLAAQPQFP------PA-- 149 (225)
T 2vq2 A
              T ss_dssp
              T ss_pred
              hhhhHHHHHHHHHHhhcchhHH
Q ss pred
Q Fri_Mar_04_23: 873 LNLLIHFRMFEEVLDVLRLGHE 894 (1037)
            873 l~~~i~~~~F~~~L~l~~~~~a
                             894 (1037)
                |..+=....|+++.|
T Consensus
            150 -----A 166 (225)
            150 ----FKELARTKMLAGQLGDA 166 (225)
T 2vq2_A
T ss_dssp
              ----ннининининитсини
              ----ННННННННННСССЬННЕ
T ss pred
No 57
                     SCOPe PROTEIN DATA BANK
                                                 Pub Med
>2fbn_A 70 kDa peptidylprolyl isomerase, putative; sulfur SAD, PFL2275C, TPR-containing domain, structural
 genomics; 1.63A {Plasmodium falciparum} SCOP: a.118.8.1
Probab=86.27 E-value=6.5 Score=39.96 Aligned_cols=94 Identities=7% Similarity=-0.026 Sum_probs=0.0
              Q ss pred
Q Fri_Mar_04_23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRH------SA
                                                                  823 (1037)
              +...+-+|..++..|+|++|..++-
T Consensus
            89 (198)
            T 2fbn A
                                                                   89 (198)
              T ss dssp
              T ss pred
              нининининоссининининининин
Q ss pred
Q Fri_Mar_04_23: 824 FYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
            824 Yy-l-Lfe----al--a-Ai----e----e----l--i----F---L-l----a 894 (1037)
Q Consensus
            T Consensus
T 2fbn_A
              T ss_dssp
              T ss_pred
```

```
PDB"
No 58
                                          Pub Med
>4cgv_A Spaghetti, RNA polymerase II-associated protein 3; chaperone, R2TP, TAH1, PIH1; 2.54A {Homo sapiens}
Probab=86.27
         E-value=4.2 Score=36.84 Aligned_cols=93 Identities=8% Similarity=-0.020 Sum_probs=0.0
               сеССсhнннннннннннеССннннннннннhhhheccccchннhhhhhheccccccchhhhecCссннннннн
Q ss pred
Q Fri Mar 04 23: 749 YLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQL
                                                                    828 (1037)
            828 (1037)
Q Consensus
             9 -----A---
T Consensus
                                                                     54 (136)
                                                                -~~~1
             9 VDSOKALVLKEKGNKYFKOGKYDEAIDCYTKG------MDADPYNPVLPTNR
T 4cgv A
                                                                     54 (136)
T ss_dssp
               ССНИНИНИНИНИНИТТСИНИНИНИНИН
T ss_pred
               сСсссининининининин
Q ss_pred
               нининьсСенининининины
Q Fri Mar 04 23: 829 SLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
            829 ~Lfe~~~al~a~Ai~~~e~~~e~~~l~~i~~F~~Ll~~a 894 (1037)
O Consensus
               ..++...|.++.|++..+.|++..+...
             55 a~~~~
                    ----A----a---p-----
                                               ---la----
T Consensus
                                                           101 (136)
T 4cgv_A
             55 ASAYFRLKKFAVAESDCNLAVALNRSYT-----KA-----YSRRGAARFALQKLEEA 101 (136)
               T ss_dssp
               T ss pred
                                     Pub Med
No 59
>2kat A Uncharacterized protein; NESG, structure, structural genomics, PSI-2, protein structure initiative; NMR
 {Bordetella parapertussis}
Probab=86.26 E-value=5.7 Score=35.94 Aligned_cols=92 Identities=12% Similarity=-0.005 Sum_probs=0.0
               сССсриннининнин
Q ss_pred
Q Fri Mar 04 23: 750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLS
                                                                    829 (1037)
                  ---fl-g---l----A---F--a------lp--l--l------l---l----
            750 ~~~
                                                                    829 (1037)
O Consensus
                                                             ----Yv--1-
               -p-----la----
                           ----A----a--
T Consensus
                                                                 ~~lg
                                                                     60 (115)
             15 GTDNMLLRFTLGKTYAEHEQFDAALPHLRAA-----LDFDPTYSVAWKWLG
T 2kat_A
                                                                     60 (115)
T ss_dssp
               ТСССИНИНИНИНИТТСИНИНИНИНИ
               T ss pred
Q ss_pred
               Q Fri_Mar_04_23: 830 LLFDRNNSQEFALKCISKSAEY--SLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
            830 ~Lfe~~~~al~~a~~Ai~~_~~~e~~~~e~~~~l~~i~~~f~~L~l~~~~a 894 (1037)
O Consensus
               .++...|.++.|++..+.|++.
               T Consensus
             61 KTLQGQGDRAGARQAWESGLAAAQSRGDQ------QV-----VKELQVFLRRLAREDAL 108 (115)
T 2kat A
T ss_dssp
               T ss_pred
               нининссенинининининин
No 60
                         EIN DATA BANK NCBI
                                     Pub Med
>4r7s_A Tetratricopeptide repeat protein; TPR family protein, structural genomics, joint center for ST genomics,
JCSG; HET: MSE; 2.39A {Parabacteroides merdae atcc 43184}
Probab=86.22 E-value=11 Score=38.69 Aligned cols=158 Identities=10% Similarity=-0.110 Sum probs=0.0
               Q ss_pred
Q Fri_Mar_04_23: 715 TENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTF 793 (1037)
O Consensus
            793 (1037)
               |.++....+..+..+..+..+.|-+.+...
                -----A---
                                  ----1--
T Consensus
             72 TKNITILENRASLYTELGETEKALNDYNTLLI---ENPEHQEALYCRGLLYIQLQNYMWAEQDFDKILEVNEKSVRARLG 148 (257)
T 4r7s A
               ТТСИНИНИНИНИТСИИНИНИНИНИНИН---НСТТСИНИНИНИНИТСИИНИНИНИНИНИНИНИТСИИНИНИН
T ss dssp
T ss_pred
               HhhhhhccccccccchhhhccCcснинниннинннинниннинниннинниннинн
Q ss pred
O Fri Mar 04 23:
            794 LEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYL
                                                                    873 (1037)
            Q Consensus
                                                                    873 (1037)
               T Consensus
            149
                                                                    213 (257)
            149 HAILEKMRGNYDESERIFNYLISEMPRDWILYEGRADLYFMMGKNARAMADIEKVFTESEPTA-----NL---
T 4r7s A
                                                                    213 (257)
               T ss_dssp
               T ss pred
               hhhнннннннннhhссhhнн
0 ss pred
Q Fri_Mar_04_23: 874 NLLIHFRMFEEVLDVLRLGHE 894 (1037)
            874 ~~~i~~~F~~~L~l~~~~a
            T Consensus
            214 ----YVLRGKIKLAQYEKERA 230 (257)
T 4r7s A
              ----ннинининниттснини
T ss dssp
               ----НИНИНИННИННН
T ss pred
```

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PDB"
                                       SCOPe
                                                                                       Pub Med
>1w3b A UDP-N-acetylqlucosamine--peptide N-acetylqlucosaminyltransferase 110; OGT, qlcnac, nucleoporin, O-linked
 glycosylation, TPR repeat, protein binding; 2.85A {Homo sapiens} SCOP: a.118.8.1
 Probab=86.07 E-value=6.7 Score=44.14 Aligned_cols=155 Identities=9% Similarity=-0.092 Sum_probs=0.0
                          СССЬЬНИНИНИННЫ сссьяний и при станова в при 
 Q ss pred
 Q Fri Mar 04 23: 715 TENSFFMTFFRSYIIENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAIND----KL
                                                                                                                      790 (1037)
                     O Consensus
                                                                                                                      790 (1037)
                      T Consensus
 T 1w3b A
 T ss dssp
                          T ss pred
 Q ss_pred
                         hнинhhhhheeceeceechhhheeCeeннининнинниннинниннинниннинниннин
 Q Fri Mar 04 23: 791 PTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHI
                                                                                                                      870 (1037)
 O Consensus
                     870 (1037)
                     T Consensus
                     108 AAALVAAGD---MEGA-VQAYVSALQYNPDLYCVRSDLGNLLKALGRLEEAKACYLKAIETQPNFA------VA-
 T 1w3b A
                                                                                                                      171 (388)
 T ss_dssp
                          T ss_pred
                          Q ss_pred
                         hhhhhннннннннннн
 Q Fri_Mar_04_23: 871 HYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
 O Consensus
                     871 ~~l~~~i~~~~F~~~L~l~~~~a
                                                       894 (1037)
                     T Consensus
                     172 -----WSNLGCVFNAQGEIWLA 188 (388)
 T 1w3b A
 T ss dssp
                         -----НИННИНННТТТСИННИ
 T ss pred
                          -----ннинининнессинин
                                        PDB
                                                    NCBI
 No 62
                                                                          Pub Med
🗌 >3ro3_A PINS homolog, G-protein-signaling modulator 2; asymmetric cell division, protein binding; 1.10A {Mus
 musculusl
 Probab=85.94 E-value=6.8 Score=37.83 Aligned cols=100 Identities=9% Similarity=0.007 Sum probs=0.0
                          hнинининнининессининининниннинн
 Q ss pred
 Q Fri_Mar_04_23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
                                                                                                                      833 (1037)
 O Consensus
                     754 \quad \text{$\sim\sim\sim$} \\ f1 - g - \sim 1 - \sim \sim A - \sim F - \sim a - \sim \sim \sim 1 \\ p - 1 - \sim 1 - \sim \sim \sim 1 - \sim 1 - \sim 1 - \sim \sim Yy - 1 - \sim Lfe
                                                                                                                      833 (1037)
                      ....-+..++.
 T Consensus
                                                                                                                      100 (164)
 T 3ro3 A
                      49 RIAYSNLGNAYIFLGEFETASEYYKKTLLLARQL-----KDR-----AVEAQSCYSLGNTYT
                                                                                                                      100 (164)
                          НИНИНИНИНИТСИИНИНИНИНИНИНИТ-----ТСН-----НИНИНИНИНИНИНИНИ
 T ss dssp
                          ннинининирссинининининининин
 T ss pred
                          Q ss pred
 Q Fri_Mar_04_23:
                     834 RNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                                                                                                 894 (1037)
                     834 -----al--a--Ai-----e-----e-----l---i----F---L-l-----a
                                                                                                 894 (1037)
                          ..|.++.|++..++|++..... + +.....
                                                                     +.++=....|+++.|
                     T Consensus
                                                                                                 148 (164)
                     101 LLQDYEKAIDYHLKHLAIAQELK-D----RIGEGRA-----CWSLGNAYTALGNHDQA
 T 3ro3 A
                                                                                                 148 (164)
                          T ss_dssp
                          ННҺҺННННННННННННННҺС--С----сНҺННН------НННННННННСССННН
 T ss_pred
 No 63
                                      PDB<sup>IN</sup>
PROTEIN DATA BANK
                                                    Pub Med
->4ule_I Eukaryotic translation initiation factor 3 subuni; EIF3 complex, beta-propeller; 2.00A {Saccharomyces
 cerevisiae} PDB: 3zwl _B
 Probab=85.92 E-value=4.6 Score=45.05 Aligned cols=75 Identities=9% Similarity=0.224 Sum probs=0.0
                          EEEEecCCCEEEEEecCCCCeeEEEecCccHHHHHHHHhcCCCCCCccceEEEEe-cCcEEEEEcCCe
 Q ss pred
 Q Fri_Mar_04_23: 164 HFLFYVSPQFSVVFLEDGGLLGLKKVDGVHYEPLLFNDNSYLKSLTRFFSRSSKSDYDSVISCKLF-HERYLIVLTQNCH
                                                                                                                      242 (1037)
                     242 (1037)
                          T Consensus
                                                                                                                        75 (347)
                      15 OVKYNKEGDLLFSCSKDSSASVWYSLNGERLGT-----LDGHT---GTIWSIDVDCFTKYCVTGSADYS
 T 4ule T
                                                                                                                       75 (347)
                          EEEECTTSSEEEEEETTSCEEEEETTTCCEEEE------ECCCC----SCEEEEEECTTSSEEEEEETTTE
 T ss_dssp
                          EEEECCCCCEEEEeeCCCcEeEE------EcCCC----cceEEEEECCCCCEEEEEcCCCC
 T ss_pred
 Q ss pred
                         EEEEEcCCCceEee
 Q Fri_Mar_04_23: 243 LKIWDLTSFTLIQDY 257 (1037)
                     243 LRiWsl~t~~~l~~~ 257 (1037)
 Q Consensus
                         +|+||+.+|+|+.+.
                      76 v~lWd~~~g~~~~
76 IKLWDVSNGQCVATW
 T Consensus
                                              90 (347)
 T 4ule_I
                                              90 (347)
 T ss dssp
                          EEEEETTTCCEEEEE
                          EEEEECCCCCEEEEe
 T ss pred
                                        PDB"
                                                                 Pub Med
```

```
🗌 >3vtx_A MAMA; tetratricopeptide repeats (TPR) containing protein, peptide protein, protein binding; 1.75A
 {Candidatus magnetobacterium bavaricum} PDB: 3vty A
Probab=85.86 E-value=4.7 Score=39.92 Aligned_cols=121 Identities=11% Similarity=0.034 Sum_probs=0.0
                        ССснинининининессининининин
 Q ss pred
                                                                                                              826 (1037)
 Q Fri_Mar_04_23: 751 RHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAIND----KLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYY
 O Consensus
                    751 ~~~~~fl~q~~l~~~~A~~F~~a~~~~~~----lp~~l~~l~~~~~l~~~l~~~~~Yy~
                                                                                                              826 (1037)
                        .+++-..+.
                                                                 -----A----al----p----
 T Consensus
                                                                                                               77 (184)
 T 3vtx_A
                      2 GETTTIYMDIGDKKRTKGDFDGAIRAYKKVLKADPNNVETLLKLGKTYMDIGL---PNDA-IESLKKFVVLDTTSAEAYY
                                                                                                               77 (184)
                         T ss_dssp
                        T ss pred
                        Q ss pred
                    827 QLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
 O Fri Mar 04 23:
 Q Consensus
                    827 ~l~~Lfe~~~~~al~~a~~Ai~~~~~
                                                        ---e----L-1---a
                                                                             |.++=....|+++.|
                        .+..++...|.++.|++..+.|++...+
                     78 ~lg~~~~~A~~~~al~~p~~~~A
78 ILGSANFMIDEKQAAIDALQRAIALNTVYA------DA------YYKLGLVYDSMGEHDKA
 T Consensus
                                                                                                126 (184)
 T 3vtx A
                                                                                                 126 (184)
 T ss dssp
                        T ss_pred
 No 65
                                    SCOPe
                                                 PDB"
                                                            NCBI
                                                                                 Pub Med
>1na0_A Designed protein CTPR3; de novo protein; HET: IPT; 1.60A (Unidentified) SCOP: k.38.1.1 PDB: 2wqh _A 3kd7 _A
   Probab=85.41 E-value=10 Score=34.38 Aligned cols=104 Identities=12% Similarity=0.215 Sum probs=0.0
                        ссенинининныессесссенининининныессининнынныессенинныессессенины
 0 ss pred
 Q Fri Mar 04 23: 730 ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWK
                                                                                                              809 (1037)
 O Consensus
                    730 --q-----fl--i--p-------fl-g---l----------A---F--a---
                                                                                                              809 (1037)
                        .+++....+.|-+.+.
 T Consensus
                        ----A----A----A----A---
                                                                          ~~a-
                                                                                                               69 (125)
                     22 OGDYDEATEYYOKALE---I.DPNNAEAWYNI.GNAYYKOGDYDEATEYYOKA-----
 T 1na0 A
                                                                                                               69 (125)
                        ТТСИНИНИНИНИН --- ИСТТСИНИНИНИНИНИТТСИНИНИНИНИН -----------------
 T ss_dssp
 T ss pred
                        Q ss_pred
                        ссиринесссия и получения в полу
 Q Fri Mar 04 23:
                    810 DLLCTFTVPYRHSAFYYOLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVL
                                                                                                              889 (1037)
 Q Consensus
                    889 (1037)
                             .---p-----l------g-----h------a----p------
 T Consensus
                                                                                            .___~1~~~~
                     70 ----LELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNA-----EA-----KQNLGNAKQKQG
 T 1na0 A
                                                                                                              125 (125)
 T ss dssp
                        T ss pred
                        -----НьсСсссьнининининининининининининининин
 No 66
                                     PDB"
                                                 NCBI
                                                            Pub Med
🗌 >4ila_A Response regulator aspartate phosphatase I; tetratricopeptide repeat, SPOOF, hydrolase; 2.44A {Bacillus
 subtilis subsp}
 Probab=85.18
               E-value=5.1 Score=45.45 Aligned_cols=97 Identities=11% Similarity=0.200 Sum_probs=0.0
                        нинининессинининин
 Q Fri_Mar_04_23:
                    758 FMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNS 837 (1037)
                    Q Consensus
                                                                                                              837 (1037)
                                                                                       ...+.+|+.+..++...|.
                           g----A----A-----A-----
 T Consensus
                                                                                                              158 (391)
 T 4ila A
                    107 FFKGMYEFRRKELISAISAYRIAESKLSEV------EDE-----IEKAEFFFKVSYVYYYMKO
                                                                                                              158 (391)
 T ss dssp
                        T ss_pred
                        ннинниннинниннинн
 Q ss_pred
 Q Fri_Mar_04_23:
                    838 QEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
 O Consensus
                    838 ---al--a--Ai-----e-----e-----l---i----F---L-l-----a
                                                                                     894 (1037)
                    T Consensus
                                                                                     203 (391)
 T 4ila_A
                    159 TYFSMNYANRALKIFREYE--EYAV--QTVRC------QFIVAGNLIDSLEYERA 203 (391)
                        ННННННННННННТТSG--GGHH--НННН------ННННННННННТТСНННН
 T ss_dssp
                        T ss pred
 No 67
                                                                     Pub Med
>2vq2_A PILW, putative fimbrial biogenesis and twitching motility protein; secretin, TPR repeat, type IV pilus,
 bacterail virulence; 1.54A (Neisseria meningitidis)
 Probab=85.16 E-value=16 Score=36.53 Aligned_cols=124 Identities=4% Similarity=-0.041 Sum probs=0.0
 Q ss_pred
                        СССһһнининнннесс-һнинннинннньсСссссСсс---ниннниннньсСснинннинныһһһьсссссс
 Q Fri_Mar_04_23:
                    715 TENSFFMTFFRSYIIENT-SHKNIRFFLENVECPFYLRHNE---VQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKL
                                                                                                              790 (1037)
 Q Consensus
                    715 ~np~~~l~~vi~q~~~~fl~i~p~~~~~fl~g~~l~~~~A~~F~a~~~~~l 790 (1037)
                        |.++....+|.++|.++|.++|.++
                            ----1-----A---
                                                                                                              139 (225)
 T Consensus
 T 2vq2_A
                     73 PDSAEINNNYGWFLCGRLNRPAESMAYFDKALA---DPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRS------
                                                                                                              139 (225)
 T ss dssp
                        ТТСНИНИНИНИНИТТТССИНИНИНИНИНТ---STTCSCHИНИНИНИНИТТСИНИНИНИНИНИ------
                        T ss pred
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Q ss pred
                                             hнинhhhhhccccccccchhhhccCcсиннинниннинсСининниннин-hhccccccccchинин
  Q Fri_Mar_04_23: 791 PTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAE-YSLKEIQIEELQDFKEKQH
                                                                                                                                                                                                                      869 (1037)
  O Consensus
                                       869 (1037)
                                                                                   ....+....+...+...|.++.|++...
                                       140 \quad ------ LAAQPQFPPAFKELARTKMLAGQLGDADYYFKKYQSRVEVLQA------DD
  T 2vq2 A
                                                                                                                                                                                                                      184 (225)
  T ss_dssp
                                               T ss_pred
  Q ss_pred
                                             hhhhhhhHHHHHHHHHHhhcchhHH
  Q Fri_Mar_04_23: 870 IHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
  O Consensus
                                      870 ---l---i----F----L-l----a 894 (1037)
                                      |..+-....|+++.|
185 -----A 201 (225)
  T Consensus
  T 2vq2_A
                                      185 -----LLLGWKIAKALGNAOAA 201 (225)
                                      -----НИНИНИННИТТСИНИН
  T ss dssp
  T ss pred
                                               -----ННННННННННСССИННН
  No 68
                                                                  SCOPe PDB
                                                                                                                                                          Pub Med
                                                                                                                      NCBI
>1hh8_A P67PHOX, NCF-2, neutrophil cytosol factor 2; cell cycle, phagocyte oxidase factor, SH3 domain, repeat,
  TPR repeat cell cycle; HET: FLC; 1.8A {Homo sapiens} SCOP: a.118.8.1 PDB: 1wm5 _A 1e96 _B*
  Probab=84.85 E-value=5.2 Score=40.91 Aligned_cols=86 Identities=9% Similarity=0.074 Sum_probs=0.0
                                               Q ss pred
  Q Fri_Mar_04_23: 753 NEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLF
                                                                                                                                                                                                                      832 (1037)
                                      832 (1037)
  O Consensus
  T Consensus
                                                                                                                                                                                                                        47 (213)
  T 1hh8 A
                                          5 EAISLWNEGVLAADKKDWKGALDAFSAV------ODP------HSRICFNIGCMY
                                                                                                                                                                                                                       47 (213)
  T ss dssp
                                               НИНИНИНИНИНТТСИИНИНИНИТS-----SSC------CHHHHHHHHHH
                                               нининининининининининин
  T ss pred
  Q ss pred
                                               Q Fri_Mar_04_23: 833 DRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
  Q Consensus
                                       833 e------al--a--Ai------e-----e-----l---i----F----L-l-----a
                                                                                                                                                                               894 (1037)
                                         T Consensus
                                                                                                                                                                                   90 (213)
                                        48 TILKNMTEAEKAFTRSINRDKHLA-----VA-----YFQRGMLYYQTEKYDLA
  T 1hh8 A
                                                                                                                                                                                 90 (213)
                                               T ss_dssp
                                               T ss pred
                                                    PDB" Pub Qed
                • = I
  No 69
                                  >2p12_A Hypothetical conserved protein TTC0263; TPR, protein binding; 2.50A {Thermus thermophilus}
  Probab=84.80 E-value=6 Score=40.80 Aligned_cols=89 Identities=12% Similarity=0.113 Sum_probs=0.0
                                               Q ss pred
  Q Fri Mar 04 23: 753 NEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLF
                                                                                                                                                                                                                      832 (1037)
                                       832 (1037)
                                              ++...+.|.+++..|++++|.++|+++
                                           4 ----a---a----a-----a-----
  T Consensus
                                                                                                                                                              -----1~~~p~~~~~1g~~~
                                                                                                                                                                                                                        49 (217)
                                           4 AEONPLRIGVOLYALGRYDAALTLFERA-----LKENPODPEALYWLARTO
  T 2pl2 A
                                                                                                                                                                                                                       49 (217)
                                               T ss_dssp
                                               СНИНИНИНИНИСССИВИНИНИНИН
  T ss_pred
                                              ньсссинининининный в соссесссининный в выпусков в напусков на пусков в напусков на пусков на пуск
  Q ss_pred
  Q Fri_Mar_04_23: 833 DRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDV------LRLGHE 894 (1037)
                                      833 e----al--a--Ai----e---e----e-----l---i----F---L-l------a 894 (1037)
  O Consensus
                                         T Consensus
                                        50 LKLGLVNPALENGKTLVARTPRYL-----GG-----YMVLSEAYVALYRQAEDRERGKGYLEQA 103 (217)
  T 2pl2 A
                                               T ss_dssp
                                               T ss pred
                                  SCOPe PDB NCBI PubMed
>2h6f A Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit; ftase, farnesyltransferase,
  ССССЬНИНИНИННЬ---сссьнинининнньньсСссссССсьнининининнес-сниининнныны
  0 ss pred
  Q Fri_Mar_04_23: 714 ITENSFFMTFFRSYII----ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCG-NFDQSYEIFQLHDYPEAIND 788 (1037)
                                       714 \quad \text{$\sim\sim$ np$} \\ \text{$\sim\sim$ 1$} \\ \text{$\sim\sim$ 1$} \\ \text{$\sim\sim$ 2$} \\ \text{$\sim\sim$ 2$} \\ \text{$\sim\sim$ 2$} \\ \text{$\sim\sim$ 3$} \\ \text{$\sim\sim$ 2$} \\ \text{$\sim\sim$ 3$} \\ \text{$\sim\sim$ 3$} \\ \text{$\sim\sim$ 4$} \\ \text{$\sim\sim$ 2$} \\ \text{$\sim\sim$ 3$} \\ \text{$\sim\sim$ 4$} \\ \text{$\sim\sim$ 3$} \\ \text{$\sim\sim$ 4$} \\ \text{$\sim\sim$ 4$
                                        +..+|...+|..+|.++|.++|.++|.++|.++|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|..+|
  T Consensus
                                                                                                                                                                                                                     166 (382)
                                        90 IIYSDKFRDVYDYFRAVLQRDERSERAFKLTRDAIE---LNAANYTVWHFRRVLLKSLQKDLHEEMNYITAIIEEQPKNY 166 (382)
  T 2h6f A
                                               ЕСССИНИНИНИНИНИНИТСССИВИНИНИНИНИ --- ИСТТСИНИНИНИНИТТССИВИНИНИНИНИНИТСТСИ
  T ss dssp
                                               hhCCHНИННИННИННННССсhнинннннннн---hCccсниннннннннннннннннннннннннннн
  T ss pred
  Q ss_pred
                                              Q Fri Mar 04 23: 789 ----KLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDF 864 (1037)
```

```
Q Consensus
                    167 OVWHHRRVLVEWLRD---PSQE-LEFIADILNQDAKNYHAWQHRQWVIQEFKLWDNELQYVDQLLKEDVRNN------ 234 (382)
 T Consensus
 T 2h6f A
                         T ss_dssp
                         T ss pred
                         hннннhhhhhhhнннннннннн
 Q ss pred
 Q Fri_Mar_04_23: 865 KEKQHIHYLNLLIHFRMFEEVLDVLRLG-----HE
                                                                 894 (1037)
 Q Consensus
                             -----l----i----F----L-l------a
                                      |.++-...+|+|+
 T Consensus
                     235 ---~A 259 (382)
                    235 ---SV------WNQRYFVISNTTGYNDRAVLERE 259 (382)
 T 2h6f A
 T ss_dssp
                         T ss_pred
                         ---нн------ннинининин
                                     SCOPe POB"
 No 71
                                                                                   Pub Med
□ >3cv0_A Peroxisome targeting signal 1 receptor PEX5; TPR motifs, TPR protein, peroxin 5, PEX5, PTS1 binding
 domain, protein-peptide complex, receptor; 2.00A {Trypanosoma brucei} SCOP: a.118.8.1 PDB: 3cvl _A 3cvn _A 3cvp _A
 Probab=84.69 E-value=16 Score=39.03 Aligned cols=129 Identities=7% Similarity=-0.006 Sum probs=0.0
                         Q ss pred
 Q Fri_Mar_04_23:
                    715\ \texttt{TENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTF}
                     715 ~~np~~~~l~~~q~~~~~fl~~i~~p~~~~~fl~g~~~l~~~A~~F~~a~~~~~lp~~
                        T Consensus
                                                                                                                 232 (327)
 T 3cv0_A
                     169 PNDAQLHASLGVLYNLSNNYDSAAANLRRAVE---LRPDDAQLWNKLGATLANGNRPQEALDAYNRA------
                                                                                                                 232 (327)
 T ss dssp
                         T ss_pred
                         Нһһһһсссссссссь һһһссСссниннинниннниннниннниннниннниннн
 Q ss pred
 Q Fri Mar 04 23:
                     794 LEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQI-----EELQDFKE
                                                                                                                 866 (1037)
 Q Consensus
                     ....+....+...+....|.++...|++...+.|++...+.
 T Consensus
                     285 (327)
                     233 ------LDINPGYVRVMYNMAVSYSNMSOYDLAAKOLVRAIYMOVGGTTPTGEASREA----T-
 T 3cv0 A
                                                                                                                 285 (327)
 T ss dssp
                         T ss_pred
                        нинрирининининин
 Q ss_pred
 Q Fri Mar 04 23: 867 KQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
                     O Consensus
                               |..+=....|+++.|
                                     ---l-----A
 T 3cv0 A
                     286 RSM-----WDFFRMLLNVMNRPDLV 305 (327)
                         ннн-----ннинининиттсини
 T ss_dssp
                         ННН------НННННННННСССНННН
 T ss pred
 No 72
                                                NCBI
                                                                      Pub Med
>4j87 A Coatomer subunit alpha; beta propeller domain, vesicle trafficking, protein transpor; 1.67A
 {Schizosaccharomyces pombe} PDB: 4j8b A 4j8q A
                E-value=7 Score=42.59 Aligned_cols=77 Identities=14% Similarity=0.248 Sum_probs=0.0
                         ERROCCCERERROCCCCREERROCCCCOORDINATION OF THE CONTROL OF THE CONTR
 Q ss pred
 Q Fri Mar 04 23: 165 FLFYVSPQFSVVFLEDGGLLGLKKVDGVHYEPLLFNDNSYLKSLTRFFSRSSKSDYDSVISCKLF-HERYLIVLTONCHL
                                                                                                                 243 (1037)
                    165 -l-a----vsl-DGqLL-l------s-l--L--lf-----vS------lftL--D--L
 O Consensus
                                                                                                                 243 (1037)
                    218 CAFHPTLPLILSAGDDRLVKLWRMTASKAWEVDTCRG------HF--NNVSCCLFHPHQELILSASEDKTI
 T 4j87 A
                                                                                                                 280 (327)
 T ss_dssp
                         EEECSSSSEEEEETTSEEEEEECSSCEEEEEEC-----CS--SCEEEEEECSSSSEEEEETTSEE
                         T ss pred
                         EEEEcCCCceEEeec
 Q ss pred
 Q Fri_Mar_04_23: 244 KIWDLTSFTLIQDYD 258 (1037)
 Q Consensus
                     244 RiWsl~t~~~l~~~d 258 (1037)
                         |+||+++++.+..
 T Consensus
                     281 ~vWd~~~~~~
                     281 RVWDLNRRTAVQTFR 295 (327)
 T 4j87 A
 T ss_dssp
                         EEEETTTCCEEEEE
 T ss_pred
                         EEEECCCCChhhhhh
                                                  NCBI
                                                                     Pub Med
🗌 >2xpi_A Anaphase-promoting complex subunit CUT9; cell cycle, TPR, ubiquitin ligase; 2.60A {Schizosaccharomyces
 pombe}
 Probab=84.57 E-value=67 Score=37.83 Aligned cols=228 Identities=7% Similarity=-0.027 Sum probs=0.0
                         Q Fri_mar_04_23: 704 SLNSNVYNASITENSFFMTFFRSYIIENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYP 783 (1037)
                    783 (1037)
 Q Consensus
```

```
402 (597)
 T Consensus
                         326 ATTTKILETDPYNLDVYPLHLASLHESGEKNKLYLISNDLVD---RHPEKAVTWLAVGIYYLCVNKISEARRYFSKSSTM
 T 2xpi_A
                                                                                                                                          402 (597)
                              НИНИНИНЕСТТССТТИНИНИНИНИТСИНИНИНИНИНИН---ИСТТЯНИНИНИНИНИТСИНИНИНИНИНИН
 T ss dssp
                              нининининосесининининининесСhининининин---hСeechининининининининининининин
 T ss pred
 Q ss_pred
                              сссс---ссhнинрру проссссссссний и просссое просседений и п
 Q Fri_Mar_04_23: 784 EAIND----KLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIE
                                                                                                                                          859 (1037)
 Q Consensus
                         859 (1037)
                                                          ....+-..+
                         T Consensus
                                                                                                                                           475 (597)
                         403 DPQFGPAWIGFAHSFAIEGE---HDQA-ISAYTTAARLFQGTHLPYLFLGMQHMQLGNILLANEYLQSSYALFQYDP---
 T 2xpi A
                                                                                                                                          475 (597)
                              T ss dssp
                              Сесенининининин
 T ss_pred
                              ссссенининныныннинининнынныннын
 Q ss_pred
 Q Fri_Mar_04_23: 860 ELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC-LSDTVRTN------FLQLLLQEDIYSRDFFSTLLRL
                                                                                                                                          925 (1037)
                         860 e-----l--1-----lv--L-1-----ay--L----r------------l--11-------lv--L---
 O Consensus
                                                                                                                                          925 (1037)
                         T Consensus
                                                                                                                            ~1~
                                                                                                                                          529 (597)
                         476 -----LL-----LNELGVVAFNKSDMQTAINHFQNALLLVKKTQSNEKPWAATWA-----NLGHAYRKL
 T 2xpi_A
                                                                                                                                          529 (597)
                              T ss_dssp
                              T ss pred
                              Q ss pred
 Q Fri_Mar_04_23:
                         926 CNAHSDNGELYLRTVDIKIVDSILSQNLRSGDWEC--FKKLYCFRMLNKSERAAAEVL 981 (1037)
                         O Consensus
                                 530 g-----A----A-----A-----
                                                                                                             573 (597)
 T Consensus
                         530 K-----MYDAAIDALNQGLLLSTNDANVHTAIALVYLHKKIPGLAITHL 573 (597)
 T 2xpi_A
                              T ss_dssp
                              T ss_pred
                                               PDB"
 No 74
                                                                            Pub Med
>2dba_A
             Smooth muscle cell associated protein-1, isoform 2; tetratricopeptide repeat, structural genomics,
 NPPSFA; NMR {Homo sapiens}
 Probab=84.45 E-value=6.4 Score=37.29 Aligned_cols=89 Identities=8% Similarity=-0.004 Sum_probs=0.0
                              сссhнинининнессссссс---сhининининнининнинниннинннинн
 Q ss pred
 Q Fri_Mar_04_23: 730 ENTSHKNIRFFLENVECPFYLRH---NEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDS
                                                                                                                                          806 (1037)
 O Consensus
                         806 (1037)
                              .+++.....|-+.+. ...+ .+...+|.+|+..|++++|.++|.++
 T Consensus
                          91 (148)
                          41 CGDYGGALAAYTQALG--LDATPQDQAVLHRNRAACHLKLEDYDKAETEASKA-----
 T 2dba A
                                                                                                                                            91 (148)
                              ТТСНИНИНИНИНТ---SCCCНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИН
 T ss dssp
 T ss_pred
                              Q ss pred
 Q Fri Mar 04 23:
                         807 IWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKE 855 (1037)
                         807 ~l~~~l~~~~~Yy~~l~~Lfe~~~~a~~Ai~~~~
                                                                                                  855 (1037)
 Q Consensus
                                         T Consensus
                          92 -----A----al---p--
                                                                                                  132 (148)
                          92 -----IEKDGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKN 132 (148)
 T 2dba A
                              T ss dssp
 T ss_pred
                              -----нносссининининининининининининининин
                                  SCOPe POB<sup>N</sup> PROTEIN DATA BANK
                                                                            NCBI
 No 75
                                                                                                      Pub Med
>1w3b_A UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110; OGT, glcnac, nucleoporin, O-linked
 glycosylation, TPR repeat, protein binding; 2.85A {Homo sapiens} SCOP: a.118.8.1
 Probab=84.41
                   E-value=12 Score=42.04 Aligned_cols=154 Identities=8% Similarity=0.025 Sum_probs=0.0
                              СССһнинининны-сссһнининниннын сСссссССсһнининниннын СССнинниннын СССниннын С
 Q ss pred
 Q Fri Mar 04 23: 715 TENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAIND----K
                                                                                                                                          789 (1037)
                              789 (1037)
                         T Consensus
                                                                                                                                          208 (388)
 T 1w3b A
                                                                                                                                          208 (388)
 T ss dssp
                              ссіннинниннинессиннинниннин---іссіннинниннинсссинниннинниннісссіннинн
 T ss pred
 Q ss_pred
                              Q Fri Mar 04 23:
                        790 LPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYOLSLLFDRNNSOEFALKCISKSAEYSLKEIOIEELODFKEKOH
                                                                                                                                          869 (1037)
                         790 lp~l~l~~a~Ai~~a~Ai~~e~~e~~
 O Consensus
                                                                                                                                          869 (1037)
                         T Consensus
                                                                                                                                          273 (388)
                         209 LGNVLKEARI---FDRA-VAAYLRALSLSPNHAVVHGNLACVYYEQGLIDLAIDTYRRAIELQPHFP------DA
 T 1w3b A
                                                                                                                                          273 (388)
                              НИНИНИТТТС---ТТИН-ИНИНИНИНИСТТСИНИНИНИНИНИТТСИНИНИНИНИНТСSSCH-------
 T ss_dssp
 T ss pred
                              Q ss pred
                              hhhhhhннннннннннн
  Q Fri_Mar_04_23: 870 IHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
 O Consensus
                         870 ~~~l~~~i~~~~F~~~L~l~~~~a 894 (1037)
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|.++=....|++++|
             274 -----A 290 (388)
T Consensus
             274 -----YCNLANALKEKGSVAEA 290 (388)
T 1w3b A
               -----ннинининниясини
T ss dssp
T ss_pred
                -----ннинининнессиния
                        PDB"
No 76
                                NCBI
                                        Pub Med
>2vsy_A XCC0866; transferase, glycosyl transferase, GT-B, OGT, protein O-GLCN; HET: NHE; 2.10A {Xanthomonas
campestris PV} PDB: 2jlb _A* 2xgm _A* 2xgo _A* 2xgs _A* 2vsn _A*
Probab=84.40 E-value=11 Score=45.25 Aligned_cols=124 Identities=5% Similarity=-0.049 Sum_probs=0.0
Probab=84.40
                СССһһниннинн-сссһниннинннин-ссссссСсһниннинннин-
Q ss pred
Q Fri_Mar_04_23: 715 TENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTF 793 (1037)
             715 ~~np~~~~l~~~vi~~~q~~~~~fl~~i~~p~~~~~~fl~g~~~l~~~~A~~~F~~a~~~~~~lp~~
             T Consensus
                                                                         83 (568)
              20 PODFVAWLMLADAELGMGDTTAGEMAVQRGLA--LHPGHPEAVARLGRVRWTQORHAEAAVLLQQA-----
T 2vsv A
                                                                         83 (568)
                -ССНИНИНИНИНИНТСНИНИНИНИНИТ---ТЅТТСНИНИНИНИНИТСНИНИНИНИНИ-----
T ss dssp
T ss_pred
                СССИНИНИНИНИНИНСССИНИНИНИНИНИНИ --- ТССССИНИНИНИНИНИНЕСССИНИНИНИНИНИ -----------
               Q ss pred
Q Fri Mar 04 23: 794 LEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYL
                                                                        873 (1037)
             Q Consensus
                                                                        873 (1037)
                           T Consensus
              84 -----SDAAPEHPGIALWLGHALEDAGQAEAAAAAYTRAHQLLPEEP----YI--- 127 (568)
T 2vsy A
                T ss dssp
T ss_pred
                Q ss_pred
               hhhHHHHHHHHHHhhcchhHH
Q Fri_Mar_04_23: 874 NLLIHFRMFEEVLDVLRLGHE 894 (1037)
             874 ~~~i~~~~F~~~L~l~~~~a
Q Consensus
                               894 (1037)
                 +.++-....|++++|
             128 ------1a-----g-----A 144 (568)
T Consensus
T 2vsy A
             128 ----TAQLLNWRRRLCDWRAL 144 (568)
T ss_dssp
               ----НИНИНИНИНИТТССТТИ
T ss_pred
                ----НИНИНИНННЫ ССИНИН
                      SCOPe POEN DATA BANK
                                                     Pub Med
                                        S NCBI
>4gco_A Protein STI-1; structural genomics, PSI-biology, midwest center for structu genomics, MCSG,
tetratricopeptide repeat domain: 1.60A (Caenorhabditis elegans) SCOP: a.118.8.0
Probab=84.37 E-value=14 Score=32.85 Aligned_cols=110 Identities=9% Similarity=-0.053 Sum_probs=0.0
                ННюсССССhhнининин----сcchнинининныноССсссСchнининининининининининин
Q Fri_Mar_04_23: 709 VYNASITENSFFMTFFRSYII---ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPE 784 (1037)
Q Consensus 709 l------q------fl-i--p---------fl-g--l------A---F--a---- 784 (1037)
                T Consensus
              1 SNARLAYINPELAQEEKNKGNEYFKKGDYPTAMRHYNEAVK---RDPENAILYSNRAACLTKLMEFQRALDDCDTC----
T 4qco A
                                                                         73 (126)
T ss_dssp
                -----СССИНИНИНИНИНИНИТСИНИНИНИНИН---НСТТСИНИНИНИНИНТСИНИНИНИНИН----
                T ss_pred
                Q ss pred
Q Fri_Mar_04_23: 785 AINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKE 855 (1037)
O Consensus
             T Consensus
                                                            ----p-- 114 (126)
              74 -----IRLDSKFIKGYIRKAACLVAMREWSKAQRAYEDALQVDPSN 114 (126)
T 4gco A
                -----ннесттснинининнеттснинининниннин
T ss dssp
                ------
T ss pred
                                PDB<sup>N</sup>
PROTEIN DATA BANK
No 78
                        SCOPe
                                        S NCBI
                                                     Pub Med
🗌 >1ihg_A Cyclophilin 40; ppiase immunophilin tetratricopeptide, isomerase; 1.80A {Bos taurus} SCOP: a.118.8.1
b.62.1.1 PDB: 1iip A
Probab=84.33 E-value=4.2 Score=46.19 Aligned cols=104 Identities=7% Similarity=-0.020 Sum probs=0.0
                Q ss pred
Q Fri_Mar_04_23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
                                                                        833 (1037)
O Consensus
             833 (1037)
             +..... | +.+..++.
T Consensus
                                                                 .
~~~la~~~
                                                                         284 (370)
             223 SEDLKNIGNTFFKSQNWEMAIKKYTKV------LRYVEG----SRA-AAEDADGAKLQPVALSCVLNIGACKL
T lihq A
                                                                        284 (370)
T ss dssp
                T ss pred
                Q ss pred
Q Fri_Mar_04_23:
             834 RNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                                                           894 (1037)
             834 -----al--a-Ai-----e-----l---i---F--L-l-----a
..+.++.|++...||+..+...
285 --g---A-----al---p------a------lg-------A
                                                           894 (1037)
T Consensus
             285 KMSDWQGAVDSCLEALEIDPSNT-----KA-----LYRRAQGWQGLKEYDQA 326 (370)
T lihg A
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T ss_dssp
                         НТТСИНИНИНИНИНТТСТТСИ------ИН------ИН-ИНИНИНИНТТСИНИН
 T ss_pred
                         рессинининининине объементы в при в
                                     SCOPe PDB<sup>M</sup> PROTEIN DATA BANK
 No 79
                                                               NCBI
                                                                                    Pub Med
->1p5q_A FKBP52, FK506-binding protein 4; isomerase; 2.80A (Homo sapiens) SCOP: a.118.8.1 d.26.1.1 PDB: 1qz2_A
 Probab=84.32 E-value=6.5 Score=43.59 Aligned cols=108 Identities=10% Similarity=-0.004 Sum probs=0.0
                         Q ss pred
 Q Fri Mar 04_23: 731 NTSHKNIRFFLENVECPFYLRHN-----EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLE 795 (1037)
                     Q Consensus
                     T Consensus
                     161 GKYKQALLQYKKIVS---WLEYESSFSNEEAQKAQALRLASHLNLAMCHLKLQAFSAAIESCNKA-----
                                                                                                                  222 (336)
 T 1p5q A
                         ТСИНИНИНИНИН---ИТТСССССЯНИНИНИНИНИНИНИНИНИТСИНИНИНИНИНИН
 T ss dssp
 T ss pred
                         0 ss pred
 Q Fri_Mar_04_23:
                     796 DLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNL
                     796 ~l~~~~~~l~~~l~~~Lfe~~~~al~~a~~Ai~~~~e~~~~e~~~~~~l~~
 Q Consensus
                                                                                                                  875 (1037)
                                        ....|+....|+.+...|.++...|++...+|++...+...
 T Consensus
                                                                                                                  266 (336)
                     223 -----LELDSNNEKGLSRRGEAHLAVNDFELARADFOKVLOLYPNNK------AA-----
 T 1p5q A
                                                                                                                  266 (336)
 T ss_dssp
                         ------ннесттснинининнининининининининининин
                                       T ss pred
                         hHHHHHHHHHHhhcchhHH
 Q ss pred
 Q Fri Mar 04 23: 876 LIHFRMFEEVLDVLRLGHE 894 (1037)
                                               894 (1037)
 O Consensus
                    876 ~i~~~F~~~L~l~~~~a
                          +..+=....+++++.
 T Consensus
                    267 --~~la~~~~~~A 283 (336)
                    267 --KTQLAVCQQRIRRQLAR 283 (336)
 T 1p5q_A
 T ss_dssp
                         --ннинининининини
 T ss pred
                         --нининининининини
                                       PDB
 No 80
                                                                       Pub Med
>3i5p A Nucleoporin NUP170; helical stack, membrane, mRNA transport, nuclear pore complex, nucleus,
 phosphoprotein, protein transport; 3.20A {Saccharomyces cerevisiae}
 Probab=84.03 E-value=6.3 Score=47.37 Aligned cols=155 Identities=13% Similarity=0.002 Sum probs=0.0
                         Q ss pred
 O Fri Mar 04 23: 823 AFYYOLSLLFDRNNSOEFALKCISKSAEYSLKEIOIEELODFKEKOHIHYLN------LLIHFRMFEE--
                                                                                                                  884 (1037)
                     823 ~Yy~-l~-Lfe~~~~~al~-a~-Ai~~~~~e~~~~e~~~~l~-----l~-----i~~~i~~~-fr~---
                                                                                                                  884 (1037)
 O Consensus
                        ..-..+...|...+.|+.|++++..+-+..++..
                                                                                                 .-+|-.||+.
                      68 ~~L~~ic~~~~l~~y~GaV~L~L~~A~~~Dp~~~~~~Al~~~~g~~~~D~~~~~R~~cY~~I~
                                                                                                          .
---L--
 T Consensus
                                                                                                                  137 (525)
                      68 EKLKEAVSMMLSVNYYPKSIEFLLNIANSMDKGK-----LACQYVANGFLENDDRKQYYDKRILVYDLVFDTLIK
 T 3i5p_A
                         T ss dssp
                         T ss pred
 Q ss_pred
                                      -----Hhhhcchhннн---hChнhннннннhhhcccснннннннннcCccccCcccChh
 Q Fri_Mar_04_23: 885 -----VLDVLRLGHEC---LSDTVRTNFLQLLLQEDIYSRDFFSTLLRLCNAHSDNGELYLRTV
                                                                                                                  940 (1037)
                     Q Consensus
                                                                                                                  940 (1037)
                    +..+-+.-.. | ...|+++|.. +.|+.++
----l-s-DelFH------LYdWli------d-LL-i---
 T Consensus
                                                                                                                  201 (525)
 T 3i5p_A
                     138 VDELAEKKOSSKTONOISISNDDEVKLROKSYEAALKYNDRLFHYH-------MYDWLVSONRE--EKLLDIE-
                                                                                                                  201 (525)
 T ss_dssp
                         TC-----HHHHHHTTCG--GGGGGCC--
                         T ss_pred
 Q ss_pred
                         ННЕННИННЕННЕСССССИННЕННЕННЕННЕННЕННЕННЕННЕННЕННЕН
                     941 DIKIVDSILSQNLRSGDWECFKKLYCFRMLNKSERAAAEVLYQYILMQADLDVIRKRKCYL--MVINV 1006 (1037)
 Q Fri Mar 04 23:
                    941 ~~~vd-iL~~ar~~~y~LYs~ri~~~R-AA~mYe~~rl~~~k~yL~~~iN~ 1006 (1037) 
--|+.-|..+.. +...+.|.-|+..|++|-+||+++|.-+.+ .....+++-.|| ++.||
202 ~sPfle~yL~~~~~dLLWryy~k~~~~AA~vL~~LA~s~~~i~L~~RieyLsrA~~~a 266 (525)
 O Consensus
 T Consensus
 T 3i5p_A
                     202 -TPFILPYLMEKAGS-SLKISNILWVYYSRRSKFFESAEILYRLATS-NFDITLFERIEFLSRANGFC
                                                                                                     266 (525)
                         -СТТНИННИНТСС----СНИНИНТНИННССЅНИНИНИНННЯS-SSCCCИНИНИНИНИННННС
 T ss_dssp
                         -Ссhнининнhhcc-сhнининнннннннннннннннннн
 T ss pred
 No 81
                                                                        Pub Med
>4ui9_F Cell division cycle protein 27 homolog; ubiquitination, cell cycle, APC/C; 3.60A {Homo sapiens}
 Probab=83.92 E-value=38 Score=42.95 Aligned_cols=219 Identities=9% Similarity=-0.013 Sum_probs=0.0
                         cCCchниннинниннесСнинниннинн
 Q ss pred
 Q Fri Mar 04 23: 750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLS 829 (1037)
                    Q Consensus
                                                                                                                  829 (1037)
                                                                                                                  574 (824)
 T Consensus
 T 4ui9 F
                                                                                                                  574 (824)
 T ss_dssp
                         T ss_pred
                         0 ss pred
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Q Fri_Mar_04_23: 830 LLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC--LSD-----TVRT 902 (1037)
  O Consensus
                                        T Consensus
                                                                                                                                                                                                                            635 (824)
  T 4ui9 F
                                                T ss_dssp
                                                T ss pred
                                                Q ss pred
                                        903 \ \text{NFLQLLLQEDIYSRDFFSTLLRLCNAHSDNGELYLRTVDIKIVDSILSQNLRSGDWEC--FKKLYCFRMLNKSERAAAEV}
  Q Fri_Mar_04_23:
                                                                                                                                                                                                                            980 (1037)
                                       691 (824)
  T Consensus
  T 4ui9 F
                                                                                                                                                                                                                            691 (824)
  T ss_dssp
                                                НИНН------НИНИНИННСС------СИНИНИНИНИНИНННОСССИНИНИНИНИНИСССИНИНИНИ
  T ss_pred
                                                НННННННННННННННННННННН
  Q ss pred
  Q Fri Mar 04 23: 981 LYQYILMQADLDVIRKRKCYLMVINVLSSFDSAYDQ 1016 (1037)
                                        981 mYe---rl-----k-yL--iN-L----d- 1016 (1037)
  Q Consensus
                                        T Consensus
                                        692 LNKAIVIDPKN-----PLCKFHRASVLFANEKYKSA 722 (824)
  T 4ui9 F
                                                НИНИННЫТТС----НИНИНИННИННИТТСИННИ
  T ss_dssp
                                                нининньноссс----нинининнинннессинин
  T ss pred
                                                                       SCOPe PODEN PROTEIN DATA BANK
  No 82
                                                                                                                                                              Pub Med
>1elw A TPR1-domain of HOP; HOP, TPR-domain, peptide-complex, helical repeat, HSP70, protein binding, chaperone;
  1.60A {Homo sapiens} SCOP: a.118.8.1
  Probab=83.88 E-value=5.9 Score=35.32 Aligned_cols=89 Identities=12% Similarity=0.063 Sum_probs=0.0
                                                сссhнинниннннеССссссССсhнинниннннннн
  Q ss pred
  Q Fri Mar 04 23: 730 ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWK
                                                                                                                                                                                                                            809 (1037)
                                        Q Consensus
                                                                                                                                                                                                                            809 (1037)
                                         .+++.....|-+.+. ...+++...+.|.++...|++++|.++|.++
17 ~~~~~A~~~~~a~~--~~1a~~~~~A~~~~~A~~~~~a-
  T Consensus
                                                                                                                                                     ~~a---
                                                                                                                                                                                                                              64 (118)
  T lelw A
                                          17 VGNTDDALOCYSEATK---LDPHNHVLYSNRSAAYAKKGDYOKAYEDGCKT------
                                                                                                                                                                                                                              64 (118)
  T ss dssp
                                                ТТСНИНИНИНИН---НСТТСИНИНИНИНИНИНИНИНИНИ------
                                                T ss_pred
                                                ссыры ссестиний и поставлений п
  Q ss pred
  Q Fri Mar 04 23: 810 DLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKE
                                                                                                                                                    855 (1037)
                                        810 --l-----Yy--l--Lfe-----al--a--Ai-----
  O Consensus
                                                                                                                                                    855 (1037)
                                                     65 ----p----p----p---
                                          65 ----VDLKPDWGKGYSRKAAALEFLNRFEEAKRTYEEGLKHEANN
  T lelw A
                                                                                                                                                    105 (118)
                                                -----НИСТТСИНИНИНИНИНИТТСИНИНИНИНИНИТТСТТС
  T ss_dssp
                                                -----ННСссссниннинниннинниннинниннинниннин
  T ss pred
                                                                       PDE NCBI Pub Med
🗌 >3u3w_A Transcriptional activator PLCR protein; ternary complex, PLCR-PAPR7-DNA, HTH DNA-binding domain, QUO
  sensing; 2.40A {Bacillus thuringlensis} PDB: 2qfc _A 4fsc _A
Probab=83.67 E-value=6.8 Score=42.29 Aligned_cols=97 Identities=14% Similarity=0.053 Sum_probs=0.0
                                                нинниннессининниннинный рассессининный рассесссий рассессии рассессий рассессии рассессий рассессий рассессий рассессий рассессий рассессии рассессий рассессии рассессий рассессии рассесии рассессии рассессии рассессии рассессии рассесии рассесии ра
  Q ss pred
  Q Fri Mar 04 23: 758 FMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNS 837 (1037)
                                        758 \ fl - g - \sim 1 - \sim \sim -A - \sim F - \sim a - \sim \sim \sim -1p - \sim 1 - \sim 1 - \sim \sim 1 - \sim \sim -2yy - \sim 1 - \sim Lfe - \sim \sim 1 - \sim 1 - \sim \sim -1 - \sim -1 - \sim \sim -1 - \sim 
  O Consensus
                                                                                                                                                                                                                            837 (1037)
                                               .-+|.+|.+++|.++|+++
                                                                                                     +....
                                        159 ~~lg~~y~~~g~~~~A~~~~a-----
                                                                                                                      ---1~~~~-----
  T Consensus
                                        159 NATANIYAENGYLKKGIDLFEOI-----LKOLE-----ALHDNEEFDVKVRYNHAKALYLDSR
  T 3u3w A
                                                                                                                                                                                                                           211 (293)
  T ss_dssp
                                                T ss pred
                                                нниннинниннинн
  Q ss pred
  Q Fri_Mar_04_23:
                                        838 QEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
  Q Consensus
                                        838 ---al--a--Ai-----e-----e----l---i---F---L-l-----a
                                                                                                                                                                           894 (1037)
                                                ++.|+++.++|++.....|+++.|
                                        T Consensus
  T 3u3w A
                                        212 YEESLYQVNKAIEISCRINSMA----LIGQL-----YYQRGECLRKLEYEEAE
                                                                                                                                                                          255 (293)
  T ss_dssp
                                                ННИНИНИНИНИНИТТВСТ----ТИНИН------НИНИНИНИНТТССИНИ
  T ss_pred
                                                NCBI Pub Med
>4jsn_D Target of rapamycin complex subunit LST8; helical repeat, kinase, WD40 repeat, protein kinase, raptor, transferase; 3.20A {Homo sapiens} PDB: 4jsp_D* 4jsv_D* 4jsx_D* 4jt5_D* 4jt6_D*
Probab=83.63 E-value=9 Score=41.83 Aligned_cols=83 Identities=10% Similarity=0.179 Sum_probs=0.0
                                                EEEEecCCCEEEEEecCCCCeeEEEecCccHHHHHHHHhcCCCCCCccceEEEEe-cCcEEEEEEcCCe
  Q Fri_Mar_04_23: 164 HFLFYVSPQFSVVFLEDGGLLGLKKVDGVHYEPLLFNDNSYLKSLTRFFSRSSKSDYDSVISCKLF-HERYLIVLTQNCH 242 (1037)
                                        Q Consensus
                                                .+...+...+...||.+-.-
```

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------v----s-d---l-s-s-D-- 293 (326)
 T Consensus
                   225 ----sp----l-s-s-D--i-iwd------
                   225 OCRFSPDSTLLATCSADOTCKIWRTSNFSLMTELSIKS------GNPGESSRGWMWGCAFSGDSQYIVTASSDNL 293 (326)
 T 4jsn D
 T ss dssp
                       EEEECTTSSEEEEEETTTEEEEEETTTCCEEEEEECCC-----SSTTSCCCCCEEEEEECTTSSEEEEEETTSE
                       EEEECCCCCEEEEecCCCceeeeeeeecc-----CCCCCcccceEEEEECCCCCEEEEccCCCC
 T ss pred
 Q ss_pred
                       EEEEEcCCCceEEee
 Q Fri_Mar_04_23: 243 LKIWDLTSFTLIQDY 257 (1037)
                   243 LRiWsl~t~~~l~~~
 Q Consensus
                                        257 (1037)
                       +|+|++++|+++.+.
                   294 v~lWd~~~g~~~~~
 T Consensus
                                         308 (326)
                   294 ARLWCVETGEIKREY 308 (326)
 T 4jsn D
 T ss dssp
                       EFFETTTCCFFFFF
                       EEEEEccCCceeeee
 T ss_pred
 No 85
->4ga2_A E3 SUMO-protein ligase ranbp2; TPR motif, nuclear pore complex component nucleocytoplasmic transport,
 transport protein; 0.95A {Pan troglodytes} PDB: 4ga0 A 4ga1 A*
Probab=83.62 E-value=7.8 Score=35.78 Aligned_cols=85 Identities=18% Similarity=0.243 Sum_probs=0.0
                       нинининессининининин
 Q Fri_Mar_04_23: 758 FMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNS
                                                                                                           837 (1037)
 Q Consensus
                   837 (1037)
                                                                                  ....+....+..+..+...
                                  ----À----
 T Consensus
                       ---à----
                                           .
~~~a-
                                                                                                            80 (150)
                    35 FYFAKLYYEAKEYDLAKKYICTY-----INVQERDPKAHRFLGLLYELEEN
 T 4ga2 A
                                                                                                            80 (150)
 T ss dssp
                       T ss pred
                       Q ss_pred
                       ННННННННННННННН
 Q Fri_Mar_04_23:
                   838 QEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRL-GHEC
                                                                                     895 (1037)
 O Consensus
                   838 ---al--a--Ai-----e-----e-----l---i----F---L-l-----ay
                                                                                     895 (1037)
                       ++.|++..+.|++..+... .. |.++=....+++ +.|.
 T Consensus
                       ~~~A~~~~~a~~~~~~~A~
                                                                                     120 (150)
                    81 TDKAVECYRRSVELNPTQK------DL-----VLKIAELLCKNDVTDGRAK
 T 4ga2_A
                                                                                     120 (150)
 T ss_dssp
                       T ss pred
 No 86
                                                                   Pub Med
>2xev_A YBGF; tetratricopeptide, alpha-helical, metal binding; 1.57A {Xanthomonas campestris}
 Probab=83.61 E-value=15 Score=32.85 Aligned cols=90 Identities=9% Similarity=0.019 Sum probs=0.0
                       нинининессининининин
 Q ss_pred
 Q Fri Mar 04 23: 758 FMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNS
                                                                                                           837 (1037)
                   837 (1037)
 O Consensus
                       |.+|.+++..|++++|.++|.++-
                                                                     T Consensus
                         ~~a~~~~~~~~~~~~~~~~~~~~a~~~~
                                                                                                            54 (129)
                     6 YNVAFDALKNGKYDDASQLFLSFL-----ELYPNGVYTPNALYWLGESYYATRN
 T 2xev A
                                                                                                            54 (129)
 T ss_dssp
                       T ss_pred
                       Q ss pred
 Q Fri_Mar_04_23:
                   838 QEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                                                                                   894 (1037)
                       838
                                                                                    894 (1037)
 T Consensus
                    95 (129)
                    55 FQLAEAQFRDLVSRYPTHD-----KAAGG-----LLKLGLSQYGEGKNTEA
 T 2xev A
                                                                                    95 (129)
 T ss_dssp
                       нининининининиссссh------hhннн-------ннининининесснини
 T ss pred
 No 87
                                                                   Pub Med
🗎 >5aio_A Transcription factor TAU 131 kDa subunit; TFIIIC, TPRS; 3.15A {Saccharomyces cerevisiae} PDB: 5aem_A
 Probab=83.59 E-value=16 Score=41.28 Aligned_cols=124 Identities=10% Similarity=-0.007 Sum_probs=0.0
 Q ss pred
                       СССЬЬНИНИНИННЫ—сесьнинининны в сесьнинин в сесьнини в сесьствой в сесьством в 
 O Fri Mar 04 23:
                   715 TENSFEMTFFRSYTT-ENTSHKNTRFFLENVECPFYLRHNEVOEFMFAMTLFSCGNFDOSYETFOLHDYPEATNDKLPTF
                                                                                                           793 (1037)
                   715 ~~np~~~~l~~~vi-~~q~~~~~fl~~i~~p~~~~~fl-g~~~l~~~A~~F~~a~~~~~lp~~
 Q Consensus
                                                                                                           793 (1037)
                    T Consensus
                                                                                                           104 (448)
 T 5aio A
                    41 ARNEAAYETI.GDTYOLOGRI.NDCCNSWELAAH---I.NASDWEEWKIVAII.SADI.DHVROATYCESRV-----
                                                                                                           104 (448)
 T ss dssp
                       T ss_pred
                       Q ss pred
 Q Fri_Mar_04_23:
                   794 LEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYL
                                                                                                           873 (1037)
                   Q Consensus
                                                                                                           873 (1037)
                                    ....+....+..+...|.++.|++...+.+..
 T Consensus
                                   -----g----l---p-----la------g-----h------l----p------
 T 5aio A
                       -----ISLNPMEWESIYRRSMLYKKTGQLARALDGFQRLYMYNPYDA-----NI--- 148 (448)
 T ss_dssp
                       T ss_pred
```

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Q ss_pred
               hhhнинниннинhhcchhин
Q Fri_Mar_04_23: 874 NLLIHFRMFEEVLDVLRLGHE 894 (1037)
O Consensus
            874 ~~~i~~~F~~~L~l~~~~a 894 (1037)
                 |..+-....|+++.|
             149 ----
                   ---la-----A
            149 ----LRELAILYVDYDRIEDS 165 (448)
T 5aio A
               ----нининининиттсини
T ss_dssp
               ----ннинининннессинин
T ss pred
No 88
                                       Pub Med
>4i17_A Hypothetical protein; TPR repeats protein, structural genomics, joint center for S genomics, JCSG,
protein structure initiative; HET: MSE; 1.83A {Bacteroides fragilis}
 Probab=83.34 E-value=9.3 Score=38.29 Aligned_cols=129 Identities=8% Similarity=-0.010 Sum_probs=0.0
               Q ss_pred
Q Fri Mar 04 23: 750 LRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAIND----KLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAF 824 (1037)
             O Consensus
              T Consensus
                                                                        78 (228)
T 4i17 A
              3 QTTDPNQLKNEGNDALNAKNYAVAFEKYSEYLKLTNNQDSVTAYNCGVCADNIKK---YKEA-ADYFDIAIKKNYNLANA
                                                                       78 (228)
               T ss_dssp
               T ss pred
               НННННННННННННННННННННННН
Q ss pred
Q Fri Mar 04 23: 825 YYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
             825 v~l~Lfe~~~~al~a~Ai~~~~e~~~e~~~~l~~i~~~f~~L~l~~~a 894 (1037)
O Consensus
               +..+..+...|.++..|++..+.|++..+.....
             T Consensus
                                                               136 (228)
T 4i17 A
             79 YIGKSAAYRDMKNNQEYIATLTEGIKAVPGNATIE----KLYAIY------YLKEGQKFQQAGNIEKA
T ss_dssp
               T ss_pred
               НИНИНИНННЫ ССИНИНИНИНИННИН СССССИНИН ---- НИНИНИ ----- НИНИНИНИННИН НИНИССИНИН
                       PDE NCBI
No 89
                                            Pub Med
->4xi0_A Magnetosome protein MAMA; magnetosome associated protein, protein-protein interaction, motif, protein
binding; 2.88A {Desulfovibrio magneticus rs-1}
Probab=83.29 E-value=6.5 Score=38.87 Aligned cols=121 Identities=7% Similarity=-0.012 Sum probs=0.0
Q ss_pred
               ССснинининининесссининининининин
Q Fri_Mar_04_23: 751 RHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAIND----KLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYY
                                                                       826 (1037)
             O Consensus
                                                                       826 (1037)
               .+.+...+..+|.+++|.+++|.++|.++|.++|...+....+ ...+ ...+ ...+
                     -~~a~~~~
                            ~~~~À~~~
                                   ----a-----A-----A-----
                                                                        79 (202)
T Consensus
              4 GDKAKLYRNISQRCLRRGSPEEALRYLKEWARHEKNDPEPLYQMGIALANLGD---YQRA-VTVFDKVLKLRPNHFMASY
T 4xi0 A
                                                                        79 (202)
               T ss dssp
               T ss_pred
               ннинннинниннинннинннинннинннинннинн
Q ss_pred
Q Fri Mar 04 23:
             827 QLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE
                                                               894 (1037)
             827 ~l~~Lfe~~~~~al~~a~~Ai~~~~~e~~~~~l~~~i~~~F~~~L~l~~~~a
Q Consensus
                                                               894 (1037)
             128 (202)
T Consensus
             80 RKGAVLLKIKQYKLALPVLEAVVAAAPADA-----RA-----YYLLGLAYDGDEQLEKG
T 4xi0 A
                                                              128 (202)
               T ss_dssp
T ss pred
               PDB™
PROTEIN DATA BANK
No 90
                               NCBI
                                       Pub Med
33ieg_A DNAJ homolog subfamily C member 3; TPR motif, chaperone, endoplasmic reticulum, TPR repeat, UNF protein
response; 2.51A {Mus musculus}
Probab=83.25 E-value=12 Score=41.82 Aligned cols=150 Identities=7% Similarity=-0.039 Sum probs=0.0
Q ss pred
               СССһһнининнин-сссһниннинниннын сСссссСсһниннинниннинниннинниннын кос-
Q Fri Mar 04_23: 715 TENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAI----- 786 (1037)
             715 ~np~~~l~~vi~~q~~~~fl~i~p~~~~fl-g~~l-~~~A~~-F~a~~~~~786 (1037)
Q Consensus
             T Consensus
                                                                    ~~a 110 (359)
             34 PDNYIAYYRRATVFLAMGKSKAALPDLTKVIA---LKMDFTAARLQRGHLLLKQGKLDEAEDDFKKVLKSNPSEQEEKEA 110 (359)
T 3ieg A
               ТТСИНИНИНИНИНИТСИНИНИНИНИН---ИСТТСИНИНИНИНИТСИНИНИНИНИНИНИТСКИЕНИНИН
T ss_dssp
               СССИНИНИНИНИНСССИНИНИНИНИНИН---сССССИНИНИНИНИНИСССИНИНИНИНИНИНИНОСССССССИНИ
T ss pred
               0 ss pred
Q Fri_Mar_04_23: 787 -----NDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAE
                                                                       850 (1037)
             787 -----lp~l~l~l~~l~~l~~l~~l~~~~Yy~~l~Lfe~~~~a~Ai~
             111 ESQLVKADEMORLRSQA---LDAFDGAD---YTAA-ITFLDKILEVCVWDAELRELRAECFIKEGEPRKAISDLKAASK
T Consensus
                                                                       182 (359)
T 3ieg A
                                                                       182 (359)
               T ss dssp
               T ss_pred
Q ss pred
               hhcccccccchHHHHhhhhhhhhHHHHHHHHHHHH
O Fri Mar 04 23: 851 YSLKEJOIEELODFKEKOHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
```

```
Q Consensus
                  851 ----a 894 (1037)
                  ..+... +. |.++-....|+++.|
183 ~~p~~~~a-----a------1g~~~~A 207 (359)
 T Consensus
                  183 LKSDNT-----EA-----FYKISTLYYQLGDHELS 207 (359)
 T 3ieg A
 T ss_dssp
                      T ss pred
                                 SCOPe PDB
 No 91
                                                                         Pub Med
>4j8e A HSC70-interacting protein; tetratricopeptide repeat, solenoid, CO-chaperone, cytosol; 2.60A {Rattus
 norvegicus} SCOP: a.118.8.0 PDB: 4j8d _A
 Probab=83.14 E-value=7.9 Score=37.53 Aligned cols=85 Identities=11% Similarity=0.055 Sum probs=0.0
                      нинининессинининининининининин
 Q ss pred
 Q Fri_Mar_04_23: 758 FMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNS
                                                                                                    837 (1037)
 O Consensus
                  837 (1037)
                     +.+|.+++..|++++|..+|.++
                                                                            ....+..+..+..+...+...|.
                   T Consensus
                                                                                                    90 (175)
                   45 KGAAIDALNDGELQKAIDLFTDA------IKLNPRLAILYAKRASVFVKLQK
 T 4i8e A
                                                                                                    90 (175)
 T ss_dssp
                      T ss_pred
                      ннинниннинниннинн
 Q ss pred
 Q Fri Mar_04_23: 838 QEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC 895 (1037)
                  838 ---al--a--Ai-----e-----e-----l---i----F---L-l-----ay 895 (1037)
 Q Consensus
                   T Consensus
                   91 PNAAIRDCDRAIEINPDSA------QP-----YKWRGKAHRLLGHWEEAA 129 (175)
 T 4i8e A
                      T ss_dssp
 T ss_pred
                      ннининининин
                                  PDB<sup>™</sup>
                                           NCBI Pub Med
 No 92
🗎 >3rkv_A Putative peptidylprolyl isomerase; structural genomics, APC102156, PSI-biology, midwest center structural
 genomics, MCSG; 2.41A {Caenorhabditis elegans}
 Probab=83.11 E-value=9.4 Score=36.29 Aligned_cols=103 Identities=13% Similarity=0.089 Sum_probs=0.0
                      Q ss pred
 Q Fri_Mar_04_23: 758 FMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNS
                                                                                                    837 (1037)
                  837 (1037)
 Q Consensus
 T Consensus
                                                                                                    78 (162)
                   15 ROKGNELFVOKDYKEAIDAYRDAL-----TRLDTLILREKPGEP----EWVELDRKNIPLYANMSQCYLNIGD
 T 3rkv A
                                                                                                    78 (162)
 T ss_dssp
                      T ss pred
 Q ss_pred
                      нинининининин
 Q Fri_Mar_04_23: 838 QEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC 895 (1037)
                  838 ---al--a--Ai-----e-----e-----l---i----F---L-l-----ay 895 (1037)
 Q Consensus
                   |.++=....+|+|+.|.
 T Consensus
                   79 LHEAEETSSEVLKREETNE-----KA------LFRRAKARIAAWKLDEAE 117 (162)
 T 3rkv_A
                      T ss_dssp
                      T ss pred
 No 93
                                                       Pub Med
                NCBI
>4ui9 F Cell division cycle protein 27 homolog; ubiquitination, cell cycle, APC/C; 3.60A {Homo sapiens}
 Probab=83.04 E-value=1e+02 Score=39.04 Aligned_cols=230 Identities=8% Similarity=0.005 Sum_probs=0.0
                      нинининнесссссинининининненнин
 Q Fri_Mar_04_23: 702 IDSLNSNVYNASITENSFFMTFFRSYIIENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHD
Q Consensus 702 i-----A---F--a-
                                                                                                   781 (1037)
                                                                                                    781 (1037)
                  ...++..+........++...++...+..++...+..++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...++...+...++...++...++...++...++...++...++...++...++...++...++...++...+...++...++...++...++...++...++...++...++...++...++...++...++...+...++...++...++...++...++...++...++...++...++...++...++...++...+.
 T Consensus
 T 4ui9 F
                  628 (824)
 T ss_dssp
                      ННИНИННИНССЅЅНИНИНИНИНИНТТСИНИНИНИНИН——-ИСТТСИНИНИНИНИНИТСИНИНИНИНИНИН
 T ss_pred
                      Q ss pred
 Q Fri_Mar_04_23: 782 YPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEEL
                                                                                                    861 (1037)
 Q Consensus
                  861 (1037)
                  +....|+..++...|.++..|++..+...
629 ------La--y---g----A--1--al---p------
 T Consensus
                                                                                                    669 (824)
                  629 -----PRHYNAWYGLGMIYYKQEKFSLAEMHFQKALDINPQSS----
 T 4ui9 F
                                                                                                    669 (824)
 T ss dssp
                      T ss pred
                      Q ss pred
                  862 QDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHEC-LSD----TVRTNFLQLLLQEDIYSRDFFSTLLRLCNAHSDNGE 934 (1037)
 Q Fri_Mar_04_23:
                  T Consensus
                  T 4ui9 F
```

```
T ss_dssp
              T ss_pred
              ------
              Q ss_pred
Q Fri_Mar_04_23: 935 LYLRTVDIKIVDSILSQNLRSGDWEC--FKKLYCFRMLNKSERAAAEVLYQYILMQADLDVIRKRKCYLMVINVLSSFDS 1012 (1037)
            O Consensus
T Consensus
T 4ui9 F
              T ss_dssp
               T ss pred
              hhcC
Q ss pred
Q Fri_Mar_04_23: 1013 AYDQ 1016 (1037)
         1013 ~~d~ 1016 (1037)
              .+++
            787 ~~eA 790 (824)
T Consensus
            787 DEEP 790 (824)
T 4ui9 F
T ss dssp
T ss_pred
              hHHH
No 94
                       PDB<sup>™</sup>
                             NCBI
                                     Pub Med
🗌 >3hym_B Cell division cycle protein 16 homolog; APC, anaphase promoting complex, cell cycle, mitosis, cyclosome,
TPR, ubiquitin, ubiquitin ligase, twinning; 2.80A (Homo sapiens)
Probab=82.98 E-value=29 Score=37.00 Aligned_cols=167 Identities=5% Similarity=-0.056 Sum_probs=0.0
              СССһһнинниннн-сс-сһниннинннн-ссссссСсһнинниннннн-сссниннниннннн-
0 ss pred
Q Fri_Mar_04_23: 715 TENSFFMTFFRSYII-EN-TSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPT
                                                                   792 (1037)
            T Consensus
                                                                   163 (330)
             87 PSNPVSWFAVGCYYLMVGHKNEHARRYLSKATT---LEKTYGPAWIAYGHSFAVESEHDQAMAAYFTAAQLMKGCHLPML
T 3hym B
                                                                   163 (330)
T ss_dssp
              T ss_pred
              Q ss pred
Q Fri Mar 04 23: 793 FLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHY
                                                                   872 (1037)
            Q Consensus
                                                                   872 (1037)
               .+..+-.....+....+.....+....|.++..|++...|.++..|++...+...
            164 -l----A-----l-----l-----A------
T Consensus
                                                                   238 (330)
            164 YIGLEYGLTNNSKLAERFFSQALSIAPEDPFVMHEVGVVAFQNGEWKTAEKWFLDALEKIKAIGNEVTVDKWE--PL--- 238 (330)
T 3hym_B
              T ss dssp
T ss_pred
              Q ss_pred
              hhhhнниннинннhhcchhни
Q Fri_Mar_04_23: 873 LNLLIHFRMFEEVLDVLRLGHE 894 (1037)
            873 l---i----F---L-l----a
Q Consensus
                             894 (1037)
                |.++=....|+++.|
                  ~~~1~~~~~~A 255 (330)
T Consensus
            239 ----LNNLGHVCRKLKKYAEA 255 (330)
T 3hym B
T ss_dssp
              -----НИНИНИННИТТСИНИ
T ss_pred
              ----ннинининининини
                     SCOPe
                                            Pub Med
                                     S NCBI
Stops A FKBP52, FK506-binding protein 4; isomerase; 2.80A (Homo sapiens) SCOP: a.118.8.1 d.26.1.1 PDB: 1qz2 A
Probab=82.84 E-value=6.4 Score=43.67 Aligned cols=103 Identities=13% Similarity=-0.071 Sum probs=0.0
Q ss_pred
              Q Fri_Mar_04_23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD 833 (1037)
O Consensus
            T Consensus
                                                                   207 (336)
T 1p5q_A
            147 STIVKERGTVYFKEGKYKQALLQYKKIVSWLE-----YES-SFSNEEAQKAQALRLASHLNLAMCHL
                                                                   207 (336)
              НИНИНИНИНИТСИИНИНИНИНИНИНИТТ-------TCC-CCCSHHHHHHHHHHHHHHHHHHH
T ss_dssp
              T ss_pred
Q ss_pred
              Q Fri_Mar_04_23: 834 RNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
O Consensus
            834 ~~~~~al~~a~~Ai~~~~~e~~~~e~~~~l~~~i~~~F~~~L~l~~~~a 894 (1037)
            ..|.++.|++...+|++...+................|+++=..+...+++|+..|
208 ~~g~~~A~~~~al~~p~~~~a-~~~a-~~~a-~~--lg~~~~~A 249 (336)
T Consensus
T 1p5g A
            208 KLQAFSAAIESCNKALELDSNNE-----KG-----LSRRGEAHLAVNDFELA 249 (336)
T ss_dssp
              T ss pred
               Нсссининининининининин
                     SCOPe PROTEIN DATA BANK NCBI
No 96
                                                Pub Med
🗆 >21ni_A Stress-induced-phosphoprotein 1; structural genomics, northeast structural genomics consortiu
PSI-biology, protein structure initiative, chaperone; NMR {Homo sapiens} SCOP: a.118.8.0
Probab=82.83 E-value=17 Score=32.72 Aligned_cols=105 Identities=6% Similarity=-0.045 Sum_probs=0.0
```

```
Q ss pred
               ссснинининненниннесссиости
Q Fri Mar 04 23: 730 ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWK
                                                                      809 (1037)
            O Consensus
                                                                      809 (1037)
             76 (133)
             29 KGDYPQAMKHYTEAIK---RNPKDAKLYSNRAACYTKLLEFQLALKDCEEC------
T 2lni A
                                                                       76 (133)
T ss_dssp
               T ss_pred
               hССИНИНИНИНИН ——cССССИНИНИНИНИНИНИНИНИНИНИНИНИНИНИ
               Q ss_pred
Q Fri_Mar_04_23:
                                                                      889 (1037)
            {\tt 810~DLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQHIHYLNLLIHFRMFEEVLDVL}
O Consensus
            889 (1037)
                  |..+-...+
             77 ----p-----1----
                                                             ~~1~~~
T Consensus
                                                                      132 (133)
T 2lni A
             77 ----IQLEPTFIKGYTRKAAALEAMKDYTKAMDVYQKALDLDSSCK-----EA-----ADGYQRCMMAQY
                                                                      132 (133)
              ----<mark>нн</mark>исттенинининининттенинининининине
T ss_dssp
T ss pred
               -----ННСССсhнинининининининининининининин
Q ss pred
Q Fri_Mar_04_23:
            890 R 890 (1037)
            890 ~
                890 (1037)
            133 ~ 133 (133)
T Consensus
            133 N 133 (133)
T 2lni A
T ss_dssp
T ss_pred
                        PDB'
No 97
                               NCBI
                                      Pub Med
🗌 >3ro3_A PINS homolog, G-protein-signaling modulator 2; asymmetric cell division, protein binding; 1.10A {Mus
musculus}
Probab=82.79 E-value=8.8 Score=37.04 Aligned cols=100 Identities=13% Similarity=-0.025 Sum probs=0.0
Q ss pred
               Q Fri_Mar_04_23:
            754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
            833 (1037)
              +....+|.++...|++++|.++|++-.....
9 ~~~~lg~~~~~g~~~~A~~~~~al~~~~~
                                                         ....-+..+..++.
T Consensus
                                                     -----lq~~~
                                                                       60 (164)
              9 GRAFGNLGNTHYLLGNFRDAVIAHEORLLIAKEF-----GDK-----AAERIAYSNLGNAYI
T 3ro3 A
                                                                       60 (164)
               T ss_dssp
T ss_pred
               Q ss pred
               O Fri Mar 04 23: 834 RNNSOEFALKCISKSAEYSLKEIOIEELODFKEKOHIHYLNLLIHFRMFEEVLDVLRLGHE 894 (1037)
            834 -----al--a--Ai-----e-----e-----l---i----F----L-l-----a
                                                         894 (1037)
O Consensus
               ..|.++.|++..++|++.....
             61 ~~g~~~A~~~~al~~~~~al~~~~A~~~A
T Consensus
             61 FLGEFETASEYYKKTLLLARQLKDRA-----VEAQS------CYSLGNTYTLLQDYEKA 108 (164)
T 3ro3 A
               T ss dssp
               ньсенининининининин
T ss pred
No 98
                                            Pub Med
>4yvo A Protein fluorescent in blue light, chloroplastic; TPR, fluorescent protein; 1.45A {Arabidopsis thaliana} Probab=82.77 E-value=7.1 Score=37.61 Aligned_cols=74 Identities=11% Similarity=0.038 Sum_probs=0.0
               Q ss_pred
Q Fri Mar 04 23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
                                                                      833 (1037)
            O Consensus
                                                                      833 (1037)
               +...+-+|.+|...|++++|.++|+++
                                   +.....
                                                    ....-|..+..++.
             92 ----a---a-----
                                         -1~~~~--
T Consensus
                                                                      143 (165)
             92 KKAARGLGASLOROGKYREATOYHSMV-----LAISKR--ESED-----SGITEAYGAIADCYT
T 4yvo A
                                                                      143 (165)
T ss_dssp
               НИНИНИНИНИТТСИНИНИНИНИ-------НИНИН----НТСС-----ТТИНИНИНИНИНИНИ
               T ss pred
               hcCCHHHHHHHHHHHHHhhccc
Q ss_pred
Q Fri_Mar_04_23:
            834 RNNSQEFALKCISKSAEYSLKE 855 (1037)
Q Consensus
            834 ~~~~al~~a~~Ai~~~~
                               855 (1037)
            ..|.++.|++...+
144 ~~g~~~A~~~~al~~~~
T Consensus
T 4yvo A
            144 ELGDLEKAGKFYDTYIARLETD
                               165 (165)
T ss_dssp
               нттснинининининиттс
T ss_pred
               HhCCHHHHHHHHHHHHHHHhhcC
                               NCBI
                                           Pub Med
>4ui9_J Cell division cycle protein 16 homolog; ubiquitination, cell cycle, APC/C; 3.60A {Homo sapiens} PDB:
 4ui9 K
Probab=82.55 E-value=71 Score=38.05 Aligned cols=227 Identities=8% Similarity=0.008 Sum probs=0.0
               СССһһнинниннн-сссһнинниннннь-сссссСсһнинннннннн-ссс-ниннннннннны
Q Fri_mar_04_23: 715 TENSFFMTFFRSYII-ENTSHKNIRFFLENVECPFYLRHNEVQEFMFAMTLFSCGN-FDQSYEIFQLHDYPEAIND---- 788 (1037)
            Q Consensus
```

```
338 (620)
 T Consensus
                      ------A-----al---p------
            262 PFHASCLPVHIGTLVELNKANELFYLSHKLVD---LYPSNPVSWFAVGCYYLMVGHKNEHARRYLSKATTLEKTYGPAWI 338 (620)
 т 411і9 л
 T ss dssp
              T ss pred
 Q ss_pred
              Q Fri_Mar_04_23: 789 KLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFDRNNSQEFALKCISKSAEYSLKEIQIEELQDFKEKQ
                                                                868 (1037)
 Q Consensus
            868 (1037)
              T Consensus
                                                                 403 (620)
 T 4ui9 J
              T ss dssp
              T ss_pred
              Нһһһһһннннннннннннннннннннннннннннн
 Q ss_pred
 Q Fri_Mar_04_23: 869 HIHYLNLLIHFRMFEEVLDVLRLGHEC--LSDTVRT------NFLQLLLQEDIYSRDFFSTLLRLCNAHSDN
                                                                932 (1037)
 O Consensus
            932 (1037)
                   .+-..+.+.|+.
                                                        ~~~~g~~----
 T Consensus
                                                                461 (620)
            404 V-----NLGHVCRKLKKY----
 T 4ui9 J
                                                                461 (620)
              H-----HHHHHHHHHHTCCHHHHHHHHHHHHHHHTTCSSCCCSTTHHHHH
 T ss_dssp
              T ss_pred
              Q ss pred
 Q Fri_Mar_04_23: 933 GELYLRTVDIKIVDSILSQNLRSGDWEC-FKKLYCFRMLNKSERAAAEVLYQYILMQADL 991 (1037)
            933 ~ll~~~~~vd~iL~~~ar~~~~y~~LYs~ri~~~~R~AA~~mYe~~~rl~~~
 Q Consensus
                                                    991 (1037)
            .+-++--....+-+, |..|=.+...|++,+|+...|+.++++...
462 -----al---p-----lg------g-----al---p-
                                                    511 (620)
 T Consensus
            462 -----AEALDYHRQALVLIPQNASTYSAIGYIHSLMGNFENAVD-YFHTALGLRRD 511 (620)
 T 4ui9 J
              T ss_dssp
              T ss_pred
No 100
                      PDB"
                                    Pub Med
>4yvq_C Protein fluorescent in blue light, chloroplastic, glutamyl-tRNA reductase 1, chloroplastic; TPR,
 protein-protein interaction; 2.40A {Arabidopsis thaliana}
 Probab=82.38 E-value=4.4 Score=38.93 Aligned_cols=74 Identities=8% Similarity=-0.016 Sum_probs=0.0
              Q ss pred
 Q Fri_Mar_04_23: 754 EVQEFMFAMTLFSCGNFDQSYEIFQLHDYPEAINDKLPTFLEDLKSENYHGDSIWKDLLCTFTVPYRHSAFYYQLSLLFD
                                                                833 (1037)
 O Consensus
            754 ~~~fl-g~~l~~~A~~F~a~~~~lp~l~~l~~l~~l~~l~~~~Yy~l~Lfe 833 (1037)
              +...+-+|.+|...|++++|.++|+++-.....
                                                      ......
 T Consensus
            ---la----
                                                                137 (159)
 T 4yvq C
            86 KKAARGLGASLQRQCKYREAIQYHSMVLAISKRE-----SED-----SGITEAYGAIADCYT
                                                                137 (159)
              НИНИНИНИНИНТСИНИНИНИНИНИНИНИНИН -------TCC-----THИНИНИНИНИНИНИ
 T ss_dssp
              T ss_pred
              hcCCHHHHHHHHHHHHHhhccc
 Q ss pred
 Q Fri Mar 04 23: 834 RNNSQEFALKCISKSAEYSLKE 855 (1037)
            834 ~~~~al~~a~~Ai~~~~~
                             855 (1037)
 Q Consensus
              ..|.++.|+++.++|++...++
 T Consensus
            138 ~~g~~~~A~~~~~al~~~~~
                             159 (159)
            138 ELGDLEKAGKFYDTYIARLETD 159 (159)
 T 4yvq_C
              нитсинининининтттсс
 T ss dssp
 T ss_pred
              нессининининининин
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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